**Table S4. Pathway mapping of annotated unigenes of RGC-1066 and M-83 varieties of guar using KAAS-KEGG automatic annotation server.**

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|  [ko01100 Metabolic pathways](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01100.args) (905) [ko01110 Biosynthesis of secondary metabolites](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01110.args) (407) [ko01120 Microbial metabolism in diverse environments](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01120.args) (157) [ko01130 Biosynthesis of antibiotics](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01130.args) (211) [ko01200 Carbon metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01200.args) (97) [ko01210 2-Oxocarboxylic acid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01210.args) (30) [ko01212 Fatty acid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01212.args) (28) [ko01230 Biosynthesis of amino acids](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01230.args) (105) [ko01220 Degradation of aromatic compounds](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01220.args) (4) [ko00010 Glycolysis / Gluconeogenesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00010.args) (36) [ko00020 Citrate cycle (TCA cycle)](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00020.args) (21) [ko00030 Pentose phosphate pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00030.args) (20) [ko00040 Pentose and glucuronateinterconversions](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00040.args) (13) [ko00051 Fructose and mannose metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00051.args) (25) [ko00052 Galactose metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00052.args) (18) [ko00053 Ascorbate and aldarate metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00053.args) (17) [ko00500 Starch and sucrose metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00500.args) (38) [ko00520 Amino sugar and nucleotide sugar metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00520.args) (44) [ko00620 Pyruvate metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00620.args) (36) [ko00630 Glyoxylate and dicarboxylate metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00630.args) (32) [ko00640 Propanoate metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00640.args) (20) [ko00650 Butanoate metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00650.args) (13) [ko00660 C5-Branched dibasic acid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00660.args) (5) [ko00562 Inositol phosphate metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00562.args) (29) [ko00190 Oxidative phosphorylation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00190.args) (88) [ko00195 Photosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00195.args) (31) [ko00196 Photosynthesis - antenna proteins](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00196.args) (7) [ko00710 Carbon fixation in photosynthetic organisms](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00710.args) (24) [ko00720 Carbon fixation pathways in prokaryotes](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00720.args) (16) [ko00680 Methane metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00680.args) (22) [ko00910 Nitrogen metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00910.args) (12) [ko00920 Sulfur metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00920.args) (16) [ko00061 Fatty acid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00061.args) (16) [ko00062 Fatty acid elongation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00062.args) (8) [ko00071 Fatty acid degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00071.args) (14) [ko00072 Synthesis and degradation of ketone bodies](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00072.args) (4) [ko00073 Cutin, suberine and wax biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00073.args) (6) [ko00100 Steroid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00100.args) (18) [ko00140 Steroid hormone biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00140.args) (5) [ko00561 Glycerolipid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00561.args) (29) [ko00564 Glycerophospholipid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00564.args) (39) [ko00565 Ether lipid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00565.args) (8) [ko00600 Sphingolipid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00600.args) (14) [ko00590 Arachidonic acid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00590.args) (9) [ko00591 Linoleic acid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00591.args) (4) [ko00592 alpha-Linolenic acid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00592.args) (14) [ko01040 Biosynthesis of unsaturated fatty acids](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01040.args) (11) [ko00230 Purine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00230.args) (98) [ko00240 Pyrimidine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00240.args) (77) [ko00250 Alanine, aspartate and glutamate metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00250.args) (29) [ko00260 Glycine, serine and threonine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00260.args) (34) [ko00270 Cysteine and methionine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00270.args) (42) [ko00280 Valine, leucine and isoleucine degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00280.args) (22) [ko00290 Valine, leucine and isoleucine biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00290.args) (10) [ko00300 Lysine biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00300.args) (9) [ko00310 Lysine degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00310.args) (16) [ko00220 Arginine biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00220.args) (23) [ko00330 Arginine and proline metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00330.args) (27) [ko00340 Histidine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00340.args) (13) [ko00350 Tyrosine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00350.args) (18) [ko00360 Phenylalanine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00360.args) (16) [ko00380 Tryptophan metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00380.args) (16) [ko00400 Phenylalanine, tyrosine and tryptophan biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00400.args) (25) [ko00410 beta-Alanine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00410.args) (17) [ko00430 Taurine and hypotaurine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00430.args) (3) [ko00440 Phosphonate and phosphinate metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00440.args) (3) [ko00450 Selenocompound metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00450.args) (10) [ko00460 Cyanoamino acid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00460.args) (10) [ko00471 D-Glutamine and D-glutamate metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00471.args) (2) [ko00473 D-Alanine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00473.args) (1) [ko00480 Glutathione metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00480.args) (19) [ko00510 N-Glycan biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00510.args) (31) [ko00513 Various types of N-glycan biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00513.args) (23) [ko00515 Mannose type O-glycan biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00515.args) (2) [ko00514 Other types of O-glycan biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00514.args) (7) [ko00532 Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatansulfate](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00532.args) (2) [ko00534 Glycosaminoglycan biosynthesis - heparansulfate / heparin](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00534.args) (3) [ko00531 Glycosaminoglycan degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00531.args) (5) [ko00563 Glycosylphosphatidylinositol (GPI)-anchor biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00563.args) (21) [ko00601 Glycosphingolipid biosynthesis - lacto and neolacto series](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00601.args) (2) [ko00603 Glycosphingolipid biosynthesis - globo and isoglobo series](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00603.args) (3) [ko00604 Glycosphingolipid biosynthesis - ganglio series](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00604.args) (2) [ko00540 Lipopolysaccharide biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00540.args) (8) [ko00550 Peptidoglycan biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00550.args) (2) [ko00511 Other glycan degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00511.args) (10) [ko00730 Thiamine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00730.args) (13) [ko00740 Riboflavin metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00740.args) (13) [ko00750 Vitamin B6 metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00750.args) (9) [ko00760 Nicotinate and nicotinamide metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00760.args) (13) [ko00770 Pantothenate and CoA biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00770.args) (18) [ko00780 Biotin metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00780.args) (8) [ko00785 Lipoic acid metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00785.args) (2) [ko00790 Folate biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00790.args) (24) [ko00670 One carbon pool by folate](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00670.args) (11) [ko00830 Retinol metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00830.args) (6) [ko00860 Porphyrin and chlorophyll metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00860.args) (35) [ko00130 Ubiquinone and other terpenoid-quinone biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00130.args) (23) [ko00900 Terpenoid backbone biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00900.args) (29) [ko00902 Monoterpenoid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00902.args) (3) [ko00909 Sesquiterpenoid and triterpenoid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00909.args) (4) [ko00904 Diterpenoid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00904.args) (6) [ko00906 Carotenoid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00906.args) (19) [ko00905 Brassinosteroid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00905.args) (5) [ko00981 Insect hormone biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00981.args) (1) [ko00908 Zeatin biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00908.args) (4) [ko00903 Limonene and pinene degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00903.args) (1) [ko00281 Geraniol degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00281.args) (1) [ko01051 Biosynthesis of ansamycins](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01051.args) (1) [ko00523 Polyketide sugar unit biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00523.args) (2) [ko00940 Phenylpropanoid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00940.args) (18) [ko00945 Stilbenoid, diarylheptanoid and gingerol biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00945.args) (4) [ko00941 Flavonoid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00941.args) (9) [ko00944 Flavone and flavonol biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00944.args) (2) [ko00942 Anthocyanin biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00942.args) (1) [ko00901 Indole alkaloid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00901.args) (3) [ko00950 Isoquinoline alkaloid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00950.args) (7) [ko00960 Tropane, piperidine and pyridine alkaloid biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00960.args) (8) [ko00232 Caffeine metabolism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00232.args) (2) [ko00965 Betalain biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00965.args) (2) [ko00966 Glucosinolate biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00966.args) (3) [ko00311 Penicillin and cephalosporin biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00311.args) (1) [ko00332 Carbapenem biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00332.args) (2) [ko00261 Monobactam biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00261.args) (6) [ko00521 Streptomycin biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00521.args) (5) [ko00524 Neomycin, kanamycin and gentamicin biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00524.args) (1) [ko00525 Acarbose and validamycin biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00525.args) (1) [ko00401 Novobiocin biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00401.args) (2) [ko00405 Phenazine biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00405.args) (2) [ko00333 Prodigiosin biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00333.args) (3) [ko00254 Aflatoxin biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00254.args) (1) [ko00362 Benzoate degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00362.args) (2) [ko00627 Aminobenzoate degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00627.args) (2) [ko00364 Fluorobenzoate degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00364.args) (1) [ko00625 Chloroalkane and chloroalkene degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00625.args) (5) [ko00361 Chlorocyclohexane and chlorobenzene degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00361.args) (1) [ko00623 Toluene degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00623.args) (1) [ko00643 Styrene degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00643.args) (4) [ko00791 Atrazine degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00791.args) (2) [ko00930 Caprolactam degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00930.args) (1) [ko00626 Naphthalene degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00626.args) (2) [ko00980 Metabolism of xenobiotics by cytochrome P450](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00980.args) (7) [ko00982 Drug metabolism - cytochrome P450](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00982.args) (5) [ko00983 Drug metabolism - other enzymes](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00983.args) (19) [ko03020 RNA polymerase](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03020.args) (30) [ko03022 Basal transcription factors](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03022.args) (30) [ko03040 Spliceosome](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03040.args) (104) [ko03010 Ribosome](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03010.args) (130) [ko00970 Aminoacyl-tRNA biosynthesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko00970.args) (27) [ko03013 RNA transport](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03013.args) (96) [ko03015 mRNA surveillance pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03015.args) (52) [ko03008 Ribosome biogenesis in eukaryotes](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03008.args) (58) [ko03060 Protein export](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03060.args) (27) [ko04141 Protein processing in endoplasmic reticulum](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04141.args) (77) [ko04130 SNARE interactions in vesicular transport](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04130.args) (18) [ko04120 Ubiquitin mediated proteolysis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04120.args) (61) [ko04122 Sulfur relay system](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04122.args) (10) [ko03050 Proteasome](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03050.args) (35) [ko03018 RNA degradation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03018.args) (53) [ko03030 DNA replication](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03030.args) (35) [ko03410 Base excision repair](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03410.args) (26) [ko03420 Nucleotide excision 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Rap1 signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04015.args) (8) [ko04010 MAPK signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04010.args) (16) [ko04013 MAPK signaling pathway - fly](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04013.args) (15) [ko04016 MAPK signaling pathway - plant](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04016.args) (41) [ko04011 MAPK signaling pathway - yeast](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04011.args) (17) [ko04012 ErbBsignaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04012.args) (8) [ko04310 Wntsignaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04310.args) (20) [ko04330 Notch signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04330.args) (8) [ko04340 Hedgehog signaling 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interaction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04512.args) (1) [ko04144 Endocytosis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04144.args) (57) [ko04145 Phagosome](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04145.args) (28) [ko04142 Lysosome](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04142.args) (38) [ko04146 Peroxisome](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04146.args) (39) [ko04140 Autophagy - animal](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04140.args) (40) [ko04138 Autophagy - yeast](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04138.args) (45) [ko04136 Autophagy - other](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04136.args) (23) [ko04137 Mitophagy - animal](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04137.args) (14) [ko04139 Mitophagy - yeast](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04139.args) (16) [ko04110 Cell cycle](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04110.args) (58) [ko04111 Cell cycle - yeast](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04111.args) (54) [ko04112 Cell cycle - Caulobacter](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04112.args) (6) [ko04113 Meiosis - yeast](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04113.args) (41) [ko04114 Oocyte meiosis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04114.args) (32) [ko04210 Apoptosis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04210.args) (16) [ko04214 Apoptosis - fly](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04214.args) (12) [ko04215 Apoptosis - multiple species](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04215.args) (3) [ko04216 Ferroptosis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04216.args) (7) [ko04217 Necroptosis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04217.args) (22) [ko04115 p53 signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04115.args) (13) [ko04218 Cellular senescence](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04218.args) (28) [ko04510 Focal adhesion](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04510.args) (11) [ko04520 Adherens junction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04520.args) (6) [ko04530 Tight junction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04530.args) (14) [ko04540 Gap junction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04540.args) (7) [ko04550 Signaling pathways regulating pluripotency of stem cells](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04550.args) (6) [ko02024 Quorum sensing](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko02024.args) (15) [ko05111 Biofilm formation - Vibrio cholerae](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05111.args) (1) [ko02025 Biofilm formation - Pseudomonas aeruginosa](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko02025.args) (4) [ko02026 Biofilm formation - Escherichia coli](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko02026.args) (4) [ko02030 Bacterial chemotaxis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko02030.args) (1) [ko04810 Regulation of actin cytoskeleton](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04810.args) (20) [ko04611 Platelet activation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04611.args) (4) [ko04620 Toll-like receptor signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04620.args) (8) [ko04624 Toll and Imdsignaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04624.args) (9) [ko04621 NOD-like receptor signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04621.args) (19) [ko04622 RIG-I-like receptor signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04622.args) (8) [ko04623 Cytosolic DNA-sensing pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04623.args) (15) [ko04625 C-type lectin receptor signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04625.args) (3) [ko04650 Natural killer cell mediated cytotoxicity](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04650.args) (6) [ko04612 Antigen processing and presentation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04612.args) (9) [ko04660 T cell receptor signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04660.args) (7) [ko04658 Th1 and Th2 cell differentiation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04658.args) (2) [ko04659 Th17 cell differentiation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04659.args) (4) [ko04657 IL-17 signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04657.args) (7) [ko04662 B cell receptor signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04662.args) (6) [ko04664 Fc epsilon RI signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04664.args) (6) [ko04666 Fc gamma R-mediated phagocytosis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04666.args) (14) [ko04670 Leukocyte transendothelial migration](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04670.args) (2) [ko04062 Chemokine signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04062.args) (7) [ko04911 Insulin secretion](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04911.args) (3) [ko04910 Insulin signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04910.args) (21) [ko04922 Glucagon signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04922.args) (17) [ko04923 Regulation of lipolysis in adipocytes](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04923.args) (3) [ko04920 Adipocytokinesignaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04920.args) (5) [ko03320 PPAR signaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko03320.args) (9) [ko04912 GnRHsignaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04912.args) (8) [ko04913 Ovarian steroidogenesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04913.args) (3) [ko04915 Estrogensignaling 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Melanogenesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04916.args) (8) [ko04924 Renin secretion](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04924.args) (4) [ko04614 Renin-angiotensin system](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04614.args) (4) [ko04925 Aldosterone synthesis and secretion](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04925.args) (6) [ko04927 Cortisol synthesis and secretion](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04927.args) (1) [ko04260 Cardiac muscle contraction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04260.args) (14) [ko04261 Adrenergic signaling in cardiomyocytes](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04261.args) (11) [ko04270 Vascular smooth muscle contraction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04270.args) (8) [ko04970 Salivary 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absorption](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04977.args) (1) [ko04978 Mineral absorption](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04978.args) (4) [ko04962 Vasopressin-regulated water reabsorption](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04962.args) (6) [ko04960 Aldosterone-regulated sodium reabsorption](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04960.args) (2) [ko04961 Endocrine and other factor-regulated calcium reabsorption](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04961.args) (7) [ko04964 Proximal tubule bicarbonate reclamation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04964.args) (3) [ko04966 Collecting duct acid secretion](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04966.args) (11) [ko04724 Glutamatergic synapse](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04724.args) (9) [ko04727 GABAergic synapse](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04727.args) (10) [ko04725 Cholinergic synapse](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04725.args) (5) [ko04728 Dopaminergic synapse](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04728.args) (12) [ko04726 Serotonergic synapse](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04726.args) (7) [ko04720 Long-term potentiation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04720.args) (11) [ko04730 Long-term depression](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04730.args) (7) [ko04723 Retrograde endocannabinoidsignaling](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04723.args) (33) [ko04721 Synaptic vesicle cycle](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04721.args) (24) [ko04722 Neurotrophinsignaling pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04722.args) (15) [ko04744 Phototransduction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04744.args) (2) [ko04745 Phototransduction - fly](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04745.args) (4) [ko04740 Olfactory transduction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04740.args) (5) [ko04742 Taste transduction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04742.args) (3) [ko04750 Inflammatory mediator regulation of TRP channels](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04750.args) (4) [ko04320 Dorso-ventral axis formation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04320.args) (3) [ko04360 Axon guidance](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04360.args) (7) [ko04380 Osteoclast differentiation](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04380.args) (7) [ko04211 Longevity regulating pathway](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04211.args) (13) [ko04212 Longevity regulating pathway - worm](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04212.args) (19) [ko04213 Longevity regulating pathway - multiple species](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04213.args) (13) [ko04710 Circadian rhythm](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04710.args) (6) [ko04713 Circadian entrainment](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04713.args) (5) [ko04711 Circadian rhythm - fly](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04711.args) (2) [ko04712 Circadian rhythm - plant](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04712.args) (21) [ko04714 Thermogenesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04714.args) (86) [ko04626 Plant-pathogen interaction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04626.args) (27) [ko05200 Pathways in cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05200.args) (40) [ko05230 Central carbon metabolism in cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05230.args) (15) [ko05231 Choline metabolism in cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05231.args) (14) [ko05202 Transcriptional misregulation in cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05202.args) (14) [ko05206 MicroRNAs in cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05206.args) (20) [ko05205 Proteoglycans in cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05205.args) (15) [ko05204 Chemical carcinogenesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05204.args) (6) [ko05203 Viral carcinogenesis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05203.args) (41) [ko05210 Colorectal cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05210.args) (15) [ko05212 Pancreatic cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05212.args) (12) [ko05225 Hepatocellular carcinoma](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05225.args) (21) [ko05226 Gastric cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05226.args) (15) [ko05214 Glioma](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05214.args) (12) [ko05216 Thyroid cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05216.args) (7) [ko05221 Acute myeloid leukemia](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05221.args) (6) [ko05220 Chronic myeloid leukemia](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05220.args) (9) [ko05217 Basal cell carcinoma](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05217.args) (3) [ko05218 Melanoma](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05218.args) (9) [ko05211 Renal cell carcinoma](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05211.args) (10) [ko05219 Bladder cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05219.args) (6) [ko05215 Prostate cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05215.args) (14) [ko05213 Endometrial cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05213.args) (10) [ko05224 Breast cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05224.args) (13) [ko05222 Small cell lung cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05222.args) (11) [ko05223 Non-small cell lung cancer](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05223.args) (10) [ko05322 Systemic lupus erythematosus](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05322.args) (8) [ko05323 Rheumatoid arthritis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05323.args) (14) [ko05340 Primary immunodeficiency](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05340.args) (3) [ko05010 Alzheimer disease](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05010.args) (59) [ko05012 Parkinson disease](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05012.args) (58) [ko05014 Amyotrophic lateral sclerosis (ALS)](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05014.args) (7) [ko05016 Huntington disease](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05016.args) (74) [ko05020 Prion diseases](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05020.args) (6) [ko05030 Cocaine addiction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05030.args) (1) [ko05031 Amphetamine addiction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05031.args) (6) [ko05032 Morphine addiction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05032.args) (3) [ko05033 Nicotine addiction](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05033.args) (1) [ko05034 Alcoholism](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05034.args) (15) [ko05418 Fluid shear stress and atherosclerosis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05418.args) (14) [ko05410 Hypertrophic cardiomyopathy (HCM)](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05410.args) (2) [ko05416 Viral myocarditis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05416.args) (4) [ko04930 Type II diabetes mellitus](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04930.args) (4) [ko04940 Type I diabetes mellitus](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04940.args) (2) [ko04932 Non-alcoholic fatty liver disease (NAFLD)](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04932.args) (45) [ko04931 Insulin resistance](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04931.args) (13) [ko04933 AGE-RAGE signaling pathway in diabetic complications](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04933.args) (5) [ko04934 Cushing syndrome](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko04934.args) (14) [ko05110 Vibrio cholerae infection](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05110.args) (19) [ko05120 Epithelial cell signaling in Helicobacter pylori infection](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05120.args) (15) [ko05130 Pathogenic Escherichia coli infection](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05130.args) (8) [ko05132 Salmonella infection](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05132.args) (10) [ko05131 Shigellosis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05131.args) (12) [ko05133 Pertussis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05133.args) (5) [ko05134 Legionellosis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05134.args) (12) [ko05152 Tuberculosis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05152.args) (23) [ko05100 Bacterial invasion of epithelial cells](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05100.args) (10) [ko05166 HTLV-I infection](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05166.args) (45) [ko05162 Measles](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05162.args) (15) [ko05164 Influenza A](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05164.args) (21) [ko05161 Hepatitis B](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05161.args) (15) [ko05160 Hepatitis C](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05160.args) (11) [ko05168 Herpes simplex infection](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05168.args) (32) [ko05163 Human cytomegalovirus infection](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05163.args) (15) [ko05167 Kaposi sarcoma-associated herpesvirus infection](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05167.args) (17) [ko05169 Epstein-Barr virus infection](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05169.args) (66) [ko05165 Human papillomavirus infection](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05165.args) (46) [ko05146 Amoebiasis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05146.args) (5) [ko05144 Malaria](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05144.args) (1) [ko05145 Toxoplasmosis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05145.args) (10) [ko05140 Leishmaniasis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05140.args) (5) [ko05142 Chagas disease (American trypanosomiasis)](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05142.args) (10) [ko05143 African trypanosomiasis](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko05143.args) (5) [ko01501 beta-Lactam resistance](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01501.args) (1) [ko01502 Vancomycin resistance](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01502.args) (2) [ko01503 Cationic antimicrobial peptide (CAMP) resistance](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01503.args) (2) [ko01521 EGFR tyrosine kinase inhibitor resistance](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01521.args) (10) [ko01524 Platinum drug resistance](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01524.args) (16) [ko01523 Antifolate resistance](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01523.args) (6) [ko01522 Endocrine resistance](https://www.genome.jp/kegg-bin/show_pathway?1531549175101874/ko01522.args) (10) |
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