Metagenome	TBZ/SUC gene expression	TBZ73/TBZ57 gene expression	TBZ109/TBZ57 gene expression	SUC57/SUC109 gene expression
Urate degradation - • • • • • • • • • • • • • • • • • •	Urate degradation - Uni- Sym- and Antiporters - Type III, Type IV, Type VI, ESAT secretion systems -	Urate degradation - Uni- Sym- and Antiporters - Type III, Type IV, Type VI, ESAT secretion systems -	Urate degradation - Uni- Sym- and Antiporters - Type III, Type IV, Type VI, ESAT secretion systems -	Urate degradation - Uni- Sym- and Antiporters - Type III, Type IV, Type VI, ESAT secretion systems -
Type III secretion system, extended - Two related proteases - tRNA sulfuration - Tricarboxylate transporter -	Type III secretion system, extended - Two related proteases - tRNA sulfuration - Tricarboxylate transporter -	Two related solutions and the state of the s	Two related proteases - tRNA sulfuration - Tricarbox ylate transporter -	Two related proteases -  tRNA sulfuration -  Tricarboxylate transporter -
Triacylglycerols	Triacylglycerols -  Transposable elements -  Translation -	Triacylglycerols - Transposable elements - Transposition - Transposition -	Triacylglycerols - Transposable elements - Translation - Transposable elements -	Triacylglycerols - Transposable elements - Translation - Transposition -
Transcription - Toxins and superantigens - TldD cluster - Three hypotheticals linked to lipoprotein biosynthesis -	Toxins and superantigens -  TldD cluster -  Three hypotheticals linked to lipoprotein biosynthesis -	Toxins and superantigens - TIdD cluster - Three hypotheticals linked to lipoprotein biosynthesis -	Toxins and superantigens - TldD cluster - Three hypotheticals linked to lipoprotein_biosynthesis -	Toxins and superantigens - TldD cluster - Three hypotheticals linked to lipoprotein_biosynthesis -
Tetrapyrroles -	Sulfatases and sulfatase modifying factor 1 (and a hypothetical) - Sugar Phosphotransferase Systems, PTS -	Sulfatases and sulfatase modifying factor 1 (and a hypothetical) - Sugar Phosphotransferase Systems, PTS -	Sulfatases and sulfatase modifying factor 1 (and a hypothetical) - Sugar Phosphotransferase Systems, PTS -	Sulfatases and sulfatase modifying factor 1 (and a hypothetical) - Sugar Phosphotransferase Systems, PTS -
Sugar alcohols - Sodium Ion-Coupled Energetics - Social motility and nonflagellar swimming in bacteria - Siderophores - Sidero	Sodium Ion-Coupled Energetics - Social motility and nonflagellar swimming in bacteria - Siderophores -	Sugar alconois - Sodium lon-Coupled Energetics - Social motility and nonflagellar swimming in bacteria - Siderophores -	Sugar actions - Sodium Ion-Coupled Energetics - Social motility and nonflagellar swimming in bacteria - Siderophores -	Sugar alconois - Sodium lon-Coupled Energetics - Social motility and nonflagellar swimming in bacteria - Siderophores -
Selenoproteins - Secretion - Sarcosine oxidase - RNA processing and modification - Sarcosine oxidase - Sar	Secretion - Sarcosine oxidase -	Selenoproteins - Secretion Sarcosine oxidase - RNA processing and modification -	Selenoproteins - Secretion - Sarcosine oxidase - RNA processing and modification -	Selenoproteins - Secretion - Sarcosine oxidase - RNA processing and modification -
Ribosome-related cluster	Ribosome-related cluster - Ribosomal Protein L28P relates to a set of uncharacterized proteins - Riboflavin, FMN, FAD -	Ribosome-related cluster - Ribosomal Protein L28P relates to a set of uncharacterized proteins - Riboflavin, FMN, FAD -	Ribosome-related cluster - Ribosomal Protein L28P relates to a set of uncharacterized proteins - Riboflavin, FMN, FAD - Riboflavin, FMN, FMN, FMN, FMN, FMN, FMN, FMN, FMN	Ribosome-related cluster - Ribosomal Protein L28P relates to a set of uncharacterized proteins - Riboflavin, FMN, FAD -
Resistance to antibiotics and toxic compounds -	Regulation of virulence - Recombination related cluster -	Resistance to antibiotics and toxic compounds - Regulation of virulence - Recombination related cluster - Quorum sensing and biofilm formation -	Resistance to antibiotics and toxic compounds - Regulation of virulence - Recombination related cluster - Quorum sensing and biofilm formation - Recombination	Resistance to antibiotics and toxic compounds - Regulation of virulence - Recombination related cluster - Quorum sensing and biofilm formation -
Quinone cofactors - • • • • • • • • • • • • • • • • • •	Quinone cofactors - Pyruvate kinase associated cluster - Pyrimidines -	Quinone cofactors - Pyrruvate kinase associated cluster - Pyrimidines -	Quinone cofactors - Pyrimidines - Pyrimidines -	Quinone cofactors - Pyruvate kinase associated cluster - Pyrimidines -
Pyridoxine	Putrescine/GABA utilization cluster-temporal,to add to SSs - Putative Isoquinoline 1-oxidoreductase subunit - Putative GGDEF domain protein related to addlutinin secretion -	Pyridoxine - Putrescine/GABA utilization cluster-temporal to add to Ss - Putative Isoquinoline 1-oxidoreductase subunit - Putative GGDEF domain protein related to agglutinin secretion -	Putrescine/GABA utilization cluster-temporal, to add to SSs - Putative Isoquinoline 1-oxidoreductase subunit - Putative GGDEF domain protein related to agglutinin secretion -	Pyridoxine - Putrescine/GABA utilization cluster-temporal, to add to SSs - Putative Isoquinoline 1-oxidoreductase subunit - Putative GGDEF domain protein related to agglutinin secretion -
Putative asociate of RNA polymerase sigma-54 factor rpoN -	Putative asociate of RNA polymerase sigma-54 factor rpoN - Purines -	Putative asociate of RNA polymerase sigma-54 factor rpoN - Purines - proteosome related - Protected and the related -	Putative asociate of RNA polymerase sigma-54 factor rpoN - Purines - Purines - Protected a related - Purines - Pur	Putative asociate of RNA polymerase sigma-54 factor rpoN - Purines - Proteosome related -
Proteolytic pathway	Protein translocation across cytoplasmic membrane  Protein secretion system, Type VIII (Extracellular nucleation/precipitation pathway, ENP)  Protein secretion system, Type VII (Chaperone/Usher pathway, CU)	Protein translocation across cytoplasmic membrane - Protein secretion system, Type VIII (Extracellular nucleation/precipitation pathway, ENP) - Protein secretion system, Type VII (Chaperone/Usher pathway, CU) -	Protein translocation across cytoplasmic membrane - Protein secretion system, Type VIII (Extracellular nucleation/precipitation pathway, ENP) - Protein secretion system, Type VII (Chaperone/Usher pathway, CU) -	Proteolytic pathway - Protein translocation across cytoplasmic membrane - Protein secretion system, Type VIII (Extracellular nucleation/precipitation pathway, ENP) - Protein secretion system, Type VII (Chaperone/Usher pathway, CU) -
Protéin secretion system, Type VI - Protein secretion system, Type III - Protein secretion system, Type II - Protein processing and modification -	Protein secretion system, Type III - Protein secretion system, Type II -	Protein secretion system, Type VI – Protein secretion system, Type III – Protein processing and system, Type III – Protein processing and system, Type III –	Protein secretion system, Type VI - Protein secretion system, Type III - Protein secretion system, Type III -	Protéin secretion system, Type VI - Protein secretion system, Type III - Protein secretion system, Type III - Protein processing and modification -
Protein folding - • • • • • • • • • • • • • • • • • •	Protein folding - Protein export? - Protein degradation -	Protein processing and modification - Protein folding - Protein export? - Protein degradation -	Protein processing and modification - Protein folding - Protein export? - Protein degradation -	Protein processing and modification - Protein folding - Protein export? - Protein degradation -
Protein biosynthesis -	Protein and nucleoprotein secretion system, Type IV - Proline and 4-hydroxyproline - Proline	Protein biosynthesis - Protein and nucleoprotein secretion system, Type IV - Programmed Cell Death and Toxin antitoxin Systems -	Protein biosynthesis - Protein and nucleoprotein secretion system, Type IV - Proline and 4-hydroxyproline - Programmed Cell Death and Toxin-authorin Systems -	Protein biosynthesis - Protein and nucleoprotein secretion system, Type IV - Proline and 4-hydroxyproline - Programmed Cell Death and Toxin antitoxin Systems -
Probably organic hydroperoxide resistance related hypothetical proteins - Probably GTP or GMP signaling related -	Programmed Cell Death and Toxin-antitoxin Systems - Probably Ybbk-related hypothetical membrane proteins - Probably organic hydroperoxide resistance related hypothetical protein - Probably GTP or GMP signaling related -	Programmed Cell Death and Toxin-antitoxin Systems - Probably Ybbk-related hypothetical membrane protein - Probably organic hydroperoxide resistance related hypothetical protein - Probably GTP or GMP signaling related -	Programmed Cell Death and Toxin-antitoxin Systems - Probably Ybbk-related hypothetical membrane proteins - Probably organic hydroperoxide resistance related hypothetical protein - Probably GTP or GMP signaling related -	Programmed Cell Death and Toxin-antitoxin Systems - Probably Ybbk-related hypothetical membrane proteins - Probably organic hydroperoxide resistance related hypothetical protein - Probably GTP or GMP signaling related -
Polysaccharides - Plant-Prokaryote DOE project - Plant Octadecanoids - Plant Hormones -	Polysaccharides - Plant-Prokaryote DOE project - Plant Octadecanoids - Plant Hormones -	Polysaccharides - Plant-Prokaryote DOE project - Plant Dant Hormones -	Plant-Prokaryote DOE project - Plant Octadecanoids - Plant Hormones - Plan	Polysaccharides - Plant-Prokaryote DOE project - Plant Octadecanoles - Plant Hormones -
Plant Alkaloids - Phospholipids - Phages, Prophages - Phages - Pha		Plant Alkaloids - Phospholipids - Phages, Prophages -	Plant Alkaloids - Phospholipids - Phages, Prophages -	Plant Alkaloids - Phospholipids - Phages, Prophages -
Phage Host Interactions - Periplasmic Stress - Periplasmic Stress - Peripheral pathways for catabolism of aromatic compounds - Pathogenicity islands -	Phage Host Interactions - Periplasmic Stress - Peripheral pathways for catabolism of aromatic compounds - Pathogenicity islands -	Phage Host Interactions - Periplasmic Stress - Peripheral pathways for catabolism of aromatic compounds - Pathogenicity islands -	Phage Host Interactions - Periplasmic Stress - Peripheral pathways for catabolism of aromatic compounds - Pathogenicity islands -	Phage Host Interactions - Periplasmic Stress - Peripheral pathways for catabolism of aromatic compounds - Pathogonicity islands -
Oxidative stress - Osmotic stress - Organic sulfur assimilation -	Osmotic stress - Organic sulfur assimilation -	TBZperSUC.log2FC Organic sulfur assimilation - TBZ73perTBZ57.TBZ73.kg		Oxidative stress - Osmotic stress - Organic sulfur assimilation -
Organic acids - One-carbon Metabolism - Nucleotidyl-phosphate metabolic cluster - NAD and NADP - O	Counts United Counts One-carbon Metabolism - Nucleotidyl-phosphate metabolic cluster - Nucleotidyl-phosphate - Nucleotidyl-pho	Organic acids - One-carbon Metabolism - Nucleotidyl-phosphate metabolic cluster - NAD and NADP -	Organic acids - One-carbon Metabolism - One-carbon Metabolism - One-carbon Metabolism - One-carbon Metabolic cluster - One-c	Organic acids - One-carbon Metabolism - Nucleotidyl-phosphate metabolic cluster - NAD and NADP -  Organic acids - One-carbon Metabolism - NAD and NADP -  SUC57perSUC109.log2FC
Monosaccharides - Molybdopterin oxidoreductase - Methylamine utilization - Methylamine utilizati	Monosaccharides -  2000  Molybdopterin oxidoreductase -  Methylamine utilization -	Monosaccharides - Molybdopterin oxidoreductase - Methylamine utilization -  7.5  Monosaccharides - Molybdopterin oxidoreductase - Methylamine utilization -  7.5	Monosaccharides - Monosaccharides - Molybdopterin oxidoreductase - Methylamine utilization - 7.5	Monosaccharides - Molybdopterin oxidoreductase - Methylamine utilization -  6
Metabolism of central aromatic intermediates - Lysine, threonine, methionine, and cysteine - Lysine Biosynthesis - Lipoic acid - Lysine Biosynthesis - Lysine Bi		10.0 Metabolism of central aromatic intermediates - Lysine, threonine, methionine, and cysteine - Lysine Biosynthesis - Lysine Biosy	Metabolism of central aromatic infermediates - Lysine, threonine, methionine, and cysteine - Lysine Biosynthesis - Lipoic acid -	Metabolism of central aromatic intermediates - Lysine, threonine, methionine, and cysteine - Lysine Biosynthesis - Lipoic acid -
Light-harvesting complexes	Light-harvesting complexes - Isoprenoids - Isoprenoid/cell wall biosynthesis: PREDICTED UNDECAPRENYL DIPHOSPHATE PHOSPHATASE - Isoprenoid/cell wall biosynthesis -	Light-harvesting complexes - Isoprenoid/cell wall biosynthesis: PREDICTED UNDECAPRENYL DIPHOSPHATE PHOSPHATE PHOSPHA		Light-harvesting complexes - Isoprenoids - I
Invasion and intracellular resistance -	Hypothetical Related to Dihydroorate Dehydrogenase - Hypothetical lipase related to Phosphatidate metabolism -	Hypothetical Related to Phosphatidate metabolism –  Hypothetical lipase related to Phosphatidate metabolism –	Invasion and intracellular resistance - Inorganic sulfur assimilation - Inorganic sulfur assimilation - Hypothetical Related to Dihydroorate Dehydrogenase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate metabolism - Increase - Hypothetical lipase related to Phosphatidate - Hypothetical lipase	Invasion and intracellular resistance - Inorganic sulfur assimilation - Hypothetical Related to Dihydroorate Dehydrogenase - Hypothetical lipase related to Phosphatidate metabolism -
Hypothetical in Lysine biosynthetic cluster - Hypothetical associated with RecF - Histidine Metabolism - Heat shock - Heat shock - Histidine Metabolism	Hypothetical associated with RecF - Histidine Metabolism -	Hypothetical in Lysine biosynthetic cluster - Hypothetical associated with RecF - Histidine Metal shock -	Hypothetical in Lysine biosynthetic cluster - Hypothetical associated with RecF - Histidine Metabolism - Heat shock	Hypothetical in Lysine biosynthetic cluster - Hypothetical associated with RecF - Histidine Metabolism - Heat shock -
Gram-Positive cell wall components -	Gram-Positive cell wall components - Gram-Negative cell wall components - Glycoside hydrolases - Glycoside hydrolases -	Gram-Positive cell wall components - Gram-Negative cell wall components - Glycoside hydrolases -	Gram-Positive cell wall components - Gram-Negative cell wall components - Glycoside hydrolases -	Gram-Positive cell wall components - Gram-Negative cell wall components - Glycoside hydrolases -
Glutamine, glutamate, aspartate, asparagine; ammonia assimilation	Flagellar moti <u>li</u> ţy in Prokaryota -	Glutamine, glutamate, aspartate, asparagine; ammonia assimilation - Folate and pterines - Flagellar motility in Prokaryota - Flagella protein? -	Glutamine, glutamate, aspartate, asparagine; ammonia assimilation - Folate and pterines - Flagellar motility in Prokaryota - Flagella protein? - F	Glutamine, glutamate, aspartate, asparagine; ammonia assimilation - Folate and pterines - Flagellar motility in Prokaryota - Flagella protein? -
Fimbriae of the Chaperone/Usher Assembly Pathway	Fimbriae of the Chaperone/Usher Assembly Pathway - Fermentation - Fatty acids -	Fimbriae of the Chaperone/Usher Assembly Pathway - Fermentation - Fatty acids -	Fimbriae of the Chaperone/Usher Assembly Pathway - Fermentation - Fatty acids - Fatty	Fimbriae of the Chaperone/Usher Assembly Pathway - Fermentation - Fatty acids -
Fatty acid metabolic cluster	Electron transport and photophosphorylation - Electron donating reactions -	Fatty acid metabolic cluster - Electron transport and photophosphorylation - Electron donating reactions - Electron accepting reactions -	Fatty acid metabolic cluster - Electron transport and photophosphorylation - Electron donating reactions - Electron accepting reactions -	Fatty acid metabolic cluster - Electron transport and photophosphorylation - Electron donating reactions - Electron accepting reactions -
Electron accepting reactions -  DNA uptake, competence -  DNA replication -  DNA repair -  DNA recombination -	DNA replication - DNA repair -	DNA uptake, competence -  DNA replication -  DNA replication -  DNA regair -	DNA uptake, competence -  DNA replication -  DNA repair -	DNA uptake, competence - DNA replication - DNA repair -
DNA polymerase III epsilon cluster - Di- and oligosaccharides - Detoxification -	Di- and oligosaccharides	DNA recombination -  DNA polymerase Ill epsilon cluster -  Di- and oligosaccharides -  Detoxification -	DNA recombination -  DNA polymerase III epsilon cluster -  Di- and oligosaccharides -  Detoxification -	DNA recombination - DNA polymerase III epsilon cluster - Di- and oligosaccharides - Detoxification -
Detection - Description - Detection - Description - Description - Description - Description - Detection - Description - Descript		Descion - Descio	Detection - Dessication stress - D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1) cluster - Cytochrome biogenesis -	Detection -  Descication stress -  D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1) cluster -  Cytochrome biogenesis -
CRISPRs and associated hypotheticals - Cold shock -	CRISPRs and associated hypotheticals - Cold shock -	CRISPs - CRISPs and associated hypotheticals - Cold shock -	CRISPs - CRISPs - CRISPs - Cold shock -	CRISPs - CRISPRs and associated hypotheticals - Cold shock -
Coenzyme M - Coenzyme F420 - Coenzyme A - COENTRY A -	Coenzyme M - Coenzyme F420 - Coenzyme A - CO2 fixation -	Coenzyme M - Coenzyme A - Coenzyme A - Coenzyme A - CO2 fixation -	Coenzyme N - Coenzyme F420 - Coenzyme A - CO2 fixation -	Coenzyme M - Coenzyme F420 - Coenzyme A - CO2 fixation -
Clustering-based subsystems - Chromosome Replication - Choline bitartrate degradation, putative - Chemotaxis, response regulators -	Clustering-based subsystems - Chromosome Replication - Choline bitartrate degradation, putative - Chemotaxis, response regulators -	Clustering-based subsystems - Chromosome Replication - Choline bitarrate degradation, putative -	Clustering-based subsystems - Chromosome Replication - Choline bitartrate degradation, putative -	Clustering-based subsystems - Chromosome Replication - Choline bitartrate degradation, putative -
Central carbohydrate metabolism -	Cell wall of Mycobacteria - Cell Division -	Chemotaxis, response regulators - Central carbohydrate metals - Cell wall of Mycobacteria - Cell Division -	Chemotaxis, response regulators - Central carbohydrate metabolism - Cell wall of Mycobacteria - Cell Division -	Chemotaxis, response regulators - Central carbohydrate metabolism - Cell wall of Mycobacteria - Cell Division -
Catabolism of an unknown compound - Carotenoid biosynthesis - Carbohydrates - Capsular and extracellular polysacchrides -		Catabolism of an unknown compound - Carotenoid biosynthesis - Carbolydraes - Carotylar and extracellular polysacchrides -	Cansular and extracellular polysachrides	Catabolism of an unknown compound - Carotenoid biosynthesis - Carbohydrates - Capsular and extracellular polysachrides -
Branched-chain ámino acids -	Biosynthesis of phenylpropanoids	Capsular and extracellular polysacchrides - Branched-chain amino acids - Biotin - Biosynthesis of phenylpropanoids -	Biosynthesis of polestal tradetables and extracellular polysacchrides - Branched-chain amino acids - Biotin - Biosynthesis of phenylpropanoids -	Biosynthesis of phenylpropanoids -  Biosynthesis of phenylpropanoids -
Biosynthesis of galactoglycans and related lipopolysacharides -	Bacteriophage structural proteins - Bacteriophage integration/excision/lysogeny -	Biosynthesis of galactoglycans and related lipopolysacharides -  Bacteriophage structural proteins -  Bacteriophage integration/excision/lysogeny -  Bacteriocins, ribosomally synthesized antibacterial peptides -	Biosynthesis of galactoglycans and related lipopolysacharides - Bacteriophage structural proteins - Bacteriophage integration/excision/lysogeny - Bacteriocins, ribosomally synthesized antibacterial peptides -	Biosynthesis of galactoglycans and related lipopolysacharides - Bacteriophage structural proteins - Bacteriophage integration/excision/lysogeny - Bacteriocins, ribosomally synthesized antibacterial peptides -
Bacterial cytostatics, différentiation factors and antibiotics - ATP synthases - Aromatic amino acids and derivatives - OFF -	Bacterial cytostatics, différentiation factors and antibiotics - ATP synthases - Aromatic amino acids and derivatives -	Bacterial cytostatics, différentiation factors and antibiotics - ATP synthases - Aromatic amino acids and derivatives -	Bacterial cytostatics, différentiation factors and antibiotics - ATP synthases - Aromatic amino acids and derivatives -	Bacterial cytostatics, différentiation factors and antibiotics - ATP synthases - Aromatic amino acids and derivatives -
Arginine; urea cycle, polyamines -	Aminosugars - Am	Arginine; urea cycle, polyamines - Anaerobic degradation of aromatic compounds - Aminosugars - alpha-proteobacterial cluster of hypotheticals -	Arginine; urea cycle, polyamines - Anaerobic degradation of aromatic compounds - Aminosugars - alpha-proteobacterial cluster of hypotheticals -	Arginine; urea cycle, polyamines - Anaerobic degradation of aromatic compounds - Aminosugars - alpha-proteobacterial cluster of hypotheticals -
Alanine, serine, and glycine - Adhesion - Acid stress - Ac	Alanine, serine, and glycine - Adhesion - Acid stress -	Alanine, serine, and glycine - Adhesion - Acid stress - ABC transporters -	Alanine, serine, and glycine - Adhesion - Acid stress - ABC transporters -	Alanine, serine, and glycine - Adhesion - Acid stress - ABC transporters -
ABC transporters - ABC transport	a de mars mars a de mars a		AbC transporters 1 as a man a man as a man as a man a	taga m m nas m m nas m m nas m m nas m m m nas m m m nas m m m m m m m m m m m m m m m m m m m
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n_30_N in_34_l in_34_l in_36_ pm_bin_n in_48_ in_56_ in_01012_s in_1012_s in_1017_ i	n_30_n   m_34_t   m_bin_36_n   m_bin_50_n   m_bin_50_n 	1.70_suk 9_sub 9_sub 1.013_sin48 1.013_sin4	1   30   1   30   1   30   1   30   30	n_30_\ in_34_\ in_36_\ in_34_\ in_36_\ in_bin_36_\ in_bin_148_\ in_bin_12\ in_bin_5_\ in_50_\
opm_bi oppm_b soppm_t groop groop raxbino maxbin metaba #abaat_l bin_42?	opm_bi groop groop axtinout:01f metaba stabat_label	oppm_bi oppm_bi oppm_bi axbinou iout.01f metabe metabe metabe in_5222	oopm_bii groopm_bii groopm_bii groopm_cgroopm_	opm_bi oppm_bi oopm_t groopm naxbino metabe metabe metabet lbin_422
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