

FUNCTIONAL ENRICHMENT ANALYSIS USING GO ANNOTATIONS

GProfiler

1. Genes/transcripts with very high (top 10%)

Top Half-life gene overview



Top Half – life detailed results

GO:BP		stats		
Term name	Term ID	P_{adj}	$-\log_{10}(P_{adj})$	Show evidence codes
small molecule catabolic process	GO:0044282	4.539×10^{-2}		

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KEGG		stats		
Term name	Term ID	P_{adj}	$-\log_{10}(P_{adj})$	Show evidence codes
Glycolysis / Gluconeogenesis	KEGG:00010	4.420×10^{-4}		
Fatty acid degradation	KEGG:00071	2.567×10^{-3}		
Metabolic pathways	KEGG:01100	7.616×10^{-3}		
Starch and sucrose metabolism	KEGG:00500	7.780×10^{-3}		
Fructose and mannose metabolism	KEGG:00051	8.099×10^{-3}		
beta-Alanine metabolism	KEGG:00410	8.431×10^{-3}		
Galactose metabolism	KEGG:00052	1.133×10^{-2}		
Valine, leucine and isoleucine degradation	KEGG:00280	1.378×10^{-2}		
Methane metabolism	KEGG:00680	2.093×10^{-2}		
Carbon metabolism	KEGG:01200	3.383×10^{-2}		

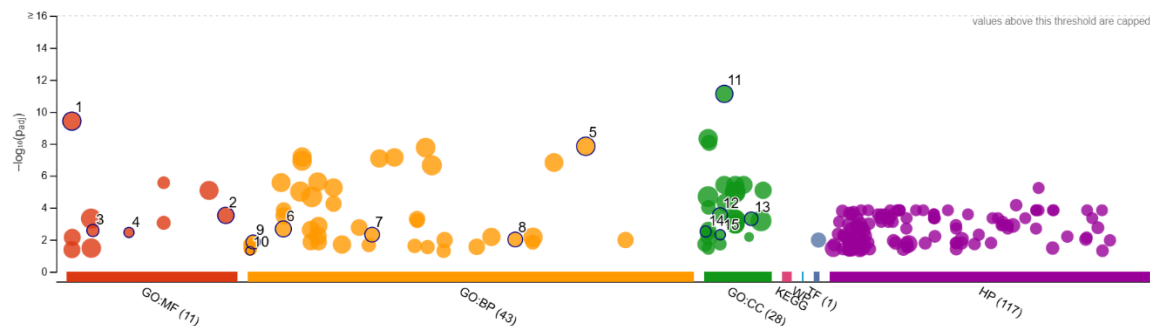
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HP		stats		
Term name	Term ID	P_{adj}	$-\log_{10}(P_{adj})$	Show evidence codes
Mitochondrial respiratory chain defects	HP:0200125	3.695×10^{-2}		

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2. Genes/transcripts with very low (bottom 10%)

Low Half-life gene overview



ID	Source	Term ID	Term Name	Padj (query_1)
1	GO:MF	GO:0003676	nucleic acid binding	3.828×10 ⁻¹⁰
2	GO:MF	GO:0140640	catalytic activity, acting on a nucleic acid	3.013×10 ⁻⁴
3	GO:MF	GO:0008173	RNA methyltransferase activity	2.661×10 ⁻³
4	GO:MF	GO:0030527	structural constituent of chromatin	3.523×10 ⁻³
5	GO:BP	GO:0141187	nucleic acid biosynthetic process	1.442×10 ⁻⁸
6	GO:BP	GO:0006325	chromatin organization	2.133×10 ⁻³
7	GO:BP	GO:0032200	telomere organization	4.829×10 ⁻³
8	GO:BP	GO:0065004	protein-DNA complex assembly	9.741×10 ⁻³
9	GO:BP	GO:0001510	RNA methylation	1.383×10 ⁻²
10	GO:BP	GO:0000452	snoRNA guided rRNA 2'-O-methylation	4.999×10 ⁻²
11	GO:CC	GO:0031981	nuclear lumen	7.569×10 ⁻¹²
12	GO:CC	GO:0030684	preribosome	2.958×10 ⁻⁴
13	GO:CC	GO:0090575	RNA polymerase II transcription regulator complex	4.917×10 ⁻⁴
14	GO:CC	GO:0000786	nucleosome	3.086×10 ⁻³
15	GO:CC	GO:0030867	rough endoplasmic reticulum membrane	4.929×10 ⁻³

version e112_eg59_p19_25aa4782
date 3/7/2025, 9:02:48 PM
organism scerevisiae

g:Profiler

Low Half – life detailed results

GO:MF		stats		
<input type="checkbox"/> Term name	Term ID	Padj	-log10(Padj)	Show evidence codes
<input checked="" type="checkbox"/> nucleic acid binding	GO:0003676	3.828×10 ⁻¹⁰		
<input type="checkbox"/> protein heterodimerization activity	GO:0046982	2.733×10 ⁻⁶		
<input type="checkbox"/> organic cyclic compound binding	GO:0097159	8.298×10 ⁻⁶		
<input checked="" type="checkbox"/> catalytic activity, acting on a nucleic acid	GO:0140640	3.013×10 ⁻⁴		
<input type="checkbox"/> binding	GO:0005488	4.813×10 ⁻⁴		
<input type="checkbox"/> protein dimerization activity	GO:0046983	8.837×10 ⁻⁴		
<input checked="" type="checkbox"/> RNA methyltransferase activity	GO:0008173	2.661×10 ⁻³		
<input checked="" type="checkbox"/> structural constituent of chromatin	GO:0030527	3.523×10 ⁻³		
<input type="checkbox"/> RNA binding	GO:0003723	7.123×10 ⁻³		
<input type="checkbox"/> protein binding	GO:0005515	3.370×10 ⁻²		
<input type="checkbox"/> DNA binding	GO:0003677	4.270×10 ⁻²		

GO:BP		stats			
<input type="checkbox"/> Term name	Term ID	Padj	$-\log_{10}(P_{adj})$	≤ 16	Show evidence codes
<input checked="" type="checkbox"/> nucleic acid biosynthetic process	GO:0141187	1.442×10^{-8}			
<input type="checkbox"/> macromolecule metabolic process	GO:0043170	1.737×10^{-8}			
<input type="checkbox"/> macromolecule biosynthetic process	GO:0009059	6.688×10^{-8}			
<input type="checkbox"/> nucleobase-containing compound biosynthetic process	GO:0034654	7.151×10^{-8}			
<input type="checkbox"/> RNA biosynthetic process	GO:0032774	8.302×10^{-8}			
<input type="checkbox"/> biosynthetic process	GO:0009058	1.185×10^{-7}			
<input type="checkbox"/> nucleic acid metabolic process	GO:0090304	1.487×10^{-7}			
<input type="checkbox"/> primary metabolic process	GO:0044238	2.224×10^{-7}			
<input type="checkbox"/> gene expression	GO:0010467	2.412×10^{-6}			
<input type="checkbox"/> nucleobase-containing compound metabolic process	GO:0006139	2.680×10^{-6}			
<input type="checkbox"/> RNA metabolic process	GO:0016070	5.521×10^{-6}			
<input type="checkbox"/> metabolic process	GO:0008152	9.815×10^{-6}			
<input type="checkbox"/> cellular process	GO:0009987	2.099×10^{-5}			
<input type="checkbox"/> rRNA metabolic process	GO:0016072	5.665×10^{-5}			
<input type="checkbox"/> rRNA processing	GO:0006364	1.440×10^{-4}			
<input type="checkbox"/> RNA processing	GO:0006396	3.217×10^{-4}			
<input type="checkbox"/> ribosome biogenesis	GO:0042254	5.143×10^{-4}			
<input type="checkbox"/> ribosomal large subunit biogenesis	GO:0042273	6.633×10^{-4}			
<input type="checkbox"/> regulation of macromolecule biosynthetic process	GO:0010556	1.341×10^{-3}			
<input type="checkbox"/> ribonucleoprotein complex biogenesis	GO:0022613	1.726×10^{-3}			
<input checked="" type="checkbox"/> chromatin organization	GO:0006325	2.133×10^{-3}			
<input type="checkbox"/> regulation of biosynthetic process	GO:0009889	2.419×10^{-3}			
<input checked="" type="checkbox"/> telomere organization	GO:0032200	4.829×10^{-3}			
<input type="checkbox"/> regulation of gene expression	GO:0010468	5.837×10^{-3}			
<input type="checkbox"/> regulation of macromolecule metabolic process	GO:0060255	6.703×10^{-3}			
<input type="checkbox"/> cellular component organization or biogenesis	GO:0071840	7.068×10^{-3}			
<input checked="" type="checkbox"/> protein-DNA complex assembly	GO:0065004	9.741×10^{-3}			
<input type="checkbox"/> regulation of macromolecule metabolic process	GO:0009059	6.688×10^{-8}			
<input type="checkbox"/> cellular component organization or biogenesis	GO:0071840	7.068×10^{-3}			
<input checked="" type="checkbox"/> protein-DNA complex assembly	GO:0065004	9.741×10^{-3}			
<input type="checkbox"/> positive regulation of DNA-templated transcription	GO:0045893	1.049×10^{-2}			
<input type="checkbox"/> positive regulation of RNA biosynthetic process	GO:1902680	1.049×10^{-2}			
<input checked="" type="checkbox"/> RNA methylation	GO:0001510	1.383×10^{-2}			
<input type="checkbox"/> positive regulation of biosynthetic process	GO:0009891	1.408×10^{-2}			
<input type="checkbox"/> positive regulation of macromolecule biosynthetic pro...	GO:0010557	1.434×10^{-2}			
<input type="checkbox"/> protein-DNA complex organization	GO:0071824	1.437×10^{-2}			
<input type="checkbox"/> maturation of 5.8S rRNA	GO:0000460	1.959×10^{-2}			
<input type="checkbox"/> regulation of metabolic process	GO:0019222	2.005×10^{-2}			
<input type="checkbox"/> heterochromatin formation	GO:0031507	2.146×10^{-2}			
<input type="checkbox"/> epigenetic regulation of gene expression	GO:0040029	2.450×10^{-2}			
<input type="checkbox"/> positive regulation of RNA metabolic process	GO:0051254	2.793×10^{-2}			
<input type="checkbox"/> macromolecule methylation	GO:0043414	2.890×10^{-2}			
<input type="checkbox"/> maturation of 5.8S rRNA from tricistronic rRNA transcri...	GO:0000466	3.464×10^{-2}			
<input type="checkbox"/> maturation of LSU-rRNA	GO:0000470	3.989×10^{-2}			
<input type="checkbox"/> negative regulation of gene expression, epigenetic	GO:0045814	4.998×10^{-2}			
<input checked="" type="checkbox"/> snoRNA guided rRNA 2'-O-methylation	GO:0000452	4.999×10^{-2}			

GO:CC		stats			
<input type="checkbox"/> Term name	Term ID	Padj	$-\log_{10}(P_{adj})$	≤ 16	Show evidence codes
<input checked="" type="checkbox"/> nuclear lumen	GO:0031981	7.569×10^{-12}			
<input type="checkbox"/> nucleus	GO:0005634	4.767×10^{-9}			
<input type="checkbox"/> nucleolus	GO:0005730	8.859×10^{-9}			
<input type="checkbox"/> intracellular organelle lumen	GO:0070013	3.740×10^{-6}			
<input type="checkbox"/> organelle lumen	GO:0043233	3.740×10^{-6}			
<input type="checkbox"/> membrane-enclosed lumen	GO:0031974	3.740×10^{-6}			
<input type="checkbox"/> nuclear protein-containing complex	GO:0140513	8.155×10^{-6}			
<input type="checkbox"/> intracellular membrane-bounded organelle	GO:0043231	9.965×10^{-6}			
<input type="checkbox"/> membrane-bounded organelle	GO:0043227	1.138×10^{-5}			

<input type="checkbox"/>	membrane-bounded organelle	GO:0043227	1.138×10 ⁻⁷	
<input type="checkbox"/>	intracellular anatomical structure	GO:0005622	2.014×10 ⁻⁵	
<input type="checkbox"/>	protein-containing complex	GO:0032991	4.810×10 ⁻⁵	
<input type="checkbox"/>	transcription regulator complex	GO:0005667	9.526×10 ⁻⁵	
<input checked="" type="checkbox"/>	preribosome	GO:0030684	2.958×10 ⁻⁴	
<input checked="" type="checkbox"/>	RNA polymerase II transcription regulator complex	GO:0090575	4.917×10 ⁻⁴	
<input type="checkbox"/>	intracellular organelle	GO:0043229	5.655×10 ⁻⁴	
<input type="checkbox"/>	organelle	GO:0043226	5.883×10 ⁻⁴	
<input type="checkbox"/>	cellular anatomical structure	GO:0110165	6.635×10 ⁻⁴	
<input type="checkbox"/>	membraneless organelle	GO:0043228	1.085×10 ⁻³	
<input type="checkbox"/>	intracellular membraneless organelle	GO:0043232	1.085×10 ⁻³	
<input type="checkbox"/>	nucleoplasm	GO:0005654	2.359×10 ⁻³	
<input checked="" type="checkbox"/>	nucleosome	GO:0000786	3.086×10 ⁻³	
<input type="checkbox"/>	rough endoplasmic reticulum	GO:0005791	4.929×10 ⁻³	
<input checked="" type="checkbox"/>	rough endoplasmic reticulum membrane	GO:0030867	4.929×10 ⁻³	
<input type="checkbox"/>	chromosome	GO:0005694	6.788×10 ⁻³	
<input type="checkbox"/>	translocon complex	GO:0071256	6.789×10 ⁻³	
<input type="checkbox"/>	preribosome, large subunit precursor	GO:0030687	1.856×10 ⁻²	
<input type="checkbox"/>	nuclear chromosome	GO:0000228	1.915×10 ⁻²	
<input type="checkbox"/>	replication fork	GO:0005657	3.387×10 ⁻²	

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TF		stats				
<input type="checkbox"/> Term name	Term ID	Padj	-log ₁₀ (Padj)	≤16	Show evidence codes	
<input type="checkbox"/> Factor: SWI4P; motif: CRCGAAAAT	TF:M08830	1.050×10 ⁻²				

HP		stats				
<input type="checkbox"/> Term name	Term ID	Padj	-log ₁₀ (Padj)	≤16	Show evidence codes	
<input type="checkbox"/> Increased circulating IgG subclass	HP:0032296	5.801×10 ⁻⁶				
<input type="checkbox"/> Raynaud phenomenon	HP:0030880	6.927×10 ⁻⁵				
<input type="checkbox"/> Generalized lymphadenopathy	HP:0008940	1.445×10 ⁻⁴				
<input type="checkbox"/> Atrophic gastritis	HP:0002582	1.445×10 ⁻⁴				
<input type="checkbox"/> Short dental root	HP:0006336	1.445×10 ⁻⁴				
<input type="checkbox"/> Aortic arch calcification	HP:0005303	1.445×10 ⁻⁴				
<input type="checkbox"/> Joint subluxation	HP:0032153	1.445×10 ⁻⁴				
<input type="checkbox"/> Decreased circulating IgG3 concentration	HP:0032137	1.445×10 ⁻⁴				
<input type="checkbox"/> Expanded metacarpals with widened medullary cavities	HP:0006232	1.445×10 ⁻⁴				
<input type="checkbox"/> Shallow acetabular fossae	HP:0003182	1.445×10 ⁻⁴				
<input type="checkbox"/> Hypoplastic distal radial epiphyses	HP:0006386	1.445×10 ⁻⁴				
<input type="checkbox"/> Expanded phalanges with widened medullary cavities	HP:0006112	1.445×10 ⁻⁴				
<input type="checkbox"/> Abnormality of the distal radial epiphysis	HP:0010597	1.445×10 ⁻⁴				
<input type="checkbox"/> Expanded metatarsals with widened medullary cavities	HP:0008102	1.445×10 ⁻⁴				
<input type="checkbox"/> Hypoplasia of the tooth germ	HP:0006353	1.445×10 ⁻⁴				
<input type="checkbox"/> Recurrent viral upper respiratory tract infections	HP:0033166	1.445×10 ⁻⁴				
<input type="checkbox"/> Recurrent viral pneumonia	HP:0033214	1.445×10 ⁻⁴				
<input type="checkbox"/> Tendon rupture	HP:0100550	1.445×10 ⁻⁴				
<input type="checkbox"/> Abnormal size of the dental root	HP:0040220	1.445×10 ⁻⁴				
<input type="checkbox"/> Increased circulating IgG3 level	HP:0032297	1.445×10 ⁻⁴				
<input type="checkbox"/> Cutis marmorata	HP:0000965	1.628×10 ⁻⁴				
<input type="checkbox"/> Unexplained fevers	HP:0001955	1.830×10 ⁻⁴				
<input type="checkbox"/> Abnormal aortic valve morphology	HP:0001646	2.245×10 ⁻⁴				
<input type="checkbox"/> Chronic CSF lymphocytosis	HP:0009704	2.596×10 ⁻⁴				
<input type="checkbox"/> Mitral valve calcification	HP:0004382	2.596×10 ⁻⁴				
<input type="checkbox"/> Neonatal alloimmune thrombocytopenia	HP:0004809	2.596×10 ⁻⁴				
<input type="checkbox"/> Increased CSF interferon alpha	HP:0009709	2.596×10 ⁻⁴				
<input type="checkbox"/> Onycholysis	HP:0001806	2.596×10 ⁻⁴				
<input type="checkbox"/> Chronic lymphatic leukemia	HP:0005550	2.596×10 ⁻⁴				

<input type="checkbox"/>	Moyamoya phenomenon	HP:0011834	2.596×10 ⁻⁴	
<input type="checkbox"/>	Abnormality of radial epiphyses	HP:0003999	2.596×10 ⁻⁴	
<input type="checkbox"/>	Abnormal gastric mucosa morphology	HP:0004295	4.411×10 ⁻⁴	
<input type="checkbox"/>	Hematemesis	HP:0002248	4.517×10 ⁻⁴	
<input type="checkbox"/>	Chilblains	HP:0009710	4.517×10 ⁻⁴	
<input type="checkbox"/>	Osteolytic defects of the phalanges of the hand	HP:0009771	4.517×10 ⁻⁴	
<input type="checkbox"/>	Osteolysis involving bones of the upper limbs	HP:0045039	4.517×10 ⁻⁴	
<input type="checkbox"/>	Psoriasisiform lesion	HP:0025526	4.517×10 ⁻⁴	
<input type="checkbox"/>	Osteolytic defects of the hand bones	HP:0009699	4.517×10 ⁻⁴	
<input type="checkbox"/>	Ground-glass opacification	HP:0025179	4.517×10 ⁻⁴	
<input type="checkbox"/>	Extrapyramidal muscular rigidity	HP:0007076	4.517×10 ⁻⁴	
<input type="checkbox"/>	Gastritis	HP:0005263	4.517×10 ⁻⁴	
<input type="checkbox"/>	Pulmonary opacity	HP:0031457	4.517×10 ⁻⁴	
<input type="checkbox"/>	Thoracic aorta calcification	HP:0004962	4.517×10 ⁻⁴	
<input type="checkbox"/>	Eruption failure	HP:0000706	7.637×10 ⁻⁴	
<input type="checkbox"/>	Aortic valve calcification	HP:0004380	7.637×10 ⁻⁴	
<input type="checkbox"/>	Cardiac valve calcification	HP:0005146	7.637×10 ⁻⁴	
<input type="checkbox"/>	Chronic leukemia	HP:0005558	7.637×10 ⁻⁴	
<input type="checkbox"/>	Enchondroma	HP:0030038	7.769×10 ⁻⁴	
<input type="checkbox"/>	Waddling gait	HP:0002515	9.422×10 ⁻⁴	
<input type="checkbox"/>	Increased circulating IgG concentration	HP:0003237	1.004×10 ⁻³	
<input type="checkbox"/>	Oligohydramnios	HP:0001562	1.128×10 ⁻³	
<input type="checkbox"/>	Abnormal left ventricular outflow tract morphology	HP:0011103	1.229×10 ⁻³	
<input type="checkbox"/>	Arrhinencephaly	HP:0002139	1.229×10 ⁻³	
<input type="checkbox"/>	Hip subluxation	HP:0030043	1.229×10 ⁻³	
<input type="checkbox"/>	Increased circulating interferon-gamma concentration	HP:0030356	1.257×10 ⁻³	
<input type="checkbox"/>	Abnormal nail attachment	HP:0025756	1.257×10 ⁻³	
<input type="checkbox"/>	Antenatal onset	HP:0030674	1.292×10 ⁻³	
<input type="checkbox"/>	Thickened calvaria	HP:0002684	1.713×10 ⁻³	
<input type="checkbox"/>	Muscle fiber atrophy	HP:0100295	1.782×10 ⁻³	
<input type="checkbox"/>	Abnormal circulating interferon concentration	HP:0011116	2.021×10 ⁻³	
<input type="checkbox"/>	Subvalvular aortic stenosis	HP:0001682	2.021×10 ⁻³	
<input type="checkbox"/>	Multifocal cerebral white matter abnormalities	HP:0007052	2.021×10 ⁻³	
<input type="checkbox"/>	Multifocal cerebral white matter abnormalities	HP:0007052	2.021×10 ⁻³	
<input type="checkbox"/>	Porencephalic cyst	HP:0002132	2.021×10 ⁻³	
<input type="checkbox"/>	Decreased circulating IgG subclass concentration	HP:0032135	2.021×10 ⁻³	
<input type="checkbox"/>	Abnormal circulating interferon-gamma concentration	HP:0030355	2.021×10 ⁻³	
<input type="checkbox"/>	Hematochezia	HP:0002573	2.021×10 ⁻³	
<input type="checkbox"/>	Multiple joint contractures	HP:0002828	2.789×10 ⁻³	
<input type="checkbox"/>	Loss of speech	HP:0002371	4.348×10 ⁻³	
<input type="checkbox"/>	Eyelid coloboma	HP:0000625	4.348×10 ⁻³	
<input type="checkbox"/>	Panniculitis	HP:0012490	4.890×10 ⁻³	
<input type="checkbox"/>	Atopic dermatitis	HP:0001047	4.890×10 ⁻³	
<input type="checkbox"/>	Respiratory failure	HP:0002878	5.649×10 ⁻³	
<input type="checkbox"/>	Broad phalanges of the hand	HP:0009768	6.180×10 ⁻³	
<input type="checkbox"/>	Acrocyanosis	HP:0001063	6.404×10 ⁻³	
<input type="checkbox"/>	Peripheral cyanosis	HP:0034033	6.404×10 ⁻³	
<input type="checkbox"/>	Spastic paraparesis	HP:0002313	6.635×10 ⁻³	
<input type="checkbox"/>	Spastic tetraparesis	HP:0001285	7.059×10 ⁻³	
<input type="checkbox"/>	Scaling skin	HP:0040189	7.386×10 ⁻³	
<input type="checkbox"/>	Pericardial effusion	HP:0001698	7.661×10 ⁻³	
<input type="checkbox"/>	Fetal onset	HP:0011461	9.093×10 ⁻³	
<input type="checkbox"/>	Abnormal circulating ferritin concentration	HP:0040133	9.364×10 ⁻³	
<input type="checkbox"/>	CSF lymphocytic pleocytosis	HP:0200149	1.096×10 ⁻²	
<input type="checkbox"/>	Broad long bones	HP:0005622	1.166×10 ⁻²	
<input type="checkbox"/>	Abnormal nasopharynx morphology	HP:0001739	1.218×10 ⁻²	
<input type="checkbox"/>	Recurrent upper respiratory tract infections	HP:0002788	1.218×10 ⁻²	
<input type="checkbox"/>	Abnormal acetabulum morphology	HP:0003170	1.499×10 ⁻²	
<input type="checkbox"/>	Abnormal circulating cytokine concentration	HP:0011112	1.599×10 ⁻²	
<input type="checkbox"/>	Abnormal immune serum protein physiology	HP:0011111	1.599×10 ⁻²	
<input type="checkbox"/>	Bloody diarrhea	HP:0025085	1.599×10 ⁻²	
<input type="checkbox"/>	Abnormal metacarpal morphology	HP:0005916	1.613×10 ⁻²	
<input type="checkbox"/>	Primary microcephaly	HP:0011451	1.635×10 ⁻²	
<input type="checkbox"/>	Demyelinating peripheral neuropathy	HP:0007108	1.645×10 ⁻²	
<input type="checkbox"/>	Abnormal cerebral artery morphology	HP:0009145	1.645×10 ⁻²	
<input type="checkbox"/>	Aplasia/Hypoplasia of the cerebrum	HP:0007364	1.798×10 ⁻²	
<input type="checkbox"/>	CSF pleocytosis	HP:0012229	1.875×10 ⁻²	
<input type="checkbox"/>	Abnormal mitral valve morphology	HP:0001633	1.918×10 ⁻²	
<input type="checkbox"/>	Hypoplasia of the maxilla	HP:0000327	2.044×10 ⁻²	
<input type="checkbox"/>	Hoarse voice	HP:0001609	2.136×10 ⁻²	
<input type="checkbox"/>	Paraparesis	HP:0002385	2.239×10 ⁻²	
<input type="checkbox"/>	Abnormal pleura morphology	HP:0002103	2.439×10 ⁻²	