

Table S1. Assembly metrics of the strains.

Strain	Genome length, Mb	Number of contigs	N50, bp
96	4,9	80	167,760
129	4,9	86	265,593
132	5,0	85	256,904
133	5,0	87	225,227
134	5,1	75	182,877
142	5,0	96	142,845
144	4,2	303	27,240
12	4,9	82	285,499
152	5,0	91	169,160



Figure S1. A diagram showing the results of overlapping clusters of orthologous genes in strains (overlapping clusters containing proteins from different strains, sorted in descending order).

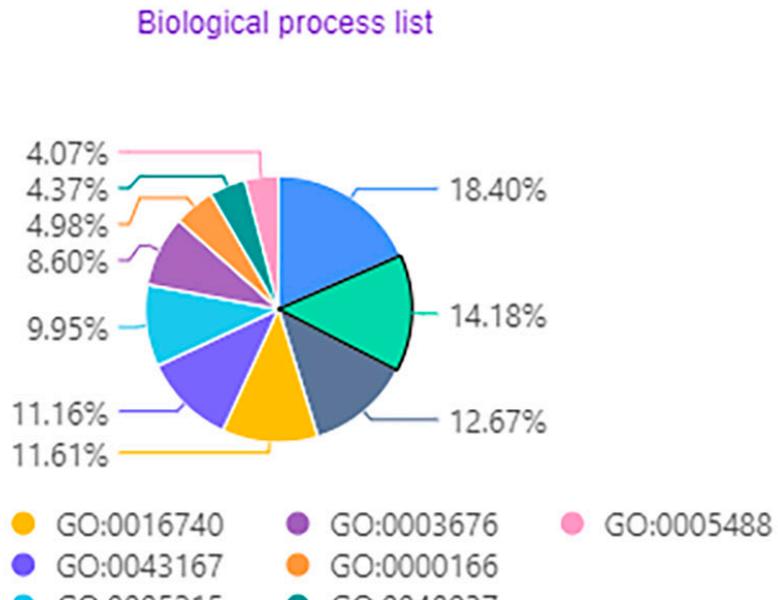
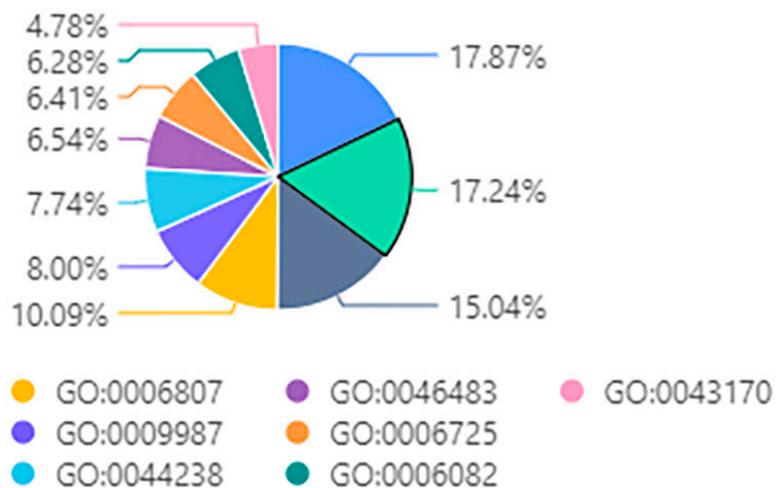


Figure S2. GO annotation core clusters for the representatives of the first group (strains 129, 144, 132, 133).

Table S2. Biological process list for the representatives of the first group.

GO	Count of unique input accessions	Name
GO:0008152	942	metabolic process
GO:0008150	909	biological_process
GO:0044237	793	cellular metabolic process
GO:0006807	532	nitrogen compound metabolic process
GO:0009987	422	cellular process
GO:0044238	408	primary metabolic process
GO:0046483	345	heterocycle metabolic process
GO:0006725	338	cellular aromatic compound metabolic process
GO:0006082	331	organic acid metabolic process
GO:0043170	252	macromolecule metabolic process
GO:0006139	235	nucleobase-containing compound metabolic process
GO:0016070	170	RNA metabolic process
GO:0065007	163	biological regulation
GO:0051186	156	cofactor metabolic process
GO:0006793	148	phosphorus metabolic process
GO:0006629	145	lipid metabolic process
GO:0044255	131	cellular lipid metabolic process
GO:0050896	114	response to stimulus
GO:0006810	109	transport
GO:0051234	109	establishment of localization
GO:0006412	96	translation
GO:0009117	83	nucleotide metabolic process
GO:0005975	65	carbohydrate metabolic process
GO:0016043	61	cellular component organization
GO:0006811	52	ion transport
GO:0009116	48	nucleoside metabolic process
GO:0043603	47	cellular amide metabolic process
GO:0019538	44	protein metabolic process
GO:0006396	40	RNA processing

GO:0006518	40	peptide metabolic process
GO:0032502	39	developmental process
GO:0006259	35	DNA metabolic process
GO:0006260	35	DNA replication
GO:0006281	35	DNA repair
GO:0006766	35	vitamin metabolic process
GO:0051179	32	localization
GO:0051704	32	multi-organism process
GO:0005976	29	polysaccharide metabolic process
GO:0007154	29	cell communication
GO:0043412	29	macromolecule modification
GO:0045333	29	cellular respiration
GO:0042180	27	cellular ketone metabolic process
GO:0006865	26	amino acid transport
GO:0006805	25	xenobiotic metabolic process
GO:0032989	25	cellular component morphogenesis
GO:0006464	24	cellular protein modification process
GO:0006091	22	generation of precursor metabolites and energy
GO:0042254	22	ribosome biogenesis
GO:0042440	20	pigment metabolic process
GO:0071555	20	cell wall organization
GO:0015031	18	protein transport
GO:0006066	17	alcohol metabolic process
GO:0065003	17	macromolecular complex assembly
GO:0009308	16	amine metabolic process
GO:0017144	15	drug metabolic process
GO:0019748	15	secondary metabolic process
GO:0032196	12	transposition
GO:0006508	11	proteolysis
GO:0006457	10	protein folding
GO:0006730	9	one-carbon metabolic process

GO:0006081	8	cellular aldehyde metabolic process
GO:0006112	8	energy reserve metabolic process
GO:0006818	8	hydrogen transport
GO:0009225	8	nucleotide-sugar metabolic process
GO:0015849	8	organic acid transport
GO:0008643	7	carbohydrate transport
GO:0022411	7	cellular component disassembly
GO:0022607	7	cellular component assembly
GO:0051189	7	prosthetic group metabolic process
GO:0051301	7	cell division
GO:0043101	6	purine-containing compound salvage
GO:0051641	6	cellular localization
GO:0006119	5	oxidative phosphorylation
GO:0006304	5	DNA modification
GO:0006662	5	glycerol ether metabolic process
GO:0032501	5	multicellular organismal process
GO:0040007	5	growth
GO:0006996	4	organelle organization
GO:0007049	4	cell cycle
GO:0008655	4	pyrimidine-containing compound salvage
GO:0015979	4	photosynthesis
GO:0016032	4	viral process
GO:0034622	4	cellular macromolecular complex assembly
GO:0042445	4	hormone metabolic process
GO:0044419	4	interspecies interaction between organisms
GO:0045229	4	external encapsulating structure organization
GO:0000003	3	reproduction
GO:0006869	3	lipid transport
GO:0007059	3	chromosome segregation
GO:0009404	3	toxin metabolic process
GO:0015074	3	DNA integration

GO:0015833	3	peptide transport
GO:0032392	3	DNA geometric change
GO:0043094	3	cellular metabolic compound salvage
GO:0051276	3	chromosome organization
GO:0006928	2	movement of cell or subcellular component
GO:0007005	2	mitochondrion organization
GO:0015976	2	carbon utilization
GO:0016049	2	cell growth
GO:0046903	2	secretion
GO:0048469	2	cell maturation
GO:0051604	2	protein maturation
GO:0000746	1	conjugation
GO:0002376	1	immune system process
GO:0006113	1	fermentation
GO:0006323	1	DNA packaging
GO:0006354	1	DNA-templated transcription, elongation
GO:0007031	1	peroxisome organization
GO:0009292	1	genetic transfer
GO:0015835	1	peptidoglycan transport
GO:0015893	1	drug transport
GO:0015920	1	lipopolysaccharide transport
GO:0015931	1	nucleobase-containing compound transport
GO:0016458	1	gene silencing
GO:0040011	1	locomotion
GO:0043449	1	cellular alkene metabolic process
GO:0045230	1	capsule organization
GO:0048285	1	organelle fission
GO:0050877	1	neurological system process
GO:0051180	1	vitamin transport
GO:0051181	1	cofactor transport
GO:0051258	1	protein polymerization

Table S3. Molecular function list for the representatives of the first group.

GO	Count of unique input accessions	Name
GO:0016491	122	oxidoreductase activity
GO:0016787	94	hydrolase activity
GO:0003674	84	molecular_function
GO:0016740	77	transferase activity
GO:0043167	74	ion binding
GO:0005215	66	transporter activity
GO:0003676	57	nucleic acid binding
GO:0000166	33	nucleotide binding
GO:0048037	29	cofactor binding
GO:0005488	27	binding
GO:0008233	21	peptidase activity
GO:0001882	18	nucleoside binding
GO:0004497	10	monooxygenase activity
GO:0003824	7	catalytic activity
GO:0004871	7	signal transducer activity
GO:0016829	6	lyase activity
GO:0016209	5	antioxidant activity
GO:0016874	5	ligase activity
GO:0004386	4	helicase activity
GO:0016853	4	isomerase activity
GO:0051213	4	dioxygenase activity
GO:0005515	3	protein binding
GO:0009055	2	electron carrier activity
GO:0031409	2	pigment binding
GO:0001871	1	pattern binding
GO:0008144	1	drug binding
GO:0008289	1	lipid binding
GO:0008641	1	small protein activating enzyme activity
GO:0019239	1	deaminase activity
GO:0030246	1	carbohydrate binding
GO:0033218	1	amide binding
GO:0043021	1	ribonucleoprotein complex binding

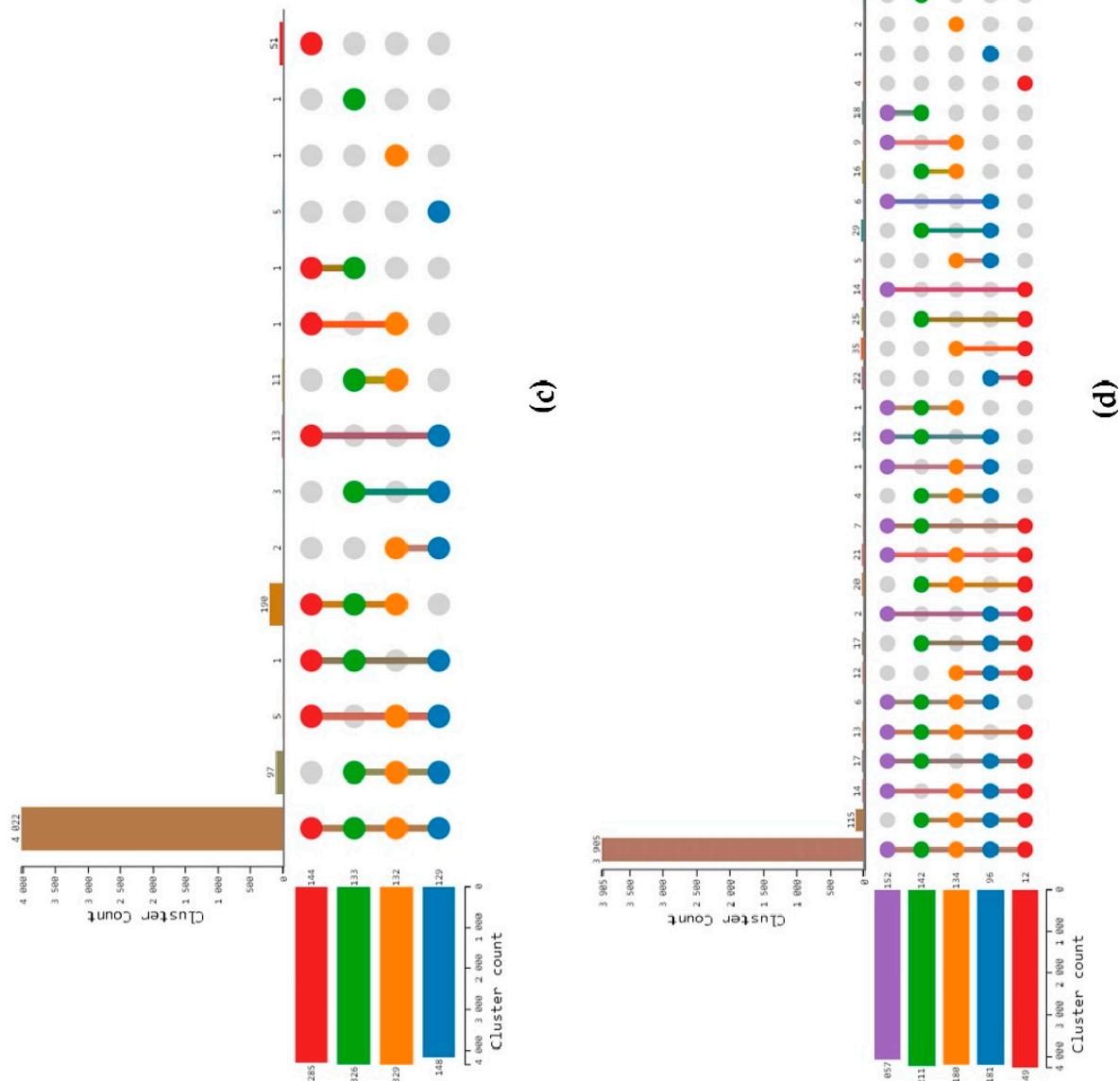
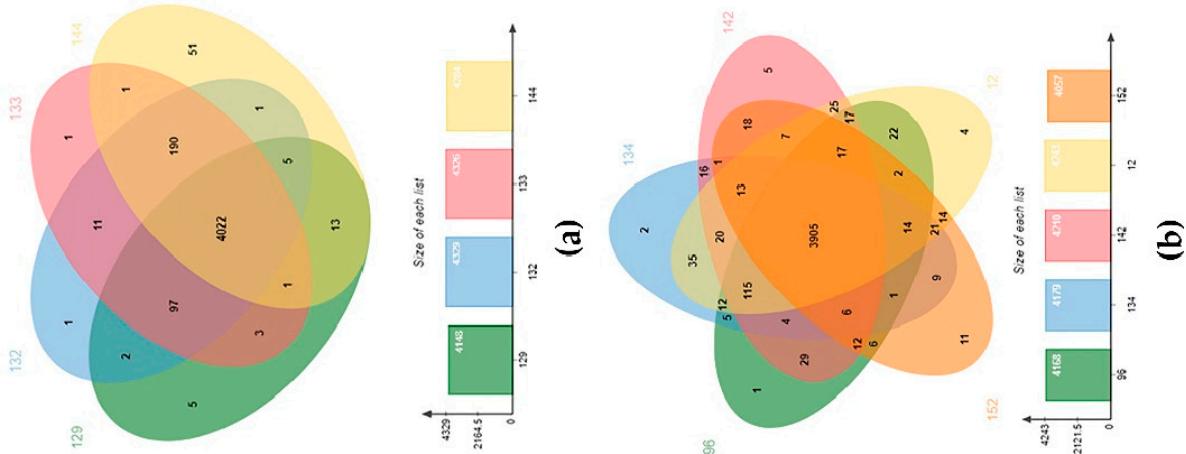


Figure S3. The representatives of the first group (a,c); of the second group (b,d): (a), (b) - Venn diagram depicting pangenome of two group strains; (c), (d) - UpSet table representing the number of orthologous clusters in each strains and the number of unique and shared homologous gene clusters.

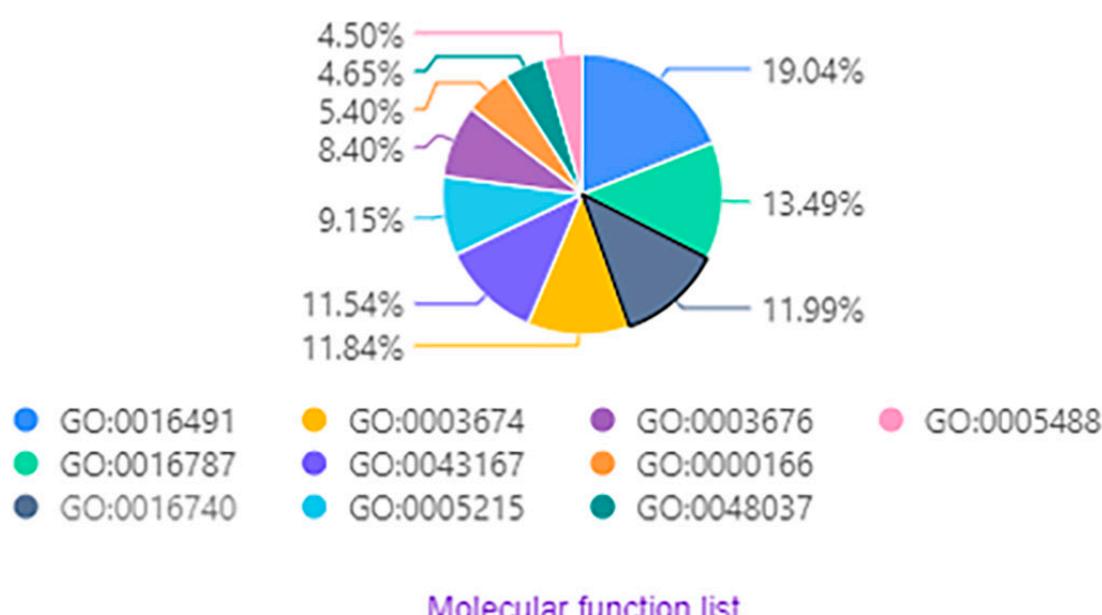
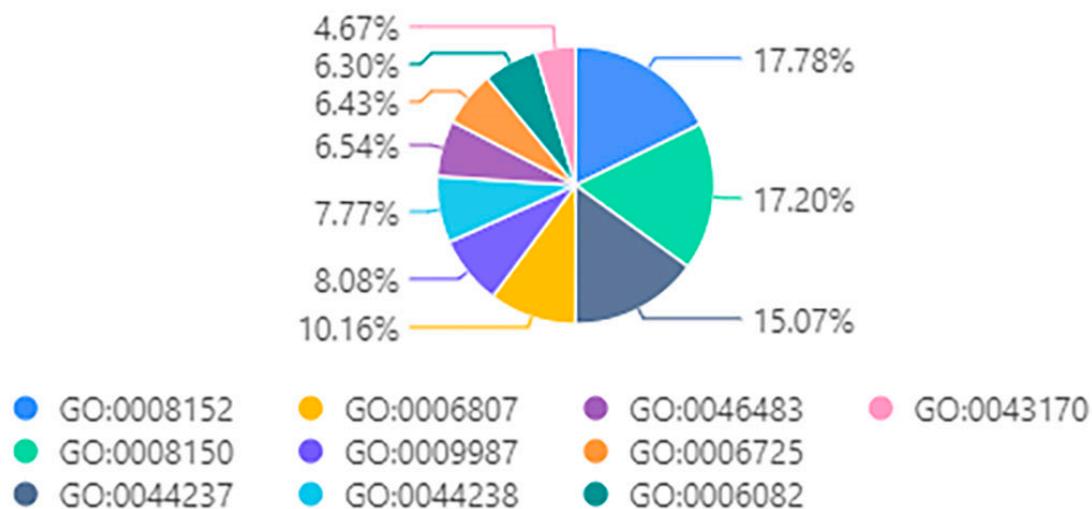


Figure S4. GO annotation core clusters for the representatives of the second group (96, 134, 142, 12, 152).

Table S4. Biological process list for the representatives of the second group.

GO	Count of unique input accessions	Name
GO:0008152	959	metabolic process
GO:0008150	928	biological_process
GO:0044237	813	cellular metabolic process
GO:0006807	548	nitrogen compound metabolic process
GO:0009987	436	cellular process
GO:0044238	419	primary metabolic process
GO:0046483	353	heterocycle metabolic process
GO:0006725	347	cellular aromatic compound metabolic process
GO:0006082	340	organic acid metabolic process
GO:0043170	252	macromolecule metabolic process
GO:0006139	241	nucleobase-containing compound metabolic process
GO:0065007	168	biological regulation
GO:0016070	166	RNA metabolic process
GO:0051186	160	cofactor metabolic process
GO:0006629	154	lipid metabolic process
GO:0006793	147	phosphorus metabolic process
GO:0044255	138	cellular lipid metabolic process
GO:0050896	115	response to stimulus
GO:0006810	108	transport
GO:0051234	108	establishment of localization
GO:0006412	97	translation
GO:0009117	85	nucleotide metabolic process
GO:0005975	71	carbohydrate metabolic process
GO:0016043	66	cellular component organization
GO:0006811	57	ion transport
GO:0009116	51	nucleoside metabolic process
GO:0032502	48	developmental process
GO:0019538	44	protein metabolic process
GO:0043603	43	cellular amide metabolic process
GO:0006396	37	RNA processing
GO:0006518	37	peptide metabolic process
GO:0006766	36	vitamin metabolic process
GO:0006259	35	DNA metabolic process
GO:0006260	34	DNA replication
GO:0006281	33	DNA repair
GO:0042180	30	cellular ketone metabolic process

GO:0051704	30	multi-organism process
GO:0005976	29	polysaccharide metabolic process
GO:0045333	29	cellular respiration
GO:0051179	29	localization
GO:0007154	27	cell communication
GO:0032989	27	cellular component morphogenesis
GO:0043412	27	macromolecule modification
GO:0006865	25	amino acid transport
GO:0042254	24	ribosome biogenesis
GO:0006091	23	generation of precursor metabolites and energy
GO:0006464	23	cellular protein modification process
GO:0042440	20	pigment metabolic process
GO:0006805	19	xenobiotic metabolic process
GO:0065003	18	macromolecular complex assembly
GO:0071555	18	cell wall organization
GO:0006066	17	alcohol metabolic process
GO:0015031	17	protein transport
GO:0009308	16	amine metabolic process
GO:0017144	16	drug metabolic process
GO:0019748	16	secondary metabolic process
GO:0006508	12	proteolysis
GO:0032196	12	transposition
GO:0006457	11	protein folding
GO:0009225	9	nucleotide-sugar metabolic process
GO:0051189	9	prosthetic group metabolic process
GO:0006081	8	cellular aldehyde metabolic process
GO:0006112	8	energy reserve metabolic process
GO:0006818	8	hydrogen transport
GO:0015849	8	organic acid transport
GO:0022607	8	cellular component assembly
GO:0032501	8	multicellular organismal process
GO:0051301	8	cell division
GO:0006730	7	one-carbon metabolic process
GO:0008643	7	carbohydrate transport
GO:0022411	7	cellular component disassembly
GO:0051641	7	cellular localization
GO:0006662	6	glycerol ether metabolic process
GO:0006996	6	organelle organization
GO:0043101	6	purine-containing compound salvage

GO:0006119	5	oxidative phosphorylation
GO:0007049	5	cell cycle
GO:0015979	5	photosynthesis
GO:0034622	5	cellular macromolecular complex assembly
GO:0040007	5	growth
GO:0045229	5	external encapsulating structure organization
GO:0007059	4	chromosome segregation
GO:0008655	4	pyrimidine-containing compound salvage
GO:0042445	4	hormone metabolic process
GO:0051276	4	chromosome organization
GO:0000003	3	reproduction
GO:0006869	3	lipid transport
GO:0009404	3	toxin metabolic process
GO:0015833	3	peptide transport
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GO:0006113	1	fermentation
GO:0006323	1	DNA packaging
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GO:0046903	1	secretion
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GO:0050877	1	neurological system process
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GO:0051181	1	cofactor transport
GO:0051258	1	protein polymerization

Table S5. Molecular function list for the representatives of the second group.

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GO:0016740	77	transferase activity
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GO:0000166	33	nucleotide binding
GO:0048037	29	cofactor binding
GO:0005488	27	binding
GO:0008233	21	peptidase activity
GO:0001882	18	nucleoside binding
GO:0004497	10	monooxygenase activity
GO:0003824	7	catalytic activity
GO:0004871	7	signal transducer activity
GO:0016829	6	lyase activity
GO:0016209	5	antioxidant activity
GO:0016874	5	ligase activity
GO:0004386	4	helicase activity
GO:0016853	4	isomerase activity
GO:0051213	4	dioxygenase activity
GO:0005515	3	protein binding
GO:0009055	2	electron carrier activity
GO:0031409	2	pigment binding
GO:0001871	1	pattern binding
GO:0008144	1	drug binding
GO:0008289	1	lipid binding
GO:0008641	1	small protein activating enzyme activity
GO:0019239	1	deaminase activity
GO:0030246	1	carbohydrate binding
GO:0033218	1	amide binding
GO:0043021	1	ribonucleoprotein complex binding