

Signature	ICGC	NES	NOM p-val	FOR q-val	TCGA	NES	NOM p-val	FOR q-val
GO_2_IRON_2_SULFUR_CLUSTER_BINDING		1.5546366	0.04752475	0.12653017		1.8305562	0.00996016	0.03105208
GO_4_IRON_4_SULFUR_CLUSTER_BINDING		1.8781075	0.00431035	0.02116238		1.8316503	0.01483051	0.03103323
GO_90S_PERIRIBOSOME		1.8662984	0.00609756	0.02314922		1.8861896	0.0078125	0.02100078
GO_AEROBIC_ELECTRON_TRANSPORT_CHAIN		1.6586405	0.02335456	0.07452937		1.7459227	0.00217391	0.05520465
GO_AEROBIC_RESPIRATION		1.9587013	0.01890756	0.01483259		1.9701035	0.0063425	0.01201548
GO_AMINO_ACID_ACTIVATION		2.0083132	0.00424629	0.01287796		2.0055063	0.00972763	0.00990288
GO_ANAPHASE_PROMOTING_COMPLEX		1.7914375	0.00212314	0.03398622		1.8604335	0.00606061	0.02421543
GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS		1.8996791	0.00310044	0.010187002		2.0735564	0.00636855	0.00636855
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I		1.5702072	0.09255533	0.11821779		1.8086798	0.01807229	0.03681691
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I		1.5075994	0.12525253	0.1587431		1.5050008	0.10176125	0.19435759
GO_APOPTOTIC_MITOCHONDRIAL_CHANGES		1.6247365	0.01310044	0.08969446		1.5322015	0.01688555	0.17342627
GO_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT		1.9090444	0.00847458	0.01781047		1.978608	0	0.01173385
GO_BASE_EXCISION_REPAIR		1.7991501	0.00662252	0.03281886		1.6633313	0.03571429	0.09130037
GO_CAUAL_BODY		1.7672838	0.00672646	0.03885208		1.4467956	0.0985577	0.24274197
GO_CATALYTIC_ACTIVITY_ACTING_ON_A_RRNA		1.7463319	0.01276596	0.04473388		2.0724566	0.00204001	0.00665854
GO_CATALYTIC_ACTIVITY_ACTING_ON_DNA		1.9750601	0.00428266	0.01349506		1.4532487	0.1124031	0.23920481
GO_CATALYTIC_ACTIVITY_ACTING_ON_RNA		2.0996804	0.00422833	0.00722887		1.9673732	0.00403226	0.01177533
GO_CATALYTIC_STEP_2_SPLICesome		2.189515	0.00215517	0.00373597		1.8721489	0.0231237	0.02278461
GO_CELL_CYCLE_DNA_REPLICATION		1.8440794	0.00858369	0.02634763		1.6371154	0.07524753	0.10547344
GO_CELL_CYCLE_G2_M_PHASE_TRANSITION		1.9311495	0.00662252	0.01691992		1.6866989	0.03118908	0.08127189
GO_CELL_REDOX_HOMEOSTASIS		1.4075692	0.12103175	0.24583554		1.4440414	0.07392197	0.24563305
GO_CELLULAR_COMPONENT_DISASSEMBLY		1.6931647	0.00617284	0.06115709		1.8823427	0	0.0215491
GO_CELLULAR_METABOLIC_COMPOUND_SALVAGE		1.5438282	0.02964427	0.1331458		1.5519315	0.04545455	0.15834711
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY		1.9894688	0.00213675	0.01319396		2.1009376	0.00204001	0.00665854
GO_CELLULAR_RESPIRATION		1.9116265	0.01301519	0.01747709		2.1236522	0	0.00515184
GO_CELLULAR_RESPONSE_TO_OXYGEN_LEVELS		1.5694808	0.04661017	0.11821197		1.5916075	0.00785855	0.13017248
GO_CHAPERONE_BINDING		1.4569552	0.06029106	0.20116156		1.5941439	0.03258656	0.12908132
GO_CHAPERONE_COMPLEX		1.8484074	0.0059761	0.02586903		1.7668012	0.02070393	0.04820181
GO_CHAPERONE_MEDIATED_PROTEIN_FOLDING		1.646454	0.0349076	0.07907362		1.4855691	0.08403362	0.20991012
GO_CHROMOSOME_SEPARATION		1.8884473	0.00643777	0.01995567		1.4835222	0.1326923	0.21085972
GO_CIS_TRANS_ISOMERASE_ACTIVITY		1.6616777	0.02531646	0.07315822		1.9003131	0	0.01837062
GO_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING		1.9272007	0	0.01708572		1.3462715	0.00421053	0.01339045
GO_CONDENSED_CHROMOSOME_CENTROMERIC_REGION		1.908657	0.00212766	0.0171083		1.4861537	0.12871288	0.20971776
GO_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE		1.8328004	0.01372549	0.02758209		1.9549553	0	0.01268143
GO_CYTOCHROME_COMPLEX		1.6537461	0.04408818	0.07639154		1.8530359	0.00443459	0.02582339
GO_CYTOCHROME_COMPLEX_ASSEMBLY		1.8497947	0.00214133	0.02585637		1.9598349	0	0.01229182
GO_CYTOPLASMIC_TRANSLATION		2.0662992	0.0060241	0.00829011		2.036124	0.00609756	0.00788216
GO_CYTOPLASMIC_TRANSLATIONAL_INITIATION		1.9730803	0	0.01357926		1.960311	0.00607288	0.01243657
GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT		1.7885567	0.00389864	0.03444242		2.0249257	0	0.00840269
GO_CYTOSOLIC_PART		2.1912854	0.00198807	0.00374339		2.2391512	0	0.00848233
GO_CYTOSOLIC_RIBOSOME		1.8334333	0.01934236	0.02763226		2.0513898	0	0.00765936
GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT		1.7661823	0.01740812	0.03899746		1.920439	0.00652174	0.01574955
GO_DAMAGED_DNA_BINDING		1.8893907	0.00898876	0.01996675		1.4742802	0.078125	0.21919294
GO_DEOXYRIBONUCLEASE_ACTIVITY		1.7681144	0.01094092	0.03875539		1.5850382	0.01689896	0.13479969
GO_DEOXYRIBOSE_PHOSPHATE_CATABOLIC_PROCESS		1.5874077	0.03821656	0.10859895		1.8053352	0.0040568	0.03754176
GO_DISULFIDE_OXIDOREDUCTASE_ACTIVITY		1.6864059	0.02970297	0.06334098		1.924583	0	0.01540211
GO_DNA_BIOSYNTHETIC_PROCESS		1.9285553	0.00218818	0.01710591		1.6534481	0.0239521	0.09628551
GO_DNA_DAMAGE_RESPONSE_DETECTION_OF_DNA_DAMAGE		1.9489381	0.00847458	0.02583457		1.9040192	0.00204001	0.01785688
GO_DNA_DEPENDENT_DNA_REPLICATION		1.9232355	0.01284797	0.01694357		1.5653175	0.00821383	0.14084604
GO_DNA_HELICASE_ACTIVITY		1.7863003	0.01758242	0.03498582		1.6330994	0.02244898	0.07404654
GO_DNA_POLYMERASE_BINDING		1.7268913	0.01452282	0.05042128		1.7880663	0.01443299	0.04230921
GO_DNA_REPLICATION_INITIATION		1.767758	0.01515152	0.0387636		1.7515402	0.02208835	0.05322875
GO_DNA_STRAND_ELONGATION		1.5571893	0.08351178	0.12483447		1.4596456	0.12883435	0.23385483
GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION		2.2400477	0.00210971	0.00361458		1.5418048	0.0625	0.16607438
GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION		2.1531723	0.00215054	0.00449691		1.9728369	0.0139165	0.04083401
GO_ELECTRON_TRANSPORT_CHAIN		1.5733513	0.06722689	0.11665197		2.1021428	0	0.00640809
GO_ENDODEOXYRIBONUCLEASE_ACTIVITY		1.7145984	0.01151879	0.05419442		1.6325722	0.02868852	0.11012238
GO_ENDONUCLEASE_ACTIVITY		1.5651922	0.0465587	0.12057386		1.8746098	0	0.02262526
GO_ENDONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCLEIC_ACIDS_AND_PRODUCING_5_PHOSPHOMONESTERS		1.933555	0.00420168	0.0167222		1.8740212	0	0.00713616
GO_ENDONUCLEASE_COMPLEX		1.9802613	0	0.01309578		1.781354	0.00606061	0.040404187
GO_ENDOPEPTIDASE_COMPLEX		1.9471263	0.00206186	0.01571803		2.0092664	0	0.00984862
GO_ENDORIBONUCLEASE_ACTIVITY		1.5107265	0.05636743	0.15654269		1.9835452	0.00210526	0.01167787
GO_ENDORIBONUCLEASE_ACTIVITY_PRODUCING_5_PHOSPHOMONESTERS		1.922281	0.00204499	0.01681793		1.9998231	0.00208768	0.01034526
GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS		1.7602427	0.01923077	0.04085524		2.0379908	0	0.00789972
GO_ERROR_FREE_TRANSLATION_SYNTHESIS		1.7249313	0.00831333	0.05097789		1.67031124	0.0172422	0.008851518
GO_ERROR_PRONE_TRANSLATION_SYNTHESIS		1.8029855	0.01040625	0.02118533		1.5298263	0.082	0.17546372
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_CHROMOSOME		1.995776	0.00204918	0.01304769		1.738035	0.0221328	0.05837833
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM		1.937211	0.01008065	0.01634823		2.0085297	0	0.00982766
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE		1.8069315	0.008	0.03155933		2.217026	0	0.00652453
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MITOCHONDRIAL_MEMBRANE		1.8276556	0.00206612	0.02812632		1.880299	0	0.02190515
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_TLOEMERE		1.8641248	0.00206186	0.02346929		1.6697475	0.03992016	0.08862737
GO_EUKARYOTIC_48S_PREINITIATION_COMPLEX		1.7928109	0	0.0336195		1.7396659	0.00798403	0.04069156
GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_3_COMPLEX		1.8314188	0.00821333	0.02768957		1.7133456	0.02217742	0.06961399
GO_EXODEOXYRIBONUCLEASE_ACTIVITY		1.6334605	0.0372807	0.08532978		1.6329989	0.03875969	0.121284037
GO_EXON_EXON_JUNCTION_COMPLEX		1.7207321	0.02226721	0.05240382		1.4371762	0.1	0.25015232
GO_EXOSOME_RNASE_COMPLEX		1.9538167	0.0021645	0.01520247		1.8516189	0.00201613	0.0260626
GO_FEMALE_MEIOTIC_NUCLEAR_DIVISION		1.592025	0.07157895	0.10645982		1.5479482	0.08964144	0.16016409
GO_FICOLIN_1_RICH_GRANULE		1.693058	0.04781705	0.0611		1.751067	0.01330799	0.05323966
GO_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY		1.553867	0.04338843	0.12677354		1.9426553	0	0.01370454
GO_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR		1.950357	0.00860215	0.01544956		1.519522	0.05443548	0.18399344
GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS		1.6646495	0.02564103	0.07199428		1.8963711	0.00401606	0.01902106
GO_HEMATOPOIETIC STEM_CELL_DIFFERENTIATION		1.6960298	0.03498372	0.05990372		1.8295451	0.00787402	0.021279604
GO_HISTONE_EXCHANGE		1.7735453	0.01742919	0.03780221		1.4818102	0.11471862	0.21253145
GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION		1.8540591	0.01101322	0.02516892		1.9737797	0.00205761	0.01184356
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX		1.9916044	0.00426439	0.0132152		2.0244234	0	0.00833269
GO_INTERLEUKIN_1_MEDIATED_SIGNALING_PATHWAY		2.0920637	0	0.00772003		1.6882825	0.02713178	0.08056341
GO_INTERSTRAND_CROSS_LINK_REPAIR		1.9147025	0.00220264	0.0174138		1.4422898	0.12138728	0.24625412
GO_INTRACELLULAR_PROTEIN_TRANSMEMBRANE_TRANSPORT		2.000829	0	0.01264928		1.9713533	0.00204001	0.01208168
GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY		1.7942084	0.01079914	0.03348633		1.5252091	0.05544554	0.17917624
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE		1.7368809	0.01118732	0.04738492		2.0655956	0.00197629	0.00707175
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE		1.6103014	0.05010893	0.09671661		1.9228024	0.00591716	0.01661259
GO_IRON_SULFUR_CLUSTER_ASSEMBLY		1.8070924	0.00668151	0.03159579		1.9043012	0	0.01792404
GO_ISOMERASE_ACTIVITY		1.5751219	0.02136752	0.11589973		1.835956	0	0.03031624
GO_LARGE_RIBOSOMAL_SUBUNIT		2.0034301	0.00203252	0.01286257		2.083209	0	0.00694732
GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS		1.9029763	0.0043573	0.01838177		1.9853064	0.00596422	0.01154037
GO_MATURATION_OF_5_8S_RRNA		1.9259416	0	0.01706409		1.9834164	0.00208333	0.01159413
GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA		1.9346548	0	0.01674035		1.9684064	0.00419287	0.01203176
GO_MATURATION_OF_18S_RRNA		1.9281425	0	0.01706408		1.9393621	0	0.01389173
GO_MATURATION_OF_SSU_RRNA		2.0549889	0	0.00900236		2.0286446	0.002	0.00803753
GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA		1.9844301	0	0.01302605		2.0045562	0	0.00991967
GO_METAL_CLUSTER_BINDING		1.7941837	0.00631579	0.03341325		2.0293977	0	0.00826139
GO_METAPHASE_ANAPHASE_TRANSITION_OF_CELL_CYCLE		1.7797961	0.02132196	0.03628285		1.4842916	0.1362764	0.21093006
GO_METAPHASE_PLATE_CONGRESSION		1.847305	0.00652174	0.02606935		1.5689954	0.07170542	0.14593206
GO_MISMATCH_REPAIR		1.4469527	0.08478261	0.20902188		1.4594288	0.08510638	0.23356476
GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_NADH_TO_UBIQUINONE		1.6293607	0.06622516	0.08720037		1.9308388	0	0.01510363
GO_MITOCHONDRIAL_GENE_EXPRESSION		2.0579221	0	0.00903079		2.1319304	0	0.00570553
GO_MITOCHONDRIAL_MATRIX		1.8472384	0.01082551	0.02599322		2.2187187	0	0.00765207
GO_MITOCHONDRIAL_MEMBRANE_ORGANIZATION		1.9874864	0.00221239	0.0131214		1.8024865	0.00191571	0.03784418

GO_NF_KAPPA8_BINDING
GO_NUCLEAR_DNA_REPLICATION
GO_NUCLEAR_ENVELOPE_ORGANIZATION
GO_NUCLEAR_ENVELOPE_REASSEMBLY
GO_NUCLEAR_EXOSOME_RNASE_COMPLEX_
GO_NUCLEAR_EXPORT
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_DEADENYLATION_DEPENDENT_DECAY
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLEOTYTIC
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY
GO_NUCLEAR_UBIQUITIN_LIGASE_COMPLEX
GO_NUCLEASE_ACTIVITY
GO_NUCLEIC_ACID_PHOSPHODIESTER_BOND_HYDROLYSIS
GO_NUCLEOBASE_BIOSYNTHETIC_PROCESS
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_CATABOLIC_PROCESS
GO_NUCLEOID
GO_NUCLEOLAR_PART
GO_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS
GO_NUCLEOSIDE_SALVAGE
GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS
GO_NUCLEOTIDE_EXCISION_REPAIR
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_GAP_FILLING
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_INCISION
GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_ASSEMBLY
GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_STABILIZATION
GO_NUCLEOTIDYLTRANSFERASE_ACTIVITY
GO_O_METHYLTRANSFERASE_ACTIVITY
GO_OUGOSACCHARIDE_LIPID_INTERMEDIATE_BIOSYNTHETIC_PROCESS
GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT
GO_ORGANELLAR_RIBOSOME
GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT
GO_ORGANELLE_ENVELOPE_LUMEN
GO_ORGANELLE_INNER_MEMBRANE
GO_OUTER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX
GO_OXIDATIVE_PHOSPHORYLATION
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_HEME_GROUP_OF_DONORS
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR
GO_OXIDOREDUCTASE_COMPLEX
GO_PEPTIDASE_COMPLEX
GO_PEPTIDYL_ARGININE_MODIFICATION
GO_PEPTIDYL_PROLINE_MODIFICATION
GO_PIGMENT_BIOSYNTHETIC_PROCESS
GO_POLYSOMAL_RIBOSOME
GO_POLYSOME
GO_POSITIVE_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS
GO_POSITIVE_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS
GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS
GO_POSITIVE_REGULATION_OF_TELOMERASE_ACTIVITY
GO_POSITIVE_REGULATION_OF_TELOMERASE_RNA_LOCALIZATION_TO_CAUAL_BODY
GO_POSITIVE_REGULATION_OF_VIRAL_PROCESS
GO_POSITIVE_REGULATION_OF_VIRAL_TRANSCRIPTION
GO_POSTREPLICATION_REPAIR
GO_PRECATALYTIC_SPLICEOSOME
GO_PPRIBOSOME
GO_PPRIBOSOME_LARGE_SUBUNIT_PRECURSOR
GO_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS
GO_PROTEASOMAL_UBIQUITIN_INDEPENDENT_PROTEIN_CATABOLIC_PROCESS
GO_PROTEASOME_ACCESSORY_COMPLEX
GO_PROTEASOME_CORE_COMPLEX
GO_PROTEIN_CONTAINING_COMPLEX_DISASSEMBLY
GO_PROTEIN_DISULFIDE_OXIDOREDUCTASE_ACTIVITY
GO_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION
GO_PROTEIN_FOLDING
GO_PROTEIN_IMPORT_24TO_MITOCHONDRIAL_MATRIX
GO_PROTEIN_INSERTION INTO_MEMBRANE
GO_PROTEIN_INSERTION INTO_MITOCHONDRIAL_MEMBRANE
GO_PROTEIN_K11_LINKED_UBIQUITINATION
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM
GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION
GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_REMOVAL
GO_PROTEIN_NEDDYLATION
GO_PROTEIN_PEPTIDYL_PROLYL_ISOMERIZATION
GO_PROTEIN_QUALITY_CONTROL_FOR_MISFOLDED_OR_INCOMPLETELY_SYNTHESIZED_PROTEINS
GO_PROTEIN_TARGETING
GO_PROTEIN_TARGETING_TO_MEMBRANE
GO_PROTEIN_TARGETING_TO_MITOCHONDRION
GO_PROTEIN_TRANSMEMBRANE_IMPORT INTO_INTRACELLULAR_ORGANELLE
GO_PROTEIN_TRANSMEMBRANE_TRANSPORT
GO_PROTEIN_TRANSPORTER_ACTIVITY
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX
GO_PSEUDOURIDINE_SYNTHESIS
GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS
GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS
GO_PYRIMIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS
GO_PYRIMIDINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS
GO_PYRIMIDINE_NUCLEOTIDE_BIOSYNTHETIC_PROCESS
GO_PYRIMIDINE_RIBONUCLEOTIDE_BIOSYNTHETIC_PROCESS
GO_REGULATION_OF_CELL_CYCLE_ARREST
GO_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION
GO_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION
GO_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS
GO_REGULATION_OF_CHROMOSOME_SEPARATION
GO_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS
GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_IN_RESPONSE_TO_STRESS
GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY
GO_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION
GO_REGULATION_OF_MITOCHONDRIAL_OUTER_MEMBRANE_PERMEABILIZATION_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY
GO_REGULATION_OF_MITOCHONDRIAL_TRANSLATION
GO_REGULATION_OF_MRNA_CATABOLIC_PROCESS
GO_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA
GO_REGULATION_OF_STEM_CELL_DIFFERENTIATION
GO_REGULATION_OF_TELOMERASE_ACTIVITY
GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_IN_RESPONSE_TO_HYPOXIA
GO_REGULATION_OF_TRANSLATIONAL_FIDELITY
GO_REGULATION_OF_TRANSLATIONAL_INITIATION
GO_REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY
GO_REGULATION_OF_VIRAL_TRANSCRIPTION
GO_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA
GO_REPLICATION_FORK
GO_REPLISOME
GO_RESPIRASOME
GO_RESPIRATORY_CHAIN_COMPLEX
GO_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN
GO_RIBONUCLEASE_ACTIVITY
GO_RIBONUCLEOPROTEIN_COMPLEX_BINDING
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION
GO_RIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS
GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS
GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY
GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS
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GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS
GO_RIBOSOMAL_SUBUNIT
GO_RIBOSOME
GO_RIBOSOME_ASSEMBLY
GO_RIBOSOME_BINDING
GO_RIBOSOME_BIOGENESIS
GO_RNA_3_END_PROCESSING
GO_RNA_5_END_PROCESSING
GO_RNA_CAP_BINDING
GO_RNA_CAPPING
GO_RNA_CATABOLIC_PROCESS
GO_RNA_DEPENDENT_DNA_BIOSYNTHETIC_PROCESS
GO_RNA_EXPORT_FROM_NUCLEUS

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GO_RNA_METHYLATION
GO_RNA_METHYLTRANSFERASE_ACTIVITY
GO_RNA_MODIFICATION
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_ENDONUCLEOLYTIC
GO_RNA_POLYMERASE_ACTIVITY
GO_RNA_POLYMERASE_COMPLEX
GO_RNA_POLYMERASE_II_CORE_COMPLEX
GO_RNA_POLYMERASE_II_HOLENZYME
GO_RNA_POLYMERASE_III_ACTIVITY
GO_RNA_POLYMERASE_III_COMPLEX
GO_RNA_SPLICING
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS
GO_ROUGH_ENDOPLASMIC_RETICULUM
GO_ROUGH_ENDOPLASMIC_RETICULUM_MEMBRANE
GO_RRNA_BINDING
GO_RRNA_CONTAINING_RIBONUCLEOPROTEIN_COMPLEX_EXPORT_FROM_NUCLEUS
GO_RRNA_METABOLIC_PROCESS
GO_RRNA_METHYLATION
GO_RRNA_MODIFICATION
GO_RRNA_TRANSCRIPTION
GO_S_ADENOSYLMETHIONINE_DEPENDENT_METHYLTRANSFERASE_ACTIVITY
GO_SCF_DEPENDENT_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS
GO_SINGLE_STRANDED_DNA_BINDING
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GO_SMALL_RIBOSOMAL_SUBUNIT
GO_SMALL_SUBUNIT_PROCESSOME
GO_SMN_SM_PROTEIN_COMPLEX
GO_SNRNA_BINDING
GO_SNRNA_3_END_PROCESSING
GO_SNRNA_BINDING
GO_SNRNA_PROCESSING
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GO_SPUCEOSOMAL_TR1_SNRNP_COMPLEX
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GO_TELOMERASE_HOLENZYME_COMPLEX
GO_TELOMERASE_RNA_BINDING
GO_TELOMERASE_RNA_LOCALIZATION
GO_TELOMERE_MAINTENANCE_VIA_SEMI_CONSERVATIVE_REPLICATION
GO_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING
GO_TELOMERE_ORGANIZATION
GO_TERMINATION_OF_RNA_POLYMERASE_I_TRANSCRIPTION
GO_TERMINATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION
GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS
GO_THREONINE_TYPE_PEPTIDASE_ACTIVITY
GO_TRANSCRIPTION_BY_RNA_POLYMERASE_I
GO_TRANSCRIPTION_BY_RNA_POLYMERASE_III
GO_TRANSCRIPTION_COUPLD_NUCLEOTIDIC_EXCISION_REPAIR
GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_I_PROMOTER
GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER
GO_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_I_PROMOTER
GO_TRANSCRIPTION_PREINITIATION_COMPLEX_ASSEMBLY
GO_TRANSFERASE_ACTIVITY_TRANSFERFERRING_ONECARBON_GROUPS
GO_TRANSLATION_ELONGATION_FACTOR_ACTIVITY
GO_TRANSLATION_FACTOR_ACTIVITY_RNA_BINDING
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GO_TRANSLATION_REGULATOR_ACTIVITY
GO_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING
GO_TRANSLATIONAL_ELONGATION
GO_TRANSLATIONAL_INITIATION
GO_TRANSLATIONAL_TERMINATION
GO_TRANSLESION_SYNTHESIS
GO_TRICARBOXYLIC_ACID_CYCLE
GO_TRNA_5_END_PROCESSING
GO_TRNA_BINDING
GO_TRNA_METABOLIC_PROCESS
GO_TRNA_METHYLATION
GO_TRNA_MODIFICATION
GO_TRNA_PROCESSING
GO_TRNA_SPECIFIC_RIBONUCLEASE_ACTIVITY
GO_TRNA_WOBBLE_BASE_MODIFICATION
GO_U1_SNRNP
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GO_U2_SNRNP
GO_U2_TYPE_CATALYTIC_STEP_2_SPUCEOSOME
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GO_U5_SNRNP
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GO_UNFOLDED_PROTEIN_BINDING
GO_VIRAL_GENE_EXPRESSION
HALLMARK_DNA_REPAIR
HALLMARK_E2F_TARGETS
HALLMARK_MTORC1_SIGNALING
HALLMARK_MYC_TARGETS_V1
HALLMARK_MYC_TARGETS_V2
HALLMARK_OXIDATIVE_PHOSPHORYLATION
HALLMARK_UNFOLDED_PROTEIN_RESPONSE
HALLMARK_UV_RESPONSE_UP
KEGG_ALZHEIMERS_DISEASE
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS
KEGG_BASE_EXCISION_REPAIR
KEGG_DNA_REPLICATION
KEGG_HOMOLOGOUS_RECOMBINATION
KEGG_HUNTINGTONS_DISEASE
KEGG_MISMATCH_REPAIR
KEGG_NUCLEOTIDE_EXCISION_REPAIR
KEGG_ONECARBON_POOL_BY_FOLATE
KEGG_OXIDATIVE_PHOSPHORYLATION
KEGG_PARKINSONS_DISEASE
KEGG_PROTEASOME
KEGG_PROTEIN_EXPORT
KEGG_PYRIDINE_METABOLISM
KEGG_RIBOSOME
KEGG_RNA_DEGRADATION
KEGG_RNA_POLYMERASE
KEGG_SPUCEOSOME
MUHAR_MYC
REACTOME_ABC_TRANSPORTER_DISORDERS
REACTOME_ABORTIVE_ELONGATION_OF_HIV_1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT
REACTOME_ACTIVATION_OF_APC_C_AND_APC_CCD20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS
REACTOME_ACTIVATION_OF_WT_KAPPA_IN_B_CELLS
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION
REACTOME_ANTIEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION
REACTOME_APC_CCD20_MEDIATED_DEGRADATION_OF_CYCLIN_B
REACTOME_APC_CCDH1_MEDIATED_DEGRADATION_OF_CD20_AND_OTHER_APC_CCDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1
REACTOME_APC_CCD20_MEDIATED_DEGRADATION_OF_NEK2A
REACTOME_ASSEMBLY_OF_THE_PRC_REPLICATIVE_COMPLEX
REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BIOSYNTHESIS
REACTOME_ASYMMETRIC_LOCALIZATION_OF_PCP_PROTEINS
REACTOME_ATF4_ACTIVATES_GENES_IN_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS
REACTOME_AUF1_HNRNP_D0_BINDS_AND_DESTABILIZES_MRNA
REACTOME_AUTOPHAGY
REACTOME_BASE_EXCISION_REPAIR
REACTOME_BUDDING_AND_MATURATION_OF_HIV_VIRION
REACTOME_BUTYRATE_RESPONSE_FACTOR_1_BRF1_BINDS_AND_DESTABILIZES_MRNA
REACTOME_C_TYPE_LECTIN_RECEPTORS_CURS
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6
REACTOME_CELL_CYCLE_CHECKPOINTS
REACTOME_CELL_CYCLE_MITOTIC
REACTOME_CELLULAR_RESPONSE_TO_HYPOXIA

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REACTION_CELLULAR_RESPONSES_TO_EXTERNAL_STIMULI
REACTION_CELLULAR_RESPONSES_TO_STRESS
REACTION_CHROMOSOME_MAINTENANCE
REACTION_CITRIC_ACID_CYCLE_TCA_CYCLE
REACTION_CLEC7A_DECTIN_1_SIGNALING
REACTION_CLEC7A_DECTIN_1_SIGNALING
REACTION_COMPLEX_I_BIOGENESIS
REACTION_COOPERATION_OF_PREFOLDIN_AND_TRIC_CCT_IN_ACTIN_AND_TUBULIN_FOLDING
REACTION_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES
REACTION_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION
REACTION_CYCLIN_A_CDK2_ASSOCIATED_EVENTS_AT_S_PHASE_ENTRY
REACTION_CYTOSOLIC_SENSORS_OF_PATHOGEN_ASSOCIATED_DNA
REACTION_CYTOSOLIC_TRNA_AMINOACYLATION
REACTION_DEADENYLATION_DEPENDENT_MRNA_DECAY
REACTION_DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING
REACTION_DEFECTIVE_CTRF_CAUSES_CYSTIC_FIBROSIS
REACTION_DEGRADATION_OF_AXIN
REACTION_DEGRADATION_OF_BETA_CATENIN_BY_THE_DESTRUCTION_COMPLEX
REACTION_DEGRADATION_OF_DVL
REACTION_DEGRADATION_OF_GLI1_BY_THE_PROTEASOME
REACTION_DISEASES_ASSOCIATED_WITH_N_GLYCOSYLATION_OF_PROTEINS
REACTION_DNA_DAMAGE_BYPASS
REACTION_DNA_DAMAGE_RECOGNITION_IN_GG_NER
REACTION_DNA_REPAIR
REACTION_DNA_REPLICATION
REACTION_DNA_REPLICATION_PRE_INITIATION
REACTION_DNA_STRAND_ELONGATION
REACTION_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR
REACTION_DOWNSTREAM_TCR_SIGNALING
REACTION_DUAL_INCISION_IN_GG_NER
REACTION_DUAL_INCISION_IN_TC_NER
REACTION_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION
REACTION_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESCRT
REACTION_EUKARYOTIC_TRANSLATION_INITIATION
REACTION_EXTENSION_OF_TELOMERES
REACTION_FANCONI_ANEMIA_PATHWAY
REACTION_FBXL7_DOWN_REGULATES_AURKA_DURING_MITOTIC_ENTRY_AND_IN_EARLY_MITOSIS
REACTION_FGFR2_ALTERNATIVE_SPLICING
REACTION_FORMATION_OF_HIV_ELONGATION_COMPLEX_IN_THE_ABSENCE_OF_HIV_TAT
REACTION_FORMATION_OF_INCISION_COMPLEX_IN_GG_NER
REACTION_FORMATION_OF_TC_NER_PRE_INCISION_COMPLEX
REACTION_FORMATION_OF_THE_EARLY_ELONGATION_COMPLEX
REACTION_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC
REACTION_G1_PHASE
REACTION_G1_S_DNA_DAMAGE_CHECKPOINTS
REACTION_G2_M_CHECKPOINTS
REACTION_GAP_FILLING_DNA_REPAIR_SYNTHESIS_AND_LIGATION_IN_GG_NER
REACTION_GENE_AND_PROTEIN_EXPRESSION_BY_JAK_STAT_SIGNALING_AFTER_INTERLEUKIN_12_STIMULATION
REACTION_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR_GG_NER
REACTION_GLYCOSYLATION_OF_PROTEINS
REACTION_HDR_THROUGH_HOMOLOGOUS_RECOMBINATION_HRR
REACTION_HEDGEHOG_LIGAND_BIOGENESIS
REACTION_HEDGEHOG_OFF_STATE
REACTION_HIV_ELONGATION_ARREST_AND_RECOVERY
REACTION_HIV_INFECTION
REACTION_HIV_LIFE_CYCLE
REACTION_HOST_INTERACTIONS_OF_HIV_FACTORS
REACTION_HSF1_ACTIVATION
REACTION_INFECTIOUS_DISEASE
REACTION_INFLUENZA_INFECTION
REACTION_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS
REACTION_INSERTION_OF_TAIL_ANCHORED_PROTEINS_INTO_THE_ENDOPLASMIC_RETICULUM_MEMBRANE
REACTION_INTERACTIONS_OF_REV_WITH_HOST_CELLULAR_PROTEINS
REACTION_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS
REACTION_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES
REACTION_INTERLEUKIN_1_FAMILY_SIGNALING
REACTION_INTERLEUKIN_1_SIGNALING
REACTION_KSRP_KHSRP_BINDS_AND_DESTABILIZES_MRNA
REACTION_LAGGING_STRAND_SYNTHESIS
REACTION_M_PHASE
REACTION_MACROAUTOPHAGY
REACTION_MAPK6_MAPK4_SIGNALING
REACTION_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES
REACTION_METABOLISM_OF_COFACTORS
REACTION_METABOLISM_OF_FOLATE_AND_PTERINES
REACTION_METABOLISM_OF_NON_CODING_RNA
REACTION_METABOLISM_OF_NUCLEOTIDES
REACTION_METABOLISM_OF_POLYAMINES
REACTION_METABOLISM_OF_PORPHYRINS
REACTION_MICRORNA_MIRNA_BIOGENESIS
REACTION_MISMATCH_REPAIR
REACTION_MITOCHONDRIAL_CALCIIUM_ION_TRANSPORT
REACTION_MITOCHONDRIAL_PROTEIN_IMPORT
REACTION_MITOCHONDRIAL_TRANSLATION
REACTION_MITOCHONDRIAL_TRNA_AMINOACYLATION
REACTION_MITOPHAGY
REACTION_MITOTIC_G1_G1_S_PHASES
REACTION_MITOTIC_G2_G2_M_PHASES
REACTION_MITOTIC_METAPHASE_AND_ANAPHASE
REACTION_MITOTIC_SPINDLE_CHECKPOINT
REACTION_MRNA_CAPPING
REACTION_MRNA_DECAY_BY_3_TO_5_EXORIBONUCLEASE
REACTION_MRNA_SPLICING
REACTION_MRNA_SPLICING_MINOR_PATHWAY
REACTION_MTORC1_MEDIATED_SIGNALING
REACTION_NEDDYLATION
REACTION_NEGATIVE_EPIGENETIC_REGULATION_OF_RRNA_EXPRESSION
REACTION_NEGATIVE_REGULATION_OF_NOTCH1_SIGNALING
REACTION_NEURODEGENERATIVE_DISEASES
REACTION_NONSENSE_MEDIATED_DECAY_NMD
REACTION_NONSENSE_MEDIATED_DECAY_NMD_INDEPENDENT_OF_THE_EXON_JUNCTION_COMPLEX_EJC
REACTION_NUCLEOBASE_BIOSYNTHESIS
REACTION_NUCLEOTIDE_EXCISION_REPAIR
REACTION_NUCLEOTIDE_SALVAGE
REACTION_ORC1_REMOVAL_FROM_CHROMATIN
REACTION_PCNA_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR
REACTION_PCP_CE_PATHWAY
REACTION_PINK_REGULATES_GENE_EXPRESSION
REACTION_PHOSPHORYLATION_OF_THE_APC_C
REACTION_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY
REACTION_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC
REACTION_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA
REACTION_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA
REACTION_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND
REACTION_PROGRAMMED_CELL_DEATH
REACTION_PROTEIN_FOLDING
REACTION_PROTEIN_LOCALIZATION
REACTION_PTEIN_REGULATION
REACTION_PURINE_CATABOLISM
REACTION_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE
REACTION_RECOGNITION_OF_DNA_DAMAGE_BY_PCNA_CONTAINING_REPLICATION_COMPLEX
REACTION_REGULATION_OF_APOPTOSIS
REACTION_REGULATION_OF_EXPRESSION_OF_SUTS_AND_ROBOS
REACTION_REGULATION_OF_MITOTIC_CELL_CYCLE
REACTION_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS
REACTION_REGULATION_OF_PTEIN_STABILITY_AND_ACTIVITY
REACTION_REGULATION_OF_RAS_BY_GAPS
REACTION_REGULATION_OF_RUNX2_EXPRESSION_AND_ACTIVITY
REACTION_REGULATION_OF_RUNX3_EXPRESSION_AND_ACTIVITY
REACTION_REGULATION_OF_TP53_ACTIVITY_THROUGH_PHOSPHORYLATION
REACTION_RESOLUTION_OF_ABASIC_SITES_AP_SITES
REACTION_RESOLUTION_OF_ABASIC_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLACEMENT_PATHWAY
REACTION_RESPIRATORY_ELECTRON_TRANSPORT
REACTION_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS
REACTION_RNA_POLYMERASE_I_PROMOTER_ESCAPE
REACTION_RNA_POLYMERASE_I_TRANSCRIPTION
REACTION_RNA_POLYMERASE_I_TRANSCRIPTION_INITIATION

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REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_TERMINATION
 REACTOME_RNA_POLYMERASE_II_PRE_TRANSCRIPTION_EVENTS
 REACTOME_RNA_POLYMERASE_II_TRANSCRIBES_SNRNA_GENES
 REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_ELONGATION
 REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING
 REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_TERMINATION
 REACTOME_RNA_POLYMERASE_III_CHAIN_ELONGATION
 REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION
 REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_1_PROMOTER
 REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER
 REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_TERMINATION
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 REACTOME_RRNA_PROCESSING
 REACTOME_RRNA_PROCESSING_IN_THE_NUCLEUS_AND_CYTOSOL
 REACTOME_RUNX1_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_DIFFERENTIATION_OF_HSCS
 REACTOME_S_PHASE
 REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21
 REACTOME_SELENOAMINO_ACID_METABOLISM
 REACTOME_SIGNALING_BY_FGFR_IIIA_TM
 REACTOME_SIGNALING_BY_NOTCH
 REACTOME_SIGNALING_BY_NOTCH4
 REACTOME_SIGNALING_BY_ROBO_RECEPTORS
 REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE
 REACTOME_STABILIZATION_OF_P53
 REACTOME_SUMOYLATION_OF_DNA_REPLICATION_PROTEINS
 REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE
 REACTOME_SYNTHESIS_OF_ACTIVE_UBIQUITIN:ROLES_OF_E1_AND_E2_ENZYMES
 REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS
 REACTOME_TELOMERE_MAINTENANCE
 REACTOME_TERMINATION_OF_TRANSLATION_DNA_SYNTHESIS
 REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT
 REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G2_CHECKPOINT
 REACTOME_TNFR2_NON_CANONICAL_NF_KB_PATHWAY
 REACTOME_TP53_REGULATES_METABOLIC_GENES
 REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_DNA_REPAIR_GENES
 REACTOME_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR_TC_NER
 REACTOME_TRANSCRIPTION_OF_THE_HIV_GENOME
 REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNK1
 REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX2
 REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX3
 REACTOME_TRANSCRIPTIONAL_REGULATION_BY_TP53
 REACTOME_TRANSLATION
 REACTOME_TRANSLESION_SYNTHESIS_BY_POLH
 REACTOME_TRANSLESION_SYNTHESIS_BY_POLK
 REACTOME_TRANSLESION_SYNTHESIS_BY_Y_FAMILY_DNA_POLYMERASES_BYPASSES_LESIONS_ON_DNA_TEMPLATE
 REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM
 REACTOME_TRISTETRAPROLIN_TTP_ZFP36_BINDS_AND_DESTABILIZES_MRNA
 REACTOME_TRNA_AMINOACYLATION
 REACTOME_TRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL
 REACTOME_TRNA_PROCESSING
 REACTOME_TRNA_PROCESSING_IN_THE_NUCLEUS
 REACTOME_UB_SPECIFIC_PROCESSING_PROTEASES
 REACTOME_UCH_PROTEINASES
 REACTOME_UNFOLDED_PROTEIN_RESPONSE_UPR
 REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G
 REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS

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