Table S7.6. Full list of Cellular Compartment Gene Ontology categories enriched in sex-biased genes (Terms from the Function Ontology with p-value ≤ 1.)

GOID	Gene Ontology term	Cluster frequency	Genome frequency of	Corrected P-	Genes annotated to the term
GO:0005634	nucleus	899 of 3038 in the list	1212 of 5465 in the genome	5.63E-49	CCG014863.1,CCG027068.1,CCG022266.1,CCG014871.1,CCG006549.1,CCG008767.3,CCG026106.1,CCG008741.1,CCG003390.1,CCG009827.1,CCG017226.1,CCG024274.1,CCG019811.1,CCG025256.1,CCG003389.1,CCG008846.1,CCG013625.1,CCG005171.1,CCG010803.1,CCG021465.1,CCG001292.1,CCG001177.1,CCG004364.1,CCG018321.1,CCG001404.1,CCG002154.1,CCG006134.1,CCG027906.1,CCG005194.1,CCG018432.1,CCG014866.1,CCG009070.1,CCG004932.1,CCG025208.1,CCG017078.1,CCG023723.1,CCG011696.1,CCG020718.1,CCG013695.1,CCG027127.1,CCG011533.1,CCG009103.1,CCG022824.1,CCG027193.1,CCG017954.1,CCG004853.1,CCG022281.1,CCG006554.2,CCG028046.1,CCG015625.1,CCG010909.1,CCG028653.1,CCG024387.1,CCG006377.1,CCG007005.1,CCG020286.1,CCG000136.1,CCG007800.1,CCG000588.1,CCG008144.1,CCG017801.1,CCG009822.1,CCG027133.1,CCG026982.1,CCG017181.1,CCG022706.1,CCG016906.1,CCG028568.1,CCG026487.1,CCG017366.1,CCG007647.1,CCG004331.1,CCG006484.1,CCG007221.2,CCG012083.1,CCG025257.1,CCG024437.1,CCG009263.1,CCG015900.1,CCG022136.1,CCG023937.1,CCG001461.1,CCG021159.1,CCG000709.1,CCG017760.1,CCG009386.1,CCG023686.1,CCG002091.1,CCG004402.1,CCG023853.1,CCG002244.1,CCG002198.1,CCG025990.1,CCG000133.1,CCG013224.2,CCG011239.1,CCG023777.1,CCG026228.2,CCG017953.2,CCG011097.1,CCG004927.1,CCG009805.2,CCG000911.1,CCG005108.1,CCG025389.1,CCG016249.1,CCG028465.1,CCG012584.1,CCG010962.1,CCG020063.1,CCG002570.1,CCG009823.1,CCG025255.1,CCG024788.1,CCG003193.1,CCG025057.1,CCG017158.1,CCG021426.1,CCG010912.1,CCG004955.1,CCG010011.1,CCG027289.1,CCG022496.1,CCG004646.1,CCG028556.1,CCG003424.1,CCG0248

GO:0005622	intracellular	2175 of 3038 in the list	3439 of 5465 in the genome	1.58E-47	CCG005254.1,CCG014531.2,CCG017420.1,CCG027068.1,CCG004973.1,CCG008767.3,CCG027509.1,CCG026106.1,CCG025108.1,CCG023989.1,CCG004583.4,CCG005974.1,CCG008041.1,CCG027906.1,CCG025208.1,CCG017078.1,CCG023723.1,CCG006992.1,CCG019382.1,CCG026413.3,CCG023474.1,CCG026871.2,CCG011533.1,CCG003767.1,CCG021911.1,CCG022281.1,CCG004819.1,CCG010905.1,CCG017622.1,CCG008270.1,CCG013537.1,CCG015625.1,CCG028653.1,CCG026795.1,CCG007005.1,CCG000588.1,CCG009822.1,CCG019571.1,CCG022706.1,CCG026487.1,CCG017366.1,CCG002452.1,CCG018788.1,CCG012083.1,CCG004859.1,CCG009263.1,CCG024119.1,CCG021159.1,CCG023686.1,CCG002198.1,CCG001579.1,CCG013641.1,CCG003563.1,CCG006089.1,CCG000133.1,CCG004927.1,CCG000911.1,CCG001876.1,CCG013465.1,CCG002937.1,CCG000789.1,CCG021426.1,CCG010912.1,CCG007669.1,CCG027289.1,CCG022496.1,CCG028556.1,CCG012844.1,CCG010136.1,CCG022449.1,CCG024000.1,CCG023854.1,CCG000487.1,CCG007523.1,CCG010112.1,CCG004986.1,CCG007750.2,CCG006479.1,CCG010656.1,CCG001395.1,CCG027736.1,CCG012500.1,CCG005627.1,CCG026778.1,CCG008383.1,CCG027000.1,CCG013123.1,CCG024760.1,CCG017891.1,CCG011015.1,CCG020320.1,CCG006081.1,CCG023046.1,CCG015167.1,CCG021720.1,CCG012959.1,CCG015869.2,CCG003009.1,CCG004647.1,CCG000807.1,CCG006050.2,CCG025369.1,CCG003566.1,CCG009923.1,CCG001440.1,CCG015800.2,CCG001789.1,CCG003775.1,CCG009928.1,CCG005635.1,CCG015908.2,CCG013491.1,CCG022749.1,CCG004912.1,CCG003955.1,CCG024058.1,CCG007724.1,CCG012229.1,CCG024679.1,CCG018742.1,CCG005920.1,CCG015312.2,CCG000490.1,CCG005269.1,CCG019520.1,CCG012542.2,CCG0142

GO:0005623	cell	2223 of 3038 in the list	3547 of 5465 in the genome	3.00E-44	CCG005254.1,CCG014531.2,CCG017420.1,CCG027068.1,CCG004973.1,CCG008767.3,CCG027509.1,CCG026106.1,CCG025108.1,CCG023989.1,CCG004583.4,CCG005974.1,CCG008041.1,CCG027906.1,CCG025208.1,CCG017078.1,CCG003362.1,CCG023723.1,CCG006992.1,CCG019382.1,CCG026413.3,CCG023474.1,CCG026871.2,CCG011533.1,CCG003767.1,CCG021911.1,CCG022281.1,CCG004819.1,CCG010905.1,CCG017622.1,CCG008270.1,CCG013537.1,CCG015625.1,CCG028653.1,CCG026795.1,CCG007005.1,CCG000588.1,CCG009822.1,CCG019571.1,CCG022706.1,CCG026487.1,CCG017366.1,CCG002452.1,CCG018788.1,CCG012083.1,CCG004859.1,CCG009263.1,CCG024119.1,CCG021159.1,CCG023686.1,CCG002198.1,CCG001579.1,CCG013641.1,CCG003563.1,CCG006089.1,CCG000133.1,CCG019647.1,CCG004927.1,CCG000911.1,CCG001876.1,CCG013465.1,CCG018688.1,CCG002937.1,CCG000789.1,CCG021426.1,CCG010912.1,CCG007669.1,CCG027289.1,CCG022496.1,CCG028556.1,CCG012844.1,CCG010136.1,CCG022449.1,CCG024000.1,CCG023854.1,CCG000487.1,CCG007523.1,CCG010112.1,CCG004986.1,CCG007750.2,CCG006479.1,CCG010656.1,CCG001395.1,CCG027736.1,CCG012500.1,CCG005627.1,CCG026778.1,CCG008383.1,CCG027000.1,CCG013123.1,CCG024760.1,CCG017891.1,CCG011015.1,CCG020320.1,CCG006081.1,CCG023046.1,CCG015167.1,CCG021720.1,CCG012959.1,CCG015869.2,CCG003009.1,CCG004647.1,CCG000807.1,CCG006050.2,CCG025369.1,CCG003566.1,CCG009923.1,CCG001440.1,CCG015800.2,CCG001789.1,CCG003775.1,CCG009928.1,CCG005635.1,CCG015908.2,CCG013491.1,CCG022749.1,CCG004912.1,CCG003955.1,CCG024058.1,CCG007724.1,CCG012229.1,CCG024679.1,CCG018742.1,CCG005920.1,CCG015312.2,CCG000490.1,CCG0052

GO:0044464	cell part	2223 of 3038 in the list	3547 of 5465 in the genome	3.00E-44	CCG005254.1,CCG014531.2,CCG017420.1,CCG027068.1,CCG004973.1,CCG008767.3,CCG027509.1,CCG026106.1,CCG025108.1,CCG023989.1,CCG004583.4,CCG005974.1,CCG008041.1,CCG027906.1,CCG025208.1,CCG017078.1,CCG003362.1,CCG023723.1,CCG006992.1,CCG019382.1,CCG026413.3,CCG023474.1,CCG026871.2,CCG011533.1,CCG003767.1,CCG021911.1,CCG022281.1,CCG004819.1,CCG010905.1,CCG017622.1,CCG008270.1,CCG013537.1,CCG015625.1,CCG028653.1,CCG026795.1,CCG007005.1,CCG000588.1,CCG009822.1,CCG019571.1,CCG022706.1,CCG026487.1,CCG017366.1,CCG002452.1,CCG018788.1,CCG012083.1,CCG004859.1,CCG009263.1,CCG024119.1,CCG021159.1,CCG023686.1,CCG002198.1,CCG001579.1,CCG013641.1,CCG003563.1,CCG006089.1,CCG000133.1,CCG019647.1,CCG004927.1,CCG000911.1,CCG001876.1,CCG013465.1,CCG018688.1,CCG002937.1,CCG000789.1,CCG021426.1,CCG010912.1,CCG007669.1,CCG027289.1,CCG022496.1,CCG028556.1,CCG012844.1,CCG010136.1,CCG022449.1,CCG024000.1,CCG023854.1,CCG000487.1,CCG007523.1,CCG010112.1,CCG004986.1,CCG007750.2,CCG006479.1,CCG010656.1,CCG001395.1,CCG027736.1,CCG012500.1,CCG005627.1,CCG026778.1,CCG008383.1,CCG027000.1,CCG013123.1,CCG024760.1,CCG017891.1,CCG011015.1,CCG020320.1,CCG006081.1,CCG023046.1,CCG015167.1,CCG021720.1,CCG012959.1,CCG015869.2,CCG003009.1,CCG004647.1,CCG000807.1,CCG006050.2,CCG025369.1,CCG003566.1,CCG009923.1,CCG001440.1,CCG015800.2,CCG001789.1,CCG003775.1,CCG009928.1,CCG005635.1,CCG015908.2,CCG013491.1,CCG022749.1,CCG004912.1,CCG003955.1,CCG024058.1,CCG007724.1,CCG012229.1,CCG024679.1,CCG018742.1,CCG005920.1,CCG015312.2,CCG000490.1,CCG0052

GO:0043227	membrane-bounded organelle	1047 of 3038 in the list	1495 of 5465 in the genome	2.24E-38	CCG011932.1,CCG027068.1,CCG022266.1,CCG014871.1,CCG006549.1,CCG008767.3,CCG026106.1,CCG019811.1,CCG025256.1,CCG009428.1,CCG001292.1,CCG001404.1,CCG027906.1,CCG018432.1,CCG014866.1,CCG004932.1,CCG025208.1,CCG017078.1,CCG023723.1,CCG027127.1,CCG011533.1,CCG009103.1,CCG022824.1,CCG027193.1,CCG004853.1,CCG022281.1,CCG006554.2,CCG028046.1,CCG015625.1,CCG002930.1,CCG028653.1,CCG007005.1,CCG020286.1,CCG000136.1,CCG007800.1,CCG000588.1,CCG008144.1,CCG009822.1,CCG026982.1,CCG005191.1,CCG022706.1,CCG008871.1,CCG028568.1,CCG026487.1,CCG017366.1,CCG006484.1,CCG012083.1,CCG024437.1,CCG009263.1,CCG024119.1,CCG021159.1,CCG009386.1,CCG023686.1,CCG002198.1,CCG025990.1,CCG000133.1,CCG011239.1,CCG026228.2,CCG016399.1,CCG011097.1,CCG004927.1,CCG009805.2,CCG000911.1,CCG012584.1,CCG010962.1,CCG020063.1,CCG009823.1,CCG025255.1,CCG003193.1,CCG021426.1,CCG010912.1,CCG004955.1,CCG027289.1,CCG022496.1,CCG028556.1,CCG010136.1,CCG023854.1,CCG027472.1,CCG027023.1,CCG007523.1,CCG010112.1,CCG010656.1,CCG000730.2,CCG000209.1,CCG001395.1,CCG012500.1,CCG005627.1,CCG018669.1,CCG005594.1,CCG026778.1,CCG011550.1,CCG008383.1,CCG002106.1,CCG013123.1,CCG024760.1,CCG027257.1,CCG007522.1,CCG017891.1,CCG011015.1,CCG023046.1,CCG020281.1,CCG021720.1,CCG002332.1,CCG005993.1,CCG003009.1,CCG025115.1,CCG011228.1,CCG025369.1,CCG010797.1,CCG004008.1,CCG010138.1,CCG015800.2,CCG001789.1,CCG009928.1,CCG005635.1,CCG021221.1,CCG000593.1,CCG013491.1,CCG004912.1,CCG002199.1,CCG006328.1,CCG024058.1,CCG023939.1,CCG008308.1,CCG027040.1,CCG027197.1,CCG0251

GO:0043231	intracellular membrane-bounded organelle	1047 of 3038 in the list	1495 of 5465 in the genome	2.24E-38	CCG011932.1,CCG027068.1,CCG022266.1,CCG014871.1,CCG006549.1,CCG008767.3,CCG026106.1,CCG019811.1,CCG025256.1,CCG009428.1,CCG001292.1,CCG001404.1,CCG027906.1,CCG018432.1,CCG014866.1,CCG004932.1,CCG025208.1,CCG017078.1,CCG023723.1,CCG027127.1,CCG011533.1,CCG009103.1,CCG022824.1,CCG027193.1,CCG004853.1,CCG022281.1,CCG006554.2,CCG028046.1,CCG015625.1,CCG002930.1,CCG028653.1,CCG007005.1,CCG020286.1,CCG000136.1,CCG007800.1,CCG000588.1,CCG008144.1,CCG009822.1,CCG026982.1,CCG005191.1,CCG022706.1,CCG008871.1,CCG028568.1,CCG026487.1,CCG017366.1,CCG006484.1,CCG012083.1,CCG024437.1,CCG009263.1,CCG024119.1,CCG021159.1,CCG009386.1,CCG023686.1,CCG002198.1,CCG025990.1,CCG000133.1,CCG011239.1,CCG026228.2,CCG016399.1,CCG011097.1,CCG004927.1,CCG009805.2,CCG000911.1,CCG012584.1,CCG010962.1,CCG020063.1,CCG009823.1,CCG025255.1,CCG003193.1,CCG021426.1,CCG010912.1,CCG004955.1,CCG027289.1,CCG022496.1,CCG028556.1,CCG010136.1,CCG023854.1,CCG027472.1,CCG027023.1,CCG007523.1,CCG010112.1,CCG010656.1,CCG000730.2,CCG000209.1,CCG001395.1,CCG012500.1,CCG005627.1,CCG018669.1,CCG005594.1,CCG026778.1,CCG011550.1,CCG008383.1,CCG002106.1,CCG013123.1,CCG024760.1,CCG027257.1,CCG007522.1,CCG017891.1,CCG011015.1,CCG023046.1,CCG020281.1,CCG021720.1,CCG002332.1,CCG005993.1,CCG003009.1,CCG025115.1,CCG011228.1,CCG025369.1,CCG010797.1,CCG004008.1,CCG010138.1,CCG015800.2,CCG001789.1,CCG009928.1,CCG005635.1,CCG021221.1,CCG000593.1,CCG013491.1,CCG004912.1,CCG002199.1,CCG006328.1,CCG024058.1,CCG023939.1,CCG008308.1,CCG027040.1,CCG027197.1,CCG0251

GO:0043226	organelle	1243 of 3038 in the list	1930 of 5465 in the genome	3.73E-20	CCG014531.2,CCG011932.1,CCG027068.1,CCG022266.1,CCG014871.1,CCG004973.1,CCG006549.1,CCG008767.3,CCG026106.1,CCG005370.1,CCG019811.1,CCG025256.1,CCG009428.1,CCG001292.1,CCG003587.1,CCG001404.1,CCG027906.1,CCG018432.1,CCG014866.1,CCG004932.1,CCG025208.1,CCG017078.1,CCG023723.1,CCG026871.2,CCG027127.1,CCG011533.1,CCG009103.1,CCG022824.1,CCG027193.1,CCG004853.1,CCG021911.1,CCG022281.1,CCG010905.1,CCG006554.2,CCG028046.1,CCG008270.1,CCG015625.1,CCG002930.1,CCG028653.1,CCG007005.1,CCG020286.1,CCG000136.1,CCG007800.1,CCG000588.1,CCG008144.1,CCG009822.1,CCG026982.1,CCG005191.1,CCG022706.1,CCG008871.1,CCG028568.1,CCG026487.1,CCG017366.1,CCG018788.1,CCG006484.1,CCG012083.1,CCG024437.1,CCG009263.1,CCG024119.1,CCG021159.1,CCG009386.1,CCG023686.1,CCG002198.1,CCG021737.1,CCG025990.1,CCG000133.1,CCG011239.1,CCG026228.2,CCG016399.1,CCG011097.1,CCG004927.1,CCG009805.2,CCG000911.1,CCG012584.1,CCG010962.1,CCG020063.1,CCG009823.1,CCG027748.1,CCG025255.1,CCG003193.1,CCG021426.1,CCG010912.1,CCG004955.1,CCG027289.1,CCG022496.1,CCG028556.1,CCG010136.1,CCG023854.1,CCG027472.1,CCG027023.1,CCG007523.1,CCG010112.1,CCG006479.1,CCG010656.1,CCG000730.2,CCG000209.1,CCG001395.1,CCG012500.1,CCG005627.1,CCG018669.1,CCG005594.1,CCG026778.1,CCG011550.1,CCG008383.1,CCG002106.1,CCG013123.1,CCG019426.1,CCG009394.1,CCG024760.1,CCG027257.1,CCG007522.1,CCG017891.1,CCG011015.1,CCG023046.1,CCG015167.1,CCG020281.1,CCG021720.1,CCG002332.1,CCG024421.3,CCG005993.1,CCG003009.1,CCG025115.1,CCG011228.1,CCG025369.1,CCG024769.1,CCG010797.1,CCG0040

GO:0043229	intracellular organelle	1243 of 3038 in the list	1930 of 5465 in the genome	3.73E-20	CCG014531.2,CCG011932.1,CCG027068.1,CCG022266.1,CCG014871.1,CCG004973.1,CCG006549.1,CCG008767.3,CCG026106.1,CCG005370.1,CCG019811.1,CCG025256.1,CCG009428.1,CCG001292.1,CCG003587.1,CCG001404.1,CCG027906.1,CCG018432.1,CCG014866.1,CCG004932.1,CCG025208.1,CCG017078.1,CCG023723.1,CCG026871.2,CCG027127.1,CCG011533.1,CCG009103.1,CCG022824.1,CCG027193.1,CCG004853.1,CCG021911.1,CCG022281.1,CCG010905.1,CCG006554.2,CCG028046.1,CCG008270.1,CCG015625.1,CCG002930.1,CCG028653.1,CCG007005.1,CCG020286.1,CCG000136.1,CCG007800.1,CCG000588.1,CCG008144.1,CCG009822.1,CCG026982.1,CCG005191.1,CCG022706.1,CCG008871.1,CCG028568.1,CCG026487.1,CCG017366.1,CCG018788.1,CCG006484.1,CCG012083.1,CCG024437.1,CCG009263.1,CCG024119.1,CCG021159.1,CCG009386.1,CCG023686.1,CCG002198.1,CCG021737.1,CCG025990.1,CCG000133.1,CCG011239.1,CCG026228.2,CCG016399.1,CCG011097.1,CCG004927.1,CCG009805.2,CCG000911.1,CCG012584.1,CCG010962.1,CCG020063.1,CCG009823.1,CCG027748.1,CCG025255.1,CCG003193.1,CCG021426.1,CCG010912.1,CCG004955.1,CCG027289.1,CCG022496.1,CCG028556.1,CCG010136.1,CCG023854.1,CCG027472.1,CCG027023.1,CCG007523.1,CCG010112.1,CCG006479.1,CCG010656.1,CCG000730.2,CCG000209.1,CCG001395.1,CCG012500.1,CCG005627.1,CCG018669.1,CCG005594.1,CCG026778.1,CCG011550.1,CCG008383.1,CCG002106.1,CCG013123.1,CCG019426.1,CCG009394.1,CCG024760.1,CCG027257.1,CCG007522.1,CCG017891.1,CCG011015.1,CCG023046.1,CCG015167.1,CCG020281.1,CCG021720.1,CCG002332.1,CCG024421.3,CCG005993.1,CCG003009.1,CCG025115.1,CCG011228.1,CCG025369.1,CCG024769.1,CCG010797.1,CCG0040

GO:0044424	intracellular part	1454 of 3038 in the list	2307 of 5465 in the genome	4.36E-19	CCG014531.2,CCG011932.1,CCG027068.1,CCG022266.1,CCG014396.1,CCG014871.1,CCG004973.1,CCG006549.1,CCG008767.3,CCG005079.1,CCG026106.1,CCG005370.1,CCG004595.1,CCG025108.1,CCG019811.1,CCG025256.1,CCG009428.1,CCG001292.1,CCG003587.1,CCG001404.1,CCG027906.1,CCG018432.1,CCG014866.1,CCG004932.1,CCG025208.1,CCG014519.1,CCG017078.1,CCG023723.1,CCG026413.3,CCG026871.2,CCG027127.1,CCG011533.1,CCG027796.1,CCG009103.1,CCG022824.1,CCG018533.1,CCG027193.1,CCG004853.1,CCG003767.1,CCG021911.1,CCG022281.1,CCG010905.1,CCG006554.2,CCG028046.1,CCG008270.1,CCG015625.1,CCG006714.1,CCG002930.1,CCG028653.1,CCG007005.1,CCG020286.1,CCG000136.1,CCG007800.1,CCG000588.1,CCG008144.1,CCG009822.1,CCG026982.1,CCG005191.1,CCG022706.1,CCG019571.1,CCG008871.1,CCG028568.1,CCG026487.1,CCG017366.1,CCG018788.1,CCG006484.1,CCG012083.1,CCG024437.1,CCG009263.1,CCG024119.1,CCG021159.1,CCG009386.1,CCG023686.1,CCG002198.1,CCG021737.1,CCG025990.1,CCG000133.1,CCG011239.1,CCG026228.2,CCG016399.1,CCG011097.1,CCG004927.1,CCG009805.2,CCG000911.1,CCG001876.1,CCG012584.1,CCG010962.1,CCG020063.1,CCG010024.1,CCG009823.1,CCG027748.1,CCG002937.1,CCG025255.1,CCG003193.1,CCG000789.1,CCG005588.1,CCG021426.1,CCG010912.1,CCG004955.1,CCG027289.1,CCG022496.1,CCG028556.1,CCG010136.1,CCG023854.1,CCG027472.1,CCG027023.1,CCG007523.1,CCG010112.1,CCG004986.1,CCG006479.1,CCG010656.1,CCG000730.2,CCG000209.1,CCG001395.1,CCG027736.1,CCG012500.1,CCG005627.1,CCG018669.1,CCG005594.1,CCG026778.1,CCG011550.1,CCG008383.1,CCG002106.1,CCG027316.1,CCG013123.1,CCG019426.1,CCG0093
GO:0044428	nuclear part	93 of 3038 in the list	115 of 5465 in the genome	2.13E-06	CCG000158.1,CCG027068.1,CCG016237.1,CCG001809.1,CC

GO:0005635	nuclear envelope	21 of 3038 in the list	21 of 5465 in the genome	0.00117	CCG010440.1,CCG011550.1,CCG008144.1,CCG009822.1,CCG001809.1,CCG000493.1,CCG012556.1,CCG013066.1,CCG022771.1,CCG009136.1,CCG020053.1,CCG028425.2,CCG026989.1,CCG004897.1,CCG006243.1,CCG008116.1,CCG017141.1,CCG023186.1,CCG003009.1,CCG017874.1,CCG017989.1
GO:0005643	nuclear pore	15 of 3038 in the list	15 of 5465 in the genome	0.04051	CCG009136.1,CCG022771.1,CCG010440.1,CCG020053.1,CCG009822.1,CCG001809.1,CCG006243.1,CCG004897.1,CCG026989.1,CCG008116.1,CCG017141.1,CCG017874.1,CCG003009.1,CCG023186.1,CCG012556.1
GO:0046930	pore complex	15 of 3038 in the list	15 of 5465 in the genome	0.04051	CCG009136.1,CCG022771.1,CCG010440.1,CCG020053.1,CCG009822.1,CCG001809.1,CCG006243.1,CCG004897.1,CCG026989.1,CCG008116.1,CCG017141.1,CCG017874.1,CCG003009.1,CCG023186.1,CCG012556.1
GO:0005874	microtubule	30 of 3038 in the list	36 of 5465 in the genome	0.11507	CCG006420.1,CCG009543.1,CCG015289.1,CCG015784.1,CCG013000.1,CCG013637.1,CCG026823.1,CCG023682.1,CCG002099.1,CCG016370.1,CCG010418.1,CCG005886.1,CCG005370.1,CCG009080.1,CCG010864.1,CCG002852.1,CCG009243.1,CCG019028.1,CCG025396.1,CCG019029.1,CCG007532.1,CCG002696.1,CCG007531.1,CCG018820.3,CCG002137.1,CCG027236.1,CCG010538.1,CCG008748.1,CCG023963.3,CCG006421.1

GO:0044422	organelle part	351 of 3038 in the list	565 of 5465 in the genome	0.1463	CCG011932.1,CCG020245.1,CCG027068.1,CCG018536.1,CCG010159.1,CCG001809.1,CCG011675.1,CCG000585.1,CCG010647.1,CCG000205.1,CCG005370.1,CCG026882.1,CCG020879.1,CCG021053.1,CCG026473.1,CCG001167.1,CCG004091.1,CCG001292.1,CCG017614.1,CCG019217.1,CCG028326.3,CCG028505.1,CCG025223.1,CCG006134.1,CCG005194.1,CCG014836.1,CCG024177.1,CCG012514.1,CCG027196.1,CCG016370.1,CCG015998.1,CCG023053.1,CCG021911.1,CCG010905.1,CCG028046.1,CCG019210.1,CCG011862.1,CCG011764.1,CCG010909.1,CCG002930.1,CCG008808.1,CCG014195.1,CCG028653.1,CCG017580.1,CCG009980.1,CCG008144.1,CCG001863.1,CCG009822.1,CCG013131.1,CCG010649.1,CCG012534.1,CCG007647.1,CCG004331.1,CCG025396.1,CCG006484.1,CCG021633.1,CCG019029.1,CCG008559.1,CCG024119.1,CCG001461.1,CCG027696.1,CCG023686.1,CCG021737.1,CCG014304.1,CCG009543.1,CCG004494.1,CCG003104.1,CCG021228.1,CCG022673.1,CCG026159.1,CCG016399.1,CCG000552.1,CCG004927.1,CCG009805.2,CCG012556.1,CCG002852.1,CCG002966.1,CCG012584.1,CCG021895.1,CCG017141.1,CCG025747.1,CCG027748.1,CCG024788.1,CCG005168.1,CCG018184.1,CCG018315.1,CCG007336.1,CCG003707.1,CCG027692.1,CCG000210.1,CCG010136.1,CCG003310.1,CCG004806.1,CCG004459.2,CCG013617.1,CCG022802.1,CCG010112.1,CCG004084.1,CCG010137.1,CCG022398.1,CCG006421.1,CCG009461.1,CCG023963.3,CCG023184.1,CCG004155.2,CCG022209.1,CCG011550.1,CCG014772.1,CCG015426.1,CCG000148.1,CCG002790.1,CCG000535.1,CCG009394.1,CCG024760.1,CCG024813.1,CCG025549.1,CCG011015.1,CCG027950.1,CCG026989.1,CCG016431.1,CCG024421.3,CCG003009.1,CCG010178.1,CCG000102.1,CCG026688.1,CCG004762.2,CCG0109

GO:0044446	intracellular organelle part	351 of 3038 in the list	565 of 5465 in the genome	0.1463	CCG011932.1,CCG020245.1,CCG027068.1,CCG018536.1,CCG010159.1,CCG001809.1,CCG011675.1,CCG000585.1,CCG010647.1,CCG000205.1,CCG005370.1,CCG026882.1,CCG020879.1,CCG021053.1,CCG026473.1,CCG001167.1,CCG004091.1,CCG001292.1,CCG017614.1,CCG019217.1,CCG028326.3,CCG028505.1,CCG025223.1,CCG006134.1,CCG005194.1,CCG014836.1,CCG024177.1,CCG012514.1,CCG027196.1,CCG016370.1,CCG015998.1,CCG023053.1,CCG021911.1,CCG010905.1,CCG028046.1,CCG019210.1,CCG011862.1,CCG011764.1,CCG010909.1,CCG002930.1,CCG008808.1,CCG014195.1,CCG028653.1,CCG017580.1,CCG009980.1,CCG008144.1,CCG001863.1,CCG009822.1,CCG013131.1,CCG010649.1,CCG012534.1,CCG007647.1,CCG004331.1,CCG025396.1,CCG006484.1,CCG021633.1,CCG019029.1,CCG008559.1,CCG024119.1,CCG001461.1,CCG027696.1,CCG023686.1,CCG021737.1,CCG014304.1,CCG009543.1,CCG004494.1,CCG003104.1,CCG021228.1,CCG022673.1,CCG026159.1,CCG016399.1,CCG000552.1,CCG004927.1,CCG009805.2,CCG012556.1,CCG002852.1,CCG002966.1,CCG012584.1,CCG021895.1,CCG017141.1,CCG025747.1,CCG027748.1,CCG024788.1,CCG005168.1,CCG018184.1,CCG018315.1,CCG007336.1,CCG003707.1,CCG027692.1,CCG000210.1,CCG010136.1,CCG003310.1,CCG004806.1,CCG004459.2,CCG013617.1,CCG022802.1,CCG010112.1,CCG004084.1,CCG010137.1,CCG022398.1,CCG006421.1,CCG009461.1,CCG023963.3,CCG023184.1,CCG004155.2,CCG022209.1,CCG011550.1,CCG014772.1,CCG015426.1,CCG000148.1,CCG002790.1,CCG000535.1,CCG009394.1,CCG024760.1,CCG024813.1,CCG025549.1,CCG011015.1,CCG027950.1,CCG026989.1,CCG016431.1,CCG024421.3,CCG003009.1,CCG010178.1,CCG000102.1,CCG026688.1,CCG004762.2,CCG0109

GO:0043233	organelle lumen	59 of 3038 in the list	81 of 5465 in the genome	0.26772	CCG000158.1,CCG021083.1,CCG004762.2,CCG016237.1,CCG011675.1,CCG026219.1,CCG017156.1,CCG000728.1,CCG020695.1,CCG026882.1,CCG007647.1,CCG006484.1,CCG003055.1,CCG021633.1,CCG023775.1,CCG010112.1,CCG011094.1,CCG019745.1,CCG016772.1,CCG017046.2,CCG014682.1,CCG001461.1,CCG001292.1,CCG011083.1,CCG020460.1,CCG028326.3,CCG028505.1,CCG000806.1,CCG006134.1,CCG023184.1,CCG025107.1,CCG024588.1,CCG007908.3,CCG001726.1,CCG002792.1,CCG016399.1,CCG024666.1,CCG028222.1,CCG015998.1,CCG010175.1,CCG009805.2,CCG025828.1,CCG016656.1,CCG017524.1,CCG023053.1,CCG027950.1,CCG001913.1,CCG002374.1,CCG025856.1,CCG019814.1,CCG001096.1,CCG010318.1,CCG025747.1,CCG014195.1,CCG028653.1,CCG005168.1,CCG018184.1,CCG018315.1,CCG011957.1
GO:0070013	intracellular organelle lumen	59 of 3038 in the list	81 of 5465 in the genome	0.26772	CCG000158.1,CCG021083.1,CCG004762.2,CCG016237.1,CCG011675.1,CCG026219.1,CCG017156.1,CCG000728.1,CCG020695.1,CCG026882.1,CCG007647.1,CCG006484.1,CCG003055.1,CCG021633.1,CCG023775.1,CCG010112.1,CCG011094.1,CCG019745.1,CCG016772.1,CCG017046.2,CCG014682.1,CCG001461.1,CCG001292.1,CCG011083.1,CCG020460.1,CCG028326.3,CCG028505.1,CCG000806.1,CCG006134.1,CCG023184.1,CCG025107.1,CCG024588.1,CCG007908.3,CCG001726.1,CCG002792.1,CCG016399.1,CCG024666.1,CCG028222.1,CCG015998.1,CCG010175.1,CCG009805.2,CCG025828.1,CCG016656.1,CCG017524.1,CCG023053.1,CCG027950.1,CCG001913.1,CCG002374.1,CCG025856.1,CCG019814.1,CCG001096.1,CCG010318.1,CCG025747.1,CCG014195.1,CCG028653.1,CCG005168.1,CCG018184.1,CCG018315.1,CCG011957.1

GO:0031981	nuclear lumen	53 of 3038 in the list	72 of 5465 in the genome	0.32068	CCG000158.1,CCG021083.1,CCG004762.2,CCG016237.1,CCG011675.1,CCG026219.1,CCG017156.1,CCG020695.1,CCG026882.1,CCG007647.1,CCG006484.1,CCG003055.1,CCG021633.1,CCG023775.1,CCG011094.1,CCG019745.1,CCG016772.1,CCG017046.2,CCG014682.1,CCG001461.1,CCG001292.1,CCG011083.1,CCG020460.1,CCG028326.3,CCG000806.1,CCG006134.1,CCG023184.1,CCG024588.1,CCG007908.3,CCG001726.1,CCG002792.1,CCG024666.1,CCG028222.1,CCG015998.1,CCG010175.1,CCG009805.2,CCG025828.1,CCG016656.1,CCG017524.1,CCG027950.1,CCG001913.1,CCG023053.1,CCG025856.1,CCG019814.1,CCG010318.1,CCG001096.1,CCG025747.1,CCG014195.1,CCG028653.1,CCG005168.1,CCG018184.1,CCG018315.1,CCG011957.1
GO:0015630	microtubule cytoskeleton	54 of 3038 in the list	74 of 5465 in the genome	0.40602	CCG015570.1,CCG006420.1,CCG026688.1,CCG015784.1,CCG013000.1,CCG013637.1,CCG026823.1,CCG023488.2,CCG023682.1,CCG012733.1,CCG019140.1,CCG003707.1,CCG010418.1,CCG005370.1,CCG009080.1,CCG009243.1,CCG027167.1,CCG019028.1,CCG025396.1,CCG019029.1,CCG001167.1,CCG002696.1,CCG025520.1,CCG021448.1,CCG027236.1,CCG008748.1,CCG006421.1,CCG023963.3,CCG016119.1,CCG009543.1,CCG015289.1,CCG002099.1,CCG003104.1,CCG005525.1,CCG021228.1,CCG016370.1,CCG019329.1,CCG005886.1,CCG000535.1,CCG022536.3,CCG002852.1,CCG010864.1,CCG021317.1,CCG008377.1,CCG007532.1,CCG007531.1,CCG021895.1,CCG018820.3,CCG002137.1,CCG019092.1,CCG024421.3,CCG010538.1,CCG008346.1,CCG018918.1

GO:0044430	cytoskeletal part	71 of 3038 in the list	101 of 5465 in the genome	0.43948	CCG015570.1,CCG006420.1,CCG013000.1,CCG026823.1,CCG023488.2,CCG003707.1,CCG004786.1,CCG019356.1,CCG005370.1,CCG009243.1,CCG019028.1,CCG004459.2,CCG004084.1,CCG001167.1,CCG002696.1,CCG025520.1,CCG002831.1,CCG027236.1,CCG006421.1,CCG023963.3,CCG012081.1,CCG002099.1,CCG015426.1,CCG016370.1,CCG000535.1,CCG022536.3,CCG010459.3,CCG021911.1,CCG007532.1,CCG008377.1,CCG007531.1,CCG018820.3,CCG010538.1,CCG024421.3,CCG011764.1,CCG008346.1,CCG026688.1,CCG015784.1,CCG013637.1,CCG023682.1,CCG024769.1,CCG012733.1,CCG019140.1,CCG010418.1,CCG024834.3,CCG009080.1,CCG027167.1,CCG025396.1,CCG000603.1,CCG019029.1,CCG021448.1,CCG008748.1,CCG009543.1,CCG016119.1,CCG015289.1,CCG003104.1,CCG021228.1,CCG005525.1,CCG019329.1,CCG005886.1,CCG023696.1,CCG002852.1,CCG010864.1,CCG021317.1,CCG026558.1,CCG021895.1,CCG002137.1,CCG019092.1,CCG008834.1,CCG016660.1,CCG018918.1
GO:0030286	dynein complex	14 of 3038 in the list	15 of 5465 in the genome	0.52826	CCG016119.1,CCG021317.1,CCG001167.1,CCG008377.1,CCG023488.2,CCG021895.1,CCG012733.1,CCG025520.1,CCG005525.1,CCG021228.1,CCG003707.1,CCG019329.1,CCG008346.1,CCG018918.1
GO:0045259	proton-transporting ATP synthase complex	14 of 3038 in the list	15 of 5465 in the genome	0.52826	CCG015410.1,CCG002038.1,CCG025107.1,CCG010112.1,CCG009142.1,CCG023640.1,CCG000148.1,CCG025348.1,CCG007724.1,CCG021934.1,CCG019619.1,CCG005924.2,CCG013643.1,CCG008422.1
GO:0019866	organelle inner membrane	30 of 3038 in the list	38 of 5465 in the genome	0.63517	CCG004155.2,CCG005677.1,CCG011932.1,CCG000102.1,CCG015410.1,CCG007862.1,CCG020245.1,CCG018684.1,CCG025107.1,CCG009142.1,CCG019590.1,CCG000148.1,CCG002790.1,CCG000205.1,CCG011381.1,CCG005924.2,CCG010939.1,CCG022802.1,CCG010112.1,CCG028425.2,CCG024119.1,CCG014053.1,CCG017614.1,CCG016304.1,CCG017125.1,CCG006459.1,CCG026514.1,CCG025163.3,CCG013643.1,CCG017989.1

GO:0030684	preribosome	10 of 3038 in the list	10 of 5465 in the genome	0.76992	CCG023263.1,CCG009214.1,CCG005176.1,CCG002735.1,CCG027579.1,CCG007962.1,CCG018636.1,CCG006357.1,CCG018474.1,CCG022629.1
GO:0031967	organelle envelope	62 of 3038 in the list	88 of 5465 in the genome	0.78362	CCG011932.1,CCG000102.1,CCG020245.1,CCG010159.1,CCG008144.1,CCG009822.1,CCG001809.1,CCG019590.1,CCG000205.1,CCG020949.1,CCG011381.1,CCG013066.1,CCG022771.1,CCG009136.1,CCG020879.1,CCG022802.1,CCG010112.1,CCG028425.2,CCG024119.1,CCG023814.2,CCG006243.1,CCG004897.1,CCG017614.1,CCG026240.1,CCG013013.1,CCG016304.1,CCG006459.1,CCG023186.1,CCG004605.1,CCG013643.1,CCG010440.1,CCG004155.2,CCG005677.1,CCG007246.2,CCG015410.1,CCG007862.1,CCG018684.1,CCG011550.1,CCG025107.1,CCG009142.1,CCG018128.1,CCG000493.1,CCG001279.1,CCG000148.1,CCG002790.1,CCG005924.2,CCG012556.1,CCG019712.1,CCG010939.1,CCG020053.1,CCG014053.1,CCG026989.1,CCG008116.1,CCG017125.1,CCG017141.1,CCG016431.1,CCG000089.1,CCG026514.1,CCG017874.1,CCG003009.1,CCG025163.3,CCG017989.1
GO:0005743	mitochondrial inner membrane	28 of 3038 in the list	36 of 5465 in the genome	1	CCG004155.2,CCG005677.1,CCG011932.1,CCG000102.1,CCG015410.1,CCG007862.1,CCG020245.1,CCG018684.1,CCG025107.1,CCG009142.1,CCG019590.1,CCG000148.1,CCG002790.1,CCG000205.1,CCG011381.1,CCG005924.2,CCG010939.1,CCG022802.1,CCG010112.1,CCG024119.1,CCG014053.1,CCG017614.1,CCG016304.1,CCG017125.1,CCG006459.1,CCG026514.1,CCG025163.3,CCG013643.1
GO:0005667	transcription factor complex	23 of 3038 in the list	29 of 5465 in the genome	1	CCG027258.1,CCG000158.1,CCG017793.1,CCG011228.1,CCG022741.1,CCG001698.1,CCG012536.1,CCG016307.1,CCG027796.1,CCG009805.2,CCG010175.1,CCG019250.1,CCG018533.1,CCG025549.1,CCG027950.1,CCG011229.1,CCG001292.1,CCG005480.2,CCG011083.1,CCG022398.1,CCG020460.1,CCG018184.1,CCG023184.1
GO:0005730	nucleolus	8 of 3038 in the list	8 of 5465 in the genome	1	CCG001726.1,CCG002792.1,CCG003055.1,CCG023053.1,CCG007908.3,CCG028653.1,CCG015998.1,CCG011957.1

GO:0032040	small-subunit processome	8 of 3038 in the list	8 of 5465 in the genome	1	CCG009214.1,CCG005176.1,CCG002735.1,CCG027579.1,CCG007962.1,CCG018636.1,CCG006357.1,CCG022629.1
GO:0000152	nuclear ubiquitin ligase complex	7 of 3038 in the list	7 of 5465 in the genome	1	CCG004331.1,CCG002269.1,CCG027068.1,CCG007403.1,CCG008808.1,CCG028046.1,CCG018116.1
GO:0005680	anaphase-promoting complex	7 of 3038 in the list	7 of 5465 in the genome	1	CCG004331.1,CCG002269.1,CCG027068.1,CCG007403.1,CCG008808.1,CCG028046.1,CCG018116.1
GO:0005753	mitochondrial proton-transporting ATP	7 of 3038 in the list	7 of 5465 in the genome	1	CCG015410.1,CCG000148.1,CCG025107.1,CCG010112.1,CCG009142.1,CCG013643.1,CCG005924.2
GO:0031974	membrane-enclosed lumen	60 of 3038 in the list	90 of 5465 in the genome	1	CCG000158.1,CCG021083.1,CCG004762.2,CCG016237.1,CCG011675.1,CCG026219.1,CCG017156.1,CCG020949.1,CCG000728.1,CCG020695.1,CCG026882.1,CCG007647.1,CCG006484.1,CCG003055.1,CCG021633.1,CCG023775.1,CCG010112.1,CCG011094.1,CCG019745.1,CCG016772.1,CCG017046.2,CCG014682.1,CCG001461.1,CCG001292.1,CCG011083.1,CCG020460.1,CCG028326.3,CCG028505.1,CCG000806.1,CCG006134.1,CCG023184.1,CCG025107.1,CCG024588.1,CCG007908.3,CCG001726.1,CCG002792.1,CCG016399.1,CCG024666.1,CCG028222.1,CCG015998.1,CCG010175.1,CCG009805.2,CCG025828.1,CCG016656.1,CCG017524.1,CCG023053.1,CCG027950.1,CCG001913.1,CCG002374.1,CCG025856.1,CCG019814.1,CCG001096.1,CCG010318.1,CCG025747.1,CCG014195.1,CCG028653.1,CCG005168.1,CCG018184.1,CCG018315.1,CCG011957.1
GO:0005654	nucleoplasm	38 of 3038 in the list	55 of 5465 in the genome	1	CCG000158.1,CCG021083.1,CCG004762.2,CCG026219.1,CCG017156.1,CCG020695.1,CCG026882.1,CCG007647.1,CCG006484.1,CCG021633.1,CCG023775.1,CCG011094.1,CCG019745.1,CCG016772.1,CCG017046.2,CCG014682.1,CCG001292.1,CCG011083.1,CCG020460.1,CCG028326.3,CCG006134.1,CCG023184.1,CCG024666.1,CCG010175.1,CCG009805.2,CCG016656.1,CCG025828.1,CCG017524.1,CCG027950.1,CCG025856.1,CCG019814.1,CCG010318.1,CCG001096.1,CCG025747.1,CCG014195.1,CCG018184.1,CCG005168.1,CCG018315.1

GO:0044451	nucleoplasm part	38 of 3038 in the list	55 of 5465 in the genome	1	CCG000158.1,CCG021083.1,CCG004762.2,CCG026219.1,CCG017156.1,CCG020695.1,CCG026882.1,CCG007647.1,CCG006484.1,CCG021633.1,CCG023775.1,CCG011094.1,CCG019745.1,CCG016772.1,CCG017046.2,CCG014682.1,CCG001292.1,CCG011083.1,CCG020460.1,CCG028326.3,CCG006134.1,CCG023184.1,CCG024666.1,CCG010175.1,CCG009805.2,CCG016656.1,CCG025828.1,CCG017524.1,CCG027950.1,CCG025856.1,CCG019814.1,CCG010318.1,CCG001096.1,CCG025747.1,CCG014195.1,CCG018184.1,CCG005168.1,CCG018315.1
GO:0045263	proton-transporting ATP synthase	6 of 3038 in the list	6 of 5465 in the genome	1	CCG000148.1,CCG025107.1,CCG010112.1,CCG009142.1,CCG013643.1,CCG008422.1
GO:0045261	proton-transporting ATP synthase	8 of 3038 in the list	9 of 5465 in the genome	1	CCG015410.1,CCG002038.1,CCG023640.1,CCG007724.1,CCG025348.1,CCG019619.1,CCG021934.1,CCG005924.2
GO:0044455	mitochondrial membrane part	16 of 3038 in the list	21 of 5465 in the genome	1	CCG011932.1,CCG015410.1,CCG007862.1,CCG025107.1,CCG009142.1,CCG019590.1,CCG000148.1,CCG011381.1,CCG005924.2,CCG010939.1,CCG010112.1,CCG017614.1,CCG017125.1,CCG016304.1,CCG026514.1,CCG013643.1
GO:0000276	mitochondrial proton-transporting ATP	5 of 3038 in the list	5 of 5465 in the genome	1	CCG000148.1,CCG025107.1,CCG010112.1,CCG009142.1,CCG013643.1

GO:1902494	catalytic complex	76 of 3038 in the list	121 of 5465 in the genome	1	CCG022047.1,CCG000789.1,CCG003060.1,CCG000158.1,CCG027068.1,CCG023488.2,CCG003707.1,CCG024695.1,CCG019599.1,CCG018116.1,CCG019745.1,CCG004091.1,CCG001167.1,CCG006505.1,CCG001292.1,CCG025520.1,CCG009685.1,CCG022453.1,CCG028505.1,CCG027539.1,CCG024232.1,CCG007485.1,CCG023184.1,CCG001101.1,CCG028615.1,CCG003362.1,CCG027316.1,CCG020230.3,CCG011658.1,CCG027950.1,CCG008377.1,CCG028046.1,CCG015929.1,CCG012959.1,CCG025277.1,CCG019558.1,CCG008808.1,CCG014195.1,CCG004134.1,CCG008346.1,CCG026212.1,CCG003215.3,CCG021083.1,CCG019394.1,CCG012733.1,CCG004212.1,CCG019571.1,CCG026146.1,CCG011382.1,CCG016189.1,CCG004331.1,CCG006484.1,CCG023775.1,CCG017046.2,CCG011083.1,CCG002269.1,CCG020460.1,CCG016119.1,CCG005525.1,CCG021228.1,CCG019329.1,CCG022214.1,CCG010175.1,CCG009805.2,CCG006884.1,CCG016656.1,CCG021317.1,CCG008557.1,CCG007403.1,CCG014228.2,CCG018688.1,CCG021895.1,CCG003192.1,CCG025747.1,CCG018184.1,CCG018918.1
GO:0000808	origin recognition complex	7 of 3038 in the list	8 of 5465 in the genome	1	CCG004012.2,CCG002942.1,CCG020652.1,CCG016237.1,CCG028222.1,CCG016576.1,CCG007336.1
GO:0005732	small nucleolar	4 of 3038 in the list	4 of 5465 in the genome	1	CCG002792.1,CCG023511.1,CCG007636.1,CCG028653.1
GO:0000428	DNA-directed RNA polymerase complex	13 of 3038 in the list	18 of 5465 in the genome	1	CCG000158.1,CCG006484.1,CCG021083.1,CCG027950.1,CCG023775.1,CCG017046.2,CCG001292.1,CCG011083.1,CCG020460.1,CCG009805.2,CCG010175.1,CCG018184.1,CCG023184.1
GO:0030880	RNA polymerase complex	13 of 3038 in the list	18 of 5465 in the genome	1	CCG000158.1,CCG006484.1,CCG021083.1,CCG027950.1,CCG023775.1,CCG017046.2,CCG001292.1,CCG011083.1,CCG020460.1,CCG009805.2,CCG010175.1,CCG018184.1,CCG023184.1
GO:0055029	nuclear DNA-directed RNA polymerase complex	13 of 3038 in the list	18 of 5465 in the genome	1	CCG000158.1,CCG006484.1,CCG021083.1,CCG027950.1,CCG023775.1,CCG017046.2,CCG001292.1,CCG011083.1,CCG020460.1,CCG009805.2,CCG010175.1,CCG018184.1,CCG023184.1

GO:0000922	spindle pole	9 of 3038 in the list	12 of 5465 in the genome	1	CCG027167.1,CCG015570.1,CCG026688.1,CCG021448.1,CCG019140.1,CCG019092.1,CCG024421.3,CCG000535.1,CCG022536.3
GO:0005815	microtubule organizing center	9 of 3038 in the list	12 of 5465 in the genome	1	CCG027167.1,CCG015570.1,CCG026688.1,CCG021448.1,CCG019140.1,CCG019092.1,CCG024421.3,CCG000535.1,CCG022536.3
GO:0005819	spindle	9 of 3038 in the list	12 of 5465 in the genome	1	CCG027167.1,CCG015570.1,CCG026688.1,CCG021448.1,CCG019140.1,CCG019092.1,CCG024421.3,CCG000535.1,CCG022536.3
GO:0044445	cytosolic part	9 of 3038 in the list	12 of 5465 in the genome	1	CCG000789.1,CCG003215.3,CCG012959.1,CCG022214.1,CCG022453.1,CCG027316.1,CCG025277.1,CCG011658.1,CCG019558.1
GO:0031966	mitochondrial membrane	32 of 3038 in the list	50 of 5465 in the genome	1	CCG011932.1,CCG000102.1,CCG020245.1,CCG019590.1,CCG000205.1,CCG011381.1,CCG022802.1,CCG010112.1,CCG024119.1,CCG023814.2,CCG017614.1,CCG026240.1,CCG013013.1,CCG016304.1,CCG006459.1,CCG013643.1,CCG005677.1,CCG004155.2,CCG007862.1,CCG015410.1,CCG025107.1,CCG018684.1,CCG009142.1,CCG001279.1,CCG002790.1,CCG000148.1,CCG005924.2,CCG010939.1,CCG014053.1,CCG017125.1,CCG026514.1,CCG025163.3
GO:0031461	cullin-RING ubiquitin ligase complex	12 of 3038 in the list	17 of 5465 in the genome	1	CCG004331.1,CCG027068.1,CCG001101.1,CCG007403.1,CCG019394.1,CCG028046.1,CCG002269.1,CCG019571.1,CCG019599.1,CCG008808.1,CCG004134.1,CCG018116.1
GO:0016459	myosin complex	15 of 3038 in the list	22 of 5465 in the genome	1	CCG004459.2,CCG021911.1,CCG000603.1,CCG012081.1,CCG004084.1,CCG026558.1,CCG024769.1,CCG015426.1,CCG002831.1,CCG011764.1,CCG004786.1,CCG024834.3,CCG010459.3,CCG016660.1,CCG023696.1
GO:0005581	collagen	3 of 3038 in the list	3 of 5465 in the genome	1	CCG020089.1,CCG004326.1,CCG004982.1
GO:0008537	proteasome activator	3 of 3038 in the list	3 of 5465 in the genome	1	CCG026177.1,CCG010543.1,CCG027736.1
GO:0022624	proteasome accessory	3 of 3038 in the list	3 of 5465 in the genome	1	CCG026177.1,CCG010543.1,CCG027736.1
GO:0043189	H4/H2A histone	3 of 3038 in the list	3 of 5465 in the genome	1	CCG025747.1,CCG019745.1,CCG014195.1
GO:1902562	H4 histone	3 of 3038 in the list	3 of 5465 in the genome	1	CCG025747.1,CCG019745.1,CCG014195.1
GO:0005681	spliceosomal complex	8 of 3038 in the list	11 of 5465 in the genome	1	CCG000754.1,CCG028285.1,CCG004008.1,CCG023686.1,CCG024810.1,CCG004927.1,CCG013802.1,CCG008858.1

GO:0044429	mitochondrial part	44 of 3038 in the list	72 of 5465 in the genome	1	CCG011932.1,CCG000102.1,CCG020245.1,CCG010159.1,CCG019590.1,CCG000205.1,CCG020949.1,CCG000728.1,CCG011381.1,CCG020879.1,CCG022802.1,CCG010112.1,CCG024119.1,CCG023814.2,CCG017614.1,CCG026240.1,CCG016304.1,CCG013013.1,CCG006459.1,CCG028505.1,CCG004605.1,CCG013643.1,CCG005677.1,CCG004155.2,CCG007246.2,CCG015410.1,CCG007862.1,CCG018684.1,CCG025107.1,CCG009142.1,CCG018128.1,CCG001279.1,CCG000148.1,CCG002790.1,CCG016399.1,CCG005924.2,CCG019712.1,CCG010939.1,CCG014053.1,CCG017125.1,CCG016431.1,CCG000089.1,CCG026514.1,CCG025163.3
GO:0016592	mediator complex	20 of 3038 in the list	31 of 5465 in the genome	1	CCG004762.2,CCG026219.1,CCG017156.1,CCG024666.1,CCG020695.1,CCG007647.1,CCG025828.1,CCG017524.1,CCG021633.1,CCG016772.1,CCG011094.1,CCG025856.1,CCG014682.1,CCG019814.1,CCG010318.1,CCG001096.1,CCG028326.3,CCG006134.1,CCG005168.1,CCG018315.1
GO:0016591	DNA-directed RNA polymerase II, holoenzyme	11 of 3038 in the list	16 of 5465 in the genome	1	CCG000158.1,CCG021083.1,CCG027950.1,CCG023775.1,CCG001292.1,CCG011083.1,CCG020460.1,CCG009805.2,CCG018184.1,CCG010175.1,CCG023184.1
GO:0044798	nuclear transcription factor complex	11 of 3038 in the list	16 of 5465 in the genome	1	CCG000158.1,CCG025549.1,CCG027950.1,CCG001292.1,CCG011083.1,CCG022398.1,CCG020460.1,CCG018184.1,CCG010175.1,CCG009805.2,CCG023184.1
GO:0005740	mitochondrial envelope	41 of 3038 in the list	67 of 5465 in the genome	1	CCG011932.1,CCG000102.1,CCG020245.1,CCG010159.1,CCG019590.1,CCG000205.1,CCG020949.1,CCG011381.1,CCG020879.1,CCG022802.1,CCG010112.1,CCG024119.1,CCG023814.2,CCG017614.1,CCG026240.1,CCG016304.1,CCG013013.1,CCG006459.1,CCG004605.1,CCG013643.1,CCG005677.1,CCG004155.2,CCG007246.2,CCG015410.1,CCG007862.1,CCG018684.1,CCG025107.1,CCG009142.1,CCG018128.1,CCG001279.1,CCG002790.1,CCG000148.1,CCG005924.2,CCG019712.1,CCG010939.1,CCG014053.1,CCG017125.1,CCG016431.1,CCG000089.1,CCG026514.1,CCG025163.3

GO:1990234	transferase complex	28 of 3038 in the list	45 of 5465 in the genome	1	CCG000789.1,CCG000158.1,CCG003215.3,CCG021083.1,CCG027316.1,CCG022214.1,CCG024695.1,CCG011658.1,CCG009805.2,CCG010175.1,CCG016656.1,CCG006484.1,CCG027950.1,CCG023775.1,CCG019745.1,CCG017046.2,CCG004091.1,CCG001292.1,CCG012959.1,CCG011083.1,CCG003192.1,CCG025747.1,CCG020460.1,CCG019558.1,CCG014195.1,CCG028505.1,CCG018184.1,CCG023184.1
GO:0031975	envelope	65 of 3038 in the list	110 of 5465 in the genome	1	CCG011932.1,CCG020245.1,CCG001584.1,CCG010159.1,CCG001809.1,CCG019590.1,CCG000205.1,CCG020949.1,CCG020879.1,CCG022802.1,CCG010112.1,CCG006243.1,CCG004897.1,CCG017614.1,CCG016304.1,CCG023186.1,CCG004605.1,CCG013643.1,CCG004155.2,CCG007246.2,CCG018684.1,CCG011550.1,CCG018128.1,CCG001279.1,CCG000148.1,CCG002790.1,CCG005924.2,CCG010939.1,CCG026989.1,CCG016431.1,CCG026514.1,CCG003009.1,CCG017989.1,CCG000102.1,CCG008144.1,CCG009822.1,CCG004844.1,CCG011381.1,CCG013066.1,CCG009136.1,CCG022771.1,CCG028425.2,CCG024119.1,CCG021686.1,CCG023814.2,CCG013013.1,CCG026240.1,CCG006459.1,CCG005677.1,CCG010440.1,CCG007862.1,CCG015410.1,CCG025107.1,CCG009142.1,CCG000493.1,CCG012556.1,CCG019712.1,CCG020053.1,CCG014053.1,CCG008116.1,CCG017125.1,CCG017141.1,CCG000089.1,CCG017874.1,CCG025163.3

GO:0005694	chromosome	90 of 3038 in the list	154 of 5465 in the genome	1	CCG016201.1,CCG004973.1,CCG016237.1,CCG007336.1,CCG011675.1,CCG019284.1,CCG008560.1,CCG010136.1,CCG021491.1,CCG010647.1,CCG003310.1,CCG022918.1,CCG013617.1,CCG026473.1,CCG012476.1,CCG014537.1,CCG010137.1,CCG005194.1,CCG009461.1,CCG024623.1,CCG025880.1,CCG014836.1,CCG010904.1,CCG024177.1,CCG004481.1,CCG012514.1,CCG024588.1,CCG027196.1,CCG014772.1,CCG004012.2,CCG026474.1,CCG027183.2,CCG000166.1,CCG011184.1,CCG025893.1,CCG018249.1,CCG020652.1,CCG015167.1,CCG010905.1,CCG022456.1,CCG010909.1,CCG010648.1,CCG011615.1,CCG018583.1,CCG017580.1,CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1,CCG010138.1,CCG010649.1,CCG008892.2,CCG025877.1,CCG020987.1,CCG027199.1,CCG027198.1,CCG003438.1,CCG012083.1,CCG008559.1,CCG018287.1,CCG027696.1,CCG010907.1,CCG007767.1,CCG012229.1,CCG010650.1,CCG024624.1,CCG002942.1,CCG009275.1,CCG004494.1,CCG002947.1,CCG010908.1,CCG015312.2,CCG005716.1,CCG027197.1,CCG022673.1,CCG026159.1,CCG027697.1,CCG020442.1,CCG010646.1,CCG028222.1,CCG017598.1,CCG001810.1,CCG024787.1,CCG027695.1,CCG008972.1,CCG001913.1,CCG012584.1,CCG016576.1,CCG008302.1,CCG024788.1
GO:0000123	histone	4 of 3038 in the list	5 of 5465 in the genome	1	CCG016656.1,CCG025747.1,CCG019745.1,CCG014195.1
GO:0005779	integral component of peroxisomal membrane	4 of 3038 in the list	5 of 5465 in the genome	1	CCG019797.1,CCG006223.1,CCG019217.1,CCG010178.1
GO:0005834	heterotrimeric G-	4 of 3038 in the list	5 of 5465 in the genome	1	CCG009446.1,CCG006412.1,CCG012573.1,CCG024952.1
GO:0019897	extrinsic component of	4 of 3038 in the list	5 of 5465 in the genome	1	CCG009446.1,CCG006412.1,CCG012573.1,CCG024952.1
GO:0031231	intrinsic component of peroxisomal membrane	4 of 3038 in the list	5 of 5465 in the genome	1	CCG019797.1,CCG006223.1,CCG019217.1,CCG010178.1
GO:0031234	extrinsic component of cytoplasmic side of	4 of 3038 in the list	5 of 5465 in the genome	1	CCG009446.1,CCG006412.1,CCG012573.1,CCG024952.1
GO:0031248	protein	4 of 3038 in the list	5 of 5465 in the genome	1	CCG016656.1,CCG025747.1,CCG019745.1,CCG014195.1
GO:0031984	organelle	4 of 3038 in the list	5 of 5465 in the genome	1	CCG011023.1,CCG014304.1,CCG019892.1,CCG021819.1
GO:0031985	Golgi cisterna	4 of 3038 in the list	5 of 5465 in the genome	1	CCG011023.1,CCG014304.1,CCG019892.1,CCG021819.1

GO:0032580	Golgi cisterna	4 of 3038 in the list	5 of 5465 in the genome	1	CCG011023.1,CCG014304.1,CCG019892.1,CCG021819.1
GO:1902493	acetyltransferase	4 of 3038 in the list	5 of 5465 in the genome	1	CCG016656.1,CCG025747.1,CCG019745.1,CCG014195.1
GO:0005578	proteinaceous extracellular matrix	10 of 3038 in the list	15 of 5465 in the genome	1	CCG003882.1,CCG020089.1,CCG004326.1,CCG026583.1,CCG015389.1,CCG008431.1,CCG004982.1,CCG025670.1,CCG013615.1,CCG006702.1
GO:0045211	postsynaptic membrane	7 of 3038 in the list	10 of 5465 in the genome	1	CCG014158.1,CCG011730.1,CCG018801.1,CCG002839.1,CCG022137.1,CCG027498.1,CCG006803.1
GO:0097060	synaptic membrane	7 of 3038 in the list	10 of 5465 in the genome	1	CCG014158.1,CCG011730.1,CCG018801.1,CCG002839.1,CCG022137.1,CCG027498.1,CCG006803.1
GO:0000172	ribonuclease MRP	2 of 3038 in the list	2 of 5465 in the genome	1	CCG023511.1,CCG007636.1
GO:0000176	nuclear exosome	2 of 3038 in the list	2 of 5465 in the genome	1	CCG000806.1,CCG001461.1
GO:0000178	exosome (RNase	2 of 3038 in the list	2 of 5465 in the genome	1	CCG000806.1,CCG001461.1
GO:0000275	mitochondrial proton-transporting ATP	2 of 3038 in the list	2 of 5465 in the genome	1	CCG015410.1,CCG005924.2
GO:0000439	core TFIIH complex	2 of 3038 in the list	2 of 5465 in the genome	1	CCG011015.1,CCG007693.1
GO:0000441	SSL2-core TFIIH	2 of 3038 in the list	2 of 5465 in the genome	1	CCG011015.1,CCG007693.1
GO:0001726	ruffle	2 of 3038 in the list	2 of 5465 in the genome	1	CCG014318.1,CCG003587.1
GO:0005605	basal lamina	2 of 3038 in the list	2 of 5465 in the genome	1	CCG015389.1,CCG008431.1
GO:0005606	laminin-1 complex	2 of 3038 in the list	2 of 5465 in the genome	1	CCG015389.1,CCG008431.1
GO:0005637	nuclear inner	2 of 3038 in the list	2 of 5465 in the genome	1	CCG028425.2,CCG017989.1
GO:0005639	integral component of nuclear inner	2 of 3038 in the list	2 of 5465 in the genome	1	CCG028425.2,CCG017989.1
GO:0005657	replication fork	2 of 3038 in the list	2 of 5465 in the genome	1	CCG018583.1,CCG015312.2
GO:0005663	DNA replication factor	2 of 3038 in the list	2 of 5465 in the genome	1	CCG018583.1,CCG015312.2
GO:0005665	DNA-directed RNA polymerase II, core	2 of 3038 in the list	2 of 5465 in the genome	1	CCG021083.1,CCG023775.1
GO:0005666	DNA-directed RNA	2 of 3038 in the list	2 of 5465 in the genome	1	CCG006484.1,CCG017046.2
GO:0005674	transcription factor	2 of 3038 in the list	2 of 5465 in the genome	1	CCG011083.1,CCG023184.1
GO:0005751	mitochondrial	2 of 3038 in the list	2 of 5465 in the genome	1	CCG011932.1,CCG007862.1
GO:0005786	signal recognition particle, endoplasmic	2 of 3038 in the list	2 of 5465 in the genome	1	CCG018217.1,CCG020806.1
GO:0005852	eukaryotic translation initiation factor 3	2 of 3038 in the list	2 of 5465 in the genome	1	CCG008592.1,CCG000294.1
GO:0005891	voltage-gated calcium	2 of 3038 in the list	2 of 5465 in the genome	1	CCG025568.1,CCG005277.1
GO:0005945	6-phosphofructokinase	2 of 3038 in the list	2 of 5465 in the genome	1	CCG022214.1,CCG003215.3

GO:0009331	glycerol-3-phosphate dehydrogenase	2 of 3038 in the list	2 of 5465 in the genome	1	CCG009685.1,CCG014228.2
GO:0016010	dystrophin-associated glycoprotein complex	2 of 3038 in the list	2 of 5465 in the genome	1	CCG027899.1,CCG022540.1
GO:0016011	dystroglycan complex	2 of 3038 in the list	2 of 5465 in the genome	1	CCG027899.1,CCG022540.1
GO:0016012	sarcoglycan complex	2 of 3038 in the list	2 of 5465 in the genome	1	CCG027899.1,CCG022540.1
GO:0016602	CCAAT-binding factor	2 of 3038 in the list	2 of 5465 in the genome	1	CCG022398.1,CCG025549.1
GO:0030677	ribonuclease P	2 of 3038 in the list	2 of 5465 in the genome	1	CCG023511.1,CCG007636.1
GO:0030688	preribosome, small	2 of 3038 in the list	2 of 5465 in the genome	1	CCG023263.1,CCG018474.1
GO:0031229	intrinsic component of nuclear inner	2 of 3038 in the list	2 of 5465 in the genome	1	CCG028425.2,CCG017989.1
GO:0031252	cell leading edge	2 of 3038 in the list	2 of 5465 in the genome	1	CCG014318.1,CCG003587.1
GO:0031429	box H/ACA snoRNP	2 of 3038 in the list	2 of 5465 in the genome	1	CCG002792.1,CCG028653.1
GO:0031965	nuclear membrane	2 of 3038 in the list	2 of 5465 in the genome	1	CCG028425.2,CCG017989.1
GO:0032777	Piccolo NuA4 histone acetyltransferase	2 of 3038 in the list	2 of 5465 in the genome	1	CCG019745.1,CCG014195.1
GO:0032806	carboxy-terminal domain protein kinase	2 of 3038 in the list	2 of 5465 in the genome	1	CCG011015.1,CCG007693.1
GO:0034704	calcium channel	2 of 3038 in the list	2 of 5465 in the genome	1	CCG025568.1,CCG005277.1
GO:0035267	NuA4 histone	2 of 3038 in the list	2 of 5465 in the genome	1	CCG019745.1,CCG014195.1
GO:0042995	cell projection	2 of 3038 in the list	2 of 5465 in the genome	1	CCG014318.1,CCG003587.1
GO:0043256	laminin complex	2 of 3038 in the list	2 of 5465 in the genome	1	CCG015389.1,CCG008431.1
GO:0043626	PCNA complex	2 of 3038 in the list	2 of 5465 in the genome	1	CCG026259.1,CCG011911.1
GO:0044452	nucleolar part	2 of 3038 in the list	2 of 5465 in the genome	1	CCG002792.1,CCG028653.1
GO:0044453	nuclear membrane part	2 of 3038 in the list	2 of 5465 in the genome	1	CCG028425.2,CCG017989.1
GO:0044796	DNA polymerase processivity factor	2 of 3038 in the list	2 of 5465 in the genome	1	CCG026259.1,CCG011911.1
GO:0045277	respiratory chain	2 of 3038 in the list	2 of 5465 in the genome	1	CCG011932.1,CCG007862.1
GO:0072588	box H/ACA RNP	2 of 3038 in the list	2 of 5465 in the genome	1	CCG002792.1,CCG028653.1
GO:0000228	nuclear chromosome	5 of 3038 in the list	7 of 5465 in the genome	1	CCG011675.1,CCG001913.1,CCG024588.1,CCG016237.1,CCG028222.1
GO:0005746	mitochondrial respiratory chain	5 of 3038 in the list	7 of 5465 in the genome	1	CCG017614.1,CCG011932.1,CCG016304.1,CCG007862.1,CCG011381.1
GO:0005759	mitochondrial matrix	5 of 3038 in the list	7 of 5465 in the genome	1	CCG025107.1,CCG010112.1,CCG016399.1,CCG028505.1,CCG000728.1

GO:0005942	phosphatidylinositol 3-kinase complex	5 of 3038 in the list	7 of 5465 in the genome	1	CCG000789.1,CCG027316.1,CCG019558.1,CCG011658.1,CCG012959.1
GO:0044420	extracellular matrix part	5 of 3038 in the list	7 of 5465 in the genome	1	CCG020089.1,CCG004326.1,CCG015389.1,CCG008431.1,CCG004982.1
GO:0070469	respiratory chain	5 of 3038 in the list	7 of 5465 in the genome	1	CCG017614.1,CCG011932.1,CCG016304.1,CCG007862.1,CCG011381.1
GO:0005829	cytosol	9 of 3038 in the list	14 of 5465 in the genome	1	CCG000789.1,CCG003215.3,CCG012959.1,CCG022214.1,CCG022453.1,CCG027316.1,CCG025277.1,CCG011658.1,CCG019558.1
GO:0005739	mitochondrion	60 of 3038 in the list	104 of 5465 in the genome	1	CCG011932.1,CCG013032.1,CCG000102.1,CCG020245.1,CCG028409.1,CCG010159.1,CCG019590.1,CCG002890.1,CCG000205.1,CCG020949.1,CCG008871.1,CCG000728.1,CCG011381.1,CCG027472.1,CCG020879.1,CCG022802.1,CCG010112.1,CCG024119.1,CCG022464.1,CCG023814.2,CCG017614.1,CCG026240.1,CCG016304.1,CCG013013.1,CCG006459.1,CCG028505.1,CCG004605.1,CCG012569.1,CCG013643.1,CCG006077.1,CCG004155.2,CCG005677.1,CCG007246.2,CCG015410.1,CCG007862.1,CCG018684.1,CCG025107.1,CCG009142.1,CCG002823.1,CCG018128.1,CCG011510.1,CCG000890.1,CCG001279.1,CCG000148.1,CCG002790.1,CCG019867.2,CCG016399.1,CCG005924.2,CCG019712.1,CCG010939.1,CCG004901.1,CCG016699.1,CCG014171.1,CCG020281.1,CCG014053.1,CCG017125.1,CCG016431.1,CCG000089.1,CCG026514.1,CCG025163.3
GO:0030054	cell junction	6 of 3038 in the list	9 of 5465 in the genome	1	CCG014318.1,CCG002453.1,CCG016125.1,CCG028356.1,CCG003587.1,CCG002276.1
GO:0000323	lytic vacuole	3 of 3038 in the list	4 of 5465 in the genome	1	CCG017994.1,CCG019082.1,CCG013509.1
GO:0005744	mitochondrial inner membrane	3 of 3038 in the list	4 of 5465 in the genome	1	CCG019590.1,CCG017125.1,CCG010939.1
GO:0005764	lysosome	3 of 3038 in the list	4 of 5465 in the genome	1	CCG017994.1,CCG019082.1,CCG013509.1

GO:0043234	protein complex	347 of 3038 in the list	620 of 5465 in the genome	1	CCG011932.1,CCG027068.1,CCG026177.1,CCG001809.1,CCG024695.1,CCG000585.1,CCG010647.1,CCG005370.1,CCG026882.1,CCG026473.1,CCG001167.1,CCG004091.1,CCG001292.1,CCG028326.3,CCG028505.1,CCG006134.1,CCG005194.1,CCG014836.1,CCG024177.1,CCG012573.1,CCG008431.1,CCG012514.1,CCG003362.1,CCG027196.1,CCG016370.1,CCG026413.3,CCG012536.1,CCG027796.1,CCG018533.1,CCG025450.1,CCG000526.1,CCG021911.1,CCG010905.1,CCG028046.1,CCG011862.1,CCG027899.1,CCG011764.1,CCG010909.1,CCG008808.1,CCG014195.1,CCG011911.1,CCG026212.1,CCG017580.1,CCG024952.1,CCG009980.1,CCG016493.2,CCG009822.1,CCG004279.1,CCG010649.1,CCG004212.1,CCG019571.1,CCG012534.1,CCG007647.1,CCG016189.1,CCG004331.1,CCG025396.1,CCG006484.1,CCG021633.1,CCG019029.1,CCG008559.1,CCG001461.1,CCG027696.1,CCG005480.2,CCG024432.2,CCG019678.1,CCG009543.1,CCG004494.1,CCG001698.1,CCG003104.1,CCG021228.1,CCG022214.1,CCG006412.1,CCG022673.1,CCG019647.1,CCG026159.1,CCG016307.1,CCG009805.2,CCG012556.1,CCG002852.1,CCG020634.1,CCG019250.1,CCG008557.1,CCG012584.1,CCG018688.1,CCG014228.2,CCG021895.1,CCG017141.1,CCG025747.1,CCG002937.1,CCG024788.1,CCG000294.1,CCG005168.1,CCG018184.1,CCG018315.1,CCG001285.1,CCG003060.1,CCG000789.1,CCG007336.1,CCG003707.1,CCG027692.1,CCG010136.1,CCG003310.1,CCG019599.1,CCG008422.1,CCG004459.2,CCG013617.1,CCG010112.1,CCG004084.1,CCG010137.1,CCG015568.1,CCG022398.1,CCG024232.1,CCG007485.1,CCG027736.1,CCG006421.1,CCG009461.1,CCG023963.3,CCG023184.1,CCG014772.1,CCG015426.1,CCG027316.1,CCG000148.1,CCG000535.1,CCG027257.1,CCG022540.1,CCG025549.1,CCG0110
GO:0005911	cell-cell junction	4 of 3038 in the list	6 of 5465 in the genome	1	CCG002453.1,CCG016125.1,CCG028356.1,CCG002276.1
GO:0005921	gap junction	4 of 3038 in the list	6 of 5465 in the genome	1	CCG002453.1,CCG016125.1,CCG028356.1,CCG002276.1
GO:0019013	viral nucleocapsid	4 of 3038 in the list	6 of 5465 in the genome	1	CCG025780.1,CCG000477.1,CCG000478.1,CCG025779.1
GO:0008287	protein serine/threonine phosphatase complex	9 of 3038 in the list	15 of 5465 in the genome	1	CCG006884.1,CCG003362.1,CCG028615.1,CCG018688.1,CCG004212.1,CCG007485.1,CCG011382.1,CCG027539.1,CCG026212.1

GO:0044427	chromosomal part	73 of 3038 in the list	130 of 5465 in the genome	1	CCG016237.1,CCG007336.1,CCG019284.1,CCG008560.1,CCG010136.1,CCG021491.1,CCG010647.1,CCG003310.1,CCG013617.1,CCG026473.1,CCG012476.1,CCG014537.1,CCG010137.1,CCG005194.1,CCG009461.1,CCG024623.1,CCG025880.1,CCG014836.1,CCG010904.1,CCG024177.1,CCG004481.1,CCG012514.1,CCG027196.1,CCG014772.1,CCG004012.2,CCG026474.1,CCG025893.1,CCG018249.1,CCG020652.1,CCG010905.1,CCG010909.1,CCG010648.1,CCG018583.1,CCG017580.1,CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1,CCG010138.1,CCG010649.1,CCG008892.2,CCG025877.1,CCG027199.1,CCG027198.1,CCG018287.1,CCG008559.1,CCG027696.1,CCG010907.1,CCG007767.1,CCG012229.1,CCG010650.1,CCG024624.1,CCG009275.1,CCG002942.1,CCG004494.1,CCG002947.1,CCG010908.1,CCG015312.2,CCG005716.1,CCG027197.1,CCG022673.1,CCG026159.1,CCG027697.1,CCG020442.1,CCG010646.1,CCG017598.1,CCG028222.1,CCG024787.1,CCG027695.1,CCG012584.1,CCG016576.1,CCG008302.1,CCG024788.1
GO:0015934	large ribosomal subunit	10 of 3038 in the list	17 of 5465 in the genome	1	CCG014051.1,CCG024813.1,CCG026048.1,CCG001863.1,CCG027913.1,CCG018126.1,CCG002238.1,CCG025223.1,CCG002966.1,CCG021737.1
GO:0005875	microtubule associated complex	15 of 3038 in the list	26 of 5465 in the genome	1	CCG016119.1,CCG021317.1,CCG001167.1,CCG008377.1,CCG023488.2,CCG021895.1,CCG012733.1,CCG025520.1,CCG003104.1,CCG005525.1,CCG021228.1,CCG003707.1,CCG019329.1,CCG008346.1,CCG018918.1
GO:0000139	Golgi membrane	17 of 3038 in the list	30 of 5465 in the genome	1	CCG014304.1,CCG019892.1,CCG021819.1,CCG009082.1,CCG026620.1,CCG017197.1,CCG011023.1,CCG000210.1,CCG025309.1,CCG012350.1,CCG016003.1,CCG007989.1,CCG027362.1,CCG011813.1,CCG019210.1,CCG020315.1,CCG016673.1

GO:0000151	ubiquitin ligase complex	17 of 3038 in the list	30 of 5465 in the genome	1	CCG003060.1,CCG027068.1,CCG001101.1,CCG019394.1,CCG019571.1,CCG020230.3,CCG019599.1,CCG018116.1,CCG004331.1,CCG016189.1,CCG008557.1,CCG007403.1,CCG028046.1,CCG006505.1,CCG002269.1,CCG008808.1,CCG004134.1
GO:0012505	endomembrane system	63 of 3038 in the list	114 of 5465 in the genome	1	CCG022047.1,CCG019892.1,CCG021819.1,CCG018536.1,CCG009082.1,CCG008144.1,CCG009822.1,CCG001809.1,CCG026620.1,CCG000663.1,CCG011023.1,CCG019367.2,CCG013131.1,CCG026370.1,CCG000210.1,CCG015800.2,CCG025309.1,CCG016003.1,CCG004806.1,CCG026146.1,CCG013066.1,CCG009136.1,CCG022771.1,CCG007330.1,CCG004091.1,CCG028425.2,CCG027362.1,CCG006243.1,CCG011813.1,CCG004897.1,CCG020315.1,CCG015087.1,CCG015843.1,CCG000010.1,CCG023186.1,CCG025233.1,CCG014304.1,CCG010440.1,CCG022209.1,CCG017241.1,CCG011550.1,CCG009434.1,CCG017197.1,CCG000493.1,CCG012350.1,CCG000552.1,CCG012556.1,CCG024760.1,CCG020053.1,CCG028332.1,CCG007989.1,CCG003110.1,CCG019210.1,CCG026989.1,CCG008116.1,CCG003192.1,CCG017141.1,CCG017874.1,CCG003009.1,CCG002930.1,CCG003251.1,CCG017989.1,CCG016673.1
GO:0000015	phosphopyruvate	2 of 3038 in the list	3 of 5465 in the genome	1	CCG022453.1,CCG025277.1
GO:0005664	nuclear origin of replication recognition	2 of 3038 in the list	3 of 5465 in the genome	1	CCG016237.1,CCG028222.1
GO:0005912	adherens junction	2 of 3038 in the list	3 of 5465 in the genome	1	CCG014318.1,CCG003587.1
GO:0005924	cell-substrate adherens	2 of 3038 in the list	3 of 5465 in the genome	1	CCG014318.1,CCG003587.1
GO:0005925	focal adhesion	2 of 3038 in the list	3 of 5465 in the genome	1	CCG014318.1,CCG003587.1
GO:0030055	cell-substrate junction	2 of 3038 in the list	3 of 5465 in the genome	1	CCG014318.1,CCG003587.1
GO:0033588	Elongator holoenzyme	2 of 3038 in the list	3 of 5465 in the genome	1	CCG018515.1,CCG023065.1
GO:0042765	GPI-anchor	2 of 3038 in the list	3 of 5465 in the genome	1	CCG022047.1,CCG026146.1
GO:0044454	nuclear chromosome	2 of 3038 in the list	3 of 5465 in the genome	1	CCG016237.1,CCG028222.1
GO:0070161	anchoring junction	2 of 3038 in the list	3 of 5465 in the genome	1	CCG014318.1,CCG003587.1
GO:0044456	synapse part	10 of 3038 in the list	18 of 5465 in the genome	1	CCG022137.1,CCG027412.1,CCG008323.1,CCG006803.1,CCG005191.1,CCG011730.1,CCG014158.1,CCG018801.1,CCG002839.1,CCG027498.1

GO:0045202	synapse	10 of 3038 in the list	18 of 5465 in the genome	1	CCG022137.1,CCG027412.1,CCG008323.1,CCG006803.1,CCG005191.1,CCG011730.1,CCG014158.1,CCG018801.1,CCG002839.1,CCG027498.1
GO:0000313	organellar ribosome	3 of 3038 in the list	5 of 5465 in the genome	1	CCG025107.1,CCG010112.1,CCG016399.1
GO:0005669	transcription factor	3 of 3038 in the list	5 of 5465 in the genome	1	CCG027950.1,CCG009805.2,CCG010175.1
GO:0005761	mitochondrial ribosome	3 of 3038 in the list	5 of 5465 in the genome	1	CCG025107.1,CCG010112.1,CCG016399.1
GO:0005801	cis-Golgi network	3 of 3038 in the list	5 of 5465 in the genome	1	CCG009428.1,CCG007989.1,CCG009362.1
GO:0031301	integral component of organelle membrane	11 of 3038 in the list	20 of 5465 in the genome	1	CCG022047.1,CCG006223.1,CCG028425.2,CCG019210.1,CCG019367.2,CCG019797.1,CCG019217.1,CCG010178.1,CCG026514.1,CCG026146.1,CCG017989.1
GO:0005778	peroxisomal membrane	5 of 3038 in the list	9 of 5465 in the genome	1	CCG018832.1,CCG019797.1,CCG006223.1,CCG019217.1,CCG010178.1
GO:0031903	microbody membrane	5 of 3038 in the list	9 of 5465 in the genome	1	CCG018832.1,CCG019797.1,CCG006223.1,CCG019217.1,CCG010178.1
GO:0044438	microbody part	5 of 3038 in the list	9 of 5465 in the genome	1	CCG018832.1,CCG019797.1,CCG006223.1,CCG019217.1,CCG010178.1
GO:0044439	peroxisomal part	5 of 3038 in the list	9 of 5465 in the genome	1	CCG018832.1,CCG019797.1,CCG006223.1,CCG019217.1,CCG010178.1
GO:0005773	vacuole	6 of 3038 in the list	11 of 5465 in the genome	1	CCG010696.1,CCG000585.1,CCG017994.1,CCG012534.1,CCG019082.1,CCG013509.1
GO:0005795	Golgi stack	6 of 3038 in the list	11 of 5465 in the genome	1	CCG011023.1,CCG014304.1,CCG003880.1,CCG019892.1,CCG021819.1,CCG021053.1

GO:0005856	cytoskeleton	87 of 3038 in the list	160 of 5465 in the genome	1	CCG015570.1,CCG006420.1,CCG028253.1,CCG013000.1,CCG026823.1,CCG023488.2,CCG003707.1,CCG024718.1,CCG004786.1,CCG019356.1,CCG005370.1,CCG009243.1,CCG019028.1,CCG004459.2,CCG001167.1,CCG004084.1,CCG002696.1,CCG003587.1,CCG006479.1,CCG025520.1,CCG002831.1,CCG027236.1,CCG006421.1,CCG023963.3,CCG007985.1,CCG012081.1,CCG013673.1,CCG002099.1,CCG015426.1,CCG016370.1,CCG014318.1,CCG000535.1,CCG022536.3,CCG010459.3,CCG021911.1,CCG007532.1,CCG008377.1,CCG028503.1,CCG007531.1,CCG018820.3,CCG010538.1,CCG024421.3,CCG011764.1,CCG008346.1,CCG026688.1,CCG021496.1,CCG015784.1,CCG013637.1,CCG023682.1,CCG024769.1,CCG012733.1,CCG019140.1,CCG010418.1,CCG020010.1,CCG024834.3,CCG009080.1,CCG015908.2,CCG027167.1,CCG025396.1,CCG000603.1,CCG019029.1,CCG004101.1,CCG021448.1,CCG008748.1,CCG009543.1,CCG016119.1,CCG015289.1,CCG028230.1,CCG018960.1,CCG003104.1,CCG005525.1,CCG021228.1,CCG019329.1,CCG005886.1,CCG023696.1,CCG002852.1,CCG010864.1,CCG009528.1,CCG021317.1,CCG026558.1,CCG021895.1,CCG002137.1,CCG019092.1,CCG008834.1,CCG016660.1,CCG028236.1,CCG018918.1
GO:0044391	ribosomal subunit	17 of 3038 in the list	32 of 5465 in the genome	1	CCG014051.1,CCG008569.1,CCG001863.1,CCG016399.1,CCG018126.1,CCG009394.1,CCG005442.1,CCG002966.1,CCG026048.1,CCG024813.1,CCG027913.1,CCG002408.1,CCG020963.1,CCG027748.1,CCG002238.1,CCG025223.1,CCG021737.1
GO:0005794	Golgi apparatus	26 of 3038 in the list	49 of 5465 in the genome	1	CCG008896.1,CCG014304.1,CCG003880.1,CCG019892.1,CCG021819.1,CCG009082.1,CCG026620.1,CCG017197.1,CCG011023.1,CCG027692.1,CCG000210.1,CCG013636.1,CCG025309.1,CCG016003.1,CCG012350.1,CCG010417.2,CCG027257.1,CCG007989.1,CCG021053.1,CCG027362.1,CCG011813.1,CCG019210.1,CCG011862.1,CCG020315.1,CCG013126.2,CCG016673.1

GO:0015629	actin cytoskeleton	20 of 3038 in the list	38 of 5465 in the genome	1	CCG012081.1,CCG024769.1,CCG015426.1,CCG014318.1,CCG004786.1,CCG019356.1,CCG024834.3,CCG010459.3,CCG023696.1,CCG004459.2,CCG000603.1,CCG021911.1,CCG004084.1,CCG026558.1,CCG006479.1,CCG003587.1,CCG002831.1,CCG011764.1,CCG008834.1,CCG016660.1
GO:0000785	chromatin	62 of 3038 in the list	116 of 5465 in the genome	1	CCG017580.1,CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1,CCG019284.1,CCG010649.1,CCG010138.1,CCG008560.1,CCG025877.1,CCG010136.1,CCG008892.2,CCG021491.1,CCG010647.1,CCG003310.1,CCG027199.1,CCG027198.1,CCG013617.1,CCG008559.1,CCG018287.1,CCG026473.1,CCG012476.1,CCG014537.1,CCG027696.1,CCG010907.1,CCG010137.1,CCG010650.1,CCG012229.1,CCG009461.1,CCG005194.1,CCG024623.1,CCG025880.1,CCG024624.1,CCG014836.1,CCG010904.1,CCG024177.1,CCG009275.1,CCG004494.1,CCG002947.1,CCG004481.1,CCG010908.1,CCG012514.1,CCG027196.1,CCG014772.1,CCG005716.1,CCG027197.1,CCG026474.1,CCG022673.1,CCG026159.1,CCG027697.1,CCG020442.1,CCG010646.1,CCG017598.1,CCG025893.1,CCG027695.1,CCG024787.1,CCG012584.1,CCG010905.1,CCG008302.1,CCG010909.1,CCG010648.1,CCG024788.1

GO:0000786	nucleosome	62 of 3038 in the list	116 of 5465 in the genome	1	CCG017580.1,CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1,CCG019284.1,CCG010649.1,CCG010138.1,CCG008560.1,CCG025877.1,CCG010136.1,CCG008892.2,CCG021491.1,CCG010647.1,CCG003310.1,CCG027199.1,CCG027198.1,CCG013617.1,CCG008559.1,CCG018287.1,CCG026473.1,CCG012476.1,CCG014537.1,CCG027696.1,CCG010907.1,CCG010137.1,CCG010650.1,CCG012229.1,CCG009461.1,CCG005194.1,CCG024623.1,CCG025880.1,CCG024624.1,CCG014836.1,CCG010904.1,CCG024177.1,CCG009275.1,CCG004494.1,CCG002947.1,CCG004481.1,CCG010908.1,CCG012514.1,CCG027196.1,CCG014772.1,CCG005716.1,CCG027197.1,CCG026474.1,CCG022673.1,CCG026159.1,CCG027697.1,CCG020442.1,CCG010646.1,CCG017598.1,CCG025893.1,CCG027695.1,CCG024787.1,CCG012584.1,CCG010905.1,CCG008302.1,CCG010909.1,CCG010648.1,CCG024788.1
GO:0044815	DNA packaging complex	62 of 3038 in the list	116 of 5465 in the genome	1	CCG017580.1,CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1,CCG019284.1,CCG010649.1,CCG010138.1,CCG008560.1,CCG025877.1,CCG010136.1,CCG008892.2,CCG021491.1,CCG010647.1,CCG003310.1,CCG027199.1,CCG027198.1,CCG013617.1,CCG008559.1,CCG018287.1,CCG026473.1,CCG012476.1,CCG014537.1,CCG027696.1,CCG010907.1,CCG010137.1,CCG010650.1,CCG012229.1,CCG009461.1,CCG005194.1,CCG024623.1,CCG025880.1,CCG024624.1,CCG014836.1,CCG010904.1,CCG024177.1,CCG009275.1,CCG004494.1,CCG002947.1,CCG004481.1,CCG010908.1,CCG012514.1,CCG027196.1,CCG014772.1,CCG005716.1,CCG027197.1,CCG026474.1,CCG022673.1,CCG026159.1,CCG027697.1,CCG020442.1,CCG010646.1,CCG017598.1,CCG025893.1,CCG027695.1,CCG024787.1,CCG012584.1,CCG010905.1,CCG008302.1,CCG010909.1,CCG010648.1,CCG024788.1

GO:1990104	DNA bending complex	62 of 3038 in the list	116 of 5465 in the genome	1	CCG017580.1,CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1,CCG019284.1,CCG010649.1,CCG010138.1,CCG008560.1,CCG025877.1,CCG010136.1,CCG008892.2,CCG021491.1,CCG010647.1,CCG003310.1,CCG027199.1,CCG027198.1,CCG013617.1,CCG008559.1,CCG018287.1,CCG026473.1,CCG012476.1,CCG014537.1,CCG027696.1,CCG010907.1,CCG010137.1,CCG010650.1,CCG012229.1,CCG009461.1,CCG005194.1,CCG024623.1,CCG025880.1,CCG024624.1,CCG014836.1,CCG010904.1,CCG024177.1,CCG009275.1,CCG004494.1,CCG002947.1,CCG004481.1,CCG010908.1,CCG012514.1,CCG027196.1,CCG014772.1,CCG005716.1,CCG027197.1,CCG026474.1,CCG022673.1,CCG026159.1,CCG027697.1,CCG020442.1,CCG010646.1,CCG017598.1,CCG025893.1,CCG027695.1,CCG024787.1,CCG012584.1,CCG010905.1,CCG008302.1,CCG010909.1,CCG010648.1,CCG024788.1
GO:0032993	protein-DNA complex	64 of 3038 in the list	120 of 5465 in the genome	1	CCG017580.1,CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1,CCG019284.1,CCG010649.1,CCG010138.1,CCG008560.1,CCG025877.1,CCG010136.1,CCG008892.2,CCG021491.1,CCG010647.1,CCG003310.1,CCG027199.1,CCG027198.1,CCG013617.1,CCG008559.1,CCG018287.1,CCG026473.1,CCG012476.1,CCG014537.1,CCG027696.1,CCG010907.1,CCG010137.1,CCG007767.1,CCG010650.1,CCG012229.1,CCG009461.1,CCG005194.1,CCG024623.1,CCG025880.1,CCG024624.1,CCG014836.1,CCG010904.1,CCG024177.1,CCG009275.1,CCG004494.1,CCG002947.1,CCG004481.1,CCG010908.1,CCG012514.1,CCG027196.1,CCG014772.1,CCG005716.1,CCG027197.1,CCG026474.1,CCG022673.1,CCG026159.1,CCG027697.1,CCG020442.1,CCG010646.1,CCG017598.1,CCG025893.1,CCG027695.1,CCG024787.1,CCG018249.1,CCG012584.1,CCG010905.1,CCG008302.1,CCG010909.1,CCG010648.1,CCG024788.1

GO:0031090	organelle membrane	84 of 3038 in the list	157 of 5465 in the genome	1	CCG022047.1,CCG018832.1,CCG011932.1,CCG019892.1,CCG020245.1,CCG021819.1,CCG018536.1,CCG000663.1,CCG011023.1,CCG019590.1,CCG000210.1,CCG000585.1,CCG000205.1,CCG004806.1,CCG022802.1,CCG007330.1,CCG010112.1,CCG004091.1,CCG011813.1,CCG017614.1,CCG020315.1,CCG016304.1,CCG015843.1,CCG019217.1,CCG000010.1,CCG013643.1,CCG004155.2,CCG022209.1,CCG018684.1,CCG009434.1,CCG001279.1,CCG000148.1,CCG002790.1,CCG005924.2,CCG024760.1,CCG010939.1,CCG028332.1,CCG019210.1,CCG026514.1,CCG010178.1,CCG002930.1,CCG017989.1,CCG016673.1,CCG000102.1,CCG009082.1,CCG026620.1,CCG013131.1,CCG019367.2,CCG026370.1,CCG015800.2,CCG025309.1,CCG012534.1,CCG016003.1,CCG026146.1,CCG011381.1,CCG028425.2,CCG024119.1,CCG027362.1,CCG023814.2,CCG026240.1,CCG019797.1,CCG013013.1,CCG015087.1,CCG006459.1,CCG014304.1,CCG025233.1,CCG005677.1,CCG015410.1,CCG007862.1,CCG017241.1,CCG025107.1,CCG009142.1,CCG017197.1,CCG010696.1,CCG012350.1,CCG000552.1,CCG006223.1,CCG007989.1,CCG003110.1,CCG014053.1,CCG003192.1,CCG017125.1,CCG025163.3,CCG003251.1
GO:0008305	integrin complex	4 of 3038 in the list	8 of 5465 in the genome	1	CCG004279.1,CCG000526.1,CCG024898.1,CCG025334.1
GO:0043235	receptor complex	4 of 3038 in the list	8 of 5465 in the genome	1	CCG004279.1,CCG000526.1,CCG024898.1,CCG025334.1
GO:0048500	signal recognition	4 of 3038 in the list	8 of 5465 in the genome	1	CCG006714.1,CCG018217.1,CCG000614.1,CCG020806.1
GO:0016272	prefoldin complex	6 of 3038 in the list	12 of 5465 in the genome	1	CCG009266.1,CCG027653.1,CCG025028.1,CCG007108.1,CCG017448.1,CCG011095.1
GO:0019028	viral capsid	6 of 3038 in the list	12 of 5465 in the genome	1	CCG025780.1,CCG000477.1,CCG014038.1,CCG000478.1,CCG013201.1,CCG025779.1
GO:0044423	virion part	6 of 3038 in the list	12 of 5465 in the genome	1	CCG025780.1,CCG000477.1,CCG014038.1,CCG000478.1,CCG013201.1,CCG025779.1
GO:0005853	eukaryotic translation elongation factor 1	3 of 3038 in the list	6 of 5465 in the genome	1	CCG005143.1,CCG000994.1,CCG027751.1
GO:0012507	ER to Golgi transport	3 of 3038 in the list	6 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1
GO:0030127	COPII vesicle coat	3 of 3038 in the list	6 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1
GO:0030134	ER to Golgi transport	3 of 3038 in the list	6 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1

GO:0000775	chromosome,	2 of 3038 in the list	4 of 5465 in the genome	1	CCG018249.1,CCG007767.1
GO:0005604	basement membrane	2 of 3038 in the list	4 of 5465 in the genome	1	CCG015389.1,CCG008431.1
GO:0005672	transcription factor	2 of 3038 in the list	4 of 5465 in the genome	1	CCG000158.1,CCG001292.1
GO:0005971	ribonucleoside-diphosphate reductase	2 of 3038 in the list	4 of 5465 in the genome	1	CCG024232.1,CCG015929.1
GO:0005783	endoplasmic reticulum	38 of 3038 in the list	73 of 5465 in the genome	1	CCG022047.1,CCG027415.1,CCG018536.1,CCG013390.1,CCG023617.1,CCG019431.1,CCG000663.1,CCG013131.1,CCG019367.2,CCG026370.1,CCG002783.1,CCG009928.1,CCG004806.1,CCG026146.1,CCG017528.1,CCG027023.1,CCG023114.1,CCG007330.1,CCG004091.1,CCG015843.1,CCG023834.2,CCG025233.1,CCG017241.1,CCG022209.1,CCG019560.1,CCG009434.1,CCG027585.1,CCG000552.1,CCG009267.1,CCG024760.1,CCG000895.1,CCG028332.1,CCG002374.1,CCG003110.1,CCG027004.1,CCG003192.1,CCG002930.1,CCG003251.1
GO:0044431	Golgi apparatus part	22 of 3038 in the list	43 of 5465 in the genome	1	CCG014304.1,CCG003880.1,CCG019892.1,CCG021819.1,CCG009082.1,CCG026620.1,CCG017197.1,CCG011023.1,CCG027692.1,CCG000210.1,CCG025309.1,CCG016003.1,CCG012350.1,CCG007989.1,CCG021053.1,CCG027362.1,CCG011813.1,CCG019210.1,CCG011862.1,CCG020315.1,CCG013126.2,CCG016673.1
GO:0031300	intrinsic component of organelle membrane	17 of 3038 in the list	34 of 5465 in the genome	1	CCG022047.1,CCG025233.1,CCG022209.1,CCG006223.1,CCG028332.1,CCG007330.1,CCG028425.2,CCG019210.1,CCG019367.2,CCG019797.1,CCG019217.1,CCG026514.1,CCG010178.1,CCG002930.1,CCG000552.1,CCG026146.1,CCG017989.1
GO:0015935	small ribosomal subunit	7 of 3038 in the list	15 of 5465 in the genome	1	CCG002408.1,CCG027748.1,CCG008569.1,CCG020963.1,CCG016399.1,CCG005442.1,CCG009394.1
GO:0019898	extrinsic component of membrane	5 of 3038 in the list	11 of 5465 in the genome	1	CCG009446.1,CCG006412.1,CCG012573.1,CCG007985.1,CCG024952.1
GO:0005774	vacuolar membrane	3 of 3038 in the list	7 of 5465 in the genome	1	CCG010696.1,CCG000585.1,CCG012534.1
GO:0016471	vacuolar proton-transporting V-type	3 of 3038 in the list	7 of 5465 in the genome	1	CCG010696.1,CCG000585.1,CCG012534.1
GO:0030176	integral component of endoplasmic reticulum	3 of 3038 in the list	7 of 5465 in the genome	1	CCG022047.1,CCG019367.2,CCG026146.1

GO:0044437	vacuolar part	3 of 3038 in the list	7 of 5465 in the genome	1	CCG010696.1,CCG000585.1,CCG012534.1
GO:0000145	exocyst	2 of 3038 in the list	5 of 5465 in the genome	1	CCG002937.1,CCG016493.2
GO:0005938	cell cortex	2 of 3038 in the list	5 of 5465 in the genome	1	CCG002937.1,CCG016493.2
GO:0008290	F-actin capping protein	2 of 3038 in the list	5 of 5465 in the genome	1	CCG019356.1,CCG008834.1
GO:0044448	cell cortex part	2 of 3038 in the list	5 of 5465 in the genome	1	CCG002937.1,CCG016493.2
GO:0033177	proton-transporting two-sector ATPase	8 of 3038 in the list	18 of 5465 in the genome	1	CCG025450.1,CCG025107.1,CCG010112.1,CCG009142.1,CCG000148.1,CCG003662.1,CCG013643.1,CCG008422.1
GO:1990204	oxidoreductase	4 of 3038 in the list	10 of 5465 in the genome	1	CCG009685.1,CCG024232.1,CCG014228.2,CCG015929.1
GO:0005886	plasma membrane	39 of 3038 in the list	80 of 5465 in the genome	1	CCG024952.1,CCG007182.1,CCG025334.1,CCG016263.1,CCG004279.1,CCG001422.1,CCG009446.1,CCG007356.1,CCG002839.1,CCG007575.1,CCG020013.1,CCG004542.1,CCG005277.1,CCG014158.1,CCG015914.1,CCG018801.1,CCG007117.1,CCG024898.1,CCG013707.1,CCG025568.1,CCG012573.1,CCG017729.1,CCG022137.1,CCG006803.1,CCG028158.1,CCG006412.1,CCG019647.1,CCG000127.1,CCG012634.1,CCG022540.1,CCG000526.1,CCG016864.1,CCG011730.1,CCG027899.1,CCG002559.1,CCG016446.1,CCG027757.1,CCG027498.1,CCG013255.1
GO:0005777	peroxisome	10 of 3038 in the list	23 of 5465 in the genome	1	CCG018832.1,CCG006223.1,CCG006391.1,CCG025521.1,CCG019797.1,CCG018851.1,CCG007979.1,CCG019217.1,CCG010178.1,CCG000591.1
GO:0042579	microbody	10 of 3038 in the list	23 of 5465 in the genome	1	CCG018832.1,CCG006223.1,CCG006391.1,CCG025521.1,CCG019797.1,CCG018851.1,CCG007979.1,CCG019217.1,CCG010178.1,CCG000591.1
GO:0008021	synaptic vesicle	3 of 3038 in the list	8 of 5465 in the genome	1	CCG027412.1,CCG008323.1,CCG005191.1
GO:0031227	intrinsic component of endoplasmic reticulum membrane	9 of 3038 in the list	21 of 5465 in the genome	1	CCG022047.1,CCG025233.1,CCG022209.1,CCG028332.1,CCG007330.1,CCG019367.2,CCG002930.1,CCG026146.1,CCG000552.1
GO:0019012	virion	6 of 3038 in the list	15 of 5465 in the genome	1	CCG025780.1,CCG000477.1,CCG014038.1,CCG000478.1,CCG013201.1,CCG025779.1

GO:0044421	extracellular region part	25 of 3038 in the list	54 of 5465 in the genome	1	CCG003774.2,CCG005113.1,CCG004025.1,CCG003882.1,CCG007376.1,CCG015746.1,CCG004326.1,CCG015389.1,CCG008431.1,CCG022425.1,CCG015747.1,CCG004982.1,CCG013615.1,CCG024731.1,CCG006702.1,CCG003745.1,CCG008759.1,CCG020089.1,CCG026583.1,CCG026537.1,CCG025670.1,CCG017112.1,CCG026865.1,CCG005060.1,CCG014689.1
GO:0033178	proton-transporting two-sector ATPase complex, catalytic	12 of 3038 in the list	29 of 5465 in the genome	1	CCG015410.1,CCG002038.1,CCG023640.1,CCG001066.1,CCG000585.1,CCG025348.1,CCG007724.1,CCG006486.1,CCG021934.1,CCG019619.1,CCG005924.2,CCG001285.1
GO:0016469	proton-transporting two-sector ATPase complex	23 of 3038 in the list	52 of 5465 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1,CCG023640.1,CCG010696.1,CCG000148.1,CCG000585.1,CCG025348.1,CCG003662.1,CCG012534.1,CCG006486.1,CCG019619.1,CCG005924.2,CCG008422.1,CCG025450.1,CCG010112.1,CCG001066.1,CCG019678.1,CCG007724.1,CCG021934.1,CCG013643.1,CCG001285.1
GO:0019773	proteasome core complex, alpha-subunit	4 of 3038 in the list	12 of 5465 in the genome	1	CCG008217.1,CCG026413.3,CCG024679.1,CCG014393.1
GO:0019867	outer membrane	4 of 3038 in the list	12 of 5465 in the genome	1	CCG026240.1,CCG001279.1,CCG013013.1,CCG001246.1
GO:0030119	AP-type membrane	4 of 3038 in the list	12 of 5465 in the genome	1	CCG027692.1,CCG007283.1,CCG021800.1,CCG013126.2
GO:0030131	clathrin adaptor	4 of 3038 in the list	12 of 5465 in the genome	1	CCG027692.1,CCG007283.1,CCG021800.1,CCG013126.2
GO:0044432	endoplasmic reticulum part	23 of 3038 in the list	53 of 5465 in the genome	1	CCG022047.1,CCG025233.1,CCG022209.1,CCG017241.1,CCG018536.1,CCG009434.1,CCG000663.1,CCG013131.1,CCG019367.2,CCG026370.1,CCG004806.1,CCG000552.1,CCG026146.1,CCG024760.1,CCG028332.1,CCG002374.1,CCG007330.1,CCG004091.1,CCG003110.1,CCG003192.1,CCG015843.1,CCG002930.1,CCG003251.1
GO:0005789	endoplasmic reticulum membrane	22 of 3038 in the list	51 of 5465 in the genome	1	CCG022047.1,CCG025233.1,CCG022209.1,CCG017241.1,CCG018536.1,CCG009434.1,CCG000663.1,CCG013131.1,CCG019367.2,CCG026370.1,CCG004806.1,CCG000552.1,CCG026146.1,CCG024760.1,CCG028332.1,CCG007330.1,CCG004091.1,CCG003110.1,CCG003192.1,CCG015843.1,CCG002930.1,CCG003251.1

GO:0042175	nuclear outer membrane-endoplasmic reticulum membrane network	22 of 3038 in the list	51 of 5465 in the genome	1	CCG022047.1,CCG025233.1,CCG022209.1,CCG017241.1,CCG018536.1,CCG009434.1,CCG000663.1,CCG013131.1,CCG019367.2,CCG026370.1,CCG004806.1,CCG000552.1,CCG026146.1,CCG024760.1,CCG028332.1,CCG007330.1,CCG004091.1,CCG003110.1,CCG003192.1,CCG015843.1,CCG002930.1,CCG003251.1
GO:0005741	mitochondrial outer	3 of 3038 in the list	10 of 5465 in the genome	1	CCG026240.1,CCG001279.1,CCG013013.1
GO:0030133	transport vesicle	3 of 3038 in the list	10 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1
GO:0030658	transport vesicle	3 of 3038 in the list	10 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1
GO:0031968	organelle outer	3 of 3038 in the list	10 of 5465 in the genome	1	CCG026240.1,CCG001279.1,CCG013013.1
GO:0044459	plasma membrane part	23 of 3038 in the list	54 of 5465 in the genome	1	CCG025568.1,CCG012573.1,CCG022137.1,CCG024952.1,CCG025334.1,CCG006803.1,CCG004279.1,CCG009446.1,CCG006412.1,CCG019647.1,CCG002839.1,CCG022540.1,CCG000526.1,CCG016864.1,CCG005277.1,CCG011730.1,CCG015914.1,CCG014158.1,CCG002559.1,CCG027899.1,CCG018801.1,CCG024898.1,CCG027498.1
GO:0005615	extracellular space	16 of 3038 in the list	41 of 5465 in the genome	1	CCG003774.2,CCG005113.1,CCG004025.1,CCG007376.1,CCG015746.1,CCG022425.1,CCG015747.1,CCG013615.1,CCG024731.1,CCG003745.1,CCG008759.1,CCG026537.1,CCG017112.1,CCG026865.1,CCG005060.1,CCG014689.1
GO:0030136	clathrin-coated vesicle	3 of 3038 in the list	12 of 5465 in the genome	1	CCG027412.1,CCG008323.1,CCG005191.1

GO:0032991	macromolecular complex	460 of 3038 in the list	888 of 5465 in the genome	1	CCG014531.2,CCG011932.1,CCG027068.1,CCG026177.1,CCG001809.1,CCG013430.1,CCG006357.1,CCG024695.1,CCG000585.1,CCG010647.1,CCG005370.1,CCG026882.1,CCG002354.1,CCG026473.1,CCG001167.1,CCG004091.1,CCG001292.1,CCG028326.3,CCG003573.1,CCG028505.1,CCG025223.1,CCG006134.1,CCG005194.1,CCG014836.1,CCG024177.1,CCG012573.1,CCG008431.1,CCG012514.1,CCG003362.1,CCG027196.1,CCG016370.1,CCG026413.3,CCG012536.1,CCG026871.2,CCG027796.1,CCG018533.1,CCG025450.1,CCG000526.1,CCG021911.1,CCG010905.1,CCG028046.1,CCG008270.1,CCG006714.1,CCG011862.1,CCG027899.1,CCG011764.1,CCG010909.1,CCG008808.1,CCG014195.1,CCG005737.1,CCG011911.1,CCG028653.1,CCG026212.1,CCG009249.1,CCG014896.1,CCG017580.1,CCG024952.1,CCG009980.1,CCG002735.1,CCG001863.1,CCG016493.2,CCG009822.1,CCG004279.1,CCG010649.1,CCG004212.1,CCG019571.1,CCG012534.1,CCG007647.1,CCG016189.1,CCG004331.1,CCG018788.1,CCG025396.1,CCG006484.1,CCG021633.1,CCG019029.1,CCG006344.1,CCG008559.1,CCG001461.1,CCG027696.1,CCG026280.1,CCG005480.2,CCG024432.2,CCG023686.1,CCG019678.1,CCG021737.1,CCG000773.1,CCG009543.1,CCG004494.1,CCG001698.1,CCG003104.1,CCG021228.1,CCG022214.1,CCG006412.1,CCG022673.1,CCG019647.1,CCG026159.1,CCG016399.1,CCG004927.1,CCG016307.1,CCG009805.2,CCG012556.1,CCG002852.1,CCG002966.1,CCG020634.1,CCG019250.1,CCG008557.1,CCG018402.1,CCG012584.1,CCG018688.1,CCG014228.2,CCG021895.1,CCG010024.1,CCG017141.1,CCG025747.1,CCG027748.1,CCG002937.1,CCG024788.1,CCG000294.1,CCG005168.1,CCG018184.1,CCG018315.1,CCG001285.1,CCG003060.1,CCG000789.1,CCG016778.1,CCG004955.1,CCG0073
GO:0030118	clathrin coat	4 of 3038 in the list	16 of 5465 in the genome	1	CCG027692.1,CCG007283.1,CCG021800.1,CCG013126.2
GO:0031012	extracellular matrix	15 of 3038 in the list	43 of 5465 in the genome	1	CCG016175.1,CCG003882.1,CCG020089.1,CCG004326.1,CCG026583.1,CCG015389.1,CCG008431.1,CCG022450.1,CCG004982.1,CCG025670.1,CCG015206.1,CCG015843.1,CCG013615.1,CCG006702.1,CCG002163.1
GO:0030120	vesicle coat	4 of 3038 in the list	17 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1,CCG011813.1

GO:0030135	coated vesicle	7 of 3038 in the list	25 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1,CCG027412.1,CCG008323.1,CCG005191.1,CCG011813.1
GO:0000502	proteasome complex	9 of 3038 in the list	30 of 5465 in the genome	1	CCG008217.1,CCG026177.1,CCG010543.1,CCG014393.1,CCG023270.1,CCG013832.1,CCG026413.3,CCG024679.1,CCG027736.1
GO:0034702	ion channel complex	6 of 3038 in the list	23 of 5465 in the genome	1	CCG025568.1,CCG015914.1,CCG002559.1,CCG019647.1,CCG016864.1,CCG005277.1
GO:0034703	cation channel complex	6 of 3038 in the list	23 of 5465 in the genome	1	CCG025568.1,CCG015914.1,CCG002559.1,CCG019647.1,CCG016864.1,CCG005277.1
GO:1902495	transmembrane transporter complex	6 of 3038 in the list	23 of 5465 in the genome	1	CCG025568.1,CCG015914.1,CCG002559.1,CCG019647.1,CCG016864.1,CCG005277.1
GO:0071944	cell periphery	44 of 3038 in the list	107 of 5465 in the genome	1	CCG001584.1,CCG024952.1,CCG007182.1,CCG025334.1,CCG016263.1,CCG016493.2,CCG004279.1,CCG001422.1,CCG009446.1,CCG007356.1,CCG002839.1,CCG004844.1,CCG007575.1,CCG020013.1,CCG004542.1,CCG005277.1,CCG021686.1,CCG014158.1,CCG015914.1,CCG018801.1,CCG007117.1,CCG024898.1,CCG013707.1,CCG025568.1,CCG012573.1,CCG017729.1,CCG022137.1,CCG006803.1,CCG028158.1,CCG006412.1,CCG019647.1,CCG000127.1,CCG012634.1,CCG022540.1,CCG000526.1,CCG016864.1,CCG011730.1,CCG027899.1,CCG002559.1,CCG016446.1,CCG002937.1,CCG027757.1,CCG027498.1,CCG013255.1

GO:0005576	extracellular region	115 of 3038 in the list	250 of 5465 in the genome	1	CCG010077.1,CCG003882.1,CCG006912.1,CCG017730.1,CCG005809.1,CCG021005.1,CCG008826.1,CCG013453.1,CCG012504.1,CCG013273.1,CCG022261.1,CCG007152.1,CCG002694.1,CCG026583.1,CCG007817.1,CCG011695.1,CCG022262.1,CCG007816.1,CCG019884.1,CCG006002.1,CCG005113.1,CCG025139.1,CCG007376.1,CCG008431.1,CCG002170.1,CCG009992.1,CCG020165.1,CCG005170.1,CCG023922.1,CCG007814.1,CCG006911.1,CCG013615.1,CCG028185.1,CCG022378.1,CCG024731.1,CCG006375.1,CCG026626.1,CCG017079.1,CCG023923.1,CCG019371.1,CCG027424.1,CCG014180.1,CCG026537.1,CCG007219.1,CCG012984.1,CCG017112.1,CCG003601.1,CCG010019.1,CCG003966.1,CCG014791.1,CCG016153.1,CCG011972.1,CCG004025.1,CCG015746.1,CCG004326.1,CCG015090.1,CCG028548.1,CCG025560.1,CCG020988.1,CCG004982.1,CCG010728.1,CCG014650.1,CCG019402.1,CCG017862.1,CCG023926.1,CCG022227.1,CCG001996.1,CCG026763.1,CCG012725.1,CCG019785.1,CCG001154.1,CCG003745.1,CCG016069.1,CCG008759.1,CCG023924.1,CCG006489.1,CCG025670.1,CCG012125.1,CCG025962.1,CCG012149.1,CCG024173.1,CCG000656.1,CCG014181.1,CCG014689.1,CCG025030.1,CCG000044.1,CCG013298.1,CCG028308.1,CCG003774.2,CCG023925.1,CCG011257.1,CCG015389.1,CCG018642.1,CCG022425.1,CCG015747.1,CCG015306.1,CCG015029.1,CCG013409.1,CCG026044.1,CCG007963.1,CCG015804.1,CCG006702.1,CCG018643.1,CCG020089.1,CCG014615.1,CCG026552.1,CCG023420.1,CCG000501.1,CCG010727.1,CCG028454.1,CCG020663.1,CCG026865.1,CCG005060.1,CCG028648.1,CCG000897.1
GO:0005887	integral component of plasma membrane	8 of 3038 in the list	29 of 5465 in the genome	1	CCG000526.1,CCG025334.1,CCG016864.1,CCG015914.1,CCG004279.1,CCG002559.1,CCG019647.1,CCG024898.1
GO:0031226	intrinsic component of plasma membrane	8 of 3038 in the list	29 of 5465 in the genome	1	CCG000526.1,CCG025334.1,CCG016864.1,CCG015914.1,CCG004279.1,CCG002559.1,CCG019647.1,CCG024898.1
GO:0012506	vesicle membrane	4 of 3038 in the list	19 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1,CCG011813.1
GO:0030659	cytoplasmic vesicle	4 of 3038 in the list	19 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1,CCG011813.1

GO:0030662	coated vesicle	4 of 3038 in the list	19 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1,CCG011813.1
GO:0044433	cytoplasmic vesicle	4 of 3038 in the list	19 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1,CCG011813.1
GO:0005839	proteasome core complex	6 of 3038 in the list	25 of 5465 in the genome	1	CCG013832.1,CCG008217.1,CCG026413.3,CCG024679.1,CCG014393.1,CCG023270.1
GO:0016023	cytoplasmic membrane-bounded	7 of 3038 in the list	28 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1,CCG027412.1,CCG008323.1,CCG005191.1,CCG011813.1
GO:0031410	cytoplasmic vesicle	7 of 3038 in the list	28 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1,CCG027412.1,CCG008323.1,CCG005191.1,CCG011813.1
GO:0031982	vesicle	7 of 3038 in the list	28 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1,CCG027412.1,CCG008323.1,CCG005191.1,CCG011813.1
GO:0031988	membrane-bounded vesicle	7 of 3038 in the list	28 of 5465 in the genome	1	CCG015800.2,CCG015087.1,CCG000010.1,CCG027412.1,CCG008323.1,CCG005191.1,CCG011813.1
GO:0008076	voltage-gated	3 of 3038 in the list	17 of 5465 in the genome	1	CCG002559.1,CCG019647.1,CCG016864.1
GO:0034705	potassium channel	3 of 3038 in the list	17 of 5465 in the genome	1	CCG002559.1,CCG019647.1,CCG016864.1
GO:0030117	membrane coat	13 of 3038 in the list	43 of 5465 in the genome	1	CCG027257.1,CCG026698.1,CCG020634.1,CCG007283.1,CCG011813.1,CCG023756.1,CCG027692.1,CCG015800.2,CCG015087.1,CCG015568.1,CCG000010.1,CCG021800.1,CCG013126.2
GO:0048475	coated membrane	13 of 3038 in the list	43 of 5465 in the genome	1	CCG027257.1,CCG026698.1,CCG020634.1,CCG007283.1,CCG011813.1,CCG023756.1,CCG027692.1,CCG015800.2,CCG015087.1,CCG015568.1,CCG000010.1,CCG021800.1,CCG013126.2

GO:0043228	non-membrane-bounded organelle	264 of 3038 in the list	547 of 5465 in the genome	1	CCG014531.2,CCG028253.1,CCG004973.1,CCG013430.1,CCG011675.1,CCG010647.1,CCG005370.1,CCG002354.1,CCG026473.1,CCG001167.1,CCG003587.1,CCG003573.1,CCG025223.1,CCG005194.1,CCG014836.1,CCG024177.1,CCG012514.1,CCG027196.1,CCG016370.1,CCG027183.2,CCG026871.2,CCG000166.1,CCG015998.1,CCG023053.1,CCG021911.1,CCG010905.1,CCG008270.1,CCG011764.1,CCG010909.1,CCG005737.1,CCG028653.1,CCG009249.1,CCG014896.1,CCG017580.1,CCG009980.1,CCG001863.1,CCG010649.1,CCG020987.1,CCG020010.1,CCG003438.1,CCG018788.1,CCG025396.1,CCG012083.1,CCG019029.1,CCG006344.1,CCG008559.1,CCG027696.1,CCG026280.1,CCG004101.1,CCG021737.1,CCG000773.1,CCG009543.1,CCG004494.1,CCG003104.1,CCG021228.1,CCG022673.1,CCG026159.1,CCG016399.1,CCG002852.1,CCG002966.1,CCG012584.1,CCG021895.1,CCG027748.1,CCG024788.1,CCG016778.1,CCG007336.1,CCG003707.1,CCG010136.1,CCG003310.1,CCG003471.1,CCG004459.2,CCG013617.1,CCG010112.1,CCG004084.1,CCG019398.1,CCG006876.1,CCG006479.1,CCG010137.1,CCG009461.1,CCG023963.3,CCG006421.1,CCG007985.1,CCG014772.1,CCG015426.1,CCG019426.1,CCG000535.1,CCG009394.1,CCG002644.1,CCG024813.1,CCG015167.1,CCG024421.3,CCG006336.1,CCG005443.1,CCG026688.1,CCG021496.1,CCG010906.1,CCG024769.1,CCG010138.1,CCG010418.1,CCG024834.3,CCG005442.1,CCG015908.2,CCG000603.1,CCG013833.1,CCG020899.1,CCG007767.1,CCG012229.1,CCG016119.1,CCG002947.1,CCG025107.1,CCG021933.1,CCG015312.2,CCG027197.1,CCG025409.1,CCG019518.1,CCG010646.1,CCG028222.1,CCG023696.1,CCG009528.1,CCG027695.1,CCG026558.1,CCG002137.1,CCG028236.1,CCG018918.1,CCG011957.1,CCG006420.1,CCG0130

GO:0043232	intracellular non-membrane-bounded organelle	264 of 3038 in the list	547 of 5465 in the genome	1	CCG014531.2,CCG028253.1,CCG004973.1,CCG013430.1,CCG011675.1,CCG010647.1,CCG005370.1,CCG002354.1,CCG026473.1,CCG001167.1,CCG003587.1,CCG003573.1,CCG025223.1,CCG005194.1,CCG014836.1,CCG024177.1,CCG012514.1,CCG027196.1,CCG016370.1,CCG027183.2,CCG026871.2,CCG000166.1,CCG015998.1,CCG023053.1,CCG021911.1,CCG010905.1,CCG008270.1,CCG011764.1,CCG010909.1,CCG005737.1,CCG028653.1,CCG009249.1,CCG014896.1,CCG017580.1,CCG009980.1,CCG001863.1,CCG010649.1,CCG020987.1,CCG020010.1,CCG003438.1,CCG018788.1,CCG025396.1,CCG012083.1,CCG019029.1,CCG006344.1,CCG008559.1,CCG027696.1,CCG026280.1,CCG004101.1,CCG021737.1,CCG000773.1,CCG009543.1,CCG004494.1,CCG003104.1,CCG021228.1,CCG022673.1,CCG026159.1,CCG016399.1,CCG002852.1,CCG002966.1,CCG012584.1,CCG021895.1,CCG027748.1,CCG024788.1,CCG016778.1,CCG007336.1,CCG003707.1,CCG010136.1,CCG003310.1,CCG003471.1,CCG004459.2,CCG013617.1,CCG010112.1,CCG004084.1,CCG019398.1,CCG006876.1,CCG006479.1,CCG010137.1,CCG009461.1,CCG023963.3,CCG006421.1,CCG007985.1,CCG014772.1,CCG015426.1,CCG019426.1,CCG000535.1,CCG009394.1,CCG002644.1,CCG024813.1,CCG015167.1,CCG024421.3,CCG006336.1,CCG005443.1,CCG026688.1,CCG021496.1,CCG010906.1,CCG024769.1,CCG010138.1,CCG010418.1,CCG024834.3,CCG005442.1,CCG015908.2,CCG000603.1,CCG013833.1,CCG020899.1,CCG007767.1,CCG012229.1,CCG016119.1,CCG002947.1,CCG025107.1,CCG021933.1,CCG015312.2,CCG027197.1,CCG025409.1,CCG019518.1,CCG010646.1,CCG028222.1,CCG023696.1,CCG009528.1,CCG027695.1,CCG026558.1,CCG002137.1,CCG028236.1,CCG018918.1,CCG011957.1,CCG006420.1,CCG0130

GO:0005737	cytoplasm	399 of 3038 in the list	804 of 5465 in the genome	1	CCG014531.2,CCG011932.1,CCG020245.1,CCG018536.1,CCG023277.1,CCG014396.1,CCG010159.1,CCG024806.1,CCG010191.3,CCG013430.1,CCG005079.1,CCG021449.1,CCG009878.1,CCG000585.1,CCG000205.1,CCG004595.1,CCG025108.1,CCG020879.1,CCG021053.1,CCG002354.1,CCG016238.1,CCG004091.1,CCG006391.1,CCG017614.1,CCG019217.1,CCG003573.1,CCG021064.1,CCG028505.1,CCG025223.1,CCG009900.1,CCG014519.1,CCG017078.1,CCG011696.1,CCG014307.1,CCG026871.2,CCG007771.1,CCG005444.1,CCG024779.1,CCG024032.1,CCG003767.1,CCG008323.1,CCG008270.1,CCG019210.1,CCG006714.1,CCG011862.1,CCG003063.1,CCG002930.1,CCG005737.1,CCG023795.2,CCG008896.1,CCG020877.1,CCG009249.1,CCG006231.1,CCG014896.1,CCG001863.1,CCG016493.2,CCG005191.1,CCG013131.1,CCG008871.1,CCG012534.1,CCG002711.1,CCG018788.1,CCG006344.1,CCG024119.1,CCG008510.1,CCG026280.1,CCG021378.1,CCG021737.1,CCG000773.1,CCG014304.1,CCG016565.1,CCG014461.1,CCG011510.1,CCG022214.1,CCG027565.1,CCG016399.1,CCG009582.1,CCG011097.1,CCG000552.1,CCG002966.1,CCG019545.1,CCG020634.1,CCG019330.1,CCG001876.1,CCG000915.1,CCG014228.2,CCG000834.1,CCG027748.1,CCG002937.1,CCG000294.1,CCG008388.1,CCG000789.1,CCG016778.1,CCG005588.1,CCG010912.1,CCG028409.1,CCG015367.1,CCG027692.1,CCG000210.1,CCG002783.1,CCG004806.1,CCG000591.1,CCG027472.1,CCG027023.1,CCG003471.1,CCG022802.1,CCG010112.1,CCG004986.1,CCG019398.1,CCG022464.1,CCG011135.1,CCG006876.1,CCG020231.1,CCG015568.1,CCG017077.1,CCG024232.1,CCG001395.1,CCG004155.2,CCG022209.1,CCG007985.1,CCG022690.1,CCG027316.1,CCG000148.1,CCG002790.1,CCG017344.1,CCG019426.1,CCG0093
GO:0033176	proton-transporting V-type ATPase complex	3 of 3038 in the list	20 of 5465 in the genome	1	CCG010696.1,CCG000585.1,CCG012534.1
GO:0030288	outer membrane-bounded periplasmic	3 of 3038 in the list	22 of 5465 in the genome	1	CCG004844.1,CCG001584.1,CCG021686.1
GO:0030312	external encapsulating	3 of 3038 in the list	22 of 5465 in the genome	1	CCG004844.1,CCG001584.1,CCG021686.1
GO:0030313	cell envelope	3 of 3038 in the list	22 of 5465 in the genome	1	CCG004844.1,CCG001584.1,CCG021686.1

GO:0042597	periplasmic space	3 of 3038 in the list	22 of 5465 in the genome	1	CCG004844.1,CCG001584.1,CCG021686.1
GO:0044462	external encapsulating	3 of 3038 in the list	22 of 5465 in the genome	1	CCG004844.1,CCG001584.1,CCG021686.1
GO:0030529	ribonucleoprotein complex	113 of 3038 in the list	266 of 5465 in the genome	1	CCG023263.1,CCG014531.2,CCG016778.1,CCG004955.1,CCG008569.1,CCG027579.1,CCG027724.1,CCG013430.1,CCG007256.1,CCG006357.1,CCG024857.1,CCG003437.1,CCG004104.1,CCG004909.1,CCG003471.1,CCG016139.1,CCG026048.1,CCG002354.1,CCG010112.1,CCG005176.1,CCG007636.1,CCG019398.1,CCG006876.1,CCG007396.1,CCG016378.1,CCG003573.1,CCG025223.1,CCG008858.1,CCG024781.1,CCG007854.1,CCG000614.1,CCG008753.1,CCG003809.1,CCG009349.1,CCG011345.1,CCG028285.1,CCG018636.1,CCG002792.1,CCG019944.1,CCG008581.1,CCG019426.1,CCG026871.2,CCG027635.1,CCG009394.1,CCG002544.1,CCG002644.1,CCG024813.1,CCG008270.1,CCG006714.1,CCG013802.1,CCG005737.1,CCG028653.1,CCG002680.1,CCG006336.1,CCG022629.1,CCG005443.1,CCG014051.1,CCG011972.1,CCG013870.1,CCG009249.1,CCG014896.1,CCG026840.1,CCG002735.1,CCG001863.1,CCG007962.1,CCG000754.1,CCG004008.1,CCG002890.1,CCG018217.1,CCG021917.1,CCG022229.1,CCG007059.1,CCG005442.1,CCG003710.1,CCG018788.1,CCG009214.1,CCG006344.1,CCG013833.1,CCG027913.1,CCG020899.1,CCG026280.1,CCG002408.1,CCG016285.1,CCG023686.1,CCG024810.1,CCG020268.1,CCG017334.1,CCG002238.1,CCG021737.1,CCG000773.1,CCG025107.1,CCG021933.1,CCG006475.1,CCG025409.1,CCG019518.1,CCG016399.1,CCG023511.1,CCG018126.1,CCG004927.1,CCG020806.1,CCG002966.1,CCG018320.1,CCG013306.1,CCG018402.1,CCG013234.1,CCG010024.1,CCG001013.1,CCG011256.1,CCG027748.1,CCG020963.1,CCG002564.1,CCG018474.1,CCG007047.1

GO:0044444	cytoplasmic part	252 of 3038 in the list	558 of 5465 in the genome	1	CCG022047.1,CCG014531.2,CCG018832.1,CCG011932.1,CCG013032.1,CCG020245.1,CCG018536.1,CCG010159.1,CCG013430.1,CCG000663.1,CCG000585.1,CCG000205.1,CCG003437.1,CCG020949.1,CCG004909.1,CCG017528.1,CCG026048.1,CCG020879.1,CCG021053.1,CCG002354.1,CCG007330.1,CCG004091.1,CCG006391.1,CCG007396.1,CCG009685.1,CCG017614.1,CCG022453.1,CCG015843.1,CCG019217.1,CCG016378.1,CCG003573.1,CCG028505.1,CCG025223.1,CCG007854.1,CCG007246.2,CCG000614.1,CCG008753.1,CCG002823.1,CCG018128.1,CCG009434.1,CCG025521.1,CCG000890.1,CCG019944.1,CCG026871.2,CCG010939.1,CCG028332.1,CCG027412.1,CCG014171.1,CCG008323.1,CCG008270.1,CCG019210.1,CCG006714.1,CCG011862.1,CCG025277.1,CCG008592.1,CCG026514.1,CCG019558.1,CCG002930.1,CCG005737.1,CCG016673.1,CCG011972.1,CCG008896.1,CCG009249.1,CCG003215.3,CCG014896.1,CCG027415.1,CCG013390.1,CCG009082.1,CCG001863.1,CCG016493.2,CCG005191.1,CCG013509.1,CCG013131.1,CCG002890.1,CCG025309.1,CCG022229.1,CCG008871.1,CCG012534.1,CCG010417.2,CCG007059.1,CCG018788.1,CCG023114.1,CCG006344.1,CCG019082.1,CCG024119.1,CCG027913.1,CCG026280.1,CCG016285.1,CCG026240.1,CCG021737.1,CCG000773.1,CCG014304.1,CCG025233.1,CCG006077.1,CCG015410.1,CCG009142.1,CCG019560.1,CCG017197.1,CCG011510.1,CCG022214.1,CCG016399.1,CCG000552.1,CCG020806.1,CCG002966.1,CCG019712.1,CCG020634.1,CCG014228.2,CCG023756.1,CCG001013.1,CCG017125.1,CCG011256.1,CCG027748.1,CCG002937.1,CCG007047.1,CCG000294.1,CCG026698.1,CCG000789.1,CCG016778.1,CCG019892.1,CCG021819.1,CCG008569.1,CCG028409.1,CCG023617.1,CCG027724.1,CCG007256.1,CCG019590.1,CCG0110

GO:0005840	ribosome	79 of 3038 in the list	225 of 5465 in the genome	1	CCG014531.2,CCG016778.1,CCG008569.1,CCG027724.1,CCG013430.1,CCG007256.1,CCG003437.1,CCG004104.1,CCG004909.1,CCG003471.1,CCG016139.1,CCG026048.1,CCG002354.1,CCG010112.1,CCG019398.1,CCG006876.1,CCG007396.1,CCG003573.1,CCG016378.1,CCG025223.1,CCG024781.1,CCG007854.1,CCG008753.1,CCG003809.1,CCG009349.1,CCG011345.1,CCG019944.1,CCG008581.1,CCG019426.1,CCG026871.2,CCG009394.1,CCG002544.1,CCG002644.1,CCG024813.1,CCG008270.1,CCG005737.1,CCG002680.1,CCG006336.1,CCG005443.1,CCG011972.1,CCG013870.1,CCG014051.1,CCG009249.1,CCG014896.1,CCG001863.1,CCG002890.1,CCG021917.1,CCG022229.1,CCG005442.1,CCG007059.1,CCG003710.1,CCG018788.1,CCG006344.1,CCG013833.1,CCG027913.1,CCG020899.1,CCG026280.1,CCG016285.1,CCG002408.1,CCG020268.1,CCG017334.1,CCG002238.1,CCG021737.1,CCG000773.1,CCG025107.1,CCG021933.1,CCG025409.1,CCG006475.1,CCG019518.1,CCG016399.1,CCG018126.1,CCG002966.1,CCG013306.1,CCG013234.1,CCG011256.1,CCG001013.1,CCG027748.1,CCG020963.1,CCG007047.1

GO:0031224	intrinsic component of membrane	463 of 3038 in the list	1012 of 5465 in the genome	1	CCG012989.1,CCG023099.1,CCG001809.1,CCG014291.1,CCG001468.1,CCG024517.1,CCG013009.1,CCG019285.1,CCG003878.1,CCG020785.1,CCG022794.1,CCG002389.1,CCG007941.1,CCG017210.1,CCG014382.1,CCG003175.1,CCG016326.1,CCG010317.1,CCG019217.1,CCG002841.1,CCG023583.1,CCG001379.1,CCG005140.1,CCG023276.2,CCG012061.1,CCG026799.1,CCG025274.1,CCG022830.1,CCG009530.1,CCG003934.1,CCG017240.1,CCG018883.1,CCG012307.1,CCG000526.1,CCG027669.1,CCG019907.1,CCG015967.1,CCG018416.1,CCG019210.1,CCG010071.1,CCG027899.1,CCG003415.1,CCG016754.1,CCG002930.1,CCG001517.1,CCG019655.1,CCG000078.1,CCG009668.1,CCG010710.1,CCG024414.1,CCG005330.1,CCG009822.1,CCG007743.1,CCG026744.1,CCG004279.1,CCG013131.1,CCG016269.1,CCG003483.1,CCG024663.1,CCG011830.1,CCG022676.1,CCG014793.1,CCG015245.1,CCG016254.1,CCG016267.1,CCG027101.1,CCG003004.1,CCG021378.1,CCG018264.1,CCG015571.1,CCG008236.1,CCG005391.2,CCG018263.1,CCG007951.1,CCG004451.1,CCG016756.1,CCG019647.1,CCG015530.1,CCG026151.1,CCG022587.1,CCG000552.1,CCG012556.1,CCG023127.1,CCG026422.2,CCG016719.1,CCG013635.1,CCG018349.1,CCG028396.1,CCG000983.1,CCG010416.1,CCG017141.1,CCG027398.1,CCG024664.1,CCG022488.2,CCG016753.1,CCG011829.1,CCG024662.1,CCG026047.1,CCG023060.1,CCG008709.1,CCG011252.1,CCG020032.1,CCG000210.1,CCG004249.1,CCG009803.1,CCG017083.1,CCG004806.1,CCG017061.1,CCG006280.1,CCG027023.1,CCG015458.1,CCG020491.1,CCG014345.2,CCG005239.1,CCG021795.1,CCG025928.1,CCG016266.1,CCG019881.1,CCG025035.1,CCG011315.1,CCG022209.1,CCG000984.1,CCG022137.1,CCG012195.1,CCG008075.1,CCG017863.3,CCG0163

GO:0016021	integral component of membrane	452 of 3038 in the list	989 of 5465 in the genome	1	CCG012989.1,CCG023099.1,CCG001809.1,CCG014291.1,CCG001468.1,CCG024517.1,CCG013009.1,CCG019285.1,CCG003878.1,CCG020785.1,CCG022794.1,CCG002389.1,CCG007941.1,CCG017210.1,CCG014382.1,CCG003175.1,CCG016326.1,CCG010317.1,CCG019217.1,CCG002841.1,CCG023583.1,CCG001379.1,CCG005140.1,CCG023276.2,CCG012061.1,CCG026799.1,CCG025274.1,CCG022830.1,CCG009530.1,CCG003934.1,CCG017240.1,CCG018883.1,CCG012307.1,CCG000526.1,CCG019907.1,CCG018416.1,CCG019210.1,CCG010071.1,CCG027899.1,CCG003415.1,CCG016754.1,CCG001517.1,CCG019655.1,CCG000078.1,CCG009668.1,CCG010710.1,CCG024414.1,CCG005330.1,CCG009822.1,CCG007743.1,CCG026744.1,CCG004279.1,CCG013131.1,CCG016269.1,CCG003483.1,CCG024663.1,CCG011830.1,CCG022676.1,CCG014793.1,CCG015245.1,CCG016254.1,CCG016267.1,CCG027101.1,CCG003004.1,CCG021378.1,CCG018264.1,CCG015571.1,CCG008236.1,CCG005391.2,CCG018263.1,CCG007951.1,CCG004451.1,CCG016756.1,CCG019647.1,CCG015530.1,CCG026151.1,CCG022587.1,CCG012556.1,CCG023127.1,CCG026422.2,CCG016719.1,CCG013635.1,CCG018349.1,CCG028396.1,CCG000983.1,CCG010416.1,CCG017141.1,CCG027398.1,CCG024664.1,CCG022488.2,CCG016753.1,CCG011829.1,CCG024662.1,CCG026047.1,CCG023060.1,CCG008709.1,CCG011252.1,CCG020032.1,CCG000210.1,CCG004249.1,CCG009803.1,CCG017083.1,CCG004806.1,CCG017061.1,CCG006280.1,CCG027023.1,CCG015458.1,CCG020491.1,CCG014345.2,CCG005239.1,CCG021795.1,CCG025928.1,CCG016266.1,CCG019881.1,CCG025035.1,CCG011315.1,CCG000984.1,CCG022137.1,CCG012195.1,CCG008075.1,CCG017863.3,CCG016306.1,CCG011827.1,CCG009811.1,CCG004125.1,CCG018271.1,CCG0106

GO:0016020	membrane	901 of 3038 in the list	2043 of 5465 in the genome	1	CCG016021.1,CCG005307.1,CCG017420.1,CCG011932.1,CCG020245.1,CCG024345.1,CCG010623.2,CCG003545.1,CCG021740.1,CCG004086.1,CCG021738.1,CCG000585.1,CCG001057.1,CCG014291.1,CCG001468.1,CCG024517.1,CCG013009.1,CCG019285.1,CCG009428.1,CCG020785.1,CCG019768.1,CCG022794.1,CCG020013.1,CCG000411.1,CCG013708.1,CCG002841.1,CCG023583.1,CCG025472.1,CCG003712.1,CCG026799.1,CCG001219.2,CCG013130.1,CCG022830.1,CCG017851.1,CCG009530.1,CCG000554.1,CCG017240.1,CCG011200.2,CCG009407.1,CCG005053.1,CCG011237.1,CCG019190.1,CCG000526.1,CCG018661.1,CCG027669.1,CCG016654.1,CCG015967.1,CCG018416.1,CCG014240.1,CCG003415.1,CCG026050.1,CCG001964.1,CCG002930.1,CCG001517.1,CCG003624.1,CCG019655.1,CCG024365.1,CCG009668.1,CCG009822.1,CCG005191.1,CCG004279.1,CCG003483.1,CCG024431.1,CCG024663.1,CCG006588.2,CCG022676.1,CCG014793.1,CCG015245.1,CCG018494.1,CCG024222.1,CCG026953.1,CCG024119.1,CCG003004.1,CCG019678.1,CCG018264.1,CCG021854.1,CCG013641.1,CCG017477.1,CCG008236.1,CCG003495.1,CCG005391.2,CCG022168.1,CCG007951.1,CCG007597.1,CCG016756.1,CCG019647.1,CCG015530.1,CCG026151.1,CCG022587.1,CCG025131.2,CCG000552.1,CCG020634.1,CCG008444.1,CCG027182.1,CCG012023.1,CCG026422.2,CCG016719.1,CCG018349.1,CCG028396.1,CCG000983.1,CCG010416.1,CCG024664.1,CCG001285.1,CCG017381.1,CCG016753.1,CCG024662.1,CCG016263.1,CCG026047.1,CCG011252.1,CCG027692.1,CCG017947.1,CCG007356.1,CCG004249.1,CCG007766.1,CCG003273.1,CCG009803.1,CCG017061.1,CCG006280.1,CCG027023.1,CCG016347.1,CCG022802.1,CCG010112.1,CCG015458.1,CCG027889.1,CCG014760.1,CCG020491.1,CCG0143

GO:0044425	membrane part	519 of 3038 in the list	1149 of 5465 in the genome	1	CCG011932.1,CCG000585.1,CCG014291.1,CCG001468.1,CCG024517.1,CCG013009.1,CCG019285.1,CCG020785.1,CCG022794.1,CCG002841.1,CCG023583.1,CCG026799.1,CCG022830.1,CCG009530.1,CCG017240.1,CCG000526.1,CCG027669.1,CCG015967.1,CCG018416.1,CCG003415.1,CCG002930.1,CCG001517.1,CCG019655.1,CCG009668.1,CCG009822.1,CCG004279.1,CCG003483.1,CCG024663.1,CCG022676.1,CCG014793.1,CCG015245.1,CCG003004.1,CCG019678.1,CCG018264.1,CCG008236.1,CCG005391.2,CCG007951.1,CCG016756.1,CCG019647.1,CCG015530.1,CCG026151.1,CCG022587.1,CCG000552.1,CCG020634.1,CCG026422.2,CCG016719.1,CCG018349.1,CCG028396.1,CCG000983.1,CCG010416.1,CCG024664.1,CCG001285.1,CCG016753.1,CCG024662.1,CCG026047.1,CCG011252.1,CCG027692.1,CCG004249.1,CCG009803.1,CCG017061.1,CCG006280.1,CCG027023.1,CCG010112.1,CCG015458.1,CCG020491.1,CCG014345.2,CCG005239.1,CCG021795.1,CCG025928.1,CCG016266.1,CCG011315.1,CCG022137.1,CCG012195.1,CCG008075.1,CCG011827.1,CCG015986.1,CCG019611.1,CCG010711.1,CCG000148.1,CCG025510.1,CCG023190.1,CCG009553.1,CCG026979.1,CCG024760.1,CCG027257.1,CCG004226.1,CCG023002.1,CCG023662.1,CCG017641.1,CCG023779.1,CCG017094.1,CCG016459.1,CCG003009.1,CCG025334.1,CCG017696.1,CCG026370.1,CCG015800.2,CCG002839.1,CCG022510.1,CCG009928.1,CCG018930.1,CCG027014.1,CCG010948.1,CCG007317.1,CCG016956.1,CCG001066.1,CCG011297.1,CCG007691.1,CCG007724.1,CCG017398.1,CCG027971.1,CCG005800.1,CCG025568.1,CCG003681.1,CCG007862.1,CCG017241.1,CCG009368.1,CCG021273.1,CCG016669.1,CCG024625.1,CCG010559.1,CCG009127.1,CCG021862.1,CCG018265.1,CCG012988.1,CCG003110.1,CCG0273