

Table 5. KEGG maps overrepresented in environmental data sets relative to fully sequenced genomes

KEGG id	Description	Freq Meta	Freq String	p-value
2030	Bacterial chemotaxis	3.955E-03	1.028E-02	0.000E+00
2040	Flagellar assembly	7.637E-03	2.568E-02	0.000E+00
3010	Ribosome	5.441E-02	9.569E-02	0.000E+00
3070	Type III secretion system	2.154E-03	1.157E-02	0.000E+00
3080	Type IV secretion system	7.391E-04	3.904E-03	0.000E+00
3090	Type II secretion system	7.138E-03	1.750E-02	0.000E+00
860	Porphylin and chlorophyll metabolism	1.907E-02	2.967E-02	8.228E-74
290	Valine, leucine and isoleucine biosynthesis	3.706E-02	2.348E-02	1.494E-71
260	Glycine, serine and threonine metabolism	5.683E-02	4.052E-02	6.741E-68
640	Propanoate metabolism	4.272E-02	2.914E-02	5.446E-62
380	Tryptophan metabolism	3.258E-02	2.088E-02	4.470E-60
780	Biotin metabolism	4.589E-03	9.323E-03	7.939E-57
512	O-Glycan biosynthesis	4.855E-03	1.044E-03	4.546E-44
533	Keratan sulfate biosyntheses	4.844E-03	1.044E-03	6.537E-44
602	Glycosphingolipid biosynthesis - neo-lactoseries	6.187E-03	2.059E-03	6.292E-40
604	Glycosphingolipid biosynthesis - ganglioseries	6.140E-03	2.030E-03	7.152E-40
30	Pentose phosphate pathway	2.067E-02	2.823E-02	2.144E-35
903	Limonene and pinene degradation	2.380E-02	1.609E-02	3.357E-35
71	Fatty acid metabolism	2.882E-02	2.035E-02	4.739E-35
195	Photosynthesis	1.384E-03	3.432E-03	3.694E-33
251	Glutamate metabolism	4.090E-02	3.114E-02	5.939E-33
790	Folate biosynthesis	1.190E-02	1.744E-02	2.363E-32
510	N-Glycan biosynthesis	8.634E-03	4.218E-03	4.657E-32
53	Ascorbate and aldarate metabolism	1.294E-02	7.650E-03	2.048E-30
120	Bile acid biosynthesis	2.078E-02	1.407E-02	2.313E-30
1052	Type I polyketide structures	2.010E-03	0.000E+00	2.551E-30
280	Valine, leucine and isoleucine degradation	3.329E-02	2.482E-02	2.649E-30
600	Sphingolipid metabolism	1.467E-02	9.065E-03	4.607E-30
4010	MAPK signaling pathway	1.862E-03	0.000E+00	4.811E-28
730	Thiamine metabolism	3.349E-03	6.134E-03	2.087E-27
310	Lysine degradation	3.426E-02	2.611E-02	3.464E-27
410	beta-Alanine metabolism	1.918E-02	1.318E-02	3.607E-26
500	Starch and sucrose metabolism	2.340E-02	3.016E-02	3.073E-25
603	Glycosphingolipid biosynthesis - globoseries	7.753E-03	4.032E-03	3.808E-25
3020	RNA polymerase	1.353E-02	8.679E-03	3.103E-24
40	Pentose and glucuronate interconversions	9.135E-03	1.323E-02	7.504E-23
20	Citrate cycle (TCA cycle)	3.275E-02	2.549E-02	2.027E-22
1051	Biosynthesis of ansamycins	1.489E-03	0.000E+00	2.562E-22
193	ATP synthesis	1.120E-02	1.554E-02	3.857E-21
3060	Protein export	1.851E-02	2.392E-02	2.633E-20
641	3-Chloroacrylic acid degradation	1.526E-03	1.001E-04	9.910E-20
51	Fructose and mannose metabolism	2.660E-02	3.280E-02	7.591E-19
970	Aminoacyl-tRNA biosynthesis	4.741E-02	3.949E-02	1.557E-18
1054	Nonribosomal peptide structures	1.158E-03	0.000E+00	3.213E-17
473	D-Alanine metabolism	2.257E-03	4.061E-03	6.060E-17
625	Tetrachloroethene degradation	5.132E-03	2.688E-03	3.402E-16
631	1,2-Dichloroethane degradation	2.259E-03	6.720E-04	6.538E-16
630	Glyoxylate and dicarboxylate metabolism	2.485E-02	1.949E-02	7.399E-16
720	Reductive carboxylate cycle (CO2 fixation)	2.923E-02	2.346E-02	1.231E-15
620	Pyruvate metabolism	5.180E-02	4.434E-02	5.271E-15
950	Alkaloid biosynthesis I	5.769E-03	3.274E-03	6.729E-15
540	Lipopolysaccharide biosynthesis	1.525E-02	1.127E-02	3.379E-14
523	Polyketide sugar unit biosynthesis	7.945E-03	5.105E-03	6.797E-14
632	Benzoate degradation via CoA ligation	3.191E-02	2.644E-02	7.740E-13
562	Inositol phosphate metabolism	5.924E-03	3.575E-03	9.599E-13
650	Butanoate metabolism	4.746E-02	4.085E-02	1.009E-12
230	Purine metabolism	8.719E-02	7.848E-02	1.830E-12
740	Riboflavin metabolism	8.028E-03	1.082E-02	4.236E-12
130	Ubiquinone biosynthesis	3.868E-02	3.290E-02	8.390E-12
660	C5-Branched dibasic acid metabolism	9.052E-03	6.306E-03	2.963E-11
520	Nucleotide sugars metabolism	2.141E-02	1.720E-02	3.621E-11
61	Fatty acid biosynthesis	2.062E-02	1.657E-02	1.058E-10
480	Glutathione metabolism	1.167E-02	8.636E-03	1.293E-10
791	Atrazine degradation	1.206E-03	2.860E-04	7.251E-10
271	Methionine metabolism	1.818E-02	1.454E-02	9.308E-10
770	Pantothenate and CoA biosynthesis	2.358E-02	1.953E-02	2.651E-09
450	Selenoamino acid metabolism	2.369E-02	1.965E-02	3.053E-09
240	Pyrimidine metabolism	7.160E-02	6.484E-02	7.310E-09
580	Phospholipid degradation	8.743E-04	1.702E-03	1.000E-08
220	Urea cycle and metabolism of amino groups	2.238E-02	1.859E-02	1.560E-08
31	Inositol metabolism	4.271E-03	2.660E-03	4.244E-08
62	Fatty acid elongation in mitochondria	1.161E-02	8.965E-03	6.304E-08
960	Alkaloid biosynthesis II	8.721E-05	5.005E-04	9.908E-08
52	Galactose metabolism	1.636E-02	1.945E-02	2.892E-07
312	beta-Lactam resistance	4.360E-06	1.716E-04	3.286E-07
563	Glycosylphosphatidylinositol(GPI)-anchor biosynthesi	4.949E-04	0.000E+00	5.856E-07
710	Carbon fixation	2.803E-02	2.458E-02	1.803E-05
4110	Cell cycle	2.420E-04	0.000E+00	2.345E-05
601	Glycosphingolipid biosynthesis - lactoseries	6.519E-04	1.430E-04	2.730E-05
590	Arachidonic acid metabolism	6.584E-04	1.573E-04	4.886E-05
4120	Ubiquitin mediated proteolysis	2.289E-04	0.000E+00	5.496E-05
940	Stilbene, coumarine and lignin biosynthesis	5.621E-03	4.132E-03	5.619E-05
471	D-Glutamine and D-glutamate metabolism	3.789E-03	5.047E-03	7.600E-05
561	Glycerolipid metabolism	3.732E-02	4.099E-02	1.750E-04
430	Taurine and hypotaurine metabolism	2.871E-03	3.889E-03	4.518E-04
4210	Apoptosis	1.940E-04	0.000E+00	5.326E-04
300	Lysine biosynthesis	2.518E-02	2.803E-02	7.956E-04