

Table SM-1. Fraction disorder in metabolic pathways, averaged over unique “gene” entries (containing one or more proteins each) and unique proteins over all the gene entries.

Pathway	Number of "gene" entries	Average fraction disorder of nodes	Number of proteins	Average fraction disorder of proteins	Pathway name
hsa00010	27	0.0666	65	0.059	Glycolysis / Gluconeogenesis
hsa00020	16	0.1187	30	0.122	Citrate cycle (TCA cycle)
hsa00030	17	0.0709	28	0.069	Pentose phosphate pathway
hsa00040	11	0.0470	33	0.041	Pentose and glucuronate interconversions
hsa00051	18	0.0650	36	0.091	Fructose and mannose metabolism
hsa00052	15	0.0663	27	0.067	Galactose metabolism
hsa00053	5	0.0504	27	0.041	Ascorbate and aldarate metabolism
hsa00061	5	0.1333	6	0.139	Fatty acid biosynthesis
hsa00062	6	0.0632	8	0.055	Fatty acid elongation in mitochondria
hsa00071	18	0.094	44	0.078	Fatty acid metabolism
hsa00072	5	0.086	9	0.081	Synthesis and degradation of ketone bodies
hsa00100	16	0.099	19	0.108	Steroid biosynthesis
hsa00120	16	0.080	16	0.080	Primary bile acid biosynthesis
hsa00130	7	0.152	7	0.152	Ubiquinone and other terpenoid-quinone biosynthesis
hsa00140	25	0.079	57	0.062	Steroid hormone biosynthesis
hsa00190	112	0.201	132	0.211	Oxidative phosphorylation
hsa00230	49	0.100	163	0.172	Purine metabolism
hsa00232	4	0.043	7	0.036	Caffeine metabolism
hsa00240	32	0.125	100	0.173	Pyrimidine metabolism
hsa00250	23	0.060	32	0.066	Alanine, aspartate and glutamate metabolism
hsa00260	28	0.071	32	0.077	Glycine, serine and threonine metabolism
hsa00270	22	0.096	36	0.111	Cysteine and methionine metabolism
hsa00280	30	0.102	44	0.097	Valine, leucine and isoleucine degradation
hsa00290	5	0.086	11	0.087	Valine, leucine and isoleucine biosynthesis
hsa00300	3	0.048	3	0.048	Lysine biosynthesis
hsa00310	17	0.128	49	0.319	Lysine degradation
hsa00330	35	0.086	55	0.090	Arginine and proline metabolism
hsa00340	15	0.080	30	0.080	Histidine metabolism
hsa00350	23	0.068	41	0.065	Tyrosine metabolism
hsa00360	11	0.062	17	0.055	Phenylalanine metabolism
hsa00380	26	0.084	42	0.084	Tryptophan metabolism
hsa00400	4	0.095	5	0.085	Phenylalanine, tyrosine and

					tryptophan biosynthesis
hsa00410	16	0.099	27	0.085	beta-Alanine metabolism
hsa00430	6	0.129	10	0.122	Taurine and hypotaurine metabolism
hsa00450	11	0.099	17	0.095	Selenocompound metabolism
hsa00460	3	0.069	7	0.085	Cyanoamino acid metabolism
hsa00471	2	0.130	4	0.129	D-Glutamine and D-glutamate metabolism
hsa00472	1	0.046	1	0.046	D-Arginine and D-ornithine metabolism
hsa00480	19	0.091	50	0.075	Glutathione metabolism
hsa00500	22	0.061	55	0.050	Starch and sucrose metabolism
hsa00510	35	0.114	49	0.137	N-Glycan biosynthesis
hsa00511	11	0.063	17	0.066	Other glycan degradation
hsa00512	9	0.150	30	0.160	Mucin type O-Glycan biosynthesis
hsa00514	17	0.129	46	0.099	Other types of O-glycan biosynthesis
hsa00520	33	0.061	48	0.054	Amino sugar and nucleotide sugar metabolism
hsa00524	2	0.056	5	0.058	Butirosin and neomycin biosynthesis
hsa00531	15	0.055	19	0.060	Glycosaminoglycan degradation
hsa00532	15	0.205	22	0.214	Glycosaminoglycan biosynthesis - chondroitin sulfate
hsa00533	10	0.173	15	0.175	Glycosaminoglycan biosynthesis - keratan sulfate
hsa00534	16	0.198	26	0.197	Glycosaminoglycan biosynthesis - heparan sulfate
hsa00561	16	0.088	50	0.115	Glycerolipid metabolism
hsa00562	24	0.248	57	0.270	Inositol phosphate metabolism
hsa00563	25	0.105	25	0.105	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis
hsa00564	36	0.141	82	0.144	Glycerophospholipid metabolism
hsa00565	12	0.118	36	0.111	Ether lipid metabolism
hsa00590	28	0.054	59	0.078	Arachidonic acid metabolism
hsa00591	4	0.050	30	0.085	Linoleic acid metabolism
hsa00592	3	0.097	20	0.111	alpha-Linolenic acid metabolism
hsa00600	23	0.099	40	0.110	Sphingolipid metabolism
hsa00601	30	0.141	26	0.130	Glycosphingolipid biosynthesis - lacto and neolacto series
hsa00603	11	0.066	14	0.067	Glycosphingolipid biosynthesis - globo series
hsa00604	15	0.110	15	0.103	Glycosphingolipid biosynthesis - ganglio series
hsa00620	21	0.081	40	0.077	Pyruvate metabolism
hsa00630	13	0.066	18	0.065	Glyoxylate and dicarboxylate metabolism
hsa00640	16	0.105	32	0.090	Propanoate metabolism
hsa00650	16	0.080	30	0.075	Butanoate metabolism
hsa00670	16	0.071	18	0.074	One carbon pool by folate

hsa00730	4	0.100	4	0.100	Thiamine metabolism
hsa00740	6	0.060	12	0.068	Riboflavin metabolism
hsa00750	5	0.057	6	0.051	Vitamin B6 metabolism
hsa00760	15	0.089	25	0.108	Nicotinate and nicotinamide metabolism
hsa00770	11	0.118	17	0.116	Pantothenate and CoA biosynthesis
hsa00780	2	0.162	2	0.162	Biotin metabolism
hsa00785	3	0.113	3	0.113	Lipoic acid metabolism
hsa00790	10	0.114	13	0.104	Folate biosynthesis
hsa00830	22	0.061	64	0.049	Retinol metabolism
hsa00860	18	0.147	43	0.102	Porphyrin and chlorophyll metabolism
hsa00900	11	0.106	15	0.109	Terpenoid backbone biosynthesis
hsa00910	9	0.079	23	0.074	Nitrogen metabolism
hsa00920	7	0.133	13	0.131	Sulfur metabolism
hsa00970	23	0.131	41	0.120	Aminoacyl-tRNA biosynthesis
hsa00980	13	0.040	71	0.038	Metabolism of xenobiotics by cytochrome P450
hsa00982	14	0.043	73	0.037	Drug metabolism - cytochrome P450
hsa00983	23	0.083	52	0.068	Drug metabolism - other enzymes
hsa01040	15	0.122	21	0.121	Biosynthesis of unsaturated fatty acids
hsa01100	581	0.096	1136	0.123	Metabolic pathways

Table SM-2. Fraction disorder in non-metabolic pathways, averaged over unique “gene” entries (containing one or more proteins each) and unique proteins over all the gene entries.

Pathway	Number of "gene" entries	Average fraction disorder of nodes	Number of proteins	Average fraction disorder of proteins	Pathway name
hsa02010	44	0.133	44	0.133	ABC transporters
hsa03008	56	0.292	82	0.325	Ribosome biogenesis in eukaryotes
hsa03010	79	0.259	90	0.267	Ribosome
hsa03013	95	0.396	153	0.367	RNA transport
hsa03015	47	0.437	84	0.379	mRNA surveillance pathway
hsa03018	54	0.313	71	0.314	RNA degradation
hsa03020	27	0.224	30	0.221	RNA polymerase
hsa03022	33	0.429	54	0.448	Basal transcription factors
hsa03030	33	0.264	36	0.257	DNA replication
hsa03040	71	0.426	128	0.426	Spliceosome
hsa03050	43	0.168	45	0.168	Proteasome
hsa03060	21	0.274	23	0.257	Protein export
hsa03320	49	0.209	71	0.179	PPAR signaling pathway
hsa03410	25	0.280	34	0.305	Base excision repair
hsa03420	29	0.283	48	0.271	Nucleotide excision repair
hsa03430	13	0.298	23	0.281	Mismatch repair
hsa03440	20	0.360	28	0.348	Homologous recombination
hsa03450	13	0.323	14	0.312	Non-homologous end-joining
hsa04010	119	0.389	268	0.322	MAPK signaling pathway
hsa04012	47	0.398	87	0.356	ErbB signaling pathway
hsa04020	40	0.236	177	0.232	Calcium signaling pathway
hsa04060	246	0.262	265	0.253	Cytokine-cytokine receptor interaction
hsa04062	49	0.300	189	0.237	Chemokine signaling pathway
hsa04070	24	0.292	78	0.262	Phosphatidylinositol signaling system
hsa04080	91	0.214	272	0.207	Neuroactive ligand-receptor interaction
hsa04110	79	0.352	128	0.338	Cell cycle
hsa04114	48	0.338	114	0.252	Oocyte meiosis
hsa04115	55	0.271	69	0.261	p53 signaling pathway
hsa04120	101	0.247	139	0.239	Ubiquitin mediated proteolysis
hsa04122	9	0.167	10	0.155	Sulfur relay system
hsa04130	24	0.464	36	0.465	SNARE interactions in vesicular transport
hsa04140	14	0.254	34	0.208	Regulation of autophagy
hsa04141	86	0.331	167	0.306	Protein processing in endoplasmic reticulum
hsa04142	62	0.111	121	0.134	Lysosome

hsa04144	78	0.383	203	0.371	Endocytosis
hsa04145	60	0.241	156	0.194	Phagosome
hsa04146	63	0.148	78	0.138	Peroxisome
hsa04150	27	0.335	52	0.299	mTOR signaling pathway
hsa04210	49	0.252	88	0.240	Apoptosis
hsa04260	14	0.361	77	0.305	Cardiac muscle contraction
hsa04270	38	0.275	116	0.230	Vascular smooth muscle contraction
hsa04310	62	0.385	151	0.333	Wnt signaling pathway
hsa04320	13	0.327	25	0.280	Dorso-ventral axis formation
hsa04330	22	0.416	47	0.414	Notch signaling pathway
hsa04340	18	0.279	56	0.271	Hedgehog signaling pathway
hsa04350	43	0.335	85	0.345	TGF-beta signaling pathway
hsa04360	61	0.241	130	0.258	Axon guidance
hsa04370	28	0.295	76	0.240	VEGF signaling pathway
hsa04380	68	0.353	128	0.332	Osteoclast differentiation
hsa04510	60	0.322	200	0.303	Focal adhesion
hsa04512	45	0.215	85	0.334	ECM-receptor interaction
hsa04514	87	0.244	136	0.240	Cell adhesion molecules (CAMs)
hsa04520	51	0.353	73	0.362	Adherens junction
hsa04530	51	0.404	133	0.340	Tight junction
hsa04540	35	0.254	90	0.194	Gap junction
hsa04610	58	0.139	69	0.157	Complement and coagulation cascades
hsa04612	27	0.288	78	0.269	Antigen processing and presentation
hsa04614	17	0.083	17	0.083	Renin-angiotensin system
hsa04620	68	0.247	102	0.222	Toll-like receptor signaling pathway
hsa04621	45	0.281	59	0.261	NOD-like receptor signaling pathway
hsa04622	50	0.293	71	0.246	RIG-I-like receptor signaling pathway
hsa04623	28	0.285	62	0.242	Cytosolic DNA-sensing pathway
hsa04630	26	0.343	155	0.278	Jak-STAT signaling pathway
hsa04640	67	0.242	88	0.226	Hematopoietic cell lineage
hsa04650	70	0.267	136	0.261	Natural killer cell mediated cytotoxicity
hsa04660	63	0.315	108	0.313	T cell receptor signaling pathway
hsa04662	43	0.320	75	0.306	B cell receptor signaling pathway
hsa04664	35	0.262	79	0.205	Fc epsilon RI signaling pathway
hsa04666	45	0.316	95	0.285	Fc gamma R-mediated phagocytosis
hsa04670	56	0.276	117	0.247	Leukocyte transendothelial migration
hsa04672	32	0.293	49	0.266	Intestinal immune network for IgA production
hsa04710	11	0.416	23	0.407	Circadian rhythm - mammal
hsa04720	25	0.305	70	0.253	Long-term potentiation
hsa04722	73	0.345	127	0.296	Neurotrophin signaling pathway

hsa04724	41	0.229	126	0.218	Glutamatergic synapse
hsa04730	25	0.247	70	0.194	Long-term depression
hsa04740	15	0.213	388	0.066	Olfactory transduction
hsa04742	18	0.183	52	0.139	Taste transduction
hsa04744	12	0.237	29	0.210	Phototransduction
hsa04810	65	0.365	214	0.306	Regulation of actin cytoskeleton
hsa04910	62	0.327	138	0.285	Insulin signaling pathway
hsa04912	40	0.264	101	0.214	GnRH signaling pathway
hsa04914	31	0.306	87	0.251	Progesterone-mediated oocyte maturation
hsa04916	33	0.321	101	0.295	Melanogenesis
hsa04920	36	0.298	69	0.285	Adipocytokine signaling pathway
hsa04930	23	0.335	48	0.283	Type II diabetes mellitus
hsa04940	20	0.255	45	0.222	Type I diabetes mellitus
hsa04950	25	0.613	25	0.613	Maturity onset diabetes of the young
hsa04960	19	0.314	42	0.266	Aldosterone-regulated sodium reabsorption
hsa04961	21	0.211	49	0.223	Endocrine and other factor-regulated calcium reabsorption
hsa04962	17	0.286	44	0.356	Vasopressin-regulated water reabsorption
hsa04964	12	0.136	23	0.129	Proximal tubule bicarbonate reclamation
hsa04966	6	0.121	27	0.170	Collecting duct acid secretion
hsa04970	39	0.294	89	0.239	Salivary secretion
hsa04971	28	0.273	74	0.229	Gastric acid secretion
hsa04972	43	0.161	101	0.148	Pancreatic secretion
hsa04973	19	0.123	44	0.121	Carbohydrate digestion and absorption
hsa04974	26	0.188	81	0.336	Protein digestion and absorption
hsa04975	21	0.167	46	0.132	Fat digestion and absorption
hsa04976	49	0.173	71	0.163	Bile secretion
hsa04977	23	0.177	24	0.177	Vitamin digestion and absorption
hsa04978	30	0.171	51	0.154	Mineral absorption
hsa05010	53	0.242	167	0.236	Alzheimer's disease
hsa05012	27	0.175	130	0.203	Parkinson's disease
hsa05014	35	0.281	53	0.257	Amyotrophic lateral sclerosis (ALS)
hsa05016	48	0.362	183	0.295	Huntington's disease
hsa05020	20	0.259	35	0.255	Prion diseases
hsa05100	36	0.339	71	0.323	Bacterial invasion of epithelial cells
hsa05110	18	0.251	54	0.202	Vibrio cholerae infection
hsa05120	33	0.281	68	0.228	Epithelial cell signaling in Helicobacter pylori infection
hsa05130	27	0.257	58	0.198	Pathogenic Escherichia coli infection
hsa05131	36	0.286	62	0.250	Shigellosis
hsa05140	40	0.304	73	0.262	Leishmaniasis
hsa05142	55	0.221	104	0.228	Chagas disease (American

					trypanosomiasis)
hsa05143	25	0.238	35	0.240	African trypanosomiasis
hsa05144	35	0.217	51	0.232	Malaria
hsa05145	53	0.222	133	0.206	Toxoplasmosis
hsa05146	40	0.230	106	0.290	Amoebiasis
hsa05150	31	0.184	56	0.208	Staphylococcus aureus infection
hsa05152	98	0.269	182	0.240	Tuberculosis
hsa05160	63	0.269	135	0.228	Hepatitis C
hsa05162	75	0.281	134	0.245	Measles
hsa05200	169	0.337	327	0.337	Pathways in cancer
hsa05210	37	0.349	62	0.342	Colorectal cancer
hsa05211	36	0.320	70	0.325	Renal cell carcinoma
hsa05212	40	0.292	70	0.287	Pancreatic cancer
hsa05213	30	0.355	52	0.360	Endometrial cancer
hsa05214	31	0.279	65	0.271	Glioma
hsa05215	40	0.357	89	0.381	Prostate cancer
hsa05216	15	0.409	29	0.465	Thyroid cancer
hsa05217	18	0.396	55	0.356	Basal cell carcinoma
hsa05218	23	0.315	71	0.307	Melanoma
hsa05219	27	0.258	42	0.270	Bladder cancer
hsa05220	39	0.367	73	0.349	Chronic myeloid leukemia
hsa05221	33	0.362	58	0.355	Acute myeloid leukemia
hsa05222	36	0.271	85	0.305	Small cell lung cancer
hsa05223	32	0.294	54	0.291	Non-small cell lung cancer
hsa05310	15	0.215	31	0.220	Asthma
hsa05320	22	0.198	54	0.166	Autoimmune thyroid disease
hsa05322	34	0.256	138	0.303	Systemic lupus erythematosus
hsa05323	43	0.260	92	0.233	Rheumatoid arthritis
hsa05330	18	0.223	39	0.201	Allograft rejection
hsa05332	14	0.250	43	0.228	Graft-versus-host disease
hsa05340	35	0.316	35	0.316	Primary immunodeficiency
hsa05410	36	0.352	83	0.313	Hypertrophic cardiomyopathy (HCM)
hsa05412	28	0.331	74	0.289	Arrhythmogenic right ventricular cardiomyopathy (ARVC)
hsa05414	36	0.343	90	0.287	Dilated cardiomyopathy
hsa05416	31	0.256	72	0.295	Viral myocarditis