Table S5. Functional annotation of the gut microbes.

Items	Description	Chow1	Chow2	Chow3	HFD1	HFD2	HFD3	HFD4	FTE1	FTE2	FTE3	FTE4	Total
Modules													
M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	9034	8054	9820	14116	8896	9956	14530	11368	5020	11904	4142	106840
M00002	Glycolysis, core module involving three-carbon compounds	6494	5618	7060	10226	6350	6986	10346	7568	3716	7868	3054	75286
M00003	Gluconeogenesis, oxaloacetate => fructose-6P	6978	6284	7780	11298	7116	8184	12400	8894	3940	9266	3216	85356
M00004	Pentose phosphate pathway (Pentose phosphate cycle)	3266	2948	4160	4328	2596	3856	5452	4966	1874	5744	1350	40540
M00005	PRPP biosynthesis, ribose 5P => PRPP	1090	942	1284	2086	1246	1334	1910	1272	542	1826	440	13972
M00007	Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P	2350	2044	3184	2934	1822	2764	3966	3538	1322	4422	896	29242
M00009	Citrate cycle (TCA cycle, Krebs cycle)	3780	3134	4308	4982	3398	3766	5630	4416	2188	5224	1582	42408
M00010	Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate	2856	2192	3006	3576	2456	2594	3850	2860	1562	3308	1188	29448
M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate	924	942	1302	1406	942	1172	1780	1556	626	1916	394	12960

M00012	Glyoxylate cycle	2000	1504	2016	2528	1734	1770	2668	2224	982	2600	820	20846
M00014	Glucuronate pathway (uronate pathway)	580	830	1260	742	508	1004	1226	1994	410	2942	134	11630
M00015	Proline biosynthesis, glutamate => proline	1868	1656	2122	2824	1616	2138	3348	2422	1104	2820	974	22892
M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	5786	5220	6044	9992	6260	6710	10872	6416	2970	7204	2716	70190
M00017	Methionine biosynthesis, apartate => homoserine => methionine	4710	3912	5192	6606	4258	4604	6972	5052	2418	5770	2046	51540
M00018	Threonine biosynthesis, aspartate => homoserine => threonine	4832	4060	5010	6136	4000	4674	6710	5116	2438	5504	2098	50578
M00019	Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine	3870	3262	4384	5730	3504	3680	6074	4946	1912	5318	2258	44938
M00021	Cysteine biosynthesis, serine => cysteine	2676	2080	2974	3586	2194	2660	3818	3036	1240	3374	886	28524
M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate	5008	3870	4842	7216	4846	4916	7784	4838	2506	5880	2000	53706
M00023	Tryptophan biosynthesis, chorismate => tryptophan	1066	1244	2124	1136	594	1602	1880	3188	772	4450	328	18384
M00024	Phenylalanine biosynthesis, chorismate => phenylalanine	902	1006	1084	2012	1250	1444	2052	1280	584	1558	450	13622
M00025	Tyrosine biosynthesis, chorismate => tyrosine	1374	1352	1484	2748	1764	2034	2506	1738	752	2346	546	18644

M00026	Histidine biosynthesis, PRPP => histidine	6054	4878	6324	8208	6054	6398	10570	6292	3512	6800	2838	67928
M00028	Ornithine biosynthesis, glutamate => ornithine	3998	3426	4688	6552	4004	4200	6932	4396	2296	5030	1832	47354
M00029	Urea cycle	1146	1356	1612	964	600	1246	1312	2636	1080	2874	1000	15826
M00030	Lysine biosynthesis, AAA pathway, 2-oxoglutarate => 2-aminoadipate => lysine	634	616	726	1124	636	800	1278	784	328	658	300	7884
M00032	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	634	616	726	1124	636	800	1278	784	328	658	300	7884
M00033	Ectoine biosynthesis, aspartate => ectoine	1508	1218	1530	2156	1256	1462	2068	1312	858	1536	578	15482
M00034	Methionine salvage pathway	2004	1746	2314	3248	1912	2122	3362	2018	1096	2130	966	22918
M00035	Methionine degradation	6264	4994	7106	5682	5366	6580	9076	10214	3384	10592	4288	73546
M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	1532	1260	1842	2498	1540	1780	3114	1576	836	1476	900	18354
M00045	Histidine degradation, histidine => N-formiminoglutamate => glutamate	816	910	910	824	636	564	446	2704	802	2130	594	11336
M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	8546	7652	9760	10686	7132	8418	12128	10312	4248	12136	3842	94860
M00049	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	3754	2662	3688	5316	3326	3668	5402	3970	1756	4890	1444	39876
M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	4274	3884	4766	6126	3782	4476	6490	5026	2256	5728	1910	48718

M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP	8046	6552	8726	10764	6792	7848	12386	9344	4256	10964	3260	88938
M00052	Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP	970	1076	1412	1750	936	1656	2214	2354	692	2876	494	16430
M00053	Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP	4464	3626	4308	5976	3920	4542	6458	5362	2142	5694	1842	48334
M00060	Lipopolysaccharide biosynthesis, KDO2-lipid A	4284	3598	4420	5936	3770	4368	7684	4224	2556	3524	2258	46622
M00063	CMP-KDO biosynthesis	2382	1992	2386	3694	2514	2650	4544	2430	1596	2130	1316	27634
M00064	ADP-L-glycero-D-manno-heptose biosynthesis	900	982	1172	1442	1218	980	1724	1688	364	2042	406	12918
M00075	N-glycan biosynthesis, complex type	214	246	270	734	396	282	190	464	56	692	24	3568
M00080	Lipopolysaccharide biosynthesis, inner core => outer core => O-antigen	796	740	1042	1358	832	1032	1876	926	454	786	492	10334
M00082	Fatty acid biosynthesis, initiation	1772	1372	1978	2108	1414	1952	2852	2330	1108	2910	680	20476
M00083	Fatty acid biosynthesis, elongation	1272	1252	1772	1538	1184	1822	1926	2654	706	3844	404	18374
M00086	beta-Oxidation, acyl-CoA synthesis	862	654	932	1416	890	1070	1756	1028	438	826	472	10344
M00089	Triacylglycerol biosynthesis	1998	2002	2540	2708	1918	2120	2512	2372	1092	2932	970	23164
M00093	Phosphatidylethanolamine (PE)	1578	1214	2116	2296	1430	1550	2916	1446	892	1344	792	17574

	biosynthesis, PA => PS => PE												
M00096	C5 isoprenoid biosynthesis, non-mevalonate pathway	5356	5070	6296	6356	4306	5118	8312	7302	3504	8152	2858	62630
M00114	Ascorbate biosynthesis, plants, glucose-6P => ascorbate	2672	2734	3490	4446	2826	3816	5822	4272	1716	4402	1422	37618
M00115	NAD biosynthesis, aspartate => NAD	2652	2666	3518	2200	1660	2140	2528	3474	1484	3192	1880	27394
M00116	Menaquinone biosynthesis, chorismate => menaquinone	1094	1016	1112	1922	1210	1608	2566	1154	662	1294	616	14254
M00117	Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinone	570	562	524	974	632	856	1260	584	308	634	316	7220
M00119	Pantothenate biosynthesis, valine/L-aspartate => pantothenate	2142	1848	2704	3776	2304	2582	4576	2350	1136	2116	1298	26832
M00120	Coenzyme A biosynthesis, pantothenate => CoA	1600	1488	1902	2776	1750	1954	3516	2056	942	2058	870	20912
M00121	Heme biosynthesis, glutamate => protoheme/siroheme	6328	5746	7616	8600	5624	7300	11094	9196	3774	9434	3260	77972
M00122	Cobalamin biosynthesis, cobinamide => cobalamin	1574	1512	1480	2502	1714	1904	3278	1654	898	1478	838	18832
M00123	Biotin biosynthesis, pimeloyl-ACP/CoA => biotin	1712	1538	1866	2590	1480	1724	3168	1748	980	1402	862	19070
M00125	Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD	888	796	1274	1432	982	1302	2096	1268	474	1500	428	12440
M00126	Tetrahydrofolate biosynthesis,	2746	2258	3364	3010	2490	3268	5236	3652	1680	4612	1248	33564

	GTP => THF												
M00127	Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P	2072	1966	2328	3774	2266	2732	4452	2996	1394	2954	1392	28326
M00129	Ascorbate biosynthesis, animals, glucose-1P => ascorbate	802	742	970	1102	722	742	1250	728	520	670	480	8728
M00133	Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine	2102	1566	1942	2592	1540	1960	3360	1820	1334	1666	1054	20936
M00135	GABA biosynthesis, eukaryotes, putrescine => GABA	108	170	284	136	46	234	306	392	156	670	62	2564
M00140	C1-unit interconversion, prokaryotes	3034	2708	3264	4332	2796	3370	5680	3878	1600	4372	1424	36458
M00141	C1-unit interconversion, eukaryotes	732	512	832	1120	588	754	1436	610	336	638	324	7882
M00153	Cytochrome d ubiquinol oxidase	986	736	860	1112	824	848	1402	716	478	670	458	9090
M00157	F-type ATPase, prokaryotes and chloroplasts	4744	5244	7206	5020	3888	4764	6142	7364	2554	7642	2760	57328
M00159	V/A-type ATPase, prokaryotes	1600	1660	2208	922	774	1000	1012	1634	626	1476	1086	13998
M00165	Reductive pentose phosphate cycle (Calvin cycle)	5748	4878	6608	8206	4980	6644	10498	7066	3156	7660	2452	67896
M00166	Reductive pentose phosphate cycle, ribulose-5P => glyceraldehyde-3P	1674	1424	1812	2566	1458	1838	3038	1680	1026	1456	848	18820
M00167	Reductive pentose phosphate cycle, glyceraldehyde-3P => ribulose-5P	4074	3454	4796	5640	3522	4806	7460	5386	2130	6204	1604	49076

M00169	CAM (Crassulacean acid metabolism), light	1218	1054	1152	2536	1364	1628	1966	2306	722	2730	546	17222
M00171	C4-dicarboxylic acid cycle, NAD - malic enzyme type	474	414	462	1330	552	684	510	1546	318	2014	218	8522
M00172	C4-dicarboxylic acid cycle, NADP - malic enzyme type	1218	1054	1152	2536	1364	1628	1966	2306	722	2730	546	17222
M00173	Reductive citrate cycle (Arnon-Buchanan cycle)	9586	8076	10988	11082	7126	8344	12212	11866	5780	12726	4958	102744
M00176	Assimilatory sulfate reduction, sulfate => H2S	278	350	440	346	182	70	78	730	152	1070	190	3886
M00178	Ribosome, bacteria	5546	5118	6598	9154	6098	6622	9894	6976	2932	7592	2678	69208
M00179	Ribosome, archaea	3352	3216	4206	5538	3626	4020	6286	4356	1852	4640	1636	42728
M00183	RNA polymerase, bacteria	3014	2668	3742	3452	2754	3142	3988	3544	1848	5178	1258	34588
M00188	NitT/TauT family transport system	2918	2182	2948	4202	3198	3102	3660	4168	1490	5318	946	34132
M00189	Molybdate transport system	968	740	928	1388	884	968	1790	780	620	756	534	10356
M00194	Maltose/maltodextrin transport system	366	296	360	144	186	226	318	576	140	796	44	3452
M00196	Raffinose/stachyose/melibiose transport system	5002	5234	7430	7102	4826	5614	6502	10490	2486	14304	1974	70964
M00197	Putative fructooligosaccharide transport system	444	448	660	292	248	520	590	1038	226	1488	58	6012
M00200	Putative sorbitol/mannitol transport system	366	296	360	144	186	226	318	576	140	796	44	3452
M00201	alpha-Glucoside transport system	366	296	360	144	186	226	318	576	140	796	44	3452
M00205	N-Acetylglucosamine transport	238	236	398	802	522	386	404	506	146	816	32	4486

	system												
M00206	Cellobiose transport system	366	296	360	144	186	226	318	576	140	796	44	3452
M00207	Putative multiple sugar transport system	11990	10822	13820	9316	7780	9726	10984	14144	5028	17732	4692	116034
M00209	Osmoprotectant transport system	180	218	256	788	458	454	284	360	64	632	48	3742
M00210	Phospholipid transport system	890	798	1070	1448	948	1150	1826	1040	634	804	432	11040
M00212	Ribose transport system	1432	2188	3058	3128	2226	3274	3560	4786	1130	7710	370	32862
M00214	Methyl-galactoside transport system	708	556	770	1570	1166	954	948	898	320	1656	90	9636
M00221	Putative simple sugar transport system	840	1448	2472	1274	1022	2332	2450	3652	812	5706	296	22304
M00222	Phosphate transport system	4748	3800	4970	5090	4066	3970	4234	5300	1754	5504	2152	45588
M00227	Glutamine transport system	830	638	832	1202	746	822	1318	846	550	706	432	8922
M00236	Putative polar amino acid transport system	2392	2238	2984	3956	2544	2978	4438	3670	1318	4568	1082	32168
M00237	Branched-chain amino acid transport system	4882	4042	5528	6978	4592	4812	7544	5580	2886	5380	2396	54620
M00238	D-Methionine transport system	524	468	648	1442	1118	700	902	996	214	1454	92	8558
M00239	Peptides/nickel transport system	4224	4356	6016	6214	4190	5752	8482	6758	2668	8232	1832	58724
M00242	Zinc transport system	2084	1576	1966	2756	1826	1936	3520	1930	1126	1710	1094	21524
M00251	Teichoic acid transport system	972	604	784	1830	1462	1082	1206	1044	310	2036	180	11510
M00254	ABC-2 type transport system	9646	9188	12436	8756	6784	11340	11710	17088	5324	22318	4338	118928
M00255	Lipoprotein-releasing system	2180	1506	1730	2412	1462	1662	3082	1774	1054	1328	1040	19230
M00256	Cell division transport system	924	764	1030	1674	1152	718	646	1112	496	1626	300	10442
M00258	Putative ABC transport system	13042	9888	13224	12260	9290	11096	11970	18286	6008	20858	6100	132022
M00259	Heme transport system	578	530	626	1102	652	722	1340	688	284	674	310	7506

M00260	DNA polymerase III complex, bacteria	9332	8820	11188	10280	7378	9348	11930	13464	5392	14866	5630	107628
M00269	PTS system, sucrose-specific II component	116	166	354	182	0	0	0	590	16	834	16	2274
M00271	PTS system, beta-glucoside-specific II component	114	160	318	196	24	84	74	524	40	700	36	2270
M00273	PTS system, fructose-specific II component	424	306	492	910	474	684	686	738	170	1272	76	6232
M00299	Spermidine/putrescine transport system	1206	1678	2396	2196	1372	2050	1898	3664	884	4972	688	23004
M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	2958	2736	3774	2202	1630	1716	1978	4130	1870	4116	2044	29154
M00308	Semi-phosphorylative Entner-Doudoroff pathway, gluconate => glycerate-3P	1674	1424	1812	2566	1458	1838	3038	1680	1026	1456	848	18820
M00309	Non-phosphorylative Entner-Doudoroff pathway, gluconate/galactonate => glycerate	964	712	1116	1454	834	882	1562	900	636	806	492	10358
M00320	Lipopolysaccharide export system	2314	1888	2546	3578	2296	2468	4414	2324	1292	2146	1172	26438
M00331	Type II general secretion pathway	3398	3104	3364	6158	4264	4478	7602	4118	1732	4032	1776	44026
M00333	Type IV secretion system	10940	9060	10828	9206	8458	9094	8608	11764	4526	15026	4954	102464
M00335	Sec (secretion) system	11514	10050	12546	14784	10078	11054	16946	15664	7420	14538	7308	131902
M00336	Twin-arginine translocation (Tat) system	1306	1032	1132	2258	1418	1444	2632	1290	632	1374	716	15234

M00344	Formaldehyde assimilation, xylulose monophosphate pathway	1794	1604	1922	3374	1874	2196	3386	2196	820	2104	780	22050
M00345	Formaldehyde assimilation, ribulose monophosphate pathway	1118	1148	1370	2242	1232	1540	2126	1778	546	2092	444	15636
M00346	Formaldehyde assimilation, serine pathway	2228	1878	2498	3822	2566	2392	4164	2680	1176	2936	1028	27368
M00357	Methanogenesis, acetate => methane	3962	3310	4168	6224	4132	4240	7102	4368	2134	4376	1964	45980
M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	27810	25386	31194	31144	21304	25968	37846	36136	15556	39536	14666	306546
M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	28732	26006	31934	32136	21890	26614	39208	36928	16218	40224	15118	315008
M00361	Nucleotide sugar biosynthesis, eukaryotes	1892	2062	2852	2126	1638	2262	2882	3370	1426	3754	1056	25320
M00362	Nucleotide sugar biosynthesis, prokaryotes	4052	3958	5310	4230	3192	4172	5710	5750	2748	6430	2136	47688
M00364	C10-C20 isoprenoid biosynthesis, bacteria	816	590	784	1234	780	1002	1506	792	368	874	426	9172
M00366	C10-C20 isoprenoid biosynthesis, plants	816	590	784	1234	780	1002	1506	792	368	874	426	9172
M00368	Ethylene biosynthesis, methionine => ethylene	844	726	954	1328	828	894	1610	796	434	742	496	9652
M00373	Ethylmalonyl pathway	204	236	228	288	108	246	126	992	146	806	104	3484
M00374	Dicarboxylate-hydroxybutyrate cycle	2080	2186	3046	3244	2136	2878	4438	3434	1270	4268	972	29952
M00376	3-Hydroxypropionate bi-cycle	1648	1214	1686	1900	1134	1534	2262	2330	934	2470	668	17780

M00377	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	2370	2348	2676	3356	2216	2626	4260	3660	1268	4428	1122	30330
M00394	RNA degradosome	3422	3172	3966	4500	2982	3028	4928	4772	2010	4448	2270	39498
M00429	Competence-related DNA transformation transporter	1570	1390	1584	1582	1166	1396	1712	2482	858	2822	1006	17568
M00432	Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate	3888	3350	4420	6006	3594	4556	7968	4224	2030	4070	1930	46036
M00434	PhoR-PhoB (phosphate starvation response) two-component regulatory system	4478	3712	4152	4922	3786	4234	5184	4478	2030	4992	2030	43998
M00436	Sulfonate transport system	188	228	278	580	394	284	258	390	64	650	16	3330
M00439	Oligopeptide transport system	1834	1540	2032	2820	2298	1792	2928	2630	996	3676	594	23140
M00478	DegS-DegU (multicellular behavior control) two-component regulatory system	62	172	292	122	74	226	242	338	74	640	12	2254
M00485	KinABCDE-Spo0FA (sporulation control) two-component regulatory system	668	812	766	572	456	604	688	1234	540	1512	676	8528
M00491	arabinogalactan oligomer/maltooligosaccharide transport system	2860	2334	2886	2714	2156	2592	3092	4076	1562	5748	966	30986
M00495	AgrC-AgrA (exoprotein synthesis) two-component regulatory system	1136	1130	1714	770	920	1340	1598	1952	658	3206	362	14786
M00498	NtrY-NtrX (nitrogen regulation)	594	602	828	916	564	682	1174	802	342	742	358	7604

	two-component regulatory system HydH-HydG (metal tolerance)												
M00499	two-component regulatory system CheA-CheYBV (chemotaxis)	5162	4344	5380	6842	4242	4210	7138	5834	3076	4684	3076	53988
M00506	two-component regulatory system YesM-YesN two-component	5748	5616	7208	7370	5510	5824	7462	7708	2676	8964	2734	66820
M00519	regulatory system Lysine biosynthesis, acetyl-DAP	1660	2404	3808	1930	1266	3460	3948	5922	1114	8728	482	34722
M00525	pathway, aspartate => lysine Lysine biosynthesis, DAP dehydrogenase pathway,	3888	3562	4002	6724	4344	4724	7312	4404	2022	4980	1840	47802
M00526	aspartate => lysine Lysine biosynthesis, DAP aminotransferase pathway,	3210	2792	3180	5306	3356	3566	5524	3278	1576	3676	1424	36888
M00527	aspartate => lysine Denitrification, nitrate =>	4582	4178	4852	7890	5144	5588	8826	5162	2412	5702	2276	56612
M00529	nitrogen Dissimilatory nitrate reduction,	746	608	922	1264	754	884	1606	814	352	762	408	9120
M00530	nitrate => ammonia Assimilatory nitrate reduction,	746	608	922	1264	754	884	1606	814	352	762	408	9120
M00531	nitrate => ammonia	318	302	386	334	348	380	484	610	260	770	150	4342
M00532	Photorespiration Isoleucine biosynthesis, pyruvate	960	748	1044	1368	712	1048	1534	1394	536	1372	376	11092
M00535	=> 2-oxobutanoate Nucleotide sugar biosynthesis,	2044	1742	2270	3002	1782	2384	4204	2300	1062	2354	936	24080
M00549	glucose => UDP-glucose	1872	1534	2076	2372	1918	1732	2646	2324	896	2926	748	21044

M00550	Ascorbate degradation, ascorbate => D-xylulose-5P	350	436	648	360	394	596	674	1008	312	1436	210	6424
M00552	D-galactonate degradation, De Ley-Doudoroff pathway, D-galactonate => glycerate-3P	1674	1424	1812	2566	1458	1838	3038	1680	1026	1456	848	18820
M00554	Nucleotide sugar biosynthesis, galactose => UDP-galactose	1566	1782	2220	1480	1194	1620	1872	2396	1116	3406	696	19348
M00555	Betaine biosynthesis, choline => betaine	60	196	278	162	16	70	48	478	26	706	2	2042
M00565	Trehalose biosynthesis, D-glucose 1P => trehalose	3156	3428	3984	4972	3632	3584	4502	5148	1572	6782	1140	41900
M00570	Isoleucine biosynthesis, threonine => 2-oxobutanoate => isoleucine	3870	3262	4384	5730	3504	3680	6074	4946	1912	5318	2258	44938
M00572	Pimeloyl-ACP biosynthesis, BioC-BioH pathway, malonyl-ACP => pimeloyl-ACP	1058	1012	1520	1270	944	1432	1528	2154	532	3230	348	15028
M00573	Biotin biosynthesis, BioI pathway, long-chain-acyl-ACP => pimeloyl-ACP => biotin	1712	1538	1866	2590	1480	1724	3168	1748	980	1402	862	19070
M00577	Biotin biosynthesis, BioW pathway, pimelate => pimeloyl-CoA => biotin	1712	1538	1866	2590	1480	1724	3168	1748	980	1402	862	19070
M00579	Phosphate acetyltransferase-acetate kinase pathway, acetyl-CoA => acetate	2680	2160	2662	3906	2482	2540	3952	2772	1254	2954	1134	28496
M00580	Pentose phosphate pathway,	58	122	216	114	60	220	260	356	66	636	22	2130

	archaea, fructose 6P => ribose 5P												
	Energy-coupling factor transport												
M00582	system	1606	1572	2162	2970	1794	2442	2860	3268	990	4534	718	24916
M00593	Inositol transport system	314	670	1102	594	278	980	1130	1612	364	2690	48	9782
	Dissimilatory sulfate reduction,												
M00596	sulfate => H2S	1544	1442	1760	2436	1638	1980	3368	1598	882	1450	814	18912
	Arabinosaccharide transport												
M00602	system	366	296	360	144	186	226	318	576	140	796	44	3452
	Putative aldouronate transport												
M00603	system	1608	1766	2538	1574	1378	2222	2576	3386	1092	5460	396	23996
	Glucose/mannose transport												
M00605	system	366	296	360	144	186	226	318	576	140	796	44	3452
	N,N'-Diacetylchitobiose transport												
M00606	system	366	296	360	144	186	226	318	576	140	796	44	3452
	Cysteine biosynthesis,												
M00609	methionine => cysteine	844	726	954	1328	828	894	1610	796	434	742	496	9652
	Incomplete reductive citrate												
	cycle, acetyl-CoA =>												
M00620	oxoglutarate	1176	1324	1894	1704	1128	1664	2358	2534	796	3360	492	18430
	beta-Lactam resistance, Bla												
M00627	system	7184	5514	6640	5578	5492	4736	5506	7160	2948	9118	2406	62282
	beta-Lactam resistance, AmpC												
M00628	system	874	858	1034	1852	1118	1224	1706	1134	426	1492	406	12124
	Galactose degradation, Leloir												
	pathway, galactose => alpha-D-												
M00632	glucose-1P	2728	3004	3672	2790	2200	2732	2874	4412	1692	5588	1116	32808

M00646	Multidrug resistance, efflux pump AcrAD-TolC	688	570	644	1332	746	942	1660	760	388	654	396	8780
M00647	Multidrug resistance, efflux pump AcrAB-TolC/SmeDEF	1982	1490	1956	2982	1798	2176	3788	1890	1012	1622	1014	21710
M00651	Vancomycin resistance, D-Ala-D-Lac type	2856	1688	2504	2718	2054	2034	2758	2572	1428	5492	772	26876
M00652	Vancomycin resistance, D-Ala-D-Ser type	674	578	924	408	386	810	1126	1440	314	2280	146	9086
M00656	VanS-VanR (VanB type vancomycin resistance) two-component regulatory system	2518	1392	2198	2468	1746	1772	2250	2082	1292	4844	702	23264
M00657	VanS-VanR (VanE type vancomycin resistance) two-component regulatory system	474	416	674	278	124	584	730	1072	206	1606	120	6284
M00669	gamma-Hexachlorocyclohexane transport system	890	798	1070	1448	948	1150	1826	1040	634	804	432	11040
M00670	Mce transport system	890	798	1070	1448	948	1150	1826	1040	634	804	432	11040
M00699	Multidrug resistance, efflux pump AmeABC	1982	1490	1956	2982	1798	2176	3788	1890	1012	1622	1014	21710
M00707	Multidrug resistance, MdlAB/SmdAB transporter	144	120	206	66	46	412	464	486	496	656	154	3250
M00718	Multidrug resistance, efflux pump MexAB-OprM	1982	1490	1956	2982	1798	2176	3788	1890	1012	1622	1014	21710
M00721	Cationic antimicrobial peptide (CAMP) resistance, arnBCADTEF operon	382	562	710	518	724	728	922	1118	282	1472	122	7540

M00726	Cationic antimicrobial peptide (CAMP) resistance, lysyl-phosphatidylglycerol (L-PG) synthase MprF	852	712	1068	1402	758	964	1648	762	428	634	420	9648
M00727	Cationic antimicrobial peptide (CAMP) resistance, N-acetylmuramoyl-L-alanine amidase AmiA and AmiC	2060	1792	2522	3130	2432	2942	3806	3156	1032	4262	770	27904
M00728	Cationic antimicrobial peptide (CAMP) resistance, envelope protein folding and degrading factors DegP and DsbA	1232	808	1262	1496	1232	1202	1944	1428	494	1588	412	13098
M00740	Methylaspartate cycle	2856	2192	3006	3576	2456	2594	3850	2860	1562	3308	1188	29448
M00741	Propanoyl-CoA metabolism, propanoyl-CoA => succinyl-CoA	204	236	228	288	108	246	126	992	146	806	104	3484
M00742	Aminoglycoside resistance, protease FtsH	4018	3856	5114	4988	3354	3782	5884	5786	1946	7526	1532	47786
M00761	Undecaprenylphosphate alpha-L-Ara4N biosynthesis, UDP-GlcA => undecaprenyl phosphate alpha-L-Ara4N	382	562	710	518	724	728	922	1118	282	1472	122	7540
M00793	dTDP-L-rhamnose biosynthesis	3946	3128	4068	5026	3618	3922	6360	5116	2468	5438	1892	44982
M00813	Lantibiotic transport system	946	976	1474	1382	952	820	808	2078	468	3060	348	13312
M00816	NisK-NisR (lantibiotic biosynthesis) two-component regulatory system	2272	1704	2072	1910	1290	1588	1628	2320	994	2704	1078	19560

KEGG pathways													
ko00010	Glycolysis / Gluconeogenesis	18532	16536	21324	27272	17672	19778	29684	24008	10510	26006	9102	220424
ko00020	Citrate cycle (TCA cycle)	8746	7142	9706	9170	6326	6910	10204	10038	5132	10626	4468	88468
ko00030	Pentose phosphate pathway	9862	8796	12102	16770	9904	12198	18114	13742	5188	16542	4030	127248
ko00040	Pentose and glucuronate interconversions	2026	2428	3538	3200	1958	3082	3852	4718	1296	6484	770	33352
ko00051	Fructose and mannose metabolism	6428	6332	8888	11098	7124	8894	12552	11640	3604	15314	2370	94244
ko00052	Galactose metabolism	11712	11984	15708	14544	11002	12356	16390	19898	6454	26136	5546	151730
ko00053	Ascorbate and aldarate metabolism	458	606	932	496	440	830	980	1400	468	2106	272	8988
ko00061	Fatty acid biosynthesis	3934	3170	4694	5428	3672	4722	6370	5906	2158	7596	1576	49226
ko00071	Fatty acid degradation	3148	2388	3374	4536	2958	3430	5824	3372	1874	3280	1588	35772
ko00130	Ubiquinone and other terpenoid-quinone biosynthesis	1094	1016	1112	1922	1210	1608	2566	1154	662	1294	616	14254
ko00190	Oxidative phosphorylation	8508	8652	11720	8888	6586	8074	10868	11698	4398	12100	4948	96440
ko00195	Photosynthesis	4744	5244	7206	5020	3888	4764	6142	7364	2554	7642	2760	57328
ko00220	Arginine biosynthesis	10132	8930	11254	13988	8888	10012	15120	12894	6080	14356	5042	116696
ko00230	Purine metabolism	49556	43012	55314	65710	44140	49872	72850	61040	25846	68160	23898	559398
ko00240	Pyrimidine metabolism	36806	32274	41184	45020	30500	35734	50980	47780	20166	53486	17998	411928
ko00250	Alanine, aspartate and glutamate metabolism	20230	17152	21766	27100	17386	19406	30082	24476	11138	27516	9638	225890
ko00260	Glycine, serine and threonine metabolism	11010	9818	12704	15550	9770	11456	17194	14062	6086	15000	4868	127518
ko00261	Monobactam biosynthesis	2528	2122	2582	4080	2628	2810	4048	2444	1244	2926	1018	28430
ko00270	Cysteine and methionine	20706	17322	23726	27092	18540	21990	33036	27146	11254	29138	11302	241252

	metabolism												
ko00280	Valine, leucine and isoleucine degradation	1844	1666	2354	2922	1694	2260	3546	2960	1138	2952	1066	24402
ko00290	Valine, leucine and isoleucine biosynthesis	7758	6612	8804	11736	7098	8236	14042	9170	3942	9388	4188	90974
ko00300	Lysine biosynthesis	11794	10286	12476	17316	11492	12392	19804	13354	6232	14234	5896	135276
ko00310	Lysine degradation	742	786	1010	1260	682	1034	1584	1176	484	1328	362	10448
ko00330	Arginine and proline metabolism	5140	4342	5406	7506	4370	5500	8894	5806	3276	6684	2638	59562
ko00332	Carbapenem biosynthesis	1664	1424	1782	2644	1508	1862	3058	1982	1018	2124	922	19988
ko00340	Histidine metabolism	6978	5958	7518	9168	6736	7196	11322	9388	4470	9600	3494	81828
ko00350	Tyrosine metabolism	3520	2896	3894	5496	3282	3768	6098	3576	2100	3928	1758	40316
ko00360	Phenylalanine metabolism	3710	3250	4154	6184	3474	4370	6796	3952	2148	4336	1934	44308
ko00380	Tryptophan metabolism	108	170	284	136	46	234	306	392	156	670	62	2564
ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis	10336	9018	11732	16016	10060	11962	17566	13058	5826	16246	4406	126226
ko00401	Novobiocin biosynthesis	2582	2262	2900	4530	2710	3170	4476	2856	1394	3724	1192	31796
ko00405	Phenazine biosynthesis	82	160	332	200	84	280	306	490	88	810	10	2842
ko00410	beta-Alanine metabolism	108	170	284	136	46	234	306	392	156	670	62	2564
ko00430	Taurine and hypotaurine metabolism	3662	3048	3632	5186	3302	3454	5594	3646	1860	3710	1602	38696
ko00450	Selenocompound metabolism	4580	4294	5672	6880	4404	4844	8036	6308	2642	6192	2588	56440
ko00460	Cyanoamino acid metabolism	4122	3856	5642	4914	3352	4570	6688	8014	2992	10628	2162	56940
ko00471	D-Glutamine and D-glutamate metabolism	2624	2378	3020	4660	3168	3156	4742	3838	1688	4364	1434	35072
ko00473	D-Alanine metabolism	2054	1774	1904	3608	2228	2516	3774	2842	1032	3124	1042	25898
ko00480	Glutathione metabolism	2444	2078	2590	2974	1788	2444	3684	2740	1584	2940	1236	26502

ko00500	Starch and sucrose metabolism	15608	14650	19876	19952	14736	18086	24470	27222	8868	36296	6056	205820
ko00510	N-Glycan biosynthesis	214	246	270	734	396	282	190	464	56	692	24	3568
ko00511	Other glycan degradation	1580	2362	3246	2636	1898	1990	2328	5372	998	7312	872	30594
ko00520	Amino sugar and nucleotide sugar metabolism	20272	19572	26452	27760	19268	21858	29070	31618	11232	39472	9832	256406
ko00521	Streptomycin biosynthesis	6420	5284	6898	8914	6348	6842	11062	8300	3566	9102	2922	75658
ko00523	Polyketide sugar unit biosynthesis	3946	3128	4068	5026	3618	3922	6360	5116	2468	5438	1892	44982
ko00524	Neomycin, kanamycin and gentamicin biosynthesis	564	506	630	368	600	558	832	950	272	1258	212	6750
ko00525	Acarbose and validamycin biosynthesis	2340	1908	2406	2926	2180	2402	4136	3098	1614	3170	1220	27400
ko00531	Glycosaminoglycan degradation	874	858	1034	1852	1118	1224	1706	1134	426	1492	406	12124
ko00540	Lipopolysaccharide biosynthesis	7664	6746	8238	11222	7596	8044	14114	8772	4540	8360	4004	89300
ko00550	Peptidoglycan biosynthesis	21408	18326	22686	24440	18250	19392	30032	25362	11348	28882	10700	230826
ko00561	Glycerolipid metabolism	3868	4178	5986	4680	3018	3678	4374	6500	2008	8706	1932	48928
ko00562	Inositol phosphate metabolism	432	376	474	754	524	528	404	688	264	812	98	5354
ko00564	Glycerophospholipid metabolism	7378	6314	8524	10440	6778	7530	11314	8254	3900	9340	3326	83098
ko00600	Sphingolipid metabolism	2698	3412	5012	3560	2422	2462	2988	6826	1242	9434	1422	41478
ko00603	Glycosphingolipid biosynthesis - globo and isoglobo series	1508	1612	2428	1390	848	872	1070	2674	616	3560	780	17358
ko00620	Pyruvate metabolism	18976	15810	20824	26050	16648	18550	28810	22436	10758	24194	9456	212512
ko00625	Chloroalkane and chloroalkene degradation	1518	1150	1678	1838	1132	1422	2382	1570	1030	1662	724	16106
ko00626	Naphthalene degradation	1410	980	1394	1702	1086	1188	2076	1178	874	992	662	13542
ko00630	Glyoxylate and dicarboxylate	8922	7320	9264	12408	7928	8562	13706	10420	4598	10240	3900	97268

	metabolism												
ko00633	Nitrotoluene degradation	1092	1170	1548	1568	1060	1504	2316	1800	608	2230	488	15384
ko00640	Propanoate metabolism	5956	5082	6772	8580	5480	6342	10008	8196	3248	9048	2738	71450
ko00650	Butanoate metabolism	7260	5828	7916	7836	5730	5102	6814	9606	3760	10690	3892	74434
ko00660	C5-Branched dibasic acid metabolism	3642	3034	4000	5074	3102	3430	5654	4922	1716	5586	1904	42064
ko00670	One carbon pool by folate	8040	6804	8476	11738	7068	8324	13462	9984	3960	10966	3336	92158
ko00680	Methane metabolism	11394	10424	13368	19060	12308	13650	21592	14998	6182	17000	5298	145274
ko00710	Carbon fixation in photosynthetic organisms	7772	6708	8880	12366	7372	9422	13538	10968	4312	12560	3188	97086
ko00720	Carbon fixation pathways in prokaryotes	17566	14948	19518	22562	14608	16744	25836	22224	10116	24000	8712	196834
ko00730	Thiamine metabolism	7114	6368	7894	10014	6614	7644	11302	9662	4208	10430	4178	85428
ko00740	Riboflavin metabolism	888	796	1274	1432	982	1302	2096	1268	474	1500	428	12440
ko00750	Vitamin B6 metabolism	2914	2506	3022	4050	2484	3306	5178	3574	1366	3558	1224	33182
ko00760	Nicotinate and nicotinamide metabolism	5830	5612	7530	5790	4306	5584	7388	8122	3504	8284	3556	65506
ko00770	Pantothenate and CoA biosynthesis	7078	6108	8384	11144	6902	7496	12744	9080	3848	9376	3992	86152
ko00780	Biotin metabolism	3566	3254	4104	4922	3100	3974	6022	4666	2024	5300	1598	42530
ko00790	Folate biosynthesis	5004	4018	5708	5796	4082	5204	8394	5898	3184	6882	2564	56734
ko00860	Porphyrin and chlorophyll metabolism	12370	10818	13162	17052	11112	13512	21356	15778	7248	15512	6222	144142
ko00900	Terpenoid backbone biosynthesis	7992	7444	9148	10184	6860	8044	12632	10332	4904	11406	4362	93308
ko00903	Limonene and pinene degradation	446	468	708	382	336	718	994	980	364	1540	152	7088
ko00908	Zeatin biosynthesis	1408	1162	1440	1608	1008	1154	1974	1780	930	1484	1032	14980

ko00910	Nitrogen metabolism	7570	6158	7754	9394	6484	7038	11842	7856	3700	8110	3352	79258
ko00920	Sulfur metabolism	6032	5414	7076	9202	6028	6764	10076	7890	3194	8680	2872	73228
ko00930	Caprolactam degradation	338	298	424	246	290	484	688	588	208	870	90	4524
ko00940	Phenylpropanoid biosynthesis	2172	2274	3536	2334	1746	2952	3716	5992	1712	8712	984	36130
ko00950	Isoquinoline alkaloid biosynthesis	1062	950	1058	1954	1168	1168	1880	1172	682	1528	548	13170
ko00960	Tropane, piperidine and pyridine alkaloid biosynthesis	2110	1916	2500	3794	2196	2580	4022	2398	1226	2936	1096	26774
ko00966	Glucosinolate biosynthesis	1158	988	1376	1616	988	1460	2576	1486	570	1580	508	14306
ko00970	Aminoacyl-tRNA biosynthesis	32208	28582	35094	35638	24512	29412	43980	40410	18000	43574	16590	348000
ko00981	Insect hormone biosynthesis	108	170	284	136	46	234	306	392	156	670	62	2564
ko00983	Drug metabolism - other enzymes	4006	3842	4624	5598	3618	4028	5462	5498	2082	6306	1802	46866
ko01040	Biosynthesis of unsaturated fatty acids	950	874	1248	1160	868	1200	1302	1730	418	2554	324	12628
ko01051	Biosynthesis of ansamycins	1976	1644	2538	2064	1318	2142	3296	2630	1152	3064	804	22628
ko01055	Biosynthesis of vancomycin group antibiotics	1170	918	1248	1526	1182	1302	2126	1466	788	1502	626	13854
ko01200	Carbon metabolism	40340	34348	45288	57416	36720	42070	63914	50828	22334	55946	18274	467478
ko01210	2-Oxocarboxylic acid metabolism	17182	14398	19086	25974	15982	17660	28772	18910	9340	20790	8334	196428
ko01212	Fatty acid metabolism	3692	3038	4430	4794	3248	4454	6136	5512	2078	6966	1500	45848
ko01220	Degradation of aromatic compounds	1748	1278	1818	1948	1376	1672	2764	1766	1082	1862	752	18066
ko01230	Biosynthesis of amino acids	67026	56748	73476	97002	61810	70650	111252	77622	36300	85970	30956	768812
ko01501	beta-Lactam resistance	19304	15670	19568	19870	15408	15474	22568	20376	9530	23666	8618	190052
ko01502	Vancomycin resistance	6366	4816	6516	7752	5440	6508	9246	8436	3136	13266	2214	73696
ko01503	Cationic antimicrobial peptide (CAMP) resistance	6508	5364	7518	9528	6944	8012	12108	8354	3248	9578	2738	79900

ko01523	Antifolate resistance	2212	1804	2582	3552	1892	2384	3808	2506	848	3120	778	25486
ko01524	Platinum drug resistance	1310	1126	1288	2102	1262	1640	2540	1758	700	1974	632	16332
ko02010	ABC transporters	41044	37340	50666	60336	41796	45954	60838	62848	23054	80984	17330	522190
ko02020	Two-component system	69438	60750	78248	85308	59090	67484	90880	82504	34640	98236	31754	758332
ko02024	Quorum sensing	30002	26806	34232	38378	27658	29874	44570	40532	17982	45118	16234	351386
ko02025	Biofilm formation - Pseudomonas aeruginosa	1208	1350	1732	1438	1228	1486	1574	2444	758	3156	714	17088
ko02026	Biofilm formation - Escherichia coli	2372	2124	2532	3182	2766	2366	2934	3698	1078	4718	884	28654
ko02030	Bacterial chemotaxis	26326	24234	30738	32338	24016	25296	30124	33992	12644	41694	12570	293972
ko02040	Flagellar assembly	42350	39058	43242	45918	32370	43024	50850	44600	23906	47570	20262	433150
ko02060	Phosphotransferase system (PTS)	874	846	1602	1552	782	1458	1640	2632	484	3968	210	16048
ko03010	Ribosome	5546	5118	6598	9154	6098	6622	9894	6976	2932	7592	2678	69208
ko03013	RNA transport	2936	2576	2970	3208	2332	2358	3542	3058	1558	3672	1002	29212
ko03018	RNA degradation	12268	10278	13204	17566	12028	12136	18440	15554	6728	16184	6192	140578
ko03020	RNA polymerase	3014	2668	3742	3452	2754	3142	3988	3544	1848	5178	1258	34588
ko03030	DNA replication	19456	17502	22658	20860	15206	17864	24158	25668	10740	28942	10662	213716
ko03060	Protein export	14064	12162	15160	18874	13404	14386	22128	19480	9114	19586	8592	166950
ko03070	Bacterial secretion system	26738	22866	27766	31824	23230	25650	35050	32116	14234	34102	14632	288208
ko03320	PPAR signaling pathway	1022	872	1340	1704	1068	1446	2176	1570	572	1612	584	13966
ko03410	Base excision repair	11626	9900	13384	12904	8986	10504	16028	13838	6780	14740	6436	125126
ko03420	Nucleotide excision repair	19054	15828	19336	20294	14108	14874	23020	23894	10384	24844	10216	195852
ko03430	Mismatch repair	24972	22378	28954	26632	18144	22806	31282	33096	14036	36638	13590	272528
ko03440	Homologous recombination	26078	23206	29814	30364	20596	23846	33096	35296	15490	38708	15600	292094
ko04016	MAPK signaling pathway - plant	1310	1126	1288	2102	1262	1640	2540	1758	700	1974	632	16332
ko04066	HIF-1 signaling pathway	2134	1878	2322	3180	2044	2258	3738	2506	1364	2378	1104	24906

ko04070	Phosphatidylinositol signaling system	674	572	892	1302	736	888	1662	708	350	634	392	8810
ko04112	Cell cycle - Caulobacter	10764	9376	11814	15964	11036	12074	18528	14122	6142	16050	5508	131378
ko04122	Sulfur relay system	4226	3606	4342	5588	3702	4258	5286	5012	2378	5826	2110	46334
ko04141	Protein processing in endoplasmic reticulum	2302	1840	2128	3104	2136	2360	3460	2834	1012	2998	850	25024
ko04142	Lysosome	84	210	388	218	92	304	318	514	90	710	18	2946
ko04146	Peroxisome	2038	1772	2462	3318	2374	2558	3610	2618	1308	2810	1014	25882
ko04151	PI3K-Akt signaling pathway	2302	1840	2128	3104	2136	2360	3460	2834	1012	2998	850	25024
ko04152	AMPK signaling pathway	734	578	768	1246	702	876	1520	774	340	648	358	8544
ko04212	Longevity regulating pathway - worm	276	228	360	222	278	508	750	992	174	1094	104	4986
ko04213	Longevity regulating pathway - multiple species	230	226	274	612	522	362	292	464	112	634	92	3820
ko04216	Ferroptosis	862	654	932	1416	890	1070	1756	1028	438	826	472	10344
ko04612	Antigen processing and presentation	2302	1840	2128	3104	2136	2360	3460	2834	1012	2998	850	25024
ko04621	NOD-like receptor signaling pathway	12336	10300	12754	13012	8106	10070	12122	11066	6112	11928	4582	112388
ko04626	Plant-pathogen interaction	12496	10518	13162	13300	8284	10446	12542	11608	6246	12714	4694	116010
ko04657	IL-17 signaling pathway	2302	1840	2128	3104	2136	2360	3460	2834	1012	2998	850	25024
ko04659	Th17 cell differentiation	2302	1840	2128	3104	2136	2360	3460	2834	1012	2998	850	25024
ko04724	Glutamatergic synapse	3358	2660	3192	3674	2392	2642	4262	3450	1712	3372	1524	32238
ko04727	GABAergic synapse	3358	2660	3192	3674	2392	2642	4262	3450	1712	3372	1524	32238
ko04910	Insulin signaling pathway	1890	1496	2064	3346	2026	2124	2938	2548	834	3288	604	23158
ko04914	Progesterone-mediated oocyte	2302	1840	2128	3104	2136	2360	3460	2834	1012	2998	850	25024

	maturation												
ko04915	Estrogen signaling pathway	2302	1840	2128	3104	2136	2360	3460	2834	1012	2998	850	25024
ko04917	Prolactin signaling pathway	904	998	1244	722	672	890	1120	1388	646	1792	484	10860
ko04920	Adipocytokine signaling pathway	862	654	932	1416	890	1070	1756	1028	438	826	472	10344
ko04922	Glucagon signaling pathway	2438	1754	2398	3686	2242	2228	3084	2640	1068	3474	812	25824
ko04930	Type II diabetes mellitus	1614	1144	1538	2504	1438	1466	2110	1430	754	1742	638	16378
ko04931	Insulin resistance	2012	1582	2168	3426	2074	2242	3100	2450	902	3300	644	23900
ko04964	Proximal tubule bicarbonate reclamation	146	178	228	236	82	158	88	606	172	682	104	2680
ko04973	Carbohydrate digestion and absorption	306	294	422	142	64	340	332	474	116	720	56	3266
ko05010	Alzheimer's disease	970	832	1036	1350	818	990	1566	916	708	818	452	10456
ko05014	Amyotrophic lateral sclerosis (ALS)	230	226	274	612	522	362	292	464	112	634	92	3820
ko05016	Huntington's disease	230	226	274	612	522	362	292	464	112	634	92	3820
ko05020	Prion diseases	230	226	274	612	522	362	292	464	112	634	92	3820
ko05111	Biofilm formation - Vibrio cholerae	6452	5668	7044	9834	6310	7270	11254	7392	3380	7510	3138	75252
ko05120	Epithelial cell signaling in Helicobacter pylori infection	1912	1910	2414	2268	1752	1142	1444	3018	1234	3088	1478	21660
ko05132	Salmonella infection	10034	8460	10626	9908	5970	7710	8662	8232	5100	8930	3732	87364
ko05134	Legionellosis	10996	9392	11932	11440	6920	8930	10826	9682	5594	10392	4316	100420
ko05150	Staphylococcus aureus infection	852	712	1068	1402	758	964	1648	762	428	634	420	9648
ko05152	Tuberculosis	1430	1270	1782	1488	1412	1284	1334	1592	562	1580	654	14388
ko05200	Pathways in cancer	2302	1840	2128	3104	2136	2360	3460	2834	1012	2998	850	25024
ko05203	Viral carcinogenesis	1614	1144	1538	2504	1438	1466	2110	1430	754	1742	638	16378

ko05206	MicroRNAs in cancer	5566	4446	6380	4590	4620	5844	7554	10024	3122	10532	3896	66574
ko05215	Prostate cancer	2302	1840	2128	3104	2136	2360	3460	2834	1012	2998	850	25024
ko05230	Central carbon metabolism in cancer	1760	1322	1766	2740	1520	1624	2198	2036	926	2424	742	19058
ko05340	Primary immunodeficiency	898	720	1008	1146	768	808	1326	746	528	680	460	9088
ko05410	Hypertrophic cardiomyopathy (HCM)	110	160	288	144	140	518	586	372	142	682	10	3152
ko05414	Dilated cardiomyopathy	110	160	288	144	140	518	586	372	142	682	10	3152
ko05418	Fluid shear stress and atherosclerosis	2302	1840	2128	3104	2136	2360	3460	2834	1012	2998	850	25024