Table S7.5. Full list of Biological Process 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 use	Corrected P-value	Genes annotated to the term
GO:0016070	RNA metabolic process	291 of 4104 in the list	409 of 8404 in the genome	5.99E-18	CCG023277.1,CCG014396.1,CCG019030.1,CCG010191.3, CCG006357.1,CCG009878.1,CCG010647.1,CCG016758.1, CCG024072.1,CCG026882.1,CCG012142.1,CCG018507.1, CCG020685.1,CCG016238.1,CCG026473.1,CCG001292.1, CCG023173.1,CCG002470.1,CCG020804.1,CCG001040.1, CCG019031.1,CCG014679.1,CCG019382.1,CCG015546.1, CCG018719.1,CCG010792.1,CCG004231.1,CCG023053.1, CCG027115.1,CCG020129.1,CCG023129.1,CCG028653.1, CCG028042.1,CCG009235.1,CCG020877.1,CCG014946.1, CCG006231.1,CCG020286.1,CCG002735.1,CCG006767.1, CCG019296.1,CCG022470.1,CCG014840.1,CCG015694.1, CCG006484.1,CCG001461.1,CCG023686.1,CCG010510.1, CCG003938.1,CCG008401.1,CCG018902.1,CCG003755.1, CCG004927.1,CCG009805.2,CCG019545.1,CCG003142.1, CCG019330.1,CCG011060.1,CCG001876.1,CCG018402.1, CCG024200.1,CCG023125.1,CCG010624.1,CCG016381.1, CCG015894.1,CCG026612.1,CCG004926.1,CCG010912.1, CCG004955.1,CCG015367.1,CCG005524.1,CCG007155.1, CCG024857.1,CCG026516.1,CCG018164.1,CCG004224.1, CCG011135.1,CCG028092.1,CCG000209.1,CCG016760.1, CCG021521.1,CCG001395.1,CCG016557.1,CCG023184.1, CCG003153.1,CCG000939.1,CCG021940.1,CCG013174.1, CCG027340.1,CCG022183.1,CCG018168.1,CCG017344.1, CCG018796.1,CCG025691.1,CCG027401.1,CCG014824.1, CCG018243.1,CCG027950.1,CCG024597.1,CCG012278.1, CCG001898.1,CCG016685.1,CCG026840.1,CCG010797.1, CCG004008.1,CCG010138.1,CCG024480.1,CCG008916.1, CCG004151.1,CCG009214.1,CCG012557.1,CCG017046.2, CCG021716.1,CCG012837.1,CCG002662.1,CCG021042.1, CCG008036.1,CCG007177.1,CCG003528.1,CCG025157.1,

GO:0033554	cellular response to stress	89 of 4104 in the list	102 of 8404 in the genome	2.66E-13	CCG027300.1,CCG021045.1,CCG006606.1,CCG004744.1, CCG021759.1,CCG026841.1,CCG019574.1,CCG026106.1, CCG018745.1,CCG022772.1,CCG022628.1,CCG027501.1, CCG005110.1,CCG024570.2,CCG013625.1,CCG019488.1, CCG007693.1,CCG006284.1,CCG003658.1,CCG018321.1, CCG006133.1,CCG012315.1,CCG007758.1,CCG000213.1, CCG017444.1,CCG004593.1,CCG005594.1,CCG001808.2, CCG005395.1,CCG008816.1,CCG024804.1,CCG016094.1, CCG023474.1,CCG005481.1,CCG011328.1,CCG004515.1, CCG024792.1,CCG000777.1,CCG019692.1,CCG011015.1, CCG012803.2,CCG003863.1,CCG004233.1,CCG000776.1, CCG018799.1,CCG006734.1,CCG018472.1,CCG005070.1, CCG005241.1,CCG014548.1,CCG015980.1,CCG004804.1, CCG001083.1,CCG027133.1,CCG004438.1,CCG017906.1, CCG007765.1,CCG002366.1,CCG009962.1,CCG007063.1, CCG024073.1,CCG006220.1,CCG012140.1,CCG018744.1, CCG006919.1,CCG023155.1,CCG012164.1,CCG004402.1, CCG017910.1,CCG000929.1,CCG002364.1,CCG001769.1, CCG000490.1,CCG027040.1,CCG005379.2,CCG028027.1, CCG021747.1,CCG020439.2,CCG005284.1,CCG003940.1, CCG018211.1,CCG024289.1,CCG001009.1,CCG000834.1,

GO:0006974	cellular response to DNA damage stimulus	87 of 4104 in the list	100 of 8404 in the genome	8.70E-13	CCG027300.1,CCG021045.1,CCG006606.1,CCG004744.1, CCG021759.1,CCG026841.1,CCG019574.1,CCG026106.1, CCG018745.1,CCG022772.1,CCG022628.1,CCG027501.1, CCG005110.1,CCG024570.2,CCG013625.1,CCG019488.1, CCG007693.1,CCG006284.1,CCG003658.1,CCG018321.1, CCG006133.1,CCG012315.1,CCG007758.1,CCG000213.1, CCG017444.1,CCG004593.1,CCG005594.1,CCG001808.2, CCG005395.1,CCG008816.1,CCG024804.1,CCG016094.1, CCG023474.1,CCG005481.1,CCG011328.1,CCG004515.1, CCG024792.1,CCG000777.1,CCG019692.1,CCG011015.1, CCG012803.2,CCG003863.1,CCG004233.1,CCG000776.1, CCG018799.1,CCG006734.1,CCG018472.1,CCG005070.1, CCG005241.1,CCG014548.1,CCG015980.1,CCG004804.1, CCG001083.1,CCG027133.1,CCG004438.1,CCG017906.1, CCG007765.1,CCG009962.1,CCG007063.1,CCG024073.1, CCG006220.1,CCG012140.1,CCG018744.1,CCG006919.1, CCG023155.1,CCG012164.1,CCG004402.1,CCG017910.1, CCG000929.1,CCG002364.1,CCG000490.1,CCG001769.1, CCG027040.1,CCG005379.2,CCG028027.1,CCG021747.1, CCG020439.2,CCG005284.1,CCG003940.1,CCG018211.1, CCG024289.1,CCG001009.1,CCG003518.3,CCG020156.1,

GO:0006281	DNA repair	85 of 4104 in the list	98 of 8404 in the genome	2.81E-12	CCG027300.1,CCG021045.1,CCG006606.1,CCG004744.1, CCG021759.1,CCG019574.1,CCG026106.1,CCG018745.1, CCG022772.1,CCG022628.1,CCG027501.1,CCG005110.1, CCG024570.2,CCG013625.1,CCG019488.1,CCG007693.1, CCG006284.1,CCG003658.1,CCG006133.1,CCG012315.1, CCG007758.1,CCG000213.1,CCG017444.1,CCG004593.1, CCG005594.1,CCG001808.2,CCG005395.1,CCG008816.1, CCG024804.1,CCG016094.1,CCG023474.1,CCG005481.1, CCG011328.1,CCG004515.1,CCG024792.1,CCG000777.1, CCG019692.1,CCG011015.1,CCG012803.2,CCG003863.1, CCG004233.1,CCG000776.1,CCG018799.1,CCG006734.1, CCG018472.1,CCG005070.1,CCG005241.1,CCG014548.1, CCG015980.1,CCG004804.1,CCG001083.1,CCG027133.1, CCG004438.1,CCG017906.1,CCG007765.1,CCG009962.1, CCG007063.1,CCG024073.1,CCG006220.1,CCG012140.1, CCG018744.1,CCG006919.1,CCG023155.1,CCG012164.1, CCG004402.1,CCG017910.1,CCG000929.1,CCG002364.1, CCG000490.1,CCG001769.1,CCG027040.1,CCG005379.2, CCG028027.1,CCG021747.1,CCG020439.2,CCG005284.1, CCG003940.1,CCG018211.1,CCG024289.1,CCG001009.1,

GO:0006396	RNA processing	134 of 4104 in the list	175 of 8404 in the genome	3.31E-11	CCG023263.1,CCG006357.1,CCG023964.1,CCG016758.1, CCG004234.1,CCG024072.1,CCG012142.1,CCG004820.1, CCG020113.1,CCG016274.1,CCG020685.1,CCG007914.1, CCG019012.1,CCG023173.1,CCG017408.1,CCG020804.1, CCG000806.1,CCG014524.1,CCG001040.1,CCG018311.1, CCG007043.1,CCG019382.1,CCG028285.1,CCG018636.1, CCG015546.1,CCG010792.1,CCG004231.1,CCG023053.1, CCG005834.1,CCG002221.1,CCG027115.1,CCG001268.1, CCG023129.1,CCG013802.1,CCG028042.1,CCG009235.1, CCG020286.1,CCG002735.1,CCG000754.1,CCG002674.1, CCG024717.1,CCG024611.1,CCG000427.1,CCG001461.1, CCG023686.1,CCG001317.1,CCG024810.1,CCG005020.1, CCG003938.1,CCG010460.1,CCG004228.1,CCG018902.1, CCG023511.1,CCG004927.1,CCG014142.1,CCG018320.1, CCG018402.1,CCG010624.1,CCG025958.1,CCG000583.2, CCG009033.1,CCG025926.1,CCG015894.1,CCG026612.1, CCG006039.1,CCG014335.1,CCG004955.1,CCG026872.2, CCG010912.1,CCG025357.1,CCG005524.1,CCG006948.1, CCG027579.1,CCG024857.1,CCG026516.1,CCG020967.1, CCG003055.1,CCG007636.1,CCG005176.1,CCG014279.1, CCG023156.1,CCG016760.1,CCG001310.1,CCG001395.1, CCG008858.1,CCG003785.1,CCG000939.1,CCG003153.1, CCG028049.1,CCG022183.1,CCG002449.1,CCG014824.1, CCG005174.1,CCG019674.1,CCG027962.1,CCG012278.1, CCG006043.1,CCG007777.1,CCG001898.1,CCG022629.1, CCG016251.1,CCG017986.1,CCG016685.1,CCG026840.1, CCG007962.1,CCG010539.1,CCG004008.1,CCG023521.1, CCG024480.1,CCG008916.1,CCG018917.1,CCG019953.1, CCG009214.1,CCG012557.1,CCG004440.1,CCG012837.1, CCG021042.1,CCG005178.3,CCG008036.1,CCG000393.1,

GO:0043412	macromolecule modification	374 of 4104 in the list	590 of 8404 in the genome	1.30E-10	CCG023297.1,CCG018536.1,CCG027737.1,CCG004887.1, CCG009151.1,CCG021449.1,CCG002687.2,CCG016952.1, CCG010985.1,CCG026174.1,CCG024745.1,CCG028333.1, CCG004091.1,CCG025472.1,CCG001788.1,CCG018432.1, CCG017266.1,CCG028198.1,CCG016689.2,CCG021479.1, CCG003362.1,CCG026300.1,CCG023381.1,CCG019735.1, CCG015296.1,CCG012077.1,CCG008381.1,CCG021616.1, CCG013914.1,CCG019210.1,CCG013402.1,CCG008301.1, CCG010776.1,CCG020055.1,CCG017984.1,CCG019378.3, CCG024612.1,CCG027636.1,CCG028653.1,CCG026212.1, CCG004569.1,CCG024139.1,CCG014946.1,CCG008040.1, CCG002156.2,CCG011071.1,CCG013109.1,CCG009002.1, CCG011949.1,CCG013345.1,CCG013131.1,CCG006465.1, CCG004212.1,CCG003248.1,CCG020010.1,CCG016189.1, CCG011322.1,CCG018494.1,CCG012083.1,CCG001311.1, CCG023251.1,CCG016480.1,CCG004101.1,CCG022627.1, CCG007457.1,CCG023331.1,CCG012332.1,CCG025715.1, CCG009687.2,CCG008401.1,CCG017127.1,CCG002957.1, CCG011587.1,CCG003755.1,CCG000552.1,CCG022056.1, CCG003532.1,CCG008557.1,CCG015186.1,CCG016327.2, CCG018688.1,CCG004903.1,CCG023458.1,CCG027943.1, CCG017113.1,CCG011886.1,CCG016095.1,CCG003520.1, CCG006928.1,CCG016738.2,CCG003060.1,CCG017381.1, CCG025433.1,CCG003554.1,CCG007874.3,CCG020978.1, CCG007331.2,CCG008404.1,CCG018201.1,CCG022628.1, CCG007766.1,CCG004806.1,CCG021179.1,CCG001108.1, CCG022370.1,CCG004123.1,CCG005531.1,CCG009038.1, CCG025707.1,CCG020078.1,CCG020837.1,CCG016294.1, CCG007485.1,CCG016557.1,CCG001051.1,CCG019139.1, CCG021825.3,CCG022209.1,CCG024922.1,CCG027340.1,

GO:0006950	response to stress	133 of 4104 in the list	182 of 8404 in the genome	1.65E-08	CCG027300.1,CCG006606.1,CCG023237.1,CCG004744.1, CCG019574.1,CCG026106.1,CCG018745.1,CCG005110.1, CCG013625.1,CCG019488.1,CCG003658.1,CCG015596.1, CCG018321.1,CCG016035.1,CCG007758.1,CCG000213.1, CCG003448.1,CCG004593.1,CCG025714.1,CCG005170.1, CCG005395.1,CCG017244.1,CCG016094.1,CCG023474.1, CCG011328.1,CCG004515.1,CCG024792.1,CCG000777.1, CCG004145.1,CCG019692.1,CCG012803.2,CCG027669.1, CCG003863.1,CCG015967.1,CCG004233.1,CCG000776.1, CCG018799.1,CCG018472.1,CCG004168.2,CCG015980.1, CCG004804.1,CCG027133.1,CCG001083.1,CCG002366.1, CCG024073.1,CCG006220.1,CCG004723.1,CCG012140.1, CCG005913.1,CCG009672.1,CCG006919.1,CCG023155.1, CCG011939.1,CCG004402.1,CCG022399.1,CCG027668.1, CCG002364.1,CCG011122.1,CCG001769.1,CCG005379.2, CCG017425.1,CCG005284.1,CCG024289.1,CCG023940.1, CCG000116.1,CCG000834.1,CCG020156.1,CCG000409.1, CCG015966.1,CCG009231.1,CCG021045.1,CCG021759.1, CCG026841.1,CCG022628.1,CCG022772.1,CCG025005.1, CCG025006.1,CCG024878.1,CCG027501.1,CCG024570.2, CCG007693.1,CCG027211.1,CCG015458.1,CCG006284.1, CCG006133.1,CCG006124.1,CCG012315.1,CCG005594.1, CCG017444.1,CCG008075.1,CCG001808.2,CCG008816.1, CCG024804.1,CCG005481.1,CCG002446.2,CCG011015.1, CCG008821.1,CCG021072.1,CCG006734.1,CCG005070.1, CCG005241.1,CCG014548.1,CCG012274.1,CCG004438.1, CCG017906.1,CCG007765.1,CCG012273.2,CCG003252.1, CCG009962.1,CCG007063.1,CCG018744.1,CCG024173.1, CCG012164.1,CCG017910.1,CCG004753.1,CCG000929.1, CCG000490.1,CCG021071.1,CCG027040.1,CCG028027.1,

GO:0006464	cellular protein modification process	342 of 4104 in the list	550 of 8404 in the genome	5.84E-08	CCG023297.1,CCG018536.1,CCG027737.1,CCG004887.1, CCG009151.1,CCG021449.1,CCG002687.2,CCG016952.1, CCG010985.1,CCG026174.1,CCG024745.1,CCG028333.1, CCG004091.1,CCG025472.1,CCG001788.1,CCG018432.1, CCG017266.1,CCG028198.1,CCG016689.2,CCG021479.1, CCG003362.1,CCG026300.1,CCG023381.1,CCG019735.1, CCG015296.1,CCG012077.1,CCG008381.1,CCG021616.1, CCG013914.1,CCG019210.1,CCG013402.1,CCG008301.1, CCG010776.1,CCG020055.1,CCG017984.1,CCG019378.3, CCG024612.1,CCG027636.1,CCG026212.1,CCG004569.1, CCG024139.1,CCG008040.1,CCG002156.2,CCG011071.1, CCG013109.1,CCG009002.1,CCG011949.1,CCG013345.1, CCG013131.1,CCG006465.1,CCG004212.1,CCG003248.1, CCG020010.1,CCG016189.1,CCG011322.1,CCG018494.1, CCG012083.1,CCG001311.1,CCG023251.1,CCG016480.1, CCG004101.1,CCG022627.1,CCG007457.1,CCG023331.1, CCG012332.1,CCG025715.1,CCG009687.2,CCG017127.1, CCG002957.1,CCG011587.1,CCG000552.1,CCG022056.1, CCG003532.1,CCG008557.1,CCG015186.1,CCG016327.2, CCG018688.1,CCG004903.1,CCG023458.1,CCG027943.1, CCG017113.1,CCG011886.1,CCG016095.1,CCG003520.1, CCG006928.1,CCG016738.2,CCG003060.1,CCG017381.1, CCG025433.1,CCG003554.1,CCG007874.3,CCG020978.1, CCG007331.2,CCG008404.1,CCG018201.1,CCG022628.1, CCG007766.1,CCG004806.1,CCG021179.1,CCG001108.1, CCG022370.1,CCG004123.1,CCG005531.1,CCG009038.1, CCG025707.1,CCG020078.1,CCG020837.1,CCG016294.1, CCG007485.1,CCG001051.1,CCG019139.1,CCG021825.3, CCG022209.1,CCG024922.1,CCG014839.1,CCG007600.1, CCG008307.1,CCG006804.1,CCG014579.1,CCG014798.2,

GO:0036211	protein modification process	342 of 4104 in the list	550 of 8404 in the genome	5.84E-08	CCG023297.1,CCG018536.1,CCG027737.1,CCG004887.1, CCG009151.1,CCG021449.1,CCG002687.2,CCG016952.1, CCG010985.1,CCG026174.1,CCG024745.1,CCG028333.1, CCG004091.1,CCG025472.1,CCG001788.1,CCG018432.1, CCG017266.1,CCG028198.1,CCG016689.2,CCG021479.1, CCG003362.1,CCG026300.1,CCG023381.1,CCG019735.1, CCG015296.1,CCG012077.1,CCG008381.1,CCG021616.1, CCG013914.1,CCG019210.1,CCG013402.1,CCG008301.1, CCG010776.1,CCG020055.1,CCG017984.1,CCG019378.3, CCG024612.1,CCG027636.1,CCG026212.1,CCG004569.1, CCG024139.1,CCG008040.1,CCG002156.2,CCG011071.1, CCG013109.1,CCG009002.1,CCG011949.1,CCG013345.1, CCG013131.1,CCG006465.1,CCG004212.1,CCG003248.1, CCG020010.1,CCG016189.1,CCG011322.1,CCG018494.1, CCG012083.1,CCG001311.1,CCG023251.1,CCG016480.1, CCG004101.1,CCG022627.1,CCG007457.1,CCG023331.1, CCG012332.1,CCG025715.1,CCG009687.2,CCG017127.1, CCG002957.1,CCG011587.1,CCG000552.1,CCG022056.1, CCG003532.1,CCG008557.1,CCG015186.1,CCG016327.2, CCG018688.1,CCG004903.1,CCG023458.1,CCG027943.1, CCG017113.1,CCG011886.1,CCG016095.1,CCG003520.1, CCG006928.1,CCG016738.2,CCG003060.1,CCG017381.1, CCG025433.1,CCG003554.1,CCG007874.3,CCG020978.1, CCG007331.2,CCG008404.1,CCG018201.1,CCG022628.1, CCG007766.1,CCG004806.1,CCG021179.1,CCG001108.1, CCG022370.1,CCG004123.1,CCG005531.1,CCG009038.1, CCG025707.1,CCG020078.1,CCG020837.1,CCG016294.1, CCG007485.1,CCG001051.1,CCG019139.1,CCG021825.3, CCG022209.1,CCG024922.1,CCG014839.1,CCG007600.1, CCG008307.1,CCG006804.1,CCG014579.1,CCG014798.2,

GO:0034660	ncRNA metabolic process	106 of 4104 in the list	141 of 8404 in the genome	1.19E-07	CCG023263.1,CCG021774.1,CCG023277.1,CCG014396.1, CCG015367.1,CCG025357.1,CCG027579.1,CCG010191.3, CCG006357.1,CCG009878.1,CCG023964.1,CCG016758.1, CCG006188.1,CCG004234.1,CCG027352.3,CCG015950.3, CCG003055.1,CCG020113.1,CCG016274.1,CCG020685.1, CCG005176.1,CCG007636.1,CCG016238.1,CCG011135.1, CCG014279.1,CCG023156.1,CCG028092.1,CCG019012.1, CCG013727.1,CCG023173.1,CCG016760.1,CCG020804.1, CCG027607.1,CCG018311.1,CCG000939.1,CCG010321.1, CCG022183.1,CCG018636.1,CCG002792.1,CCG017344.1, CCG000138.1,CCG015577.3,CCG002449.1,CCG014824.1, CCG023053.1,CCG002221.1,CCG019674.1,CCG023129.1, CCG000414.1,CCG012278.1,CCG028653.1,CCG006043.1, CCG002018.1,CCG022629.1,CCG016251.1,CCG020877.1, CCG006231.1,CCG008321.1,CCG020286.1,CCG002735.1, CCG007962.1,CCG010539.1,CCG001811.1,CCG023521.1, CCG008916.1,CCG004949.1,CCG002674.1,CCG019953.1, CCG005204.1,CCG009214.1,CCG000540.1,CCG001317.1, CCG021716.1,CCG004440.1,CCG005020.1,CCG021820.1, CCG010460.1,CCG006570.1,CCG002662.1,CCG000352.1, CCG004228.1,CCG023315.1,CCG003528.1,CCG016652.1, CCG010541.1,CCG010565.1,CCG023511.1,CCG000655.1, CCG005097.1,CCG005849.1,CCG014142.1,CCG003296.1, CCG019545.1,CCG009393.1,CCG019330.1,CCG022269.1, CCG001876.1,CCG026725.1,CCG026570.1,CCG000583.2,

GO:0006793	phosphorus metabolic process	444 of 4104 in the list	750 of 8404 in the genome	1.72E-06	CCG017420.1,CCG023297.1,CCG027737.1,CCG004887.1, CCG002687.2,CCG019020.1,CCG016952.1,CCG012875.1, CCG020879.1,CCG010985.1,CCG026174.1,CCG024745.1, CCG000970.1,CCG011006.1,CCG027119.1,CCG012558.1, CCG001788.1,CCG024297.1,CCG017266.1,CCG028198.1, CCG016689.2,CCG021479.1,CCG003362.1,CCG026300.1, CCG025307.1,CCG023381.1,CCG019735.1,CCG007993.1, CCG015296.1,CCG016370.1,CCG016653.1,CCG011237.1, CCG008381.1,CCG021616.1,CCG013216.1,CCG013402.1, CCG021110.1,CCG010776.1,CCG020055.1,CCG017984.1, CCG019378.3,CCG024612.1,CCG027636.1,CCG026212.1, CCG004569.1,CCG024139.1,CCG008040.1,CCG002156.2, CCG009002.1,CCG011949.1,CCG013345.1,CCG013131.1, CCG006465.1,CCG004212.1,CCG003248.1,CCG020010.1, CCG011322.1,CCG018113.1,CCG025396.1,CCG018494.1, CCG028131.1,CCG026953.1,CCG001311.1,CCG023251.1, CCG004101.1,CCG022627.1,CCG024432.2,CCG002675.1, CCG019678.1,CCG007457.1,CCG023331.1,CCG013641.1, CCG012332.1,CCG025715.1,CCG003495.1,CCG009687.2, CCG017127.1,CCG002957.1,CCG003683.2,CCG011587.1, CCG025131.2,CCG000552.1,CCG023452.1,CCG014116.1, CCG002852.1,CCG024903.1,CCG013610.1,CCG015186.1, CCG009518.1,CCG016327.2,CCG018688.1,CCG014228.2, CCG007362.1,CCG004903.1,CCG023458.1,CCG026865.1, CCG027943.1,CCG017113.1,CCG011886.1,CCG016095.1, CCG003520.1,CCG001285.1,CCG006928.1,CCG004532.1, CCG016738.2,CCG000789.1,CCG025433.1,CCG003554.1, CCG007874.3,CCG026047.1,CCG020978.1,CCG010014.1, CCG008404.1,CCG018201.1,CCG006529.1,CCG022628.1, CCG004806.1,CCG008287.1,CCG021179.1,CCG001108.1,

GO:0006796	phosphate-containing compound metabolic process	441 of 4104 in the list	747 of 8404 in the genome	3.30E-06	CCG017420.1,CCG023297.1,CCG027737.1,CCG004887.1, CCG002687.2,CCG019020.1,CCG016952.1,CCG012875.1, CCG020879.1,CCG010985.1,CCG026174.1,CCG024745.1, CCG000970.1,CCG011006.1,CCG027119.1,CCG012558.1, CCG001788.1,CCG024297.1,CCG017266.1,CCG028198.1, CCG016689.2,CCG021479.1,CCG003362.1,CCG026300.1, CCG025307.1,CCG023381.1,CCG019735.1,CCG007993.1, CCG015296.1,CCG016370.1,CCG016653.1,CCG011237.1, CCG008381.1,CCG021616.1,CCG013402.1,CCG021110.1, CCG010776.1,CCG020055.1,CCG017984.1,CCG019378.3, CCG024612.1,CCG027636.1,CCG026212.1,CCG004569.1, CCG024139.1,CCG008040.1,CCG002156.2,CCG009002.1, CCG011949.1,CCG013345.1,CCG013131.1,CCG006465.1, CCG004212.1,CCG003248.1,CCG020010.1,CCG011322.1, CCG025396.1,CCG018494.1,CCG028131.1,CCG026953.1, CCG001311.1,CCG023251.1,CCG004101.1,CCG022627.1, CCG024432.2,CCG002675.1,CCG019678.1,CCG007457.1, CCG023331.1,CCG013641.1,CCG012332.1,CCG025715.1, CCG003495.1,CCG009687.2,CCG017127.1,CCG002957.1, CCG011587.1,CCG025131.2,CCG000552.1,CCG023452.1, CCG014116.1,CCG002852.1,CCG024903.1,CCG013610.1, CCG015186.1,CCG009518.1,CCG016327.2,CCG018688.1, CCG014228.2,CCG007362.1,CCG004903.1,CCG023458.1, CCG026865.1,CCG027943.1,CCG017113.1,CCG011886.1, CCG016095.1,CCG003520.1,CCG001285.1,CCG006928.1, CCG004532.1,CCG016738.2,CCG000789.1,CCG025433.1, CCG003554.1,CCG007874.3,CCG026047.1,CCG020978.1, CCG010014.1,CCG008404.1,CCG018201.1,CCG006529.1, CCG022628.1,CCG004806.1,CCG008287.1,CCG021179.1, CCG001108.1,CCG007533.1,CCG008422.1,CCG004123.1,

GO:0034470	ncRNA processing	56 of 4104 in the list	68 of 8404 in the genome	1.04E-05	CCG016251.1,CCG023263.1,CCG020286.1,CCG025357.1, CCG002735.1,CCG027579.1,CCG010539.1,CCG007962.1, CCG006357.1,CCG023521.1,CCG008916.1,CCG023964.1, CCG016758.1,CCG004234.1,CCG002674.1,CCG019953.1, CCG009214.1,CCG003055.1,CCG020113.1,CCG016274.1, CCG005176.1,CCG007636.1,CCG014279.1,CCG023156.1, CCG019012.1,CCG023173.1,CCG001317.1,CCG004440.1, CCG016760.1,CCG005020.1,CCG010460.1,CCG020804.1, CCG004228.1,CCG018311.1,CCG000939.1,CCG022183.1, CCG018636.1,CCG010541.1,CCG023511.1,CCG002449.1, CCG000655.1,CCG005097.1,CCG005849.1,CCG014142.1, CCG014824.1,CCG009393.1,CCG023053.1,CCG026725.1, CCG002221.1,CCG000583.2,CCG027125.1,CCG023129.1, CCG018474.1,CCG012278.1,CCG006043.1,CCG022629.1

GO:0044763	single-organism cellular process	1273 of 4104 in the list	2370 of 8404 in the genome	1.27E-05	CCG005254.1,CCG017420.1,CCG014340.1,CCG005375.1, CCG014396.1,CCG026106.1,CCG021740.1,CCG005370.1, CCG001468.1,CCG004595.1,CCG012875.1,CCG025108.1, CCG026174.1,CCG022794.1,CCG003587.1,CCG026360.1, CCG018432.1,CCG017266.1,CCG016689.2,CCG014466.1, CCG017851.1,CCG009530.1,CCG020956.1,CCG017240.1, CCG015101.1,CCG016094.1,CCG023474.1,CCG027127.1, CCG022025.2,CCG005053.1,CCG011237.1,CCG018533.1, CCG000526.1,CCG022281.1,CCG018416.1,CCG013308.1, CCG023579.1,CCG021110.1,CCG026050.1,CCG024612.1, CCG009668.1,CCG004548.1,CCG024663.1,CCG021681.1, CCG012083.1,CCG026953.1,CCG010622.1,CCG024119.1, CCG019678.1,CCG023464.1,CCG018264.1,CCG001579.1, CCG013641.1,CCG016924.1,CCG000732.1,CCG003317.1, CCG005391.2,CCG007951.1,CCG018585.3,CCG007597.1, CCG016399.1,CCG005284.1,CCG024903.1,CCG013610.1, CCG009959.1,CCG001876.1,CCG002231.1,CCG016719.1, CCG000983.1,CCG009823.1,CCG002937.1,CCG000876.1, CCG024664.1,CCG004532.1,CCG000789.1,CCG017381.1, CCG005588.1,CCG016753.1,CCG011547.1,CCG011252.1, CCG007356.1,CCG009333.1,CCG008939.1,CCG015407.1, CCG010112.1,CCG028092.1,CCG006479.1,CCG020491.1, CCG014345.2,CCG019825.2,CCG024155.1,CCG019884.1, CCG021990.1,CCG005594.1,CCG008075.1,CCG012195.1, CCG010561.1,CCG011827.1,CCG006787.1,CCG022871.1, CCG020654.1,CCG002135.1,CCG019611.1,CCG006804.1, CCG007023.1,CCG009553.1,CCG024760.1,CCG024918.1, CCG023662.1,CCG011015.1,CCG007958.1,CCG023779.1, CCG016459.1,CCG012959.1,CCG006013.1,CCG017112.1, CCG024421.3,CCG016836.2,CCG025897.1,CCG019890.1,

GO:0006399	tRNA metabolic process	83 of 4104 in the list	112 of 8404 in the genome	3.98E-05	CCG021774.1,CCG023277.1,CCG014396.1,CCG015367.1, CCG025357.1,CCG010191.3,CCG009878.1,CCG023964.1, CCG016758.1,CCG006188.1,CCG004234.1,CCG027352.3, CCG015950.3,CCG020113.1,CCG007636.1,CCG016238.1, CCG014279.1,CCG011135.1,CCG023156.1,CCG028092.1, CCG013727.1,CCG019012.1,CCG023173.1,CCG020804.1, CCG027607.1,CCG018311.1,CCG000939.1,CCG010321.1, CCG022183.1,CCG017344.1,CCG000138.1,CCG015577.3, CCG002449.1,CCG014824.1,CCG002221.1,CCG023129.1, CCG000414.1,CCG012278.1,CCG006043.1,CCG002018.1, CCG016251.1,CCG020877.1,CCG008321.1,CCG006231.1, CCG020286.1,CCG010539.1,CCG001811.1,CCG023521.1, CCG008916.1,CCG004949.1,CCG002674.1,CCG005204.1, CCG001317.1,CCG021716.1,CCG004440.1,CCG005020.1, CCG021820.1,CCG010460.1,CCG006570.1,CCG002662.1, CCG000352.1,CCG004228.1,CCG023315.1,CCG003528.1, CCG010541.1,CCG010565.1,CCG023511.1,CCG000655.1, CCG014142.1,CCG003296.1,CCG019545.1,CCG009393.1, CCG019330.1,CCG001876.1,CCG022269.1,CCG026725.1, CCG026570.1,CCG000583.2,CCG027125.1,CCG008789.1,

GO:0044710	single-organism metabolic process	973 of 4104 in the list	1786 of 8404 in the genome	4.72E-05	CCG012202.1,CCG017420.1,CCG027300.1,CCG014396.1, CCG000184.1,CCG008603.1,CCG026106.1,CCG015926.1, CCG028623.1,CCG009878.1,CCG019182.1,CCG020913.1, CCG004595.1,CCG012875.1,CCG024517.1,CCG025108.1, CCG009904.1,CCG026174.1,CCG013625.1,CCG016238.1, CCG016220.1,CCG010284.1,CCG013059.1,CCG025836.1, CCG025472.1,CCG012949.1,CCG024297.1,CCG018432.1, CCG012578.1,CCG007424.2,CCG009496.1,CCG011763.1, CCG005616.1,CCG010038.1,CCG025307.1,CCG020956.1, CCG016370.1,CCG025346.1,CCG017624.1,CCG016094.1, CCG023474.1,CCG017255.1,CCG000948.1,CCG022025.2, CCG005053.1,CCG011237.1,CCG024123.2,CCG000944.1, CCG007420.1,CCG011722.1,CCG021110.1,CCG010246.1, CCG003063.1,CCG017651.1,CCG024612.1,CCG015450.1, CCG018253.1,CCG020660.1,CCG027133.1,CCG018625.1, CCG011231.2,CCG025396.1,CCG012083.1,CCG013816.1, CCG026953.1,CCG023451.1,CCG005913.1,CCG024119.1, CCG018290.1,CCG012339.1,CCG004402.1,CCG019678.1, CCG018257.1,CCG022399.1,CCG017982.1,CCG011895.1, CCG013641.1,CCG006821.1,CCG002113.1,CCG003495.1, CCG009662.1,CCG013318.1,CCG022214.1,CCG011891.1, CCG012840.1,CCG000775.1,CCG025131.2,CCG005284.1, CCG000552.1,CCG023452.1,CCG002852.1,CCG024903.1, CCG019545.1,CCG013610.1,CCG001876.1,CCG009518.1, CCG002231.1,CCG008902.1,CCG000834.1,CCG026865.1, CCG025096.1,CCG025015.2,CCG008388.1,CCG001285.1, CCG004532.1,CCG000789.1,CCG019844.1,CCG017381.1, CCG026016.1,CCG005588.1,CCG015367.1,CCG026047.1, CCG011547.1,CCG005162.1,CCG015537.1,CCG008437.1, CCG011491.1,CCG022772.1,CCG009333.1,CCG012619.1,

GO:0008033	tRNA processing	39 of 4104 in the list	46 of 8404 in the genome	0.00043	CCG016251.1,CCG020286.1,CCG025357.1,CCG010539.1, CCG023521.1,CCG008916.1,CCG023964.1,CCG016758.1, CCG004234.1,CCG002674.1,CCG020113.1,CCG007636.1, CCG014279.1,CCG023156.1,CCG019012.1,CCG023173.1, CCG001317.1,CCG004440.1,CCG005020.1,CCG010460.1, CCG020804.1,CCG004228.1,CCG018311.1,CCG000939.1, CCG022183.1,CCG010541.1,CCG023511.1,CCG002449.1, CCG000655.1,CCG014142.1,CCG014824.1,CCG009393.1, CCG026725.1,CCG002221.1,CCG000583.2,CCG027125.1,
GO:0006091	generation of precursor metabolites and energy	52 of 4104 in the list	66 of 8404 in the genome	0.00055	CCG020616.1,CCG024798.1,CCG023685.1,CCG005588.1, CCG000102.1,CCG003215.3,CCG001649.1,CCG012727.1, CCG011547.1,CCG010373.1,CCG006864.1,CCG007981.1, CCG008130.1,CCG000431.1,CCG019953.1,CCG001842.1, CCG023350.1,CCG020879.1,CCG003220.2,CCG006203.1, CCG018614.1,CCG024119.1,CCG022453.1,CCG012249.1, CCG006459.1,CCG024297.1,CCG022035.1,CCG004155.2, CCG005677.1,CCG018684.1,CCG018128.1,CCG004244.1, CCG020956.1,CCG007023.1,CCG022214.1,CCG002790.1, CCG013339.1,CCG011237.1,CCG019712.1,CCG009771.2, CCG022430.1,CCG017200.1,CCG004760.1,CCG014053.1, CCG001072.1,CCG025277.1,CCG016431.1,CCG000089.1,

GO:0009987	cellular process	2373 of 4104 in the list	4632 of 8404 in the genome	0.00067	CCG005254.1,CCG014531.2,CCG017420.1,CCG027068.1, CCG004973.1,CCG004887.1,CCG026106.1,CCG016952.1, CCG012875.1,CCG025108.1,CCG004468.1,CCG023989.1, CCG012726.1,CCG024584.1,CCG017266.1,CCG025208.1, CCG021479.1,CCG003362.1,CCG023381.1,CCG019382.1, CCG017851.1,CCG017240.1,CCG015101.1,CCG016094.1, CCG026413.3,CCG023474.1,CCG026871.2,CCG010792.1, CCG022025.2,CCG005053.1,CCG021616.1,CCG022281.1, CCG010905.1,CCG008270.1,CCG021110.1,CCG026050.1, CCG024612.1,CCG028653.1,CCG013109.1,CCG006465.1, CCG019571.1,CCG015694.1,CCG021681.1,CCG018788.1, CCG002982.1,CCG012083.1,CCG024119.1,CCG023686.1, CCG001579.1,CCG013641.1,CCG015350.1,CCG007951.1, CCG021948.1,CCG007597.1,CCG004927.1,CCG024903.1, CCG021137.1,CCG022056.1,CCG013610.1,CCG001876.1, CCG013465.1,CCG018688.1,CCG024200.1,CCG016719.1, CCG000983.1,CCG023458.1,CCG002937.1,CCG000876.1, CCG004926.1,CCG006928.1,CCG004532.1,CCG000789.1, CCG017381.1,CCG010912.1,CCG016753.1,CCG001704.1, CCG005524.1,CCG011547.1,CCG013640.1,CCG008404.1, CCG010136.1,CCG022370.1,CCG010112.1,CCG022513.2, CCG007750.2,CCG025707.1,CCG028092.1,CCG006479.1, CCG014345.2,CCG019825.2,CCG001395.1,CCG024155.1, CCG016557.1,CCG021990.1,CCG012195.1,CCG027000.1, CCG011827.1,CCG006787.1,CCG020654.1,CCG006804.1, CCG006264.1,CCG024760.1,CCG011015.1,CCG015167.1, CCG014222.1,CCG012959.1,CCG000612.1,CCG006013.1, CCG025897.1,CCG023983.1,CCG010046.1,CCG004308.1, CCG002466.1,CCG001440.1,CCG017696.1,CCG006921.1, CCG003775.1,CCG009928.1,CCG008152.1,CCG014982.1,

GO:0006468	protein phosphorylation	196 of 4104 in the list	319 of 8404 in the genome	0.00293	CCG000757.1,CCG002799.1,CCG023297.1,CCG025284.1, CCG027737.1,CCG004887.1,CCG005421.1,CCG025148.1, CCG003589.1,CCG002236.1,CCG028602.1,CCG020372.1, CCG007183.1,CCG016952.1,CCG010985.1,CCG026174.1, CCG006244.2,CCG024745.1,CCG013616.1,CCG009699.2, CCG017266.1,CCG028198.1,CCG016689.2,CCG021479.1, CCG009508.1,CCG019420.2,CCG023381.1,CCG019735.1, CCG015296.1,CCG024301.1,CCG028451.1,CCG018341.1, CCG008919.1,CCG008381.1,CCG021616.1,CCG022599.1, CCG023108.1,CCG013402.1,CCG018202.1,CCG017672.1, CCG017984.1,CCG019378.3,CCG004698.1,CCG027636.1, CCG004569.1,CCG024139.1,CCG004782.1,CCG008040.1, CCG024840.1,CCG021507.1,CCG002226.1,CCG011562.1, CCG009002.1,CCG013345.1,CCG011949.1,CCG006465.1, CCG003248.1,CCG018139.1,CCG011322.1,CCG018494.1, CCG017765.1,CCG008098.1,CCG025614.1,CCG001311.1, CCG023251.1,CCG011482.1,CCG020473.1,CCG025250.1, CCG012974.1,CCG024960.1,CCG028197.1,CCG013826.1, CCG007457.1,CCG023331.1,CCG004397.1,CCG012332.1, CCG022834.1,CCG010096.1,CCG020326.1,CCG021881.1, CCG028497.1,CCG018960.1,CCG025715.1,CCG009687.2, CCG025054.1,CCG017127.1,CCG010943.1,CCG002957.1, CCG004215.1,CCG011587.1,CCG013403.1,CCG020636.1, CCG000440.1,CCG027239.1,CCG015186.1,CCG016327.2, CCG004903.1,CCG023458.1,CCG014005.1,CCG027943.1, CCG018477.1,CCG017113.1,CCG011886.1,CCG016095.1, CCG003520.1,CCG006928.1,CCG016738.2,CCG025433.1, CCG003554.1,CCG020978.1,CCG003498.1,CCG008404.1, CCG018201.1,CCG022628.1,CCG021179.1,CCG026494.1, CCG001108.1,CCG005360.1,CCG001043.1,CCG004123.1,

GO:0007017	microtubule-based process	71 of 4104 in the list	99 of 8404 in the genome	0.00306	CCG015570.1,CCG006420.1,CCG013000.1,CCG026823.1, CCG023488.2,CCG003707.1,CCG010695.1,CCG005370.1, CCG009243.1,CCG019028.1,CCG023319.1,CCG001167.1, CCG002696.1,CCG025520.1,CCG001881.1,CCG027236.1, CCG025751.1,CCG006421.1,CCG023963.3,CCG005696.1, CCG011262.1,CCG008801.1,CCG024300.1,CCG000825.1, CCG016370.1,CCG000535.1,CCG022536.3,CCG010363.1, CCG007532.1,CCG008377.1,CCG007531.1,CCG018820.3, CCG010538.1,CCG024421.3,CCG008346.1,CCG026688.1, CCG015784.1,CCG014305.1,CCG013637.1,CCG023682.1, CCG012733.1,CCG017480.1,CCG019140.1,CCG010418.1, CCG009080.1,CCG027167.1,CCG025396.1,CCG019029.1, CCG021818.1,CCG001770.1,CCG010622.1,CCG021448.1, CCG010657.1,CCG008748.1,CCG009543.1,CCG016119.1, CCG015289.1,CCG021228.1,CCG005525.1,CCG019329.1, CCG005886.1,CCG003024.1,CCG002852.1,CCG010864.1, CCG006361.2,CCG021317.1,CCG017837.1,CCG021895.1
GO:0042254	ribosome biogenesis	39 of 4104 in the list	48 of 8404 in the genome	0.0038	CCG023263.1,CCG014531.2,CCG020286.1,CCG018407.1, CCG002735.1,CCG027579.1,CCG005477.1,CCG007962.1, CCG006357.1,CCG019953.1,CCG009214.1,CCG003055.1, CCG016274.1,CCG000540.1,CCG005176.1,CCG007636.1, CCG002681.1,CCG016760.1,CCG018046.1,CCG007518.1, CCG016652.1,CCG018636.1,CCG002792.1,CCG023511.1, CCG008299.1,CCG015998.1,CCG005097.1,CCG005849.1, CCG014824.1,CCG004044.1,CCG011449.1,CCG023053.1, CCG023663.1,CCG022486.1,CCG002564.1,CCG018474.1, CCG000658.1,CCG011057.1,CCG002680.1
GO:0006289	nucleotide-excision repair	17 of 4104 in the list	17 of 8404 in the genome	0.00548	CCG005241.1,CCG000213.1,CCG000929.1,CCG001808.2, CCG001769.1,CCG027133.1,CCG001083.1,CCG005395.1, CCG005379.2,CCG022772.1,CCG024804.1,CCG024792.1, CCG006284.1,CCG003658.1,CCG012164.1,CCG004402.1,

GO:0022613	ribonucleoprotein complex biogenesis	40 of 4104 in the list	50 of 8404 in the genome	0.00594	CCG023263.1,CCG014531.2,CCG020286.1,CCG018407.1, CCG002735.1,CCG027579.1,CCG005477.1,CCG007962.1, CCG006357.1,CCG019953.1,CCG009214.1,CCG003055.1, CCG016274.1,CCG000540.1,CCG005176.1,CCG007636.1, CCG002681.1,CCG016760.1,CCG018046.1,CCG007518.1, CCG016652.1,CCG018636.1,CCG002792.1,CCG010792.1, CCG023511.1,CCG008299.1,CCG015998.1,CCG005097.1, CCG005849.1,CCG014824.1,CCG004044.1,CCG011449.1, CCG023053.1,CCG023663.1,CCG022486.1,CCG002564.1,

GO:0016310	phosphorylation	219 of 4104 in the list	365 of 8404 in the genome	0.00854	CCG000757.1,CCG023685.1,CCG002799.1,CCG023297.1, CCG019820.1,CCG025284.1,CCG027737.1,CCG004887.1, CCG006864.1,CCG005421.1,CCG025148.1,CCG003589.1, CCG002236.1,CCG028602.1,CCG020372.1,CCG007183.1, CCG016952.1,CCG020879.1,CCG010985.1,CCG026174.1, CCG006244.2,CCG024745.1,CCG013616.1,CCG009699.2, CCG024297.1,CCG010996.1,CCG017266.1,CCG028198.1, CCG016689.2,CCG021479.1,CCG009508.1,CCG019420.2, CCG023381.1,CCG019735.1,CCG015296.1,CCG024301.1, CCG028451.1,CCG018341.1,CCG008919.1,CCG011237.1, CCG008381.1,CCG021616.1,CCG022599.1,CCG023108.1, CCG013402.1,CCG018202.1,CCG021110.1,CCG017672.1, CCG017984.1,CCG019378.3,CCG004698.1,CCG027636.1, CCG004569.1,CCG024139.1,CCG004782.1,CCG008040.1, CCG024840.1,CCG021507.1,CCG002226.1,CCG023393.1, CCG011562.1,CCG009002.1,CCG011949.1,CCG013345.1, CCG006465.1,CCG003248.1,CCG018139.1,CCG011322.1, CCG018494.1,CCG017765.1,CCG008098.1,CCG025614.1, CCG001311.1,CCG023251.1,CCG011482.1,CCG020473.1, CCG025250.1,CCG012974.1,CCG024960.1,CCG028197.1, CCG013826.1,CCG007457.1,CCG023331.1,CCG004397.1, CCG012332.1,CCG022834.1,CCG010096.1,CCG020326.1, CCG021881.1,CCG028497.1,CCG018960.1,CCG025715.1, CCG009687.2,CCG025054.1,CCG017127.1,CCG010943.1, CCG002957.1,CCG004215.1,CCG011587.1,CCG013403.1, CCG020636.1,CCG000440.1,CCG027239.1,CCG024903.1, CCG015186.1,CCG016327.2,CCG004903.1,CCG023458.1, CCG014005.1,CCG027943.1,CCG018477.1,CCG017113.1, CCG011886.1,CCG016095.1,CCG003520.1,CCG006928.1, CCG000789.1,CCG016738.2,CCG025433.1,CCG003554.1,

GO:0071840	cellular component organization or biogenesis	220 of 4104 in the list	367 of 8404 in the genome	0.00889	CCG023263.1,CCG014531.2,CCG006420.1,CCG018832.1, CCG006211.1,CCG004973.1,CCG013000.1,CCG026823.1, CCG005477.1,CCG003361.1,CCG011675.1,CCG006357.1, CCG010647.1,CCG019356.1,CCG020949.1,CCG005370.1, CCG019028.1,CCG016274.1,CCG007941.1,CCG026473.1, CCG012476.1,CCG002696.1,CCG014817.2,CCG014537.1, CCG003587.1,CCG013028.1,CCG027236.1,CCG019217.1, CCG024028.1,CCG005194.1,CCG024623.1,CCG014836.1, CCG015767.2,CCG024177.1,CCG000614.1,CCG009641.1, CCG004481.1,CCG006686.1,CCG012514.1,CCG027196.1, CCG000575.1,CCG002099.1,CCG018636.1,CCG002792.1, CCG016370.1,CCG014318.1,CCG010792.1,CCG003485.1, CCG015998.1,CCG025893.1,CCG023053.1,CCG010905.1, CCG022456.1,CCG006714.1,CCG027899.1,CCG010538.1, CCG010909.1,CCG028653.1,CCG018647.1,CCG020286.1, CCG017580.1,CCG015784.1,CCG009980.1,CCG002735.1, CCG023682.1,CCG015968.1,CCG013509.1,CCG019140.1, CCG018893.1,CCG010649.1,CCG025877.1,CCG018767.1, CCG020987.1,CCG015560.1,CCG002366.1,CCG009080.1, CCG027198.1,CCG009089.1,CCG027167.1,CCG000469.1, CCG025396.1,CCG000587.1,CCG012083.1,CCG018326.1, CCG019029.1,CCG008559.1,CCG019082.1,CCG027696.1, CCG002681.1,CCG021448.1,CCG010650.1,CCG000708.1, CCG025990.1,CCG024624.1,CCG009543.1,CCG004494.1, CCG015289.1,CCG010908.1,CCG005716.1,CCG022673.1, CCG026159.1,CCG023511.1,CCG009582.1,CCG015398.1, CCG020442.1,CCG020806.1,CCG001810.1,CCG002852.1, CCG024787.1,CCG000915.1,CCG012584.1,CCG021366.1, CCG000834.1,CCG018859.3,CCG008302.1,CCG019092.1, CCG002564.1,CCG024788.1,CCG015570.1,CCG006899.1,
GO:0006261	DNA-dependent DNA replication	19 of 4104 in the list	20 of 8404 in the genome	0.01398	CCG025352.1,CCG025208.1,CCG017380.1,CCG026841.1, CCG006549.1,CCG014280.1,CCG003904.1,CCG020651.1, CCG013917.1,CCG015694.1,CCG015711.1,CCG016381.1, CCG009896.1,CCG026258.1,CCG018321.1,CCG022735.1, CCG023633.1,CCG015599.1,CCG006164.1

GO:0016311	dephosphorylation	53 of 4104 in the list	72 of 8404 in the genome	0.01658	CCG002156.2,CCG008411.1,CCG024246.1,CCG007874.3, CCG021496.1,CCG012754.1,CCG010014.1,CCG009398.1, CCG013128.1,CCG021269.1,CCG004212.1,CCG008194.1, CCG020010.1,CCG026143.1,CCG011382.1,CCG002687.2, CCG021890.1,CCG004101.1,CCG022627.1,CCG015077.1, CCG012046.1,CCG016460.1,CCG000839.1,CCG011683.1, CCG027539.1,CCG007485.1,CCG001788.1,CCG001051.1, CCG003693.1,CCG013101.1,CCG007177.1,CCG028615.1, CCG003362.1,CCG026300.1,CCG013007.1,CCG007358.1, CCG006691.1,CCG002105.1,CCG021178.1,CCG006884.1, CCG021369.1,CCG008652.1,CCG014945.1,CCG000926.1, CCG018688.1,CCG008081.1,CCG021617.1,CCG010776.1, CCG020055.1,CCG020784.1,CCG012377.1,CCG026212.1

GO:0044085	cellular component biogenesis	138 of 4104 in the list	221 of 8404 in the genome	0.02816	CCG023263.1,CCG014531.2,CCG006420.1,CCG013000.1, CCG005477.1,CCG003361.1,CCG006357.1,CCG010647.1, CCG005370.1,CCG016274.1,CCG026473.1,CCG012476.1, CCG002696.1,CCG014537.1,CCG005194.1,CCG024623.1, CCG014836.1,CCG024177.1,CCG004481.1,CCG012514.1, CCG027196.1,CCG002099.1,CCG018636.1,CCG002792.1, CCG016370.1,CCG010792.1,CCG003485.1,CCG015998.1, CCG025893.1,CCG023053.1,CCG010905.1,CCG010909.1, CCG028653.1,CCG020286.1,CCG017580.1,CCG009980.1, CCG002735.1,CCG015968.1,CCG018893.1,CCG010649.1, CCG025877.1,CCG015560.1,CCG002366.1,CCG009080.1, CCG027198.1,CCG025396.1,CCG008559.1,CCG027696.1, CCG002681.1,CCG010650.1,CCG000708.1,CCG025990.1, CCG024624.1,CCG009543.1,CCG004494.1,CCG015289.1, CCG010908.1,CCG005716.1,CCG022673.1,CCG026159.1, CCG023511.1,CCG020442.1,CCG002852.1,CCG024787.1, CCG012584.1,CCG000834.1,CCG018859.3,CCG008302.1, CCG002564.1,CCG024788.1,CCG018407.1,CCG027579.1, CCG019284.1,CCG021491.1,CCG010136.1,CCG008560.1, CCG003310.1,CCG009243.1,CCG013617.1,CCG003055.1, CCG007636.1,CCG000433.1,CCG005176.1,CCG010137.1, CCG016760.1,CCG009461.1,CCG023963.3,CCG006421.1, CCG025880.1,CCG007395.1,CCG010904.1,CCG018046.1, CCG014772.1,CCG026474.1,CCG017033.1,CCG014824.1, CCG011449.1,CCG007532.1,CCG009637.1,CCG015583.1, CCG007531.1,CCG018820.3,CCG026579.1,CCG022486.1, CCG010648.1,CCG022629.1,CCG013637.1,CCG007962.1, CCG010906.1,CCG010138.1,CCG010418.1,CCG008892.2, CCG027199.1,CCG019953.1,CCG009214.1,CCG000540.1, CCG018287.1,CCG010907.1,CCG008748.1,CCG012229.1,
GO:0032259	methylation	25 of 4104 in the list	29 of 8404 in the genome	0.03325	CCG014335.1,CCG000417.1,CCG011888.1,CCG008401.1, CCG026248.1,CCG009425.1,CCG021449.1,CCG003755.1, CCG021244.2,CCG022674.1,CCG004234.1,CCG017176.1, CCG015398.1,CCG023905.2,CCG025940.1,CCG002946.1, CCG010791.1,CCG012083.1,CCG016016.1,CCG001369.2, CCG024098.1,CCG023156.1,CCG025991.2,CCG014986.1,

GO:0045333	cellular respiration	28 of 4104 in the list	34 of 8404 in the genome	0.06065	CCG024798.1,CCG004155.2,CCG023685.1,CCG000102.1, CCG018684.1,CCG001649.1,CCG012727.1,CCG018128.1, CCG011547.1,CCG006864.1,CCG020956.1,CCG004244.1, CCG011237.1,CCG019712.1,CCG009771.2,CCG001842.1, CCG020879.1,CCG023350.1,CCG014053.1,CCG001072.1, CCG012249.1,CCG016431.1,CCG006459.1,CCG000089.1, CCG027631.1,CCG020707.1,CCG025163.3,CCG024297.1
GO:0048523	negative regulation of cellular process	46 of 4104 in the list	63 of 8404 in the genome	0.08496	CCG003216.1,CCG026798.1,CCG024952.1,CCG028409.1, CCG023484.1,CCG026841.1,CCG025758.1,CCG010489.1, CCG009446.1,CCG015062.1,CCG003390.1,CCG025132.1, CCG005898.1,CCG019102.1,CCG003765.1,CCG019427.1, CCG001794.1,CCG020974.1,CCG005486.1,CCG017498.1, CCG001079.1,CCG004073.1,CCG018321.1,CCG021064.1, CCG012573.1,CCG008308.1,CCG002823.1,CCG006063.1, CCG014461.1,CCG016445.1,CCG011501.1,CCG001795.1, CCG000890.1,CCG006412.1,CCG005487.1,CCG005485.1, CCG004838.1,CCG004343.1,CCG006714.1,CCG025026.1, CCG023431.1,CCG016835.2,CCG025057.1,CCG014323.1, CCG021794.1,CCG015450.1
GO:0007018	microtubule-based movement	50 of 4104 in the list	70 of 8404 in the genome	0.1075	CCG006420.1,CCG014305.1,CCG013637.1,CCG023488.2, CCG017480.1,CCG012733.1,CCG003707.1,CCG010695.1, CCG010418.1,CCG009080.1,CCG009243.1,CCG025396.1, CCG023319.1,CCG021818.1,CCG001770.1,CCG010622.1, CCG001167.1,CCG002696.1,CCG025520.1,CCG001881.1, CCG010657.1,CCG008748.1,CCG025751.1,CCG006421.1, CCG005696.1,CCG023963.3,CCG016119.1,CCG008801.1, CCG015289.1,CCG024300.1,CCG000825.1,CCG005525.1, CCG021228.1,CCG016370.1,CCG019329.1,CCG005886.1, CCG003024.1,CCG002852.1,CCG010864.1,CCG010363.1, CCG006361.2,CCG021317.1,CCG008377.1,CCG017837.1, CCG007532.1,CCG007531.1,CCG021895.1,CCG018820.3, CCG008346.1,CCG018918.1

GO:0006928	cellular component movement	51 of 4104 in the list	72 of 8404 in the genome	0.13035	CCG006420.1,CCG014305.1,CCG013637.1,CCG023488.2, CCG017480.1,CCG012733.1,CCG003707.1,CCG010695.1, CCG010418.1,CCG009080.1,CCG009243.1,CCG025396.1, CCG023319.1,CCG021818.1,CCG001770.1,CCG010622.1, CCG001167.1,CCG002696.1,CCG025520.1,CCG001881.1, CCG010657.1,CCG008748.1,CCG025751.1,CCG006421.1, CCG005696.1,CCG023963.3,CCG016119.1,CCG008801.1, CCG015289.1,CCG024300.1,CCG000825.1,CCG005525.1, CCG021228.1,CCG016370.1,CCG019329.1,CCG005886.1, CCG003024.1,CCG002852.1,CCG010864.1,CCG010363.1, CCG013982.1,CCG006361.2,CCG021317.1,CCG008377.1, CCG017837.1,CCG007532.1,CCG007531.1,CCG021895.1, CCG018820.2,CCG008346.1,CCG018918.1
GO:0032774	RNA biosynthetic process	84 of 4104 in the list	129 of 8404 in the genome	0.1377	CCG000158.1,CCG017812.1,CCG006211.1,CCG016968.1, CCG007155.1,CCG021944.1,CCG010647.1,CCG005846.1, CCG011129.1,CCG026882.1,CCG018164.1,CCG018507.1, CCG015039.1,CCG004224.1,CCG026473.1,CCG000489.1, CCG001292.1,CCG000209.1,CCG021521.1,CCG002470.1, CCG006164.1,CCG018617.1,CCG023184.1,CCG020377.1, CCG008027.1,CCG021940.1,CCG006686.1,CCG013174.1, CCG018168.1,CCG007856.1,CCG019333.1,CCG018719.1, CCG018796.1,CCG025691.1,CCG027401.1,CCG018243.1, CCG027950.1,CCG024597.1,CCG027115.1,CCG020129.1, CCG018768.2,CCG021083.1,CCG020286.1,CCG020044.1, CCG010797.1,CCG001509.1,CCG001477.1,CCG006767.1, CCG010138.1,CCG000824.1,CCG019296.1,CCG014840.1, CCG004151.1,CCG015694.1,CCG006484.1,CCG015704.1, CCG018326.1,CCG023775.1,CCG010509.1,CCG017046.2, CCG011083.1,CCG010510.1,CCG020460.1,CCG019541.1, CCG010650.1,CCG024624.1,CCG024392.1,CCG009894.1, CCG011710.1,CCG011384.1,CCG025157.1,CCG027197.1, CCG003112.1,CCG010175.1,CCG009805.2,CCG003142.1, CCG024200.1,CCG023125.1,CCG016776.1,CCG016381.1,

GO:0009451	RNA modification	30 of 4104 in the list	38 of 8404 in the genome	0.146	CCG016251.1,CCG014335.1,CCG014946.1,CCG008401.1, CCG027340.1,CCG022183.1,CCG019389.1,CCG009425.1, CCG016652.1,CCG002792.1,CCG003755.1,CCG004234.1, CCG017176.1,CCG005097.1,CCG019953.1,CCG016274.1, CCG000540.1,CCG024750.2,CCG019292.1,CCG020589.1, CCG011971.1,CCG023156.1,CCG019012.1,CCG027125.1, CCG004440.1,CCG005020.1,CCG018019.1,CCG028653.1,

GO:0010467	gene expression	362 of 4104 in the list	649 of 8404 in the genome	0.14601	CCG014531.2,CCG023277.1,CCG014396.1,CCG004807.1, CCG010191.3,CCG013430.1,CCG006357.1,CCG009878.1, CCG010647.1,CCG016758.1,CCG024072.1,CCG026882.1, CCG012142.1,CCG018507.1,CCG020685.1,CCG002354.1, CCG016238.1,CCG026473.1,CCG001292.1,CCG023173.1, CCG026825.1,CCG002470.1,CCG003573.1,CCG020804.1, CCG025223.1,CCG001040.1,CCG019382.1,CCG026871.2, CCG015546.1,CCG018719.1,CCG010792.1,CCG004231.1, CCG023053.1,CCG008270.1,CCG027115.1,CCG020129.1, CCG023129.1,CCG005737.1,CCG028042.1,CCG009235.1, CCG020877.1,CCG009249.1,CCG006231.1,CCG020286.1, CCG014896.1,CCG002735.1,CCG001863.1,CCG006767.1, CCG019296.1,CCG008871.1,CCG014840.1,CCG014819.1, CCG018788.1,CCG006484.1,CCG026602.1,CCG006344.1, CCG001461.1,CCG026280.1,CCG023686.1,CCG010510.1, CCG003938.1,CCG021737.1,CCG000773.1,CCG018902.1, CCG004927.1,CCG009805.2,CCG002966.1,CCG019545.1, CCG003142.1,CCG019330.1,CCG001876.1,CCG000915.1, CCG018402.1,CCG024200.1,CCG023125.1,CCG010624.1, CCG027748.1,CCG015894.1,CCG000294.1,CCG026612.1, CCG004926.1,CCG016778.1,CCG010912.1,CCG004955.1, CCG015367.1,CCG005524.1,CCG007155.1,CCG024857.1, CCG020032.1,CCG000368.1,CCG026516.1,CCG003471.1, CCG018164.1,CCG004224.1,CCG010112.1,CCG019398.1, CCG011135.1,CCG006876.1,CCG028092.1,CCG000209.1, CCG016760.1,CCG021521.1,CCG001395.1,CCG023184.1, CCG003153.1,CCG000939.1,CCG021940.1,CCG013174.1, CCG022183.1,CCG018168.1,CCG017344.1,CCG019426.1, CCG018796.1,CCG025691.1,CCG009394.1,CCG027401.1, CCG002644.1,CCG014824.1,CCG024813.1,CCG018243.1,

GO:0048519	negative regulation of biological process	46 of 4104 in the list	64 of 8404 in the genome	0.15964	CCG003216.1,CCG026798.1,CCG024952.1,CCG028409.1, CCG023484.1,CCG026841.1,CCG025758.1,CCG010489.1, CCG009446.1,CCG015062.1,CCG003390.1,CCG025132.1, CCG005898.1,CCG019102.1,CCG003765.1,CCG019427.1, CCG001794.1,CCG020974.1,CCG005486.1,CCG017498.1, CCG001079.1,CCG004073.1,CCG018321.1,CCG021064.1, CCG012573.1,CCG008308.1,CCG002823.1,CCG006063.1, CCG014461.1,CCG016445.1,CCG011501.1,CCG001795.1, CCG000890.1,CCG006412.1,CCG005487.1,CCG005485.1, CCG004838.1,CCG004343.1,CCG006714.1,CCG025026.1, CCG023431.1,CCG016835.2,CCG025057.1,CCG014323.1, CCG021704.1,CCG015459.1
GO:0015985	energy coupled proton transport, down electrochemical gradient	15 of 4104 in the list	16 of 8404 in the genome	0.20058	CCG015410.1,CCG002038.1,CCG025107.1,CCG010112.1, CCG009142.1,CCG023640.1,CCG000148.1,CCG025348.1, CCG007724.1,CCG025989.2,CCG021934.1,CCG019619.1, CCG005924.2,CCG013643.1,CCG008422.1
GO:0015986	ATP synthesis coupled proton transport	15 of 4104 in the list	16 of 8404 in the genome	0.20058	CCG015410.1,CCG002038.1,CCG025107.1,CCG010112.1, CCG009142.1,CCG023640.1,CCG000148.1,CCG025348.1, CCG007724.1,CCG025989.2,CCG021934.1,CCG019619.1, CCG005924.2,CCG013643.1,CCG008422.1

GO:0018130	heterocycle biosynthetic process	169 of 4104 in the list	286 of 8404 in the genome	0.2776	CCG000158.1,CCG017812.1,CCG006211.1,CCG016968.1, CCG017331.1,CCG021944.1,CCG010647.1,CCG005846.1, CCG025989.2,CCG021335.1,CCG011129.1,CCG026882.1, CCG025493.1,CCG018507.1,CCG015039.1,CCG026174.1, CCG000016.1,CCG026473.1,CCG001292.1,CCG016220.1, CCG002470.1,CCG006164.1,CCG018617.1,CCG020377.1, CCG008027.1,CCG026536.1,CCG006686.1,CCG007993.1, CCG023780.2,CCG007856.1,CCG001423.1,CCG018719.1, CCG005053.1,CCG025940.1,CCG008860.1,CCG008609.1, CCG010944.1,CCG027115.1,CCG021110.1,CCG020129.1, CCG015746.1,CCG020286.1,CCG020044.1,CCG023640.1, CCG001477.1,CCG021086.2,CCG006767.1,CCG019296.1, CCG000824.1,CCG025348.1,CCG019619.1,CCG014840.1, CCG015694.1,CCG006484.1,CCG018326.1,CCG028131.1, CCG023775.1,CCG010509.1,CCG011083.1,CCG024432.2, CCG010510.1,CCG019541.1,CCG010650.1,CCG010460.1, CCG024624.1,CCG024392.1,CCG009894.1,CCG015410.1, CCG003865.1,CCG011710.1,CCG009142.1,CCG011384.1, CCG026898.1,CCG023452.1,CCG009805.2,CCG010175.1, CCG014116.1,CCG017111.1,CCG003142.1,CCG013610.1, CCG003173.1,CCG009518.1,CCG023125.1,CCG024200.1, CCG016776.1,CCG016381.1,CCG006791.1,CCG000468.1, CCG026865.1,CCG004926.1,CCG026047.1,CCG017175.1, CCG007155.1,CCG007610.1,CCG011491.1,CCG006529.1, CCG007533.1,CCG008422.1,CCG018164.1,CCG004224.1, CCG000489.1,CCG010112.1,CCG000209.1,CCG021521.1, CCG020441.1,CCG013643.1,CCG023184.1,CCG021940.1, CCG002038.1,CCG010561.1,CCG013174.1,CCG018168.1, CCG000148.1,CCG019333.1,CCG018453.1,CCG013365.1, CCG025691.1,CCG018796.1,CCG005924.2,CCG027401.1,

GO:0015980	energy derivation by oxidation of organic compounds	32 of 4104 in the list	42 of 8404 in the genome	0.28958	CCG024798.1,CCG023685.1,CCG000102.1,CCG001649.1, CCG012727.1,CCG011547.1,CCG006864.1,CCG008130.1, CCG001842.1,CCG020879.1,CCG023350.1,CCG012249.1, CCG006459.1,CCG024297.1,CCG004155.2,CCG018684.1, CCG018128.1,CCG004244.1,CCG020956.1,CCG011237.1, CCG022430.1,CCG009771.2,CCG019712.1,CCG004760.1, CCG014053.1,CCG001072.1,CCG016431.1,CCG000089.1, CCG027631.1,CCG025015.2,CCG025163.3,CCG020707.1

GO:0044271	cellular nitrogen compound biosynthetic process	177 of 4104 in the list	302 of 8404 in the genome	0.35805	CCG000158.1,CCG010174.2,CCG017812.1,CCG006211.1, CCG016968.1,CCG017331.1,CCG021944.1,CCG010647.1, CCG005846.1,CCG025989.2,CCG021335.1,CCG011129.1, CCG026882.1,CCG025493.1,CCG018507.1,CCG015039.1, CCG026174.1,CCG000016.1,CCG026473.1,CCG001292.1, CCG002470.1,CCG006164.1,CCG018617.1,CCG002495.1, CCG020377.1,CCG008027.1,CCG026536.1,CCG006686.1, CCG007993.1,CCG023780.2,CCG007856.1,CCG018719.1, CCG005053.1,CCG025940.1,CCG027282.1,CCG008609.1, CCG009515.2,CCG010944.1,CCG027115.1,CCG021110.1, CCG020129.1,CCG015746.1,CCG020286.1,CCG020044.1, CCG023640.1,CCG001477.1,CCG028391.1,CCG021086.2, CCG006767.1,CCG019296.1,CCG000824.1,CCG025348.1, CCG019619.1,CCG014840.1,CCG015694.1,CCG006484.1, CCG018326.1,CCG028131.1,CCG023775.1,CCG010509.1, CCG011083.1,CCG010510.1,CCG019541.1,CCG010650.1, CCG010460.1,CCG024624.1,CCG024392.1,CCG006821.1, CCG009894.1,CCG015410.1,CCG011710.1,CCG003865.1, CCG009142.1,CCG011384.1,CCG026898.1,CCG023452.1, CCG002883.1,CCG009805.2,CCG010175.1,CCG014116.1, CCG003142.1,CCG013610.1,CCG003173.1,CCG009518.1, CCG023125.1,CCG024200.1,CCG016776.1,CCG016381.1, CCG006791.1,CCG000468.1,CCG026865.1,CCG004926.1, CCG022191.1,CCG026047.1,CCG017175.1,CCG007155.1, CCG007610.1,CCG011491.1,CCG006529.1,CCG009333.1, CCG002555.1,CCG007533.1,CCG008422.1,CCG018164.1, CCG004224.1,CCG010112.1,CCG000489.1,CCG000209.1, CCG021521.1,CCG020441.1,CCG013643.1,CCG023184.1, CCG021940.1,CCG002038.1,CCG010561.1,CCG013174.1, CCG018168.1,CCG000148.1,CCG019333.1,CCG018453.1,

GO:1901362	organic cyclic compound biosynthetic process	171 of 4104 in the list	291 of 8404 in the genome	0.37607	CCG000158.1,CCG017812.1,CCG006211.1,CCG016968.1, CCG017331.1,CCG021944.1,CCG010647.1,CCG005846.1, CCG025989.2,CCG021335.1,CCG011129.1,CCG026882.1, CCG025493.1,CCG018507.1,CCG015039.1,CCG026174.1, CCG000016.1,CCG026473.1,CCG001292.1,CCG016220.1, CCG002470.1,CCG006164.1,CCG018617.1,CCG020377.1, CCG008027.1,CCG026536.1,CCG006686.1,CCG007993.1, CCG023780.2,CCG007856.1,CCG001423.1,CCG018719.1, CCG005053.1,CCG025940.1,CCG008860.1,CCG008609.1, CCG010944.1,CCG027115.1,CCG021110.1,CCG020129.1, CCG015746.1,CCG020286.1,CCG020044.1,CCG023640.1, CCG001477.1,CCG021086.2,CCG006767.1,CCG019296.1, CCG000824.1,CCG025348.1,CCG019619.1,CCG014840.1, CCG015694.1,CCG006484.1,CCG018326.1,CCG028131.1, CCG023775.1,CCG010509.1,CCG011083.1,CCG024432.2, CCG010510.1,CCG019541.1,CCG010650.1,CCG010460.1, CCG024624.1,CCG024392.1,CCG009894.1,CCG015410.1, CCG003865.1,CCG011710.1,CCG009142.1,CCG011384.1, CCG026898.1,CCG023452.1,CCG009805.2,CCG010175.1, CCG014116.1,CCG017111.1,CCG003142.1,CCG013610.1, CCG003173.1,CCG009518.1,CCG023125.1,CCG024200.1, CCG016776.1,CCG016381.1,CCG006791.1,CCG000468.1, CCG026865.1,CCG004926.1,CCG026047.1,CCG017175.1, CCG007155.1,CCG007610.1,CCG011491.1,CCG006529.1, CCG007533.1,CCG008422.1,CCG018164.1,CCG004224.1, CCG000489.1,CCG010112.1,CCG000209.1,CCG021521.1, CCG020441.1,CCG013643.1,CCG023184.1,CCG021940.1, CCG002038.1,CCG010561.1,CCG013174.1,CCG018168.1, CCG000148.1,CCG019333.1,CCG018453.1,CCG013365.1, CCG025691.1,CCG018796.1,CCG005924.2,CCG027401.1,

GO:0044237	cellular metabolic process	1617 of 4104 in the list	3157 of 8404 in the genome	0.40868	CCG014531.2,CCG017420.1,CCG027068.1,CCG014396.1, CCG006549.1,CCG004887.1,CCG026106.1,CCG016952.1, CCG012875.1,CCG025108.1,CCG026174.1,CCG004468.1, CCG023989.1,CCG012726.1,CCG024584.1,CCG001292.1, CCG018432.1,CCG001040.1,CCG017266.1,CCG028198.1, CCG016689.2,CCG025208.1,CCG021479.1,CCG003362.1, CCG014515.1,CCG019113.1,CCG023381.1,CCG019382.1, CCG019735.1,CCG020956.1,CCG016094.1,CCG026413.3, CCG023474.1,CCG026871.2,CCG010792.1,CCG012623.1, CCG022025.2,CCG005053.1,CCG011237.1,CCG021616.1, CCG005738.1,CCG013876.1,CCG010905.1,CCG008270.1, CCG021110.1,CCG024612.1,CCG027636.1,CCG028653.1, CCG004569.1,CCG020286.1,CCG013109.1,CCG021086.2, CCG006465.1,CCG015074.1,CCG019571.1,CCG008871.1, CCG015694.1,CCG018113.1,CCG018788.1,CCG006484.1, CCG002982.1,CCG012083.1,CCG026953.1,CCG026602.1, CCG024119.1,CCG023686.1,CCG019678.1,CCG007457.1, CCG021737.1,CCG025990.1,CCG013641.1,CCG015350.1, CCG021948.1,CCG020651.1,CCG005284.1,CCG004927.1, CCG009805.2,CCG024903.1,CCG021137.1,CCG022056.1, CCG013610.1,CCG001876.1,CCG012584.1,CCG015186.1, CCG013465.1,CCG016327.2,CCG018688.1,CCG024200.1, CCG010624.1,CCG002231.1,CCG023458.1,CCG027748.1, CCG017001.1,CCG021767.1,CCG003520.1,CCG004926.1, CCG006928.1,CCG004532.1,CCG000789.1,CCG017381.1, CCG005588.1,CCG010912.1,CCG004955.1,CCG007874.3, CCG001704.1,CCG005524.1,CCG011547.1,CCG010014.1, CCG013640.1,CCG008404.1,CCG018201.1,CCG010136.1, CCG009333.1,CCG008287.1,CCG009574.1,CCG022370.1, CCG010112.1,CCG009038.1,CCG022513.2,CCG007750.2,

GO:0006351	transcription, DNA-templated	80 of 4104 in the list	125 of 8404 in the genome	0.45285	CCG000158.1,CCG017812.1,CCG006211.1,CCG016968.1, CCG007155.1,CCG021944.1,CCG010647.1,CCG005846.1, CCG011129.1,CCG026882.1,CCG018164.1,CCG018507.1, CCG015039.1,CCG004224.1,CCG026473.1,CCG000489.1, CCG001292.1,CCG000209.1,CCG021521.1,CCG002470.1, CCG018617.1,CCG023184.1,CCG020377.1,CCG008027.1, CCG021940.1,CCG006686.1,CCG013174.1,CCG018168.1, CCG007856.1,CCG019333.1,CCG018719.1,CCG018796.1, CCG025691.1,CCG027401.1,CCG018243.1,CCG027950.1, CCG024597.1,CCG027115.1,CCG020129.1,CCG018768.2, CCG021083.1,CCG020286.1,CCG020044.1,CCG010797.1, CCG001509.1,CCG001477.1,CCG006767.1,CCG010138.1, CCG000824.1,CCG019296.1,CCG014840.1,CCG004151.1, CCG006484.1,CCG015704.1,CCG018326.1,CCG023775.1, CCG010509.1,CCG017046.2,CCG011083.1,CCG010510.1, CCG020460.1,CCG019541.1,CCG010650.1,CCG024624.1, CCG024392.1,CCG009894.1,CCG011710.1,CCG011384.1, CCG025157.1,CCG027197.1,CCG003112.1,CCG010175.1, CCG009805.2,CCG003142.1,CCG024200.1,CCG023125.1,
GO:0006310	DNA recombination	16 of 4104 in the list	18 of 8404 in the genome	0.50567	CCG019648.1,CCG017444.1,CCG021045.1,CCG000490.1, CCG008622.1,CCG020439.2,CCG023474.1,CCG009962.1, CCG010116.1,CCG000777.1,CCG008498.1,CCG006919.1, CCG018650.1,CCG028267.1,CCG000776.1,CCG018799.1
GO:0022900	electron transport chain	16 of 4104 in the list	18 of 8404 in the genome	0.50567	CCG004155.2,CCG005677.1,CCG023685.1,CCG000102.1, CCG018684.1,CCG001649.1,CCG006864.1,CCG002790.1, CCG011237.1,CCG020879.1,CCG018614.1,CCG024119.1, CCG014053.1,CCG006459.1,CCG025163.3,CCG024297.1

GO:0034654	nucleobase-containing compound biosynthetic process	136 of 4104 in the list	228 of 8404 in the genome	0.62752	CCG000158.1,CCG017812.1,CCG006211.1,CCG016968.1, CCG021944.1,CCG010647.1,CCG005846.1,CCG025989.2, CCG011129.1,CCG026882.1,CCG025493.1,CCG018507.1, CCG015039.1,CCG026174.1,CCG000016.1,CCG026473.1, CCG001292.1,CCG002470.1,CCG006164.1,CCG018617.1, CCG020377.1,CCG008027.1,CCG006686.1,CCG007993.1, CCG007856.1,CCG018719.1,CCG010944.1,CCG027115.1, CCG021110.1,CCG020129.1,CCG015746.1,CCG020286.1, CCG020044.1,CCG023640.1,CCG001477.1,CCG006767.1, CCG019296.1,CCG000824.1,CCG025348.1,CCG019619.1, CCG014840.1,CCG015694.1,CCG006484.1,CCG018326.1, CCG028131.1,CCG023775.1,CCG010509.1,CCG011083.1, CCG010510.1,CCG019541.1,CCG010650.1,CCG010460.1, CCG024624.1,CCG024392.1,CCG009894.1,CCG015410.1, CCG011710.1,CCG009142.1,CCG011384.1,CCG026898.1, CCG023452.1,CCG009805.2,CCG010175.1,CCG014116.1, CCG003142.1,CCG013610.1,CCG009518.1,CCG023125.1, CCG024200.1,CCG016776.1,CCG016381.1,CCG006791.1, CCG000468.1,CCG026865.1,CCG004926.1,CCG026047.1, CCG007155.1,CCG006529.1,CCG007533.1,CCG008422.1, CCG018164.1,CCG004224.1,CCG000489.1,CCG010112.1, CCG000209.1,CCG021521.1,CCG013643.1,CCG023184.1, CCG002038.1,CCG021940.1,CCG013174.1,CCG018168.1, CCG019333.1,CCG000148.1,CCG013365.1,CCG025691.1, CCG018796.1,CCG005924.2,CCG027401.1,CCG027950.1, CCG018243.1,CCG024597.1,CCG017330.1,CCG021934.1, CCG014379.1,CCG018768.2,CCG021083.1,CCG004180.1, CCG017995.1,CCG010797.1,CCG001509.1,CCG010138.1, CCG004151.1,CCG015704.1,CCG013999.1,CCG021336.1, CCG007417.1,CCG017046.2,CCG004440.1,CCG020460.1,
GO:0006270	DNA replication initiation	13 of 4104 in the list	14 of 8404 in the genome	0.74422	CCG025352.1,CCG025208.1,CCG017380.1,CCG006549.1, CCG015711.1,CCG014280.1,CCG003904.1,CCG026258.1, CCG020651.1,CCG022735.1,CCG023633.1,CCG015599.1,

GO:0016072	rRNA metabolic process	23 of 4104 in the list	29 of 8404 in the genome	0.81785	CCG023263.1,CCG020286.1,CCG002735.1,CCG027579.1, CCG007962.1,CCG018636.1,CCG006357.1,CCG023511.1, CCG005097.1,CCG005849.1,CCG019953.1,CCG014824.1, CCG009214.1,CCG003055.1,CCG020685.1,CCG016274.1, CCG023053.1,CCG007636.1,CCG005176.1,CCG019674.1, CCG016760.1,CCG018474.1,CCG022629.1
GO:0006996	organelle organization	144 of 4104 in the list	244 of 8404 in the genome	0.8347	CCG018832.1,CCG006211.1,CCG004973.1,CCG026823.1, CCG003361.1,CCG011675.1,CCG010647.1,CCG019356.1, CCG020949.1,CCG019028.1,CCG026473.1,CCG012476.1, CCG014817.2,CCG014537.1,CCG003587.1,CCG013028.1, CCG027236.1,CCG019217.1,CCG024028.1,CCG005194.1, CCG024623.1,CCG014836.1,CCG024177.1,CCG009641.1, CCG004481.1,CCG006686.1,CCG012514.1,CCG027196.1, CCG000575.1,CCG014318.1,CCG025893.1,CCG010905.1, CCG022456.1,CCG027899.1,CCG010538.1,CCG010909.1, CCG018647.1,CCG017580.1,CCG015784.1,CCG009980.1, CCG023682.1,CCG015968.1,CCG013509.1,CCG019140.1, CCG018893.1,CCG010649.1,CCG025877.1,CCG018767.1, CCG020987.1,CCG015560.1,CCG002366.1,CCG027198.1, CCG027167.1,CCG000469.1,CCG000587.1,CCG012083.1, CCG018326.1,CCG019029.1,CCG008559.1,CCG019082.1, CCG027696.1,CCG021448.1,CCG010650.1,CCG000708.1, CCG025990.1,CCG024624.1,CCG004494.1,CCG010908.1, CCG005716.1,CCG022673.1,CCG026159.1,CCG015398.1, CCG020442.1,CCG001810.1,CCG024787.1,CCG012584.1, CCG021366.1,CCG000834.1,CCG008302.1,CCG019092.1, CCG024788.1,CCG015570.1,CCG006899.1,CCG002479.1, CCG019284.1,CCG008560.1,CCG021491.1,CCG010136.1, CCG003310.1,CCG013617.1,CCG000433.1,CCG010137.1, CCG020315.1,CCG009461.1,CCG011262.1,CCG025880.1, CCG010904.1,CCG018482.1,CCG014772.1,CCG026474.1, CCG000535.1,CCG022536.3,CCG018249.1,CCG015167.1, CCG009637.1,CCG024421.3,CCG026579.1,CCG010648.1, CCG010178.1,CCG026688.1,CCG027348.1,CCG020863.1, CCG010906.1,CCG026620.1,CCG010138.1,CCG008892.2, CCG027199.1,CCG001369.2,CCG005579.1,CCG018287.1,

GO:0007346	regulation of mitotic cell cycle	10 of 4104 in the list	10 of 8404 in the genome	0.83752	CCG004331.1,CCG009521.1,CCG013849.1,CCG027068.1, CCG017923.1,CCG009035.1,CCG002269.1,CCG012743.1, CCG026404.1,CCG018116.1
GO:0010564	regulation of cell cycle process	10 of 4104 in the list	10 of 8404 in the genome	0.83752	CCG004331.1,CCG009521.1,CCG013849.1,CCG027068.1, CCG017923.1,CCG009035.1,CCG002269.1,CCG012743.1, CCG026404.1,CCG018116.1
GO:1901987	regulation of cell cycle phase transition	10 of 4104 in the list	10 of 8404 in the genome	0.83752	CCG004331.1,CCG009521.1,CCG013849.1,CCG027068.1, CCG017923.1,CCG009035.1,CCG002269.1,CCG012743.1, CCG026404.1,CCG018116.1
GO:1901990	regulation of mitotic cell cycle phase transition	10 of 4104 in the list	10 of 8404 in the genome	0.83752	CCG004331.1,CCG009521.1,CCG013849.1,CCG027068.1, CCG017923.1,CCG009035.1,CCG002269.1,CCG012743.1, CCG026404.1,CCG018116.1
GO:0006364	rRNA processing	21 of 4104 in the list	26 of 8404 in the genome	0.90572	CCG023263.1,CCG020286.1,CCG002735.1,CCG027579.1, CCG007962.1,CCG018636.1,CCG006357.1,CCG023511.1, CCG005097.1,CCG005849.1,CCG019953.1,CCG014824.1, CCG009214.1,CCG003055.1,CCG016274.1,CCG023053.1, CCG007636.1,CCG005176.1,CCG016760.1,CCG018474.1,
GO:0006470	protein dephosphorylation	41 of 4104 in the list	59 of 8404 in the genome	1	CCG002156.2,CCG024246.1,CCG007874.3,CCG021496.1, CCG012754.1,CCG009398.1,CCG013128.1,CCG021269.1, CCG004212.1,CCG008194.1,CCG020010.1,CCG026143.1, CCG011382.1,CCG002687.2,CCG004101.1,CCG022627.1, CCG015077.1,CCG016460.1,CCG000839.1,CCG027539.1, CCG007485.1,CCG001788.1,CCG001051.1,CCG003693.1, CCG013101.1,CCG007177.1,CCG028615.1,CCG003362.1, CCG026300.1,CCG013007.1,CCG006691.1,CCG002105.1, CCG006884.1,CCG021369.1,CCG014945.1,CCG000926.1, CCG018688.1,CCG010776.1,CCG020055.1,CCG012377.1,
GO:0051726	regulation of cell cycle	29 of 4104 in the list	39 of 8404 in the genome	1	CCG013849.1,CCG027068.1,CCG008308.1,CCG028049.1, CCG006063.1,CCG017923.1,CCG026888.1,CCG001795.1, CCG013274.1,CCG012743.1,CCG004783.1,CCG027441.1, CCG018116.1,CCG005849.1,CCG004331.1,CCG009521.1, CCG000116.1,CCG009035.1,CCG004682.1,CCG001794.1, CCG001854.1,CCG016760.1,CCG002269.1,CCG020898.1, CCG013794.1,CCG025057.1,CCG011648.1,CCG026404.1,

GO:0044267	cellular protein metabolic process	610 of 4104 in the list	1150 of 8404 in the genome	1	CCG014531.2,CCG027068.1,CCG014396.1,CCG004887.1, CCG013430.1,CCG009878.1,CCG002687.2,CCG016952.1, CCG026174.1,CCG016238.1,CCG012726.1,CCG025472.1, CCG018432.1,CCG017266.1,CCG028198.1,CCG016689.2, CCG021479.1,CCG003362.1,CCG026300.1,CCG023381.1, CCG019735.1,CCG026413.3,CCG016271.1,CCG026871.2, CCG012077.1,CCG008381.1,CCG021616.1,CCG005738.1, CCG013876.1,CCG008270.1,CCG008301.1,CCG017984.1, CCG024612.1,CCG005737.1,CCG027636.1,CCG026212.1, CCG004569.1,CCG024139.1,CCG008040.1,CCG002156.2, CCG013109.1,CCG011238.1,CCG011949.1,CCG006465.1, CCG015074.1,CCG004212.1,CCG003248.1,CCG019571.1, CCG008871.1,CCG004331.1,CCG018788.1,CCG018494.1, CCG002982.1,CCG012083.1,CCG001311.1,CCG026602.1, CCG006344.1,CCG016480.1,CCG022627.1,CCG007457.1, CCG021737.1,CCG012332.1,CCG002957.1,CCG024897.1, CCG000552.1,CCG002966.1,CCG019545.1,CCG022056.1, CCG001876.1,CCG015186.1,CCG016327.2,CCG018688.1, CCG023458.1,CCG027748.1,CCG027943.1,CCG000294.1, CCG003520.1,CCG006928.1,CCG016738.2,CCG017381.1, CCG003554.1,CCG007874.3,CCG001704.1,CCG015367.1, CCG013640.1,CCG008404.1,CCG018201.1,CCG007766.1, CCG021179.1,CCG001108.1,CCG009574.1,CCG022370.1, CCG018164.1,CCG010112.1,CCG009038.1,CCG007750.2, CCG025707.1,CCG028092.1,CCG020078.1,CCG021521.1, CCG019139.1,CCG024922.1,CCG015580.1,CCG027000.1, CCG006804.1,CCG018168.1,CCG006264.1,CCG019426.1, CCG025889.1,CCG024790.1,CCG007254.1,CCG009394.1, CCG023684.1,CCG024760.1,CCG009177.1,CCG014222.1, CCG001217.1,CCG000612.1,CCG025892.1,CCG021138.1,

GO:0019438	aromatic compound biosynthetic process	155 of 4104 in the list	267 of 8404 in the genome	1	CCG000158.1,CCG017812.1,CCG006211.1,CCG016968.1, CCG017331.1,CCG021944.1,CCG010647.1,CCG005846.1, CCG025989.2,CCG021335.1,CCG011129.1,CCG026882.1, CCG025493.1,CCG018507.1,CCG015039.1,CCG026174.1, CCG000016.1,CCG026473.1,CCG001292.1,CCG002470.1, CCG006164.1,CCG018617.1,CCG020377.1,CCG008027.1, CCG026536.1,CCG006686.1,CCG007993.1,CCG023780.2, CCG007856.1,CCG018719.1,CCG005053.1,CCG008609.1, CCG010944.1,CCG027115.1,CCG021110.1,CCG020129.1, CCG015746.1,CCG020286.1,CCG020044.1,CCG023640.1, CCG001477.1,CCG021086.2,CCG006767.1,CCG019296.1, CCG000824.1,CCG025348.1,CCG019619.1,CCG014840.1, CCG015694.1,CCG006484.1,CCG018326.1,CCG028131.1, CCG023775.1,CCG010509.1,CCG011083.1,CCG010510.1, CCG019541.1,CCG010650.1,CCG010460.1,CCG024624.1, CCG024392.1,CCG009894.1,CCG015410.1,CCG011710.1, CCG009142.1,CCG011384.1,CCG026898.1,CCG023452.1, CCG009805.2,CCG010175.1,CCG014116.1,CCG003142.1, CCG013610.1,CCG003173.1,CCG009518.1,CCG023125.1, CCG024200.1,CCG016776.1,CCG016381.1,CCG006791.1, CCG000468.1,CCG026865.1,CCG004926.1,CCG026047.1, CCG007155.1,CCG007610.1,CCG011491.1,CCG006529.1, CCG007533.1,CCG008422.1,CCG018164.1,CCG004224.1, CCG000489.1,CCG010112.1,CCG000209.1,CCG021521.1, CCG020441.1,CCG013643.1,CCG023184.1,CCG021940.1, CCG002038.1,CCG010561.1,CCG013174.1,CCG018168.1, CCG019333.1,CCG018453.1,CCG000148.1,CCG013365.1, CCG025691.1,CCG018796.1,CCG005924.2,CCG027401.1, CCG027950.1,CCG018243.1,CCG024597.1,CCG004257.1, CCG017330.1,CCG021934.1,CCG010319.1,CCG014379.1,

GO:0065009	regulation of molecular function	51 of 4104 in the list	77 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG011044.1,CCG012519.1,CCG004132.1,CCG017369.1, CCG013274.1,CCG012743.1,CCG024000.1,CCG016965.1, CCG022676.1,CCG027878.1,CCG004151.1,CCG009450.1, CCG024809.1,CCG009024.1,CCG009521.1,CCG015333.1, CCG002971.1,CCG009035.1,CCG004682.1,CCG001854.1, CCG002109.1,CCG021151.1,CCG020898.1,CCG013794.1, CCG005105.1,CCG026404.1,CCG022394.1,CCG009894.1, CCG016027.1,CCG011341.1,CCG013849.1,CCG019462.1, CCG028049.1,CCG017923.1,CCG017560.1,CCG025554.1, CCG004783.1,CCG013303.1,CCG007631.1,CCG016181.1, CCG013203.1,CCG018776.1,CCG010260.1,CCG002864.1, CCG011648.1,CCG018184.1,CCG021794.1
GO:0000226	microtubule cytoskeleton organization	18 of 4104 in the list	22 of 8404 in the genome	1	CCG015570.1,CCG026688.1,CCG015784.1,CCG026823.1, CCG023682.1,CCG019140.1,CCG000535.1,CCG022536.3, CCG019028.1,CCG027167.1,CCG019029.1,CCG021448.1, CCG002137.1,CCG019092.1,CCG024421.3,CCG010538.1,
GO:0008380	RNA splicing	18 of 4104 in the list	22 of 8404 in the genome	1	CCG003785.1,CCG000939.1,CCG000393.1,CCG000754.1, CCG028285.1,CCG004008.1,CCG026516.1,CCG010792.1, CCG004927.1,CCG009393.1,CCG000183.1,CCG000583.2, CCG023686.1,CCG024810.1,CCG013802.1,CCG003938.1,
GO:0006560	proline metabolic process	9 of 4104 in the list	9 of 8404 in the genome	1	CCG017111.1,CCG007203.1,CCG017894.1,CCG002231.1, CCG016220.1,CCG015921.1,CCG001423.1,CCG003871.1,
GO:0043414	macromolecule methylation	16 of 4104 in the list	19 of 8404 in the genome	1	CCG014335.1,CCG012083.1,CCG002946.1,CCG001369.2, CCG008401.1,CCG026248.1,CCG023156.1,CCG009425.1, CCG021449.1,CCG025991.2,CCG003755.1,CCG022674.1, CCG004234.1,CCG017176.1,CCG015398.1,CCG025942.1

GO:1901605	alpha-amino acid metabolic process	56 of 4104 in the list	86 of 8404 in the genome	1	CCG007203.1,CCG010174.2,CCG019954.3,CCG025465.1, CCG010111.1,CCG011491.1,CCG015921.1,CCG009333.1, CCG021923.1,CCG020154.1,CCG023501.1,CCG009084.2, CCG025108.1,CCG028131.1,CCG017894.1,CCG011721.1, CCG013043.1,CCG008510.1,CCG016220.1,CCG019834.1, CCG015568.1,CCG016315.1,CCG020441.1,CCG006059.1, CCG017543.1,CCG006821.1,CCG000682.1,CCG008932.1, CCG010561.1,CCG025307.1,CCG018907.1,CCG001423.1, CCG027551.3,CCG000472.1,CCG022025.2,CCG025636.2, CCG008860.1,CCG017201.1,CCG017111.1,CCG006994.1, CCG025731.1,CCG015276.2,CCG011789.1,CCG022773.2, CCG001082.1,CCG024133.1,CCG002231.1,CCG011722.1, CCG015943.1,CCG026030.1,CCG026155.1,CCG003063.1, CCG025897.1,CCG003871.1,CCG015567.1,CCG008388.1

GO:0006520	cellular amino acid metabolic process	114 of 4104 in the list	192 of 8404 in the genome	1	CCG021774.1,CCG010174.2,CCG019078.1,CCG023277.1, CCG014396.1,CCG015367.1,CCG010191.3,CCG010111.1, CCG011491.1,CCG009878.1,CCG009333.1,CCG021923.1, CCG006188.1,CCG023501.1,CCG027352.3,CCG015950.3, CCG025108.1,CCG016238.1,CCG011135.1,CCG028092.1, CCG013727.1,CCG019834.1,CCG016220.1,CCG015568.1, CCG020441.1,CCG027607.1,CCG010561.1,CCG026910.1, CCG010321.1,CCG025307.1,CCG008776.1,CCG018907.1, CCG001423.1,CCG017344.1,CCG000138.1,CCG027551.3, CCG000472.1,CCG015577.3,CCG022025.2,CCG008860.1, CCG006994.1,CCG025731.1,CCG018108.1,CCG001082.1, CCG026099.1,CCG024133.1,CCG011722.1,CCG026030.1, CCG003063.1,CCG025897.1,CCG000414.1,CCG002018.1, CCG007203.1,CCG020877.1,CCG006231.1,CCG008321.1, CCG019954.3,CCG025465.1,CCG001811.1,CCG015921.1, CCG017708.1,CCG004949.1,CCG020154.1,CCG005938.1, CCG009084.2,CCG005204.1,CCG028131.1,CCG017894.1, CCG011721.1,CCG013043.1,CCG008510.1,CCG022407.1, CCG021716.1,CCG021820.1,CCG016315.1,CCG021610.1, CCG006059.1,CCG006570.1,CCG002662.1,CCG000352.1, CCG014436.2,CCG017543.1,CCG006821.1,CCG019243.1, CCG000682.1,CCG023315.1,CCG008932.1,CCG002897.1, CCG003528.1,CCG025439.1,CCG010565.1,CCG025636.2, CCG017201.1,CCG017111.1,CCG015276.2,CCG003296.1, CCG011789.1,CCG019545.1,CCG022773.2,CCG019330.1, CCG022269.1,CCG001876.1,CCG002231.1,CCG026570.1, CCG015943.1,CCG016955.1,CCG026155.1,CCG008789.1,
GO:0009142	nucleoside triphosphate biosynthetic process	19 of 4104 in the list	24 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG000148.1,CCG006529.1, CCG025348.1,CCG025989.2,CCG019619.1,CCG005924.2, CCG008422.1,CCG010112.1,CCG007417.1,CCG021110.1, CCG007724.1,CCG021934.1,CCG013643.1

GO:0009145	purine nucleoside triphosphate biosynthetic process	19 of 4104 in the list	24 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG000148.1,CCG006529.1, CCG025348.1,CCG025989.2,CCG019619.1,CCG005924.2, CCG008422.1,CCG010112.1,CCG007417.1,CCG021110.1, CCG007724.1,CCG021934.1,CCG013643.1
GO:0009201	ribonucleoside triphosphate biosynthetic process	19 of 4104 in the list	24 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG000148.1,CCG006529.1, CCG025348.1,CCG025989.2,CCG019619.1,CCG005924.2, CCG008422.1,CCG010112.1,CCG007417.1,CCG021110.1, CCG007724.1,CCG021934.1,CCG013643.1
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	19 of 4104 in the list	24 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG000148.1,CCG006529.1, CCG025348.1,CCG025989.2,CCG019619.1,CCG005924.2, CCG008422.1,CCG010112.1,CCG007417.1,CCG021110.1, CCG007724.1,CCG021934.1,CCG013643.1

GO:0051276	chromosome organization	93 of 4104 in the list	154 of 8404 in the genome	1	CCG006899.1,CCG006211.1,CCG004973.1,CCG003361.1, CCG011675.1,CCG019284.1,CCG008560.1,CCG010136.1, CCG021491.1,CCG010647.1,CCG003310.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG014537.1, CCG010137.1,CCG013028.1,CCG005194.1,CCG009461.1, CCG024623.1,CCG025880.1,CCG014836.1,CCG010904.1, CCG024177.1,CCG018482.1,CCG004481.1,CCG006686.1, CCG012514.1,CCG027196.1,CCG014772.1,CCG000575.1, CCG026474.1,CCG025893.1,CCG015167.1,CCG009637.1, CCG010905.1,CCG022456.1,CCG026579.1,CCG010909.1, CCG010648.1,CCG017580.1,CCG009980.1,CCG027348.1, CCG020863.1,CCG010906.1,CCG015968.1,CCG018893.1, CCG010649.1,CCG010138.1,CCG025877.1,CCG018767.1, CCG008892.2,CCG020987.1,CCG015560.1,CCG027199.1, CCG027198.1,CCG018326.1,CCG012083.1,CCG000587.1, CCG001369.2,CCG008559.1,CCG018287.1,CCG027696.1, CCG010907.1,CCG025991.2,CCG012229.1,CCG010650.1, CCG000708.1,CCG025990.1,CCG024624.1,CCG009275.1, CCG004494.1,CCG002947.1,CCG010908.1,CCG005716.1, CCG027197.1,CCG022673.1,CCG026159.1,CCG027697.1, CCG020442.1,CCG010646.1,CCG015398.1,CCG017598.1, CCG001810.1,CCG024787.1,CCG027695.1,CCG001913.1,

GO:0016043	cellular component organization	183 of 4104 in the list	323 of 8404 in the genome	1	CCG006420.1,CCG018832.1,CCG006211.1,CCG004973.1, CCG013000.1,CCG026823.1,CCG003361.1,CCG011675.1, CCG010647.1,CCG019356.1,CCG020949.1,CCG005370.1, CCG019028.1,CCG007941.1,CCG026473.1,CCG012476.1, CCG002696.1,CCG014817.2,CCG014537.1,CCG003587.1, CCG013028.1,CCG027236.1,CCG019217.1,CCG024028.1, CCG005194.1,CCG024623.1,CCG014836.1,CCG015767.2, CCG024177.1,CCG000614.1,CCG009641.1,CCG004481.1, CCG006686.1,CCG012514.1,CCG027196.1,CCG000575.1, CCG002099.1,CCG016370.1,CCG014318.1,CCG010792.1, CCG003485.1,CCG025893.1,CCG010905.1,CCG022456.1, CCG006714.1,CCG027899.1,CCG010538.1,CCG010909.1, CCG018647.1,CCG017580.1,CCG015784.1,CCG009980.1, CCG023682.1,CCG015968.1,CCG013509.1,CCG019140.1, CCG018893.1,CCG010649.1,CCG025877.1,CCG018767.1, CCG020987.1,CCG015560.1,CCG002366.1,CCG009080.1, CCG027198.1,CCG009089.1,CCG027167.1,CCG000469.1, CCG025396.1,CCG000587.1,CCG012083.1,CCG018326.1, CCG019029.1,CCG008559.1,CCG019082.1,CCG027696.1, CCG021448.1,CCG010650.1,CCG000708.1,CCG025990.1, CCG024624.1,CCG009543.1,CCG004494.1,CCG015289.1, CCG010908.1,CCG005716.1,CCG022673.1,CCG026159.1, CCG009582.1,CCG015398.1,CCG020442.1,CCG020806.1, CCG001810.1,CCG002852.1,CCG024787.1,CCG000915.1, CCG012584.1,CCG021366.1,CCG000834.1,CCG018859.3, CCG008302.1,CCG019092.1,CCG024788.1,CCG015570.1, CCG006899.1,CCG002479.1,CCG019284.1,CCG008560.1, CCG021491.1,CCG010136.1,CCG003310.1,CCG009243.1, CCG013617.1,CCG000433.1,CCG010137.1,CCG020315.1, CCG009461.1,CCG011262.1,CCG023963.3,CCG006421.1,
GO:0001522	pseudouridine synthesis	11 of 4104 in the list	12 of 8404 in the genome	1	CCG014946.1,CCG000540.1,CCG019292.1,CCG020589.1, CCG011971.1,CCG019389.1,CCG016652.1,CCG002792.1, CCG028653.1,CCG018019.1,CCG016557.1

GO:0019220	regulation of phosphate metabolic process	53 of 4104 in the list	82 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG012519.1,CCG004132.1,CCG028409.1,CCG017369.1, CCG013274.1,CCG024695.1,CCG012743.1,CCG024000.1, CCG016965.1,CCG022676.1,CCG027878.1,CCG009450.1, CCG024809.1,CCG009024.1,CCG009521.1,CCG015333.1, CCG002971.1,CCG009035.1,CCG004682.1,CCG001854.1, CCG002109.1,CCG021151.1,CCG020898.1,CCG013794.1, CCG005105.1,CCG026404.1,CCG022394.1,CCG016027.1, CCG011341.1,CCG013849.1,CCG019462.1,CCG028049.1, CCG002823.1,CCG017923.1,CCG000890.1,CCG017560.1, CCG004783.1,CCG025554.1,CCG013303.1,CCG007631.1, CCG016181.1,CCG013203.1,CCG018776.1,CCG010260.1, CCG011162.1,CCG002864.1,CCG011648.1,CCG018184.1
GO:0051174	regulation of phosphorus metabolic process	53 of 4104 in the list	82 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG012519.1,CCG004132.1,CCG028409.1,CCG017369.1, CCG013274.1,CCG024695.1,CCG012743.1,CCG024000.1, CCG016965.1,CCG022676.1,CCG027878.1,CCG009450.1, CCG024809.1,CCG009024.1,CCG009521.1,CCG015333.1, CCG002971.1,CCG009035.1,CCG004682.1,CCG001854.1, CCG002109.1,CCG021151.1,CCG020898.1,CCG013794.1, CCG005105.1,CCG026404.1,CCG022394.1,CCG016027.1, CCG011341.1,CCG013849.1,CCG019462.1,CCG028049.1, CCG002823.1,CCG017923.1,CCG000890.1,CCG017560.1, CCG004783.1,CCG025554.1,CCG013303.1,CCG007631.1, CCG016181.1,CCG013203.1,CCG018776.1,CCG010260.1, CCG011162.1,CCG002864.1,CCG011648.1,CCG018184.1
GO:0006754	ATP biosynthetic process	15 of 4104 in the list	18 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG010112.1, CCG009142.1,CCG023640.1,CCG000148.1,CCG025348.1, CCG007724.1,CCG025989.2,CCG021934.1,CCG019619.1, CCG005924.2,CCG013643.1,CCG008422.1

GO:0050790	regulation of catalytic activity	49 of 4104 in the list	75 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG011044.1,CCG012519.1,CCG004132.1,CCG017369.1, CCG013274.1,CCG012743.1,CCG024000.1,CCG016965.1, CCG022676.1,CCG027878.1,CCG009450.1,CCG024809.1, CCG009024.1,CCG009521.1,CCG015333.1,CCG002971.1, CCG009035.1,CCG004682.1,CCG001854.1,CCG002109.1, CCG021151.1,CCG020898.1,CCG013794.1,CCG005105.1, CCG026404.1,CCG022394.1,CCG016027.1,CCG011341.1, CCG013849.1,CCG019462.1,CCG028049.1,CCG017923.1, CCG017560.1,CCG025554.1,CCG004783.1,CCG013303.1, CCG007631.1,CCG016181.1,CCG013203.1,CCG018776.1,

GO:0055114	oxidation-reduction process	458 of 4104 in the list	859 of 8404 in the genome	1	CCG006974.1,CCG017633.1,CCG012202.1,CCG019078.1, CCG000520.1,CCG014901.1,CCG000184.1,CCG018055.1, CCG015926.1,CCG019182.1,CCG020913.1,CCG003729.1, CCG004595.1,CCG025108.1,CCG015758.1,CCG009904.1, CCG020879.1,CCG006391.1,CCG016220.1,CCG010284.1, CCG017981.1,CCG013059.1,CCG025836.1,CCG012949.1, CCG020804.1,CCG006639.1,CCG024297.1,CCG012578.1, CCG007424.2,CCG009496.1,CCG026536.1,CCG018943.2, CCG010038.1,CCG025307.1,CCG013289.1,CCG007720.1, CCG012579.1,CCG020956.1,CCG022067.1,CCG025346.1, CCG017624.1,CCG000948.1,CCG020227.1,CCG022025.2, CCG005053.1,CCG011237.1,CCG025833.1,CCG006994.1, CCG024123.2,CCG015290.1,CCG000944.1,CCG007420.1, CCG011722.1,CCG003063.1,CCG023245.1,CCG015331.1, CCG019909.1,CCG015763.2,CCG015450.1,CCG018253.1, CCG010179.1,CCG017162.1,CCG021468.1,CCG018255.1, CCG020660.1,CCG018625.1,CCG011231.2,CCG013816.1, CCG028131.1,CCG023451.1,CCG027557.1,CCG005913.1, CCG009672.1,CCG024119.1,CCG007260.1,CCG018290.1, CCG020911.1,CCG012339.1,CCG026670.1,CCG018257.1, CCG022399.1,CCG027312.1,CCG017982.1,CCG011895.1, CCG024532.1,CCG002113.1,CCG015133.1,CCG004434.1, CCG011891.1,CCG017425.1,CCG000775.1,CCG017111.1, CCG013610.1,CCG023940.1,CCG017979.1,CCG025827.1, CCG008215.1,CCG014228.2,CCG002231.1,CCG008902.1, CCG016900.1,CCG006972.1,CCG017116.1,CCG025096.1, CCG025015.2,CCG018446.1,CCG019844.1,CCG026016.1, CCG005588.1,CCG011547.1,CCG005162.1,CCG020414.1, CCG015537.1,CCG011491.1,CCG005955.1,CCG008895.1, CCG024878.1,CCG002783.1,CCG000391.1,CCG013575.1,

GO:0046578	regulation of Ras protein signal transduction	60 of 4104 in the list	95 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG006050.2, CCG025433.1,CCG021263.1,CCG012519.1,CCG026214.1, CCG004132.1,CCG017369.1,CCG009980.1,CCG010808.1, CCG009512.1,CCG025470.1,CCG022334.1,CCG008892.2, CCG024000.1,CCG016965.1,CCG022676.1,CCG027878.1, CCG024809.1,CCG009024.1,CCG015333.1,CCG010849.1, CCG003602.1,CCG004884.2,CCG022749.1,CCG002971.1, CCG018380.1,CCG002109.1,CCG018015.1,CCG010329.2, CCG021151.1,CCG005105.1,CCG001579.1,CCG021483.1, CCG028651.1,CCG022394.1,CCG016027.1,CCG011341.1, CCG019462.1,CCG008035.1,CCG000596.1,CCG019585.1, CCG025554.1,CCG013303.1,CCG012670.1,CCG007631.1, CCG025667.2,CCG016181.1,CCG013203.1,CCG018776.1, CCG022420.1,CCG009510.1,CCG021294.1,CCG010260.1, CCG010157.1,CCG002864.1,CCG020983.1,CCG011422.1
GO:0006979	response to oxidative stress	18 of 4104 in the list	23 of 8404 in the genome	1	CCG011122.1,CCG021071.1,CCG012274.1,CCG012273.2, CCG017425.1,CCG024878.1,CCG003364.1,CCG004145.1, CCG023940.1,CCG004723.1,CCG009672.1,CCG005913.1, CCG001530.1,CCG027211.1,CCG021072.1,CCG000409.1,
GO:0016568	chromatin modification	18 of 4104 in the list	23 of 8404 in the genome	1	CCG006899.1,CCG018482.1,CCG006686.1,CCG006211.1, CCG020863.1,CCG027348.1,CCG000575.1,CCG011675.1, CCG015398.1,CCG018326.1,CCG012083.1,CCG000587.1, CCG001913.1,CCG001369.2,CCG000122.1,CCG025991.2,
GO:0006418	tRNA aminoacylation for protein translation	44 of 4104 in the list	67 of 8404 in the genome	1	CCG020877.1,CCG021774.1,CCG006231.1,CCG008321.1, CCG023277.1,CCG014396.1,CCG015367.1,CCG010191.3, CCG001811.1,CCG009878.1,CCG006188.1,CCG004949.1, CCG027352.3,CCG015950.3,CCG005204.1,CCG016238.1, CCG011135.1,CCG013727.1,CCG028092.1,CCG021716.1, CCG021820.1,CCG002662.1,CCG006570.1,CCG027607.1, CCG000352.1,CCG023315.1,CCG003528.1,CCG010321.1, CCG000138.1,CCG017344.1,CCG010565.1,CCG015577.3, CCG003296.1,CCG019545.1,CCG019330.1,CCG001876.1, CCG022269.1,CCG026570.1,CCG008789.1,CCG000414.1, CCG002018.1,CCG023510.1,CCG013068.1,CCG024526.1

GO:0043038	amino acid activation	44 of 4104 in the list	67 of 8404 in the genome	1	CCG020877.1,CCG021774.1,CCG006231.1,CCG008321.1, CCG023277.1,CCG014396.1,CCG015367.1,CCG010191.3, CCG001811.1,CCG009878.1,CCG006188.1,CCG004949.1, CCG027352.3,CCG015950.3,CCG005204.1,CCG016238.1, CCG011135.1,CCG013727.1,CCG028092.1,CCG021716.1, CCG021820.1,CCG002662.1,CCG006570.1,CCG027607.1, CCG000352.1,CCG023315.1,CCG003528.1,CCG010321.1, CCG000138.1,CCG017344.1,CCG010565.1,CCG015577.3, CCG003296.1,CCG019545.1,CCG019330.1,CCG001876.1, CCG022269.1,CCG026570.1,CCG008789.1,CCG000414.1,
GO:0043039	tRNA aminoacylation	44 of 4104 in the list	67 of 8404 in the genome	1	CCG020877.1,CCG021774.1,CCG006231.1,CCG008321.1, CCG023277.1,CCG014396.1,CCG015367.1,CCG010191.3, CCG001811.1,CCG009878.1,CCG006188.1,CCG004949.1, CCG027352.3,CCG015950.3,CCG005204.1,CCG016238.1, CCG011135.1,CCG013727.1,CCG028092.1,CCG021716.1, CCG021820.1,CCG002662.1,CCG006570.1,CCG027607.1, CCG000352.1,CCG023315.1,CCG003528.1,CCG010321.1, CCG000138.1,CCG017344.1,CCG010565.1,CCG015577.3, CCG003296.1,CCG019545.1,CCG019330.1,CCG001876.1, CCG022269.1,CCG026570.1,CCG008789.1,CCG000414.1,

GO:0031323	regulation of cellular metabolic process	314 of 4104 in the list	579 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022266.1,CCG003824.3, CCG008767.3,CCG008741.1,CCG024695.1,CCG003390.1, CCG027427.1,CCG007493.1,CCG002971.1,CCG021465.1, CCG003175.1,CCG004682.1,CCG023752.1,CCG018321.1, CCG028326.3,CCG013794.1,CCG006134.1,CCG009970.1, CCG011341.1,CCG019462.1,CCG016745.1,CCG021436.1, CCG016445.1,CCG012536.1,CCG000659.1,CCG027127.1, CCG018719.1,CCG015425.1,CCG027796.1,CCG022824.1, CCG018533.1,CCG024710.1,CCG022281.1,CCG011465.1, CCG018776.1,CCG006714.1,CCG020129.1,CCG027186.1, CCG011911.1,CCG004132.1,CCG000588.1,CCG022045.1, CCG013274.1,CCG028568.1,CCG022676.1,CCG007647.1, CCG024809.1,CCG021633.1,CCG012083.1,CCG000562.1, CCG005480.2,CCG017760.1,CCG016859.1,CCG005486.1, CCG020898.1,CCG017591.1,CCG002198.1,CCG021284.1, CCG016924.1,CCG013849.1,CCG000133.1,CCG013224.2, CCG002273.1,CCG001698.1,CCG023777.1,CCG014461.1, CCG026228.2,CCG005487.1,CCG021054.1,CCG016307.1, CCG009805.2,CCG016749.1,CCG028465.1,CCG019250.1, CCG005396.1,CCG025747.1,CCG009823.1,CCG021456.1, CCG014928.1,CCG005168.1,CCG018184.1,CCG018315.1, CCG027580.1,CCG025433.1,CCG024271.1,CCG012519.1, CCG028409.1,CCG025758.1,CCG009458.1,CCG022496.1, CCG015062.1,CCG024000.1,CCG016965.1,CCG018164.1, CCG015333.1,CCG001301.1,CCG023199.2,CCG001431.2, CCG001341.1,CCG022398.1,CCG021521.1,CCG009562.2, CCG010139.1,CCG021940.1,CCG024639.1,CCG015846.1, CCG008833.1,CCG018168.1,CCG014509.1,CCG004783.1, CCG025691.1,CCG018042.1,CCG014463.1,CCG026788.1, CCG020543.1,CCG025549.1,CCG011015.1,CCG027950.1,

GO:1901566	organonitrogen compound biosynthetic process	109 of 4104 in the list	186 of 8404 in the genome	1	CCG022191.1,CCG010174.2,CCG017331.1,CCG017175.1, CCG007610.1,CCG011491.1,CCG002555.1,CCG009333.1, CCG006529.1,CCG025989.2,CCG021335.1,CCG008422.1, CCG024517.1,CCG025493.1,CCG010112.1,CCG016220.1, CCG015568.1,CCG020441.1,CCG013643.1,CCG002495.1, CCG026536.1,CCG002038.1,CCG010561.1,CCG023780.2, CCG000148.1,CCG018453.1,CCG001423.1,CCG013365.1, CCG022025.2,CCG005924.2,CCG005053.1,CCG025940.1, CCG008860.1,CCG025731.1,CCG018108.1,CCG027282.1, CCG026099.1,CCG008609.1,CCG024133.1,CCG009515.2, CCG004257.1,CCG017330.1,CCG021110.1,CCG025897.1, CCG021934.1,CCG010319.1,CCG017559.1,CCG007203.1, CCG027212.1,CCG019954.3,CCG017995.1,CCG004180.1, CCG026752.1,CCG023640.1,CCG002556.1,CCG028391.1, CCG021086.2,CCG015921.1,CCG025348.1,CCG019619.1, CCG016005.1,CCG005938.1,CCG013999.1,CCG028131.1, CCG021336.1,CCG017894.1,CCG007417.1,CCG013043.1, CCG024432.2,CCG004440.1,CCG007724.1,CCG022072.1, CCG016315.1,CCG021610.1,CCG010460.1,CCG006821.1, CCG000682.1,CCG008932.1,CCG015410.1,CCG002897.1, CCG003865.1,CCG025107.1,CCG009142.1,CCG026898.1, CCG026812.1,CCG023452.1,CCG002883.1,CCG018659.2, CCG025636.2,CCG014116.1,CCG017201.1,CCG017111.1, CCG015276.2,CCG022773.2,CCG013610.1,CCG003173.1, CCG016614.1,CCG028305.1,CCG009518.1,CCG004188.3, CCG002231.1,CCG015943.1,CCG006791.1,CCG016955.1,
GO:0006096	glycolysis	16 of 4104 in the list	20 of 8404 in the genome	1	CCG022035.1,CCG020616.1,CCG005588.1,CCG003215.3, CCG010373.1,CCG007981.1,CCG007023.1,CCG022214.1, CCG000431.1,CCG013339.1,CCG019953.1,CCG017200.1, CCG003220.2,CCG006203.1,CCG022453.1,CCG025277.1
GO:0006099	tricarboxylic acid cycle	16 of 4104 in the list	20 of 8404 in the genome	1	CCG024798.1,CCG012727.1,CCG018128.1,CCG011547.1, CCG020956.1,CCG004244.1,CCG019712.1,CCG009771.2, CCG001842.1,CCG023350.1,CCG001072.1,CCG012249.1, CCG016431.1,CCG000089.1,CCG027631.1,CCG020707.1

GO:0009060	aerobic respiration	16 of 4104 in the list	20 of 8404 in the genome	1	CCG024798.1,CCG012727.1,CCG018128.1,CCG011547.1, CCG020956.1,CCG004244.1,CCG019712.1,CCG009771.2, CCG001842.1,CCG023350.1,CCG001072.1,CCG012249.1, CCG016431.1,CCG000089.1,CCG027631.1,CCG020707.1
GO:0016052	carbohydrate catabolic process	21 of 4104 in the list	28 of 8404 in the genome	1	CCG022035.1,CCG020616.1,CCG005588.1,CCG003215.3, CCG025307.1,CCG010373.1,CCG007981.1,CCG007023.1, CCG022214.1,CCG000431.1,CCG013339.1,CCG009084.2, CCG019953.1,CCG017200.1,CCG006358.1,CCG003220.2, CCG006203.1,CCG005177.1,CCG022453.1,CCG025277.1,
GO:0051258	protein polymerization	21 of 4104 in the list	28 of 8404 in the genome	1	CCG006420.1,CCG009543.1,CCG015289.1,CCG013000.1, CCG013637.1,CCG016370.1,CCG010418.1,CCG005886.1, CCG005370.1,CCG009080.1,CCG010864.1,CCG002852.1, CCG009243.1,CCG025396.1,CCG007532.1,CCG007531.1, CCG002696.1,CCG018820.3,CCG008748.1,CCG023963.3,
GO:0006325	chromatin organization	88 of 4104 in the list	147 of 8404 in the genome	1	CCG006899.1,CCG006211.1,CCG003361.1,CCG011675.1, CCG019284.1,CCG008560.1,CCG010136.1,CCG021491.1, CCG010647.1,CCG003310.1,CCG013617.1,CCG000433.1, CCG026473.1,CCG012476.1,CCG014537.1,CCG010137.1, CCG013028.1,CCG009461.1,CCG005194.1,CCG024623.1, CCG025880.1,CCG014836.1,CCG010904.1,CCG024177.1, CCG018482.1,CCG004481.1,CCG006686.1,CCG012514.1, CCG027196.1,CCG014772.1,CCG000575.1,CCG026474.1, CCG025893.1,CCG009637.1,CCG010905.1,CCG026579.1, CCG010909.1,CCG010648.1,CCG017580.1,CCG009980.1, CCG027348.1,CCG020863.1,CCG010906.1,CCG015968.1, CCG018893.1,CCG010138.1,CCG010649.1,CCG018767.1, CCG008892.2,CCG025877.1,CCG015560.1,CCG027199.1, CCG027198.1,CCG018326.1,CCG012083.1,CCG000587.1, CCG001369.2,CCG018287.1,CCG008559.1,CCG027696.1, CCG010907.1,CCG025991.2,CCG012229.1,CCG010650.1, CCG000708.1,CCG025990.1,CCG024624.1,CCG009275.1, CCG004494.1,CCG002947.1,CCG010908.1,CCG005716.1, CCG027197.1,CCG022673.1,CCG026159.1,CCG027697.1, CCG020442.1,CCG010646.1,CCG015398.1,CCG017598.1, CCG024787.1,CCG027695.1,CCG001913.1,CCG012584.1,

GO:0022904	respiratory electron transport chain	12 of 4104 in the list	14 of 8404 in the genome	1	CCG004155.2,CCG023685.1,CCG000102.1,CCG020879.1, CCG018684.1,CCG001649.1,CCG014053.1,CCG006864.1, CCG006459.1,CCG025163.3,CCG024297.1,CCG011237.1
GO:0044712	single-organism catabolic process	115 of 4104 in the list	198 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG005588.1,CCG002549.1, CCG007060.1,CCG013000.1,CCG010373.1,CCG013766.1, CCG010111.1,CCG024327.1,CCG000591.1,CCG024092.1, CCG015386.1,CCG019020.1,CCG009243.1,CCG025108.1, CCG006358.1,CCG003220.2,CCG006203.1,CCG006391.1, CCG002925.1,CCG019834.1,CCG025387.1,CCG022453.1, CCG023005.1,CCG024375.1,CCG003748.1,CCG009607.1, CCG011006.1,CCG027119.1,CCG007827.1,CCG014434.1, CCG006421.1,CCG023963.3,CCG022035.1,CCG021990.1, CCG025027.1,CCG015949.1,CCG025307.1,CCG025521.1, CCG016370.1,CCG007023.1,CCG019103.1,CCG019629.2, CCG006311.1,CCG002917.1,CCG005147.1,CCG004988.1, CCG001082.1,CCG020909.1,CCG007532.1,CCG018447.1, CCG007531.1,CCG016966.1,CCG018820.3,CCG011722.1, CCG025277.1,CCG025179.1,CCG003063.1,CCG006777.1, CCG007203.1,CCG020616.1,CCG003215.3,CCG025973.1, CCG013637.1,CCG007981.1,CCG001440.1,CCG015351.1, CCG010418.1,CCG020154.1,CCG002366.1,CCG009080.1, CCG004869.1,CCG000431.1,CCG009084.2,CCG019953.1, CCG025396.1,CCG026953.1,CCG011721.1,CCG006924.1, CCG021220.1,CCG008510.1,CCG008748.1,CCG006059.1, CCG017543.1,CCG013641.1,CCG019243.1,CCG016027.1, CCG015289.1,CCG003495.1,CCG021411.1,CCG001859.1, CCG026336.1,CCG022214.1,CCG005886.1,CCG025131.2, CCG016542.1,CCG013339.1,CCG026154.1,CCG015654.1, CCG002852.1,CCG010864.1,CCG001445.1,CCG011789.1, CCG013765.1,CCG017200.1,CCG002231.1,CCG005177.1,

GO:0019222	regulation of metabolic process	317 of 4104 in the list	587 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022266.1,CCG003824.3, CCG008767.3,CCG008741.1,CCG024695.1,CCG003390.1, CCG027427.1,CCG007493.1,CCG002971.1,CCG021465.1, CCG003175.1,CCG004682.1,CCG023752.1,CCG018321.1, CCG028326.3,CCG013794.1,CCG006134.1,CCG009970.1, CCG011341.1,CCG019462.1,CCG016745.1,CCG021436.1, CCG016445.1,CCG012536.1,CCG000659.1,CCG027127.1, CCG018719.1,CCG015425.1,CCG027796.1,CCG022824.1, CCG018533.1,CCG024710.1,CCG022281.1,CCG011465.1, CCG018776.1,CCG006714.1,CCG020129.1,CCG027186.1, CCG011911.1,CCG004132.1,CCG000588.1,CCG022045.1, CCG013274.1,CCG028568.1,CCG022676.1,CCG007647.1, CCG024809.1,CCG021633.1,CCG012083.1,CCG000562.1, CCG005480.2,CCG017760.1,CCG016859.1,CCG005486.1, CCG020898.1,CCG017591.1,CCG002198.1,CCG021284.1, CCG016924.1,CCG013849.1,CCG000133.1,CCG013224.2, CCG002273.1,CCG001698.1,CCG023777.1,CCG014461.1, CCG026228.2,CCG005487.1,CCG021054.1,CCG016307.1, CCG009805.2,CCG016749.1,CCG028465.1,CCG019250.1, CCG005396.1,CCG025747.1,CCG009823.1,CCG021456.1, CCG014928.1,CCG005168.1,CCG018184.1,CCG018315.1, CCG027580.1,CCG025433.1,CCG024271.1,CCG011044.1, CCG012519.1,CCG028409.1,CCG025758.1,CCG009458.1, CCG022496.1,CCG015062.1,CCG024000.1,CCG016965.1, CCG018164.1,CCG015333.1,CCG001301.1,CCG023199.2, CCG001431.2,CCG001341.1,CCG022398.1,CCG021521.1, CCG009562.2,CCG010139.1,CCG021940.1,CCG024639.1, CCG015846.1,CCG008833.1,CCG018168.1,CCG014509.1, CCG004783.1,CCG025691.1,CCG018042.1,CCG014463.1, CCG026788.1,CCG020543.1,CCG025549.1,CCG011015.1,

GO:0032268	regulation of cellular protein metabolic process	28 of 4104 in the list	40 of 8404 in the genome	1	CCG013849.1,CCG003216.1,CCG028049.1,CCG017923.1, CCG016445.1,CCG013274.1,CCG015062.1,CCG024695.1, CCG005487.1,CCG005485.1,CCG012743.1,CCG004783.1, CCG009521.1,CCG003765.1,CCG009035.1,CCG004682.1, CCG001854.1,CCG006714.1,CCG005486.1,CCG026155.1, CCG020898.1,CCG023431.1,CCG013794.1,CCG016835.2, CCG011648.1,CCG026404.1,CCG018184.1,CCG021794.1

GO:0044699	single-organism process	1853 of 4104 in the list	3675 of 8404 in the genome	1	CCG005254.1,CCG017420.1,CCG014340.1,CCG005375.1, CCG014396.1,CCG017209.1,CCG026106.1,CCG021740.1, CCG004086.1,CCG021738.1,CCG005370.1,CCG001468.1, CCG004595.1,CCG012875.1,CCG025108.1,CCG009904.1, CCG026174.1,CCG022794.1,CCG003587.1,CCG013059.1, CCG025836.1,CCG026360.1,CCG003712.1,CCG012949.1, CCG018432.1,CCG017266.1,CCG011763.1,CCG005616.1, CCG016689.2,CCG017078.1,CCG026799.1,CCG014466.1, CCG017851.1,CCG009530.1,CCG020956.1,CCG017240.1, CCG015101.1,CCG016094.1,CCG023474.1,CCG017255.1, CCG000948.1,CCG027127.1,CCG022025.2,CCG005053.1, CCG011237.1,CCG018533.1,CCG019190.1,CCG000526.1, CCG007420.1,CCG022281.1,CCG016654.1,CCG018416.1, CCG013308.1,CCG023579.1,CCG006714.1,CCG021110.1, CCG010246.1,CCG026050.1,CCG001964.1,CCG024612.1, CCG009668.1,CCG018253.1,CCG004548.1,CCG018625.1, CCG024663.1,CCG011231.2,CCG021681.1,CCG012083.1, CCG026953.1,CCG006489.1,CCG023451.1,CCG010622.1, CCG005913.1,CCG024119.1,CCG012339.1,CCG019678.1, CCG018257.1,CCG023464.1,CCG018264.1,CCG001579.1, CCG013641.1,CCG016924.1,CCG000732.1,CCG003317.1, CCG000133.1,CCG005391.2,CCG007951.1,CCG018585.3, CCG007597.1,CCG019647.1,CCG012840.1,CCG000775.1, CCG026151.1,CCG016399.1,CCG005284.1,CCG024903.1, CCG013610.1,CCG009959.1,CCG001876.1,CCG002231.1, CCG016719.1,CCG008902.1,CCG000983.1,CCG010416.1, CCG009823.1,CCG025096.1,CCG002937.1,CCG000876.1, CCG024664.1,CCG004532.1,CCG000789.1,CCG019844.1, CCG017381.1,CCG005588.1,CCG016753.1,CCG011547.1, CCG015537.1,CCG011252.1,CCG007356.1,CCG009333.1,
GO:1901615	organic hydroxy compound metabolic process	25 of 4104 in the list	35 of 8404 in the genome	1	CCG026536.1,CCG018054.1,CCG005286.1,CCG015949.1, CCG026331.1,CCG013318.1,CCG018055.1,CCG020559.1, CCG016653.1,CCG008317.1,CCG011327.1,CCG015587.1, CCG012875.1,CCG015680.1,CCG024095.1,CCG006358.1, CCG018029.3,CCG023757.1,CCG025827.1,CCG018923.1, CCG024433.1,CCG005177.1,CCG014174.1,CCG015679.1,

GO:0009966	regulation of signal transduction	83 of 4104 in the list	139 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG025433.1,CCG021263.1, CCG012519.1,CCG026798.1,CCG026214.1,CCG023484.1, CCG009512.1,CCG022334.1,CCG009446.1,CCG024000.1, CCG016965.1,CCG027878.1,CCG015333.1,CCG010849.1, CCG003602.1,CCG004884.2,CCG002338.1,CCG002971.1, CCG019427.1,CCG018015.1,CCG001079.1,CCG010329.2, CCG021064.1,CCG021483.1,CCG028651.1,CCG012573.1, CCG011341.1,CCG019462.1,CCG008035.1,CCG011501.1, CCG004343.1,CCG019585.1,CCG012670.1,CCG012835.1, CCG013203.1,CCG018776.1,CCG022420.1,CCG018222.1, CCG009510.1,CCG010260.1,CCG010157.1,CCG002166.1, CCG002864.1,CCG011422.1,CCG006050.2,CCG022083.1, CCG000807.1,CCG024952.1,CCG004132.1,CCG010808.1, CCG009980.1,CCG017369.1,CCG025470.1,CCG008892.2, CCG004805.1,CCG022676.1,CCG024809.1,CCG009450.1, CCG009024.1,CCG022749.1,CCG018380.1,CCG002109.1, CCG021151.1,CCG017498.1,CCG025178.1,CCG005105.1, CCG001579.1,CCG022394.1,CCG016027.1,CCG017560.1, CCG006412.1,CCG000596.1,CCG019947.1,CCG025554.1, CCG013303.1,CCG007631.1,CCG025667.2,CCG016181.1,

GO:0010646	regulation of cell communication	83 of 4104 in the list	139 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG025433.1,CCG021263.1, CCG012519.1,CCG026798.1,CCG026214.1,CCG023484.1, CCG009512.1,CCG022334.1,CCG009446.1,CCG024000.1, CCG016965.1,CCG027878.1,CCG015333.1,CCG010849.1, CCG003602.1,CCG004884.2,CCG002338.1,CCG002971.1, CCG019427.1,CCG018015.1,CCG001079.1,CCG010329.2, CCG021064.1,CCG021483.1,CCG028651.1,CCG012573.1, CCG011341.1,CCG019462.1,CCG008035.1,CCG011501.1, CCG004343.1,CCG019585.1,CCG012670.1,CCG012835.1, CCG013203.1,CCG018776.1,CCG022420.1,CCG018222.1, CCG009510.1,CCG010260.1,CCG010157.1,CCG002166.1, CCG002864.1,CCG011422.1,CCG006050.2,CCG022083.1, CCG000807.1,CCG024952.1,CCG004132.1,CCG010808.1, CCG009980.1,CCG017369.1,CCG025470.1,CCG008892.2, CCG004805.1,CCG022676.1,CCG024809.1,CCG009450.1, CCG009024.1,CCG022749.1,CCG018380.1,CCG002109.1, CCG021151.1,CCG017498.1,CCG025178.1,CCG005105.1, CCG001579.1,CCG022394.1,CCG016027.1,CCG017560.1, CCG006412.1,CCG000596.1,CCG019947.1,CCG025554.1, CCG013303.1,CCG007631.1,CCG025667.2,CCG016181.1,

GO:0048583	regulation of response to stimulus	83 of 4104 in the list	139 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG025433.1,CCG021263.1, CCG012519.1,CCG026798.1,CCG026214.1,CCG023484.1, CCG009512.1,CCG022334.1,CCG009446.1,CCG024000.1, CCG016965.1,CCG027878.1,CCG015333.1,CCG010849.1, CCG003602.1,CCG004884.2,CCG002338.1,CCG002971.1, CCG019427.1,CCG018015.1,CCG001079.1,CCG010329.2, CCG021064.1,CCG021483.1,CCG028651.1,CCG012573.1, CCG011341.1,CCG019462.1,CCG008035.1,CCG011501.1, CCG004343.1,CCG019585.1,CCG012670.1,CCG012835.1, CCG013203.1,CCG018776.1,CCG022420.1,CCG018222.1, CCG009510.1,CCG010260.1,CCG010157.1,CCG002166.1, CCG002864.1,CCG011422.1,CCG006050.2,CCG022083.1, CCG000807.1,CCG024952.1,CCG004132.1,CCG010808.1, CCG009980.1,CCG017369.1,CCG025470.1,CCG008892.2, CCG004805.1,CCG022676.1,CCG024809.1,CCG009450.1, CCG009024.1,CCG022749.1,CCG018380.1,CCG002109.1, CCG021151.1,CCG017498.1,CCG025178.1,CCG005105.1, CCG001579.1,CCG022394.1,CCG016027.1,CCG017560.1, CCG006412.1,CCG000596.1,CCG019947.1,CCG025554.1, CCG013303.1,CCG007631.1,CCG025667.2,CCG016181.1,
GO:0001510	RNA methylation	7 of 4104 in the list	7 of 8404 in the genome	1	CCG003755.1,CCG014335.1,CCG004234.1,CCG017176.1, CCG008401.1,CCG023156.1,CCG009425.1
GO:0006561	proline biosynthetic process	7 of 4104 in the list	7 of 8404 in the genome	1	CCG017111.1,CCG016220.1,CCG015921.1,CCG001423.1, CCG017894.1,CCG003871.1,CCG008860.1
GO:0009156	ribonucleoside monophosphate biosynthetic process	26 of 4104 in the list	37 of 8404 in the genome	1	CCG015410.1,CCG015746.1,CCG002038.1,CCG025107.1, CCG009142.1,CCG023640.1,CCG015747.1,CCG000148.1, CCG025348.1,CCG025989.2,CCG019619.1,CCG018659.2, CCG005924.2,CCG007533.1,CCG008422.1,CCG013610.1, CCG016614.1,CCG028305.1,CCG010112.1,CCG017330.1, CCG006791.1,CCG026865.1,CCG007724.1,CCG021934.1,
GO:0009127	purine nucleoside monophosphate biosynthetic process	23 of 4104 in the list	32 of 8404 in the genome	1	CCG015410.1,CCG015746.1,CCG002038.1,CCG025107.1, CCG009142.1,CCG023640.1,CCG015747.1,CCG000148.1, CCG025348.1,CCG025989.2,CCG019619.1,CCG018659.2, CCG005924.2,CCG008422.1,CCG028305.1,CCG010112.1, CCG017330.1,CCG006791.1,CCG026865.1,CCG007724.1, CCG021934.1,CCG013643.1,CCG017295.1

GO:0009168	purine ribonucleoside monophosphate biosynthetic process	23 of 4104 in the list	32 of 8404 in the genome	1	CCG015410.1,CCG015746.1,CCG002038.1,CCG025107.1, CCG009142.1,CCG023640.1,CCG015747.1,CCG000148.1, CCG025348.1,CCG025989.2,CCG019619.1,CCG018659.2, CCG005924.2,CCG008422.1,CCG028305.1,CCG010112.1, CCG017330.1,CCG006791.1,CCG026865.1,CCG007724.1, CCG021934.1,CCG013643.1,CCG017295.1
GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	15 of 4104 in the list	19 of 8404 in the genome	1	CCG009521.1,CCG013849.1,CCG028049.1,CCG017923.1, CCG009035.1,CCG004682.1,CCG001854.1,CCG013274.1, CCG020898.1,CCG012743.1,CCG013794.1,CCG004783.1, CCG011648.1,CCG026404.1,CCG018184.1
GO:0071900	regulation of protein serine/threonine kinase activity	15 of 4104 in the list	19 of 8404 in the genome	1	CCG009521.1,CCG013849.1,CCG028049.1,CCG017923.1, CCG009035.1,CCG004682.1,CCG001854.1,CCG013274.1, CCG020898.1,CCG012743.1,CCG013794.1,CCG004783.1, CCG011648.1,CCG026404.1,CCG018184.1

GO:0044281	small molecule metabolic process	312 of 4104 in the list	580 of 8404 in the genome	1	CCG017420.1,CCG019078.1,CCG023277.1,CCG014396.1, CCG010191.3,CCG017331.1,CCG028623.1,CCG009878.1, CCG019020.1,CCG012875.1,CCG025108.1,CCG026174.1, CCG016238.1,CCG006391.1,CCG023354.1,CCG017097.1, CCG016220.1,CCG011006.1,CCG027119.1,CCG026536.1, CCG025307.1,CCG007993.1,CCG016370.1,CCG016653.1, CCG022025.2,CCG025940.1,CCG006994.1,CCG011722.1, CCG021110.1,CCG003063.1,CCG019909.1,CCG020877.1, CCG006231.1,CCG025396.1,CCG028131.1,CCG026953.1, CCG008510.1,CCG018290.1,CCG019678.1,CCG027312.1, CCG013641.1,CCG006821.1,CCG003495.1,CCG009662.1, CCG013318.1,CCG025131.2,CCG023452.1,CCG025636.2, CCG014116.1,CCG002852.1,CCG017111.1,CCG019545.1, CCG013610.1,CCG019330.1,CCG022773.2,CCG010986.1, CCG001876.1,CCG009518.1,CCG002231.1,CCG007362.1, CCG026865.1,CCG008388.1,CCG001285.1,CCG015367.1, CCG026047.1,CCG017175.1,CCG011491.1,CCG006529.1, CCG012619.1,CCG009333.1,CCG000591.1,CCG007533.1, CCG008422.1,CCG010112.1,CCG011135.1,CCG028092.1, CCG015568.1,CCG020441.1,CCG006421.1,CCG023963.3, CCG021990.1,CCG010561.1,CCG026910.1,CCG000148.1, CCG017344.1,CCG000472.1,CCG004988.1,CCG018615.3, CCG006998.1,CCG018108.1,CCG026099.1,CCG016415.1, CCG026030.1,CCG025897.1,CCG006009.1,CCG021934.1, CCG007203.1,CCG004308.1,CCG002466.1,CCG017995.1, CCG006600.1,CCG001440.1,CCG012408.1,CCG015921.1, CCG020559.1,CCG010418.1,CCG016222.1,CCG026852.1, CCG013999.1,CCG017894.1,CCG007417.1,CCG013043.1, CCG018289.1,CCG001066.1,CCG021716.1,CCG008960.1, CCG007724.1,CCG006059.1,CCG002662.1,CCG022027.1,
GO:0009124	nucleoside monophosphate biosynthetic process	27 of 4104 in the list	39 of 8404 in the genome	1	CCG015410.1,CCG015746.1,CCG002038.1,CCG025107.1, CCG009142.1,CCG004180.1,CCG023640.1,CCG015747.1, CCG000148.1,CCG025348.1,CCG025989.2,CCG019619.1, CCG018659.2,CCG005924.2,CCG007533.1,CCG008422.1, CCG013610.1,CCG016614.1,CCG028305.1,CCG010112.1, CCG017330.1,CCG006791.1,CCG026865.1,CCG007724.1,

GO:0023051	regulation of signaling	84 of 4104 in the list	142 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG025433.1,CCG021263.1, CCG012519.1,CCG026798.1,CCG026214.1,CCG023484.1, CCG009512.1,CCG022334.1,CCG009446.1,CCG024000.1, CCG016965.1,CCG027878.1,CCG015333.1,CCG010849.1, CCG003602.1,CCG004884.2,CCG002338.1,CCG002971.1, CCG019427.1,CCG018015.1,CCG001079.1,CCG010329.2, CCG021064.1,CCG021483.1,CCG028651.1,CCG012573.1, CCG011341.1,CCG019462.1,CCG008035.1,CCG011501.1, CCG004343.1,CCG019585.1,CCG012670.1,CCG012835.1, CCG018268.1,CCG013203.1,CCG018776.1,CCG022420.1, CCG009510.1,CCG018222.1,CCG010260.1,CCG010157.1, CCG002166.1,CCG002864.1,CCG011422.1,CCG000807.1, CCG006050.2,CCG022083.1,CCG024952.1,CCG004132.1, CCG010808.1,CCG009980.1,CCG017369.1,CCG025470.1, CCG008892.2,CCG004805.1,CCG022676.1,CCG024809.1, CCG009450.1,CCG009024.1,CCG022749.1,CCG018380.1, CCG002109.1,CCG021151.1,CCG017498.1,CCG025178.1, CCG005105.1,CCG001579.1,CCG022394.1,CCG016027.1, CCG017560.1,CCG006412.1,CCG000596.1,CCG019947.1, CCG025554.1,CCG013303.1,CCG007631.1,CCG025667.2,
GO:0031324	negative regulation of cellular metabolic process	24 of 4104 in the list	34 of 8404 in the genome	1	CCG003216.1,CCG028409.1,CCG002823.1,CCG026841.1, CCG025758.1,CCG016445.1,CCG014461.1,CCG010489.1, CCG000890.1,CCG015062.1,CCG003390.1,CCG025132.1, CCG005487.1,CCG005485.1,CCG005898.1,CCG004838.1, CCG003765.1,CCG005486.1,CCG006714.1,CCG018321.1, CCG023431.1,CCG016835.2,CCG014323.1,CCG021794.1
GO:0046034	ATP metabolic process	24 of 4104 in the list	34 of 8404 in the genome	1	CCG004308.1,CCG015410.1,CCG017693.1,CCG002038.1, CCG025107.1,CCG009142.1,CCG023640.1,CCG026314.1, CCG000148.1,CCG004309.1,CCG025348.1,CCG025989.2, CCG006486.1,CCG019619.1,CCG005924.2,CCG008422.1, CCG010112.1,CCG001066.1,CCG019866.1,CCG019678.1, CCG007724.1,CCG021934.1,CCG013643.1,CCG001285.1

GO:0007010	cytoskeleton organization	35 of 4104 in the list	53 of 8404 in the genome	1	CCG015570.1,CCG018647.1,CCG002479.1,CCG026688.1, CCG015784.1,CCG026823.1,CCG023682.1,CCG019140.1, CCG019356.1,CCG027167.1,CCG019028.1,CCG000469.1, CCG005579.1,CCG019029.1,CCG014817.2,CCG003587.1, CCG021448.1,CCG027236.1,CCG024028.1,CCG011262.1, CCG009090.1,CCG009641.1,CCG003708.1,CCG016992.2, CCG014318.1,CCG000535.1,CCG022536.3,CCG021366.1, CCG027899.1,CCG002137.1,CCG019092.1,CCG010538.1,
GO:0009161	ribonucleoside monophosphate metabolic process	35 of 4104 in the list	53 of 8404 in the genome	1	CCG004308.1,CCG017693.1,CCG015746.1,CCG023640.1, CCG026314.1,CCG004309.1,CCG025348.1,CCG025989.2, CCG019619.1,CCG007533.1,CCG008422.1,CCG010112.1, CCG001066.1,CCG019866.1,CCG019678.1,CCG007724.1, CCG013643.1,CCG017295.1,CCG015410.1,CCG025107.1, CCG002038.1,CCG009142.1,CCG015747.1,CCG000148.1, CCG006486.1,CCG005924.2,CCG018659.2,CCG013610.1, CCG016614.1,CCG028305.1,CCG017330.1,CCG006791.1,

GO:0050896	response to stimulus	446 of 4104 in the list	845 of 8404 in the genome	1	CCG005254.1,CCG010628.1,CCG017420.1,CCG027300.1, CCG028253.1,CCG014340.1,CCG012989.1,CCG006606.1, CCG008603.1,CCG026106.1,CCG026054.2,CCG008741.1, CCG000646.1,CCG019020.1,CCG013398.1,CCG026174.1, CCG020785.1,CCG013625.1,CCG011006.1,CCG002841.1, CCG018321.1,CCG010275.1,CCG026360.1,CCG024680.1, CCG011717.1,CCG014378.1,CCG000213.1,CCG017266.1, CCG012573.1,CCG016689.2,CCG016745.1,CCG020709.1, CCG025714.1,CCG005170.1,CCG014466.1,CCG007993.1, CCG015101.1,CCG016094.1,CCG000659.1,CCG023474.1, CCG027127.1,CCG007335.1,CCG004515.1,CCG018533.1, CCG000647.1,CCG019692.1,CCG000526.1,CCG022281.1, CCG027669.1,CCG015967.1,CCG026537.1,CCG021661.1, CCG010071.1,CCG013308.1,CCG023579.1,CCG009510.1, CCG018799.1,CCG019717.1,CCG025176.1,CCG000078.1, CCG008685.1,CCG026109.1,CCG024952.1,CCG009980.1, CCG014506.1,CCG027133.1,CCG016252.1,CCG004279.1, CCG024663.1,CCG003745.1,CCG018494.1,CCG008759.1, CCG026953.1,CCG005913.1,CCG009672.1,CCG009427.1, CCG011939.1,CCG004402.1,CCG019493.1,CCG002520.1, CCG017591.1,CCG022399.1,CCG023464.1,CCG021284.1, CCG001579.1,CCG028136.1,CCG013641.1,CCG000732.1, CCG003317.1,CCG002364.1,CCG003495.1,CCG017127.1, CCG007951.1,CCG006412.1,CCG017425.1,CCG025131.2, CCG005284.1,CCG016307.1,CCG023940.1,CCG008444.1, CCG017701.1,CCG028486.1,CCG000834.1,CCG018859.3, CCG026695.1,CCG014712.1,CCG000876.1,CCG014928.1, CCG024664.1,CCG015638.1,CCG000789.1,CCG026055.1, CCG024271.1,CCG021045.1,CCG024662.1,CCG021759.1, CCG026047.1,CCG020978.1,CCG025005.1,CCG022772.1,
GO:0006298	mismatch repair	9 of 4104 in the list	10 of 8404 in the genome	1	CCG006220.1,CCG013625.1,CCG003863.1,CCG003518.3, CCG017906.1,CCG020156.1,CCG022628.1,CCG005284.1,
GO:0006584	catecholamine metabolic process	11 of 4104 in the list	13 of 8404 in the genome	1	CCG015680.1,CCG018029.3,CCG018054.1,CCG005286.1, CCG025827.1,CCG018923.1,CCG024433.1,CCG018055.1, CCG015679.1,CCG024665.1,CCG011327.1

GO:0009712	catechol-containing compound metabolic process	11 of 4104 in the list	13 of 8404 in the genome	1	CCG015680.1,CCG018029.3,CCG018054.1,CCG005286.1, CCG025827.1,CCG018923.1,CCG024433.1,CCG018055.1, CCG015679.1,CCG024665.1,CCG011327.1
GO:0018958	phenol-containing compound metabolic process	11 of 4104 in the list	13 of 8404 in the genome	1	CCG015680.1,CCG018029.3,CCG018054.1,CCG005286.1, CCG025827.1,CCG018923.1,CCG024433.1,CCG018055.1, CCG015679.1,CCG024665.1,CCG011327.1
GO:0080090	regulation of primary metabolic process	308 of 4104 in the list	574 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022266.1,CCG008767.3, CCG008741.1,CCG024695.1,CCG003390.1,CCG027427.1, CCG007493.1,CCG002971.1,CCG021465.1,CCG003175.1, CCG004682.1,CCG023752.1,CCG018321.1,CCG028326.3, CCG013794.1,CCG006134.1,CCG009970.1,CCG011341.1, CCG019462.1,CCG016745.1,CCG021436.1,CCG016445.1, CCG012536.1,CCG000659.1,CCG027127.1,CCG018719.1, CCG015425.1,CCG027796.1,CCG022824.1,CCG018533.1, CCG024710.1,CCG022281.1,CCG011465.1,CCG018776.1, CCG006714.1,CCG020129.1,CCG027186.1,CCG011911.1, CCG004132.1,CCG000588.1,CCG022045.1,CCG013274.1, CCG028568.1,CCG022676.1,CCG007647.1,CCG024809.1, CCG021633.1,CCG012083.1,CCG000562.1,CCG005480.2, CCG017760.1,CCG016859.1,CCG005486.1,CCG020898.1, CCG017591.1,CCG002198.1,CCG021284.1,CCG016924.1, CCG013849.1,CCG000133.1,CCG013224.2,CCG002273.1, CCG001698.1,CCG023777.1,CCG014461.1,CCG026228.2, CCG005487.1,CCG021054.1,CCG016307.1,CCG009805.2, CCG016749.1,CCG028465.1,CCG019250.1,CCG005396.1, CCG025747.1,CCG009823.1,CCG021456.1,CCG014928.1, CCG005168.1,CCG018184.1,CCG018315.1,CCG027580.1, CCG025433.1,CCG024271.1,CCG012519.1,CCG028409.1, CCG025758.1,CCG009458.1,CCG022496.1,CCG015062.1, CCG024000.1,CCG016965.1,CCG018164.1,CCG015333.1, CCG001301.1,CCG023199.2,CCG001431.2,CCG001341.1, CCG022398.1,CCG021521.1,CCG009562.2,CCG010139.1, CCG021940.1,CCG024639.1,CCG015846.1,CCG008833.1, CCG018168.1,CCG014509.1,CCG004783.1,CCG025691.1, CCG018042.1,CCG014463.1,CCG026788.1,CCG020543.1, CCG025549.1,CCG011015.1,CCG027950.1,CCG002045.1,

GO:0009123	nucleoside monophosphate metabolic process	36 of 4104 in the list	55 of 8404 in the genome	1	CCG004308.1,CCG017693.1,CCG015746.1,CCG004180.1, CCG023640.1,CCG026314.1,CCG004309.1,CCG025348.1, CCG025989.2,CCG019619.1,CCG007533.1,CCG008422.1, CCG010112.1,CCG001066.1,CCG019866.1,CCG019678.1, CCG007724.1,CCG013643.1,CCG017295.1,CCG015410.1, CCG025107.1,CCG002038.1,CCG009142.1,CCG015747.1, CCG000148.1,CCG006486.1,CCG005924.2,CCG018659.2, CCG013610.1,CCG016614.1,CCG028305.1,CCG017330.1,
GO:0009126	purine nucleoside monophosphate metabolic process	32 of 4104 in the list	48 of 8404 in the genome	1	CCG004308.1,CCG015410.1,CCG017693.1,CCG015746.1, CCG002038.1,CCG025107.1,CCG009142.1,CCG023640.1, CCG015747.1,CCG026314.1,CCG000148.1,CCG004309.1, CCG025348.1,CCG025989.2,CCG006486.1,CCG019619.1, CCG018659.2,CCG005924.2,CCG008422.1,CCG028305.1, CCG010112.1,CCG017330.1,CCG001066.1,CCG006791.1, CCG026865.1,CCG019866.1,CCG019678.1,CCG007724.1, CCG021934.1,CCG013643.1,CCG001285.1,CCG017295.1
GO:0009167	purine ribonucleoside monophosphate metabolic process	32 of 4104 in the list	48 of 8404 in the genome	1	CCG004308.1,CCG015410.1,CCG017693.1,CCG015746.1, CCG002038.1,CCG025107.1,CCG009142.1,CCG023640.1, CCG015747.1,CCG026314.1,CCG000148.1,CCG004309.1, CCG025348.1,CCG025989.2,CCG006486.1,CCG019619.1, CCG018659.2,CCG005924.2,CCG008422.1,CCG028305.1, CCG010112.1,CCG017330.1,CCG001066.1,CCG006791.1, CCG026865.1,CCG019866.1,CCG019678.1,CCG007724.1, CCG021934.1,CCG013643.1,CCG001285.1,CCG017295.1
GO:0043549	regulation of kinase activity	16 of 4104 in the list	21 of 8404 in the genome	1	CCG013849.1,CCG028049.1,CCG017923.1,CCG013274.1, CCG012743.1,CCG004783.1,CCG009521.1,CCG009035.1, CCG004682.1,CCG001854.1,CCG020898.1,CCG013794.1, CCG011648.1,CCG018184.1,CCG026404.1,CCG021794.1
GO:0045859	regulation of protein kinase activity	16 of 4104 in the list	21 of 8404 in the genome	1	CCG013849.1,CCG028049.1,CCG017923.1,CCG013274.1, CCG012743.1,CCG004783.1,CCG009521.1,CCG009035.1, CCG004682.1,CCG001854.1,CCG020898.1,CCG013794.1, CCG011648.1,CCG018184.1,CCG026404.1,CCG021794.1

GO:0051338	regulation of transferase activity	16 of 4104 in the list	21 of 8404 in the genome	1	CCG013849.1,CCG028049.1,CCG017923.1,CCG013274.1, CCG012743.1,CCG004783.1,CCG009521.1,CCG009035.1, CCG004682.1,CCG001854.1,CCG020898.1,CCG013794.1, CCG011648.1,CCG018184.1,CCG026404.1,CCG021794.1
GO:0006007	glucose catabolic process	19 of 4104 in the list	26 of 8404 in the genome	1	CCG022035.1,CCG020616.1,CCG005588.1,CCG003215.3, CCG025307.1,CCG010373.1,CCG007981.1,CCG007023.1, CCG022214.1,CCG000431.1,CCG013339.1,CCG009084.2, CCG019953.1,CCG017200.1,CCG003220.2,CCG006203.1, CCG022453.1,CCG003748.1,CCG025277.1
GO:0019320	hexose catabolic process	19 of 4104 in the list	26 of 8404 in the genome	1	CCG022035.1,CCG020616.1,CCG005588.1,CCG003215.3, CCG025307.1,CCG010373.1,CCG007981.1,CCG007023.1, CCG022214.1,CCG000431.1,CCG013339.1,CCG009084.2, CCG019953.1,CCG017200.1,CCG003220.2,CCG006203.1, CCG022453.1,CCG003748.1,CCG025277.1
GO:0044724	single-organism carbohydrate catabolic process	19 of 4104 in the list	26 of 8404 in the genome	1	CCG022035.1,CCG020616.1,CCG005588.1,CCG003215.3, CCG025307.1,CCG010373.1,CCG007981.1,CCG007023.1, CCG022214.1,CCG000431.1,CCG013339.1,CCG009084.2, CCG019953.1,CCG017200.1,CCG003220.2,CCG006203.1, CCG022453.1,CCG003748.1,CCG025277.1
GO:0046365	monosaccharide catabolic process	19 of 4104 in the list	26 of 8404 in the genome	1	CCG022035.1,CCG020616.1,CCG005588.1,CCG003215.3, CCG025307.1,CCG010373.1,CCG007981.1,CCG007023.1, CCG022214.1,CCG000431.1,CCG013339.1,CCG009084.2, CCG019953.1,CCG017200.1,CCG003220.2,CCG006203.1, CCG022453.1,CCG003748.1,CCG025277.1
GO:1901607	alpha-amino acid biosynthetic process	33 of 4104 in the list	50 of 8404 in the genome	1	CCG007203.1,CCG010174.2,CCG019954.3,CCG011491.1, CCG015921.1,CCG009333.1,CCG028131.1,CCG017894.1, CCG013043.1,CCG016220.1,CCG015568.1,CCG016315.1, CCG020441.1,CCG008932.1,CCG000682.1,CCG006821.1, CCG010561.1,CCG001423.1,CCG022025.2,CCG025636.2, CCG008860.1,CCG017201.1,CCG025731.1,CCG015276.2, CCG017111.1,CCG022773.2,CCG024133.1,CCG002231.1, CCG015943.1,CCG026155.1,CCG025897.1,CCG003871.1,

GO:0009163	nucleoside biosynthetic process	30 of 4104 in the list	45 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG026812.1,CCG000148.1, CCG006529.1,CCG025348.1,CCG025989.2,CCG019619.1, CCG018659.2,CCG005924.2,CCG008422.1,CCG013610.1, CCG013999.1,CCG021336.1,CCG016614.1,CCG010112.1, CCG007417.1,CCG006791.1,CCG021110.1,CCG016955.1, CCG027125.1,CCG004440.1,CCG007724.1,CCG021934.1,
GO:0042455	ribonucleoside biosynthetic process	30 of 4104 in the list	45 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG026812.1,CCG000148.1, CCG006529.1,CCG025348.1,CCG025989.2,CCG019619.1, CCG018659.2,CCG005924.2,CCG008422.1,CCG013610.1, CCG013999.1,CCG021336.1,CCG016614.1,CCG010112.1, CCG007417.1,CCG006791.1,CCG021110.1,CCG016955.1, CCG027125.1,CCG004440.1,CCG007724.1,CCG021934.1,
GO:1901659	glycosyl compound biosynthetic process	30 of 4104 in the list	45 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG026812.1,CCG000148.1, CCG006529.1,CCG025348.1,CCG025989.2,CCG019619.1, CCG018659.2,CCG005924.2,CCG008422.1,CCG013610.1, CCG013999.1,CCG021336.1,CCG016614.1,CCG010112.1, CCG007417.1,CCG006791.1,CCG021110.1,CCG016955.1, CCG027125.1,CCG004440.1,CCG007724.1,CCG021934.1,
GO:0009890	negative regulation of biosynthetic process	20 of 4104 in the list	28 of 8404 in the genome	1	CCG003216.1,CCG026841.1,CCG025758.1,CCG016445.1, CCG014461.1,CCG010489.1,CCG015062.1,CCG003390.1, CCG025132.1,CCG005487.1,CCG005485.1,CCG005898.1, CCG004838.1,CCG003765.1,CCG005486.1,CCG006714.1, CCG018321.1,CCG023431.1,CCG016835.2,CCG014323.1
GO:0010558	negative regulation of macromolecule biosynthetic process	20 of 4104 in the list	28 of 8404 in the genome	1	CCG003216.1,CCG026841.1,CCG025758.1,CCG016445.1, CCG014461.1,CCG010489.1,CCG015062.1,CCG003390.1, CCG025132.1,CCG005487.1,CCG005485.1,CCG005898.1, CCG004838.1,CCG003765.1,CCG005486.1,CCG006714.1, CCG018321.1,CCG023431.1,CCG016835.2,CCG014323.1

GO:0031327	negative regulation of cellular biosynthetic process	20 of 4104 in the list	28 of 8404 in the genome	1	CCG003216.1,CCG026841.1,CCG025758.1,CCG016445.1, CCG014461.1,CCG010489.1,CCG015062.1,CCG003390.1, CCG025132.1,CCG005487.1,CCG005485.1,CCG005898.1, CCG004838.1,CCG003765.1,CCG005486.1,CCG006714.1, CCG018321.1,CCG023431.1,CCG016835.2,CCG014323.1
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	20 of 4104 in the list	28 of 8404 in the genome	1	CCG003216.1,CCG026841.1,CCG025758.1,CCG016445.1, CCG014461.1,CCG010489.1,CCG015062.1,CCG003390.1, CCG025132.1,CCG005487.1,CCG005485.1,CCG005898.1, CCG004838.1,CCG003765.1,CCG005486.1,CCG006714.1, CCG018321.1,CCG023431.1,CCG016835.2,CCG014323.1
GO:0072527	pyrimidine-containing compound metabolic process	17 of 4104 in the list	23 of 8404 in the genome	1	CCG004180.1,CCG017995.1,CCG017175.1,CCG006529.1, CCG016222.1,CCG023452.1,CCG005938.1,CCG014116.1, CCG025940.1,CCG013610.1,CCG018108.1,CCG025493.1, CCG016614.1,CCG007417.1,CCG021110.1,CCG010960.2,
GO:0006275	regulation of DNA replication	6 of 4104 in the list	6 of 8404 in the genome	1	CCG026259.1,CCG018321.1,CCG011911.1,CCG026841.1, CCG025758.1,CCG014323.1
GO:0006420	arginyl-tRNA aminoacylation	6 of 4104 in the list	6 of 8404 in the genome	1	CCG020877.1,CCG015577.3,CCG012968.1,CCG023510.1, CCG027352.3,CCG028092.1
GO:0008643	carbohydrate transport	6 of 4104 in the list	6 of 8404 in the genome	1	CCG000210.1,CCG023190.1,CCG025309.1,CCG012350.1, CCG009082.1,CCG016673.1
GO:0010389	regulation of G2/M transition of mitotic cell cycle	6 of 4104 in the list	6 of 8404 in the genome	1	CCG009521.1,CCG013849.1,CCG012743.1,CCG026404.1, CCG017923.1,CCG009035.1
GO:0051052	regulation of DNA metabolic process	6 of 4104 in the list	6 of 8404 in the genome	1	CCG026259.1,CCG018321.1,CCG011911.1,CCG026841.1, CCG025758.1,CCG014323.1

GO:1901564	organonitrogen compound metabolic process	348 of 4104 in the list	656 of 8404 in the genome	1	CCG017420.1,CCG019078.1,CCG023277.1,CCG014396.1, CCG010191.3,CCG018055.1,CCG006912.1,CCG017331.1, CCG009878.1,CCG005809.1,CCG019020.1,CCG012875.1, CCG024517.1,CCG025108.1,CCG016238.1,CCG004020.1, CCG016220.1,CCG011006.1,CCG007816.1,CCG026536.1, CCG020799.1,CCG025307.1,CCG016370.1,CCG006911.1, CCG022025.2,CCG005053.1,CCG025940.1,CCG023890.1, CCG006994.1,CCG019371.1,CCG011722.1,CCG021110.1, CCG003601.1,CCG010019.1,CCG003063.1,CCG016153.1, CCG020877.1,CCG006231.1,CCG021086.2,CCG025396.1, CCG028131.1,CCG026953.1,CCG008510.1,CCG024432.2, CCG014181.1,CCG019678.1,CCG013641.1,CCG006821.1, CCG003495.1,CCG025131.2,CCG023452.1,CCG025636.2, CCG014116.1,CCG002852.1,CCG017111.1,CCG019545.1, CCG013610.1,CCG019330.1,CCG022773.2,CCG003173.1, CCG010986.1,CCG001876.1,CCG018643.1,CCG025827.1, CCG009518.1,CCG002231.1,CCG028454.1,CCG020663.1, CCG011996.1,CCG008388.1,CCG001285.1,CCG022191.1, CCG015367.1,CCG017175.1,CCG007610.1,CCG011491.1, CCG002555.1,CCG009333.1,CCG006529.1,CCG017730.1, CCG007533.1,CCG008422.1,CCG007817.1,CCG010112.1, CCG011135.1,CCG028092.1,CCG015568.1,CCG020441.1, CCG006421.1,CCG023963.3,CCG010561.1,CCG026910.1, CCG020165.1,CCG023922.1,CCG007814.1,CCG000148.1, CCG017344.1,CCG000472.1,CCG006375.1,CCG018108.1, CCG017079.1,CCG026099.1,CCG023779.1,CCG016415.1, CCG026030.1,CCG003966.1,CCG025897.1,CCG021934.1, CCG010319.1,CCG007203.1,CCG004308.1,CCG027212.1, CCG017995.1,CCG015921.1,CCG010418.1,CCG016222.1, CCG022227.1,CCG023926.1,CCG017862.1,CCG026852.1,

GO:0034622	cellular macromolecular complex assembly	94 of 4104 in the list	163 of 8404 in the genome	1	CCG006420.1,CCG013000.1,CCG003361.1,CCG019284.1, CCG008560.1,CCG010136.1,CCG021491.1,CCG010647.1, CCG003310.1,CCG005370.1,CCG009243.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG002696.1, CCG014537.1,CCG010137.1,CCG006421.1,CCG023963.3, CCG005194.1,CCG009461.1,CCG024623.1,CCG025880.1, CCG014836.1,CCG010904.1,CCG024177.1,CCG004481.1, CCG012514.1,CCG027196.1,CCG014772.1,CCG002099.1, CCG026474.1,CCG016370.1,CCG010792.1,CCG025893.1, CCG009637.1,CCG007532.1,CCG010905.1,CCG007531.1, CCG018820.3,CCG026579.1,CCG010909.1,CCG010648.1, CCG017580.1,CCG013637.1,CCG009980.1,CCG010906.1, CCG015968.1,CCG018893.1,CCG010649.1,CCG010138.1, CCG025877.1,CCG010418.1,CCG008892.2,CCG015560.1, CCG027199.1,CCG009080.1,CCG027198.1,CCG025396.1, CCG008559.1,CCG018287.1,CCG027696.1,CCG010907.1, CCG008748.1,CCG012229.1,CCG010650.1,CCG000708.1, CCG025990.1,CCG024624.1,CCG009543.1,CCG009275.1, CCG004494.1,CCG002947.1,CCG015289.1,CCG010908.1, CCG005716.1,CCG007518.1,CCG027197.1,CCG022673.1, CCG005886.1,CCG026159.1,CCG027697.1,CCG020442.1, CCG010646.1,CCG017598.1,CCG002852.1,CCG010864.1,
GO:0009892	negative regulation of metabolic process	24 of 4104 in the list	35 of 8404 in the genome	1	CCG003216.1,CCG028409.1,CCG002823.1,CCG026841.1, CCG025758.1,CCG016445.1,CCG014461.1,CCG010489.1, CCG000890.1,CCG015062.1,CCG003390.1,CCG025132.1, CCG005487.1,CCG005485.1,CCG005898.1,CCG004838.1, CCG003765.1,CCG005486.1,CCG006714.1,CCG018321.1, CCG023431.1,CCG016835.2,CCG014323.1,CCG021794.1
GO:0051246	regulation of protein metabolic process	28 of 4104 in the list	42 of 8404 in the genome	1	CCG013849.1,CCG003216.1,CCG028049.1,CCG017923.1, CCG016445.1,CCG013274.1,CCG015062.1,CCG024695.1, CCG005487.1,CCG005485.1,CCG012743.1,CCG004783.1, CCG009521.1,CCG003765.1,CCG009035.1,CCG004682.1, CCG001854.1,CCG006714.1,CCG005486.1,CCG026155.1, CCG020898.1,CCG023431.1,CCG013794.1,CCG016835.2, CCG011648.1,CCG026404.1,CCG018184.1,CCG021794.1

GO:0006119	oxidative phosphorylation	10 of 4104 in the list	12 of 8404 in the genome	1	CCG023685.1,CCG000102.1,CCG020879.1,CCG001649.1, CCG014053.1,CCG006864.1,CCG006459.1,CCG025163.3, CCG024297.1,CCG011237.1
GO:0042773	ATP synthesis coupled electron transport	10 of 4104 in the list	12 of 8404 in the genome	1	CCG023685.1,CCG000102.1,CCG020879.1,CCG001649.1, CCG014053.1,CCG006864.1,CCG006459.1,CCG025163.3, CCG024297.1,CCG011237.1
GO:0022607	cellular component assembly	101 of 4104 in the list	177 of 8404 in the genome	1	CCG006420.1,CCG013000.1,CCG003361.1,CCG019284.1, CCG008560.1,CCG010136.1,CCG021491.1,CCG010647.1, CCG003310.1,CCG005370.1,CCG009243.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG002696.1, CCG014537.1,CCG010137.1,CCG006421.1,CCG023963.3, CCG005194.1,CCG009461.1,CCG007395.1,CCG024623.1, CCG025880.1,CCG014836.1,CCG010904.1,CCG024177.1, CCG004481.1,CCG012514.1,CCG027196.1,CCG014772.1, CCG002099.1,CCG026474.1,CCG016370.1,CCG010792.1, CCG017033.1,CCG003485.1,CCG025893.1,CCG009637.1, CCG007532.1,CCG010905.1,CCG015583.1,CCG007531.1, CCG018820.3,CCG026579.1,CCG010909.1,CCG010648.1, CCG017580.1,CCG013637.1,CCG009980.1,CCG010906.1, CCG015968.1,CCG018893.1,CCG010649.1,CCG010138.1, CCG025877.1,CCG010418.1,CCG008892.2,CCG015560.1, CCG027199.1,CCG002366.1,CCG009080.1,CCG027198.1, CCG025396.1,CCG008559.1,CCG018287.1,CCG027696.1, CCG010907.1,CCG008748.1,CCG010650.1,CCG012229.1, CCG000708.1,CCG025990.1,CCG024624.1,CCG009543.1, CCG009275.1,CCG004494.1,CCG002947.1,CCG015289.1, CCG010908.1,CCG005716.1,CCG007518.1,CCG027197.1, CCG022673.1,CCG005886.1,CCG026159.1,CCG027697.1, CCG020442.1,CCG010646.1,CCG017598.1,CCG002852.1, CCG010864.1,CCG024787.1,CCG027695.1,CCG012584.1,
GO:0042221	response to chemical	26 of 4104 in the list	39 of 8404 in the genome	1	CCG026055.1,CCG024271.1,CCG008742.1,CCG022741.1, CCG016745.1,CCG017154.1,CCG026054.2,CCG008741.1, CCG017795.1,CCG000659.1,CCG014509.1,CCG027127.1, CCG016307.1,CCG019520.1,CCG018533.1,CCG022281.1, CCG019185.1,CCG013113.1,CCG013809.1,CCG020586.1, CCG010702.1,CCG012009.1,CCG020224.1,CCG004878.1,

GO:0008652	cellular amino acid biosynthetic process	37 of 4104 in the list	59 of 8404 in the genome	1	CCG007203.1,CCG010174.2,CCG019954.3,CCG011491.1, CCG015921.1,CCG009333.1,CCG028131.1,CCG017894.1, CCG013043.1,CCG016220.1,CCG015568.1,CCG016315.1, CCG021610.1,CCG020441.1,CCG006821.1,CCG008932.1, CCG000682.1,CCG002897.1,CCG010561.1,CCG001423.1, CCG022025.2,CCG025636.2,CCG008860.1,CCG017201.1, CCG017111.1,CCG025731.1,CCG015276.2,CCG022773.2, CCG026099.1,CCG024133.1,CCG002231.1,CCG015943.1, CCG016955.1,CCG026155.1,CCG025897.1,CCG003871.1, CCG015567.1
GO:0009719	response to endogenous stimulus	20 of 4104 in the list	29 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG022741.1,CCG016745.1, CCG008741.1,CCG017795.1,CCG000659.1,CCG014509.1, CCG027127.1,CCG016307.1,CCG019520.1,CCG018533.1, CCG019185.1,CCG022281.1,CCG020586.1,CCG010702.1, CCG012009.1,CCG020224.1,CCG004878.1,CCG014928.1
GO:0010033	response to organic substance	20 of 4104 in the list	29 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG022741.1,CCG016745.1, CCG008741.1,CCG017795.1,CCG000659.1,CCG014509.1, CCG027127.1,CCG016307.1,CCG019520.1,CCG018533.1, CCG019185.1,CCG022281.1,CCG020586.1,CCG010702.1, CCG012009.1,CCG020224.1,CCG004878.1,CCG014928.1
GO:0070887	cellular response to chemical stimulus	20 of 4104 in the list	29 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG022741.1,CCG016745.1, CCG008741.1,CCG017795.1,CCG000659.1,CCG014509.1, CCG027127.1,CCG016307.1,CCG019520.1,CCG018533.1, CCG019185.1,CCG022281.1,CCG020586.1,CCG010702.1, CCG012009.1,CCG020224.1,CCG004878.1,CCG014928.1
GO:0071310	cellular response to organic substance	20 of 4104 in the list	29 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG022741.1,CCG016745.1, CCG008741.1,CCG017795.1,CCG000659.1,CCG014509.1, CCG027127.1,CCG016307.1,CCG019520.1,CCG018533.1, CCG019185.1,CCG022281.1,CCG020586.1,CCG010702.1, CCG012009.1,CCG020224.1,CCG004878.1,CCG014928.1
GO:0071495	cellular response to endogenous stimulus	20 of 4104 in the list	29 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG022741.1,CCG016745.1, CCG008741.1,CCG017795.1,CCG000659.1,CCG014509.1, CCG027127.1,CCG016307.1,CCG019520.1,CCG018533.1, CCG019185.1,CCG022281.1,CCG020586.1,CCG010702.1, CCG012009.1,CCG020224.1,CCG004878.1,CCG014928.1

GO:0000375	RNA splicing, via transesterification reactions	11 of 4104 in the list	14 of 8404 in the genome	1	CCG000393.1,CCG000183.1,CCG000754.1,CCG028285.1, CCG023686.1,CCG024810.1,CCG010792.1,CCG013802.1, CCG004927.1,CCG003938.1,CCG001898.1
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	11 of 4104 in the list	14 of 8404 in the genome	1	CCG000393.1,CCG000183.1,CCG000754.1,CCG028285.1, CCG023686.1,CCG024810.1,CCG010792.1,CCG013802.1, CCG004927.1,CCG003938.1,CCG001898.1
GO:0000398	mRNA splicing, via spliceosome	11 of 4104 in the list	14 of 8404 in the genome	1	CCG000393.1,CCG000183.1,CCG000754.1,CCG028285.1, CCG023686.1,CCG024810.1,CCG010792.1,CCG013802.1, CCG004927.1,CCG003938.1,CCG001898.1
GO:0006357	regulation of transcription from RNA polymerase II promoter	24 of 4104 in the list	36 of 8404 in the genome	1	CCG018515.1,CCG023065.1,CCG014461.1,CCG026219.1, CCG010489.1,CCG017156.1,CCG024666.1,CCG020695.1, CCG007647.1,CCG014982.1,CCG025828.1,CCG017524.1, CCG021633.1,CCG011094.1,CCG016772.1,CCG025856.1, CCG014682.1,CCG019814.1,CCG001096.1,CCG014983.1, CCG028326.3,CCG005168.1,CCG006134.1,CCG018315.1
GO:0031329	regulation of cellular catabolic process	33 of 4104 in the list	52 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG022394.1,CCG016027.1,CCG011341.1,CCG019462.1, CCG012519.1,CCG004132.1,CCG003824.3,CCG017369.1, CCG024000.1,CCG025554.1,CCG016965.1,CCG022676.1, CCG013303.1,CCG027878.1,CCG024809.1,CCG009024.1, CCG007631.1,CCG023747.3,CCG015333.1,CCG002971.1, CCG016181.1,CCG013203.1,CCG018776.1,CCG002109.1, CCG021151.1,CCG015233.1,CCG010260.1,CCG002864.1,
GO:0016071	mRNA metabolic process	29 of 4104 in the list	45 of 8404 in the genome	1	CCG017986.1,CCG010912.1,CCG000393.1,CCG026872.2, CCG007177.1,CCG005524.1,CCG000754.1,CCG028285.1, CCG018917.1,CCG023511.1,CCG010792.1,CCG004231.1, CCG004927.1,CCG007690.1,CCG012557.1,CCG004284.1, CCG000183.1,CCG007636.1,CCG025958.1,CCG023686.1, CCG024810.1,CCG001268.1,CCG017408.1,CCG013802.1, CCG003938.1,CCG004448.2,CCG001395.1,CCG026612.1,

GO:0051056	regulation of small GTPase mediated signal transduction	66 of 4104 in the list	113 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG025433.1,CCG021263.1, CCG012519.1,CCG026214.1,CCG009512.1,CCG022334.1, CCG024000.1,CCG016965.1,CCG027878.1,CCG015333.1, CCG010849.1,CCG003602.1,CCG004884.2,CCG002338.1, CCG002971.1,CCG018015.1,CCG010329.2,CCG021483.1, CCG028651.1,CCG011341.1,CCG019462.1,CCG008035.1, CCG019585.1,CCG012670.1,CCG013203.1,CCG018776.1, CCG022420.1,CCG018222.1,CCG009510.1,CCG010260.1, CCG010157.1,CCG002166.1,CCG002864.1,CCG011422.1, CCG006050.2,CCG022083.1,CCG000807.1,CCG004132.1, CCG010808.1,CCG009980.1,CCG017369.1,CCG025470.1, CCG008892.2,CCG022676.1,CCG024809.1,CCG009024.1, CCG022749.1,CCG018380.1,CCG002109.1,CCG021151.1, CCG025178.1,CCG005105.1,CCG001579.1,CCG022394.1, CCG016027.1,CCG000596.1,CCG019947.1,CCG025554.1, CCG013303.1,CCG007631.1,CCG025667.2,CCG016181.1
GO:1902531	regulation of intracellular signal transduction	66 of 4104 in the list	113 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG025433.1,CCG021263.1, CCG012519.1,CCG026214.1,CCG009512.1,CCG022334.1, CCG024000.1,CCG016965.1,CCG027878.1,CCG015333.1, CCG010849.1,CCG003602.1,CCG004884.2,CCG002338.1, CCG002971.1,CCG018015.1,CCG010329.2,CCG021483.1, CCG028651.1,CCG011341.1,CCG019462.1,CCG008035.1, CCG019585.1,CCG012670.1,CCG013203.1,CCG018776.1, CCG022420.1,CCG018222.1,CCG009510.1,CCG010260.1, CCG010157.1,CCG002166.1,CCG002864.1,CCG011422.1, CCG006050.2,CCG022083.1,CCG000807.1,CCG004132.1, CCG010808.1,CCG009980.1,CCG017369.1,CCG025470.1, CCG008892.2,CCG022676.1,CCG024809.1,CCG009024.1, CCG022749.1,CCG018380.1,CCG002109.1,CCG021151.1, CCG025178.1,CCG005105.1,CCG001579.1,CCG022394.1, CCG016027.1,CCG000596.1,CCG019947.1,CCG025554.1, CCG013303.1,CCG007631.1,CCG025667.2,CCG016181.1

GO:0042451	purine nucleoside biosynthetic process	25 of 4104 in the list	38 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG026812.1,CCG000148.1, CCG006529.1,CCG025348.1,CCG025989.2,CCG019619.1, CCG018659.2,CCG005924.2,CCG008422.1,CCG013999.1, CCG021336.1,CCG010112.1,CCG007417.1,CCG006791.1, CCG021110.1,CCG016955.1,CCG007724.1,CCG021934.1,
GO:0046129	purine ribonucleoside biosynthetic process	25 of 4104 in the list	38 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG026812.1,CCG000148.1, CCG006529.1,CCG025348.1,CCG025989.2,CCG019619.1, CCG018659.2,CCG005924.2,CCG008422.1,CCG013999.1, CCG021336.1,CCG010112.1,CCG007417.1,CCG006791.1, CCG021110.1,CCG016955.1,CCG007724.1,CCG021934.1,
GO:0010605	negative regulation of macromolecule metabolic process	21 of 4104 in the list	31 of 8404 in the genome	1	CCG003216.1,CCG026841.1,CCG025758.1,CCG016445.1, CCG014461.1,CCG010489.1,CCG015062.1,CCG003390.1, CCG025132.1,CCG005487.1,CCG005485.1,CCG005898.1, CCG004838.1,CCG003765.1,CCG005486.1,CCG006714.1, CCG018321.1,CCG023431.1,CCG016835.2,CCG014323.1,

GO:0019219	regulation of nucleobase-containing compound metabolic process	288 of 4104 in the list	544 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022266.1,CCG008767.3, CCG008741.1,CCG003390.1,CCG027427.1,CCG007493.1, CCG002971.1,CCG021465.1,CCG003175.1,CCG023752.1, CCG018321.1,CCG028326.3,CCG013794.1,CCG006134.1, CCG009970.1,CCG011341.1,CCG019462.1,CCG016745.1, CCG021436.1,CCG012536.1,CCG000659.1,CCG027127.1, CCG018719.1,CCG015425.1,CCG027796.1,CCG022824.1, CCG018533.1,CCG024710.1,CCG022281.1,CCG011465.1, CCG018776.1,CCG020129.1,CCG027186.1,CCG011911.1, CCG004132.1,CCG000588.1,CCG022045.1,CCG013274.1, CCG028568.1,CCG022676.1,CCG007647.1,CCG024809.1, CCG021633.1,CCG012083.1,CCG000562.1,CCG005480.2, CCG017760.1,CCG016859.1,CCG020898.1,CCG017591.1, CCG002198.1,CCG021284.1,CCG016924.1,CCG000133.1, CCG013224.2,CCG002273.1,CCG001698.1,CCG023777.1, CCG014461.1,CCG026228.2,CCG021054.1,CCG016307.1, CCG009805.2,CCG016749.1,CCG028465.1,CCG019250.1, CCG005396.1,CCG025747.1,CCG009823.1,CCG021456.1, CCG014928.1,CCG005168.1,CCG018184.1,CCG018315.1, CCG027580.1,CCG025433.1,CCG024271.1,CCG012519.1, CCG028409.1,CCG025758.1,CCG009458.1,CCG022496.1, CCG024000.1,CCG016965.1,CCG018164.1,CCG015333.1, CCG001301.1,CCG023199.2,CCG001431.2,CCG001341.1, CCG022398.1,CCG021521.1,CCG009562.2,CCG010139.1, CCG021940.1,CCG024639.1,CCG015846.1,CCG008833.1, CCG018168.1,CCG014509.1,CCG004783.1,CCG025691.1, CCG018042.1,CCG014463.1,CCG026788.1,CCG020543.1, CCG025549.1,CCG011015.1,CCG027950.1,CCG002045.1, CCG025572.1,CCG004378.1,CCG002864.1,CCG014243.1, CCG009023.1,CCG018847.1,CCG014323.1,CCG027258.1,

GO:0051171	regulation of nitrogen compound metabolic process	288 of 4104 in the list	544 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022266.1,CCG008767.3, CCG008741.1,CCG003390.1,CCG027427.1,CCG007493.1, CCG002971.1,CCG021465.1,CCG003175.1,CCG023752.1, CCG018321.1,CCG028326.3,CCG013794.1,CCG006134.1, CCG009970.1,CCG011341.1,CCG019462.1,CCG016745.1, CCG021436.1,CCG012536.1,CCG000659.1,CCG027127.1, CCG018719.1,CCG015425.1,CCG027796.1,CCG022824.1, CCG018533.1,CCG024710.1,CCG022281.1,CCG011465.1, CCG018776.1,CCG020129.1,CCG027186.1,CCG011911.1, CCG004132.1,CCG000588.1,CCG022045.1,CCG013274.1, CCG028568.1,CCG022676.1,CCG007647.1,CCG024809.1, CCG021633.1,CCG012083.1,CCG000562.1,CCG005480.2, CCG017760.1,CCG016859.1,CCG020898.1,CCG017591.1, CCG002198.1,CCG021284.1,CCG016924.1,CCG000133.1, CCG013224.2,CCG002273.1,CCG001698.1,CCG023777.1, CCG014461.1,CCG026228.2,CCG021054.1,CCG016307.1, CCG009805.2,CCG016749.1,CCG028465.1,CCG019250.1, CCG005396.1,CCG025747.1,CCG009823.1,CCG021456.1, CCG014928.1,CCG005168.1,CCG018184.1,CCG018315.1, CCG027580.1,CCG025433.1,CCG024271.1,CCG012519.1, CCG028409.1,CCG025758.1,CCG009458.1,CCG022496.1, CCG024000.1,CCG016965.1,CCG018164.1,CCG015333.1, CCG001301.1,CCG023199.2,CCG001431.2,CCG001341.1, CCG022398.1,CCG021521.1,CCG009562.2,CCG010139.1, CCG021940.1,CCG024639.1,CCG015846.1,CCG008833.1, CCG018168.1,CCG014509.1,CCG004783.1,CCG025691.1, CCG018042.1,CCG014463.1,CCG026788.1,CCG020543.1, CCG025549.1,CCG011015.1,CCG027950.1,CCG002045.1, CCG025572.1,CCG004378.1,CCG002864.1,CCG014243.1, CCG009023.1,CCG018847.1,CCG014323.1,CCG027258.1,
GO:0006400	tRNA modification	9 of 4104 in the list	11 of 8404 in the genome	1	CCG016251.1,CCG027125.1,CCG004440.1,CCG005020.1, CCG004234.1,CCG010460.1,CCG022183.1,CCG023156.1,
GO:0048518	positive regulation of biological process	9 of 4104 in the list	11 of 8404 in the genome	1	CCG018164.1,CCG007246.2,CCG023747.3,CCG027118.1, CCG003824.3,CCG026216.1,CCG021944.1,CCG015233.1,
GO:0048522	positive regulation of cellular process	9 of 4104 in the list	11 of 8404 in the genome	1	CCG018164.1,CCG007246.2,CCG023747.3,CCG027118.1, CCG003824.3,CCG026216.1,CCG021944.1,CCG015233.1,

GO:0006206	pyrimidine nucleobase metabolic process	5 of 4104 in the list	5 of 8404 in the genome	1	CCG017175.1,CCG018108.1,CCG016614.1,CCG005938.1, CCG025940.1
GO:0006207	'de novo' pyrimidine nucleobase biosynthetic process	5 of 4104 in the list	5 of 8404 in the genome	1	CCG017175.1,CCG018108.1,CCG016614.1,CCG005938.1, CCG025940.1
GO:0006403	RNA localization	5 of 4104 in the list	5 of 8404 in the genome	1	CCG009454.1,CCG011567.1,CCG017874.1,CCG021221.1, CCG026989.1
GO:0009066	aspartate family amino acid metabolic process	5 of 4104 in the list	5 of 8404 in the genome	1	CCG006821.1,CCG010174.2,CCG009333.1,CCG024133.1, CCG027551.3
GO:0015931	nucleobase-containing compound transport	5 of 4104 in the list	5 of 8404 in the genome	1	CCG009454.1,CCG011567.1,CCG017874.1,CCG021221.1, CCG026989.1
GO:0016073	snRNA metabolic process	5 of 4104 in the list	5 of 8404 in the genome	1	CCG002792.1,CCG020286.1,CCG000540.1,CCG028653.1, CCG016652.1
GO:0019856	pyrimidine nucleobase biosynthetic process	5 of 4104 in the list	5 of 8404 in the genome	1	CCG017175.1,CCG018108.1,CCG016614.1,CCG005938.1, CCG025940.1
GO:0050657	nucleic acid transport	5 of 4104 in the list	5 of 8404 in the genome	1	CCG009454.1,CCG011567.1,CCG017874.1,CCG021221.1, CCG026989.1
GO:0050658	RNA transport	5 of 4104 in the list	5 of 8404 in the genome	1	CCG009454.1,CCG011567.1,CCG017874.1,CCG021221.1, CCG026989.1
GO:0051028	mRNA transport	5 of 4104 in the list	5 of 8404 in the genome	1	CCG009454.1,CCG011567.1,CCG017874.1,CCG021221.1, CCG026989.1
GO:0051236	establishment of RNA localization	5 of 4104 in the list	5 of 8404 in the genome	1	CCG009454.1,CCG011567.1,CCG017874.1,CCG021221.1, CCG026989.1

GO:0051716	cellular response to stimulus	396 of 4104 in the list	759 of 8404 in the genome	1	CCG005254.1,CCG010628.1,CCG017420.1,CCG027300.1, CCG028253.1,CCG014340.1,CCG012989.1,CCG006606.1, CCG008603.1,CCG026106.1,CCG008741.1,CCG000646.1, CCG019020.1,CCG013398.1,CCG026174.1,CCG020785.1, CCG013625.1,CCG011006.1,CCG002841.1,CCG018321.1, CCG010275.1,CCG026360.1,CCG011717.1,CCG000213.1, CCG017266.1,CCG012573.1,CCG016689.2,CCG016745.1, CCG020709.1,CCG014466.1,CCG007993.1,CCG015101.1, CCG016094.1,CCG000659.1,CCG023474.1,CCG027127.1, CCG007335.1,CCG004515.1,CCG018533.1,CCG000647.1, CCG019692.1,CCG000526.1,CCG022281.1,CCG027669.1, CCG015967.1,CCG026537.1,CCG021661.1,CCG010071.1, CCG013308.1,CCG023579.1,CCG009510.1,CCG018799.1, CCG019717.1,CCG025176.1,CCG000078.1,CCG008685.1, CCG026109.1,CCG024952.1,CCG009980.1,CCG014506.1, CCG027133.1,CCG016252.1,CCG004279.1,CCG024663.1, CCG003745.1,CCG018494.1,CCG008759.1,CCG026953.1, CCG009427.1,CCG004402.1,CCG019493.1,CCG002520.1, CCG017591.1,CCG023464.1,CCG021284.1,CCG001579.1, CCG028136.1,CCG013641.1,CCG000732.1,CCG003317.1, CCG002364.1,CCG003495.1,CCG017127.1,CCG007951.1, CCG006412.1,CCG025131.2,CCG005284.1,CCG016307.1, CCG008444.1,CCG017701.1,CCG028486.1,CCG000834.1, CCG018859.3,CCG026695.1,CCG014712.1,CCG000876.1, CCG014928.1,CCG024664.1,CCG015638.1,CCG000789.1, CCG024271.1,CCG021045.1,CCG024662.1,CCG021759.1, CCG026047.1,CCG020978.1,CCG022772.1,CCG022628.1, CCG008939.1,CCG024570.2,CCG005531.1,CCG017725.1, CCG000111.2,CCG014345.2,CCG001759.1,CCG006133.1, CCG028477.1,CCG025899.1,CCG019881.1,CCG025035.1,

GO:0006461	protein complex assembly	91 of 4104 in the list	161 of 8404 in the genome	1	CCG006420.1,CCG013000.1,CCG003361.1,CCG019284.1, CCG008560.1,CCG010136.1,CCG021491.1,CCG010647.1, CCG003310.1,CCG005370.1,CCG009243.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG002696.1, CCG014537.1,CCG010137.1,CCG006421.1,CCG023963.3, CCG005194.1,CCG009461.1,CCG024623.1,CCG025880.1, CCG014836.1,CCG010904.1,CCG024177.1,CCG004481.1, CCG012514.1,CCG027196.1,CCG014772.1,CCG002099.1, CCG026474.1,CCG016370.1,CCG025893.1,CCG009637.1, CCG007532.1,CCG010905.1,CCG007531.1,CCG018820.3, CCG026579.1,CCG010909.1,CCG010648.1,CCG017580.1, CCG013637.1,CCG009980.1,CCG010906.1,CCG015968.1, CCG018893.1,CCG010649.1,CCG010138.1,CCG010418.1, CCG008892.2,CCG025877.1,CCG015560.1,CCG027199.1, CCG009080.1,CCG027198.1,CCG025396.1,CCG008559.1, CCG018287.1,CCG027696.1,CCG010907.1,CCG008748.1, CCG012229.1,CCG010650.1,CCG000708.1,CCG025990.1, CCG024624.1,CCG009543.1,CCG009275.1,CCG004494.1, CCG002947.1,CCG015289.1,CCG010908.1,CCG005716.1, CCG027197.1,CCG022673.1,CCG005886.1,CCG026159.1, CCG027697.1,CCG020442.1,CCG010646.1,CCG017598.1, CCG002852.1,CCG010864.1,CCG024787.1,CCG027695.1,

GO:0070271	protein complex biogenesis	91 of 4104 in the list	161 of 8404 in the genome	1	CCG006420.1,CCG013000.1,CCG003361.1,CCG019284.1, CCG008560.1,CCG010136.1,CCG021491.1,CCG010647.1, CCG003310.1,CCG005370.1,CCG009243.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG002696.1, CCG014537.1,CCG010137.1,CCG006421.1,CCG023963.3, CCG005194.1,CCG009461.1,CCG024623.1,CCG025880.1, CCG014836.1,CCG010904.1,CCG024177.1,CCG004481.1, CCG012514.1,CCG027196.1,CCG014772.1,CCG002099.1, CCG026474.1,CCG016370.1,CCG025893.1,CCG009637.1, CCG007532.1,CCG010905.1,CCG007531.1,CCG018820.3, CCG026579.1,CCG010909.1,CCG010648.1,CCG017580.1, CCG013637.1,CCG009980.1,CCG010906.1,CCG015968.1, CCG018893.1,CCG010649.1,CCG010138.1,CCG010418.1, CCG008892.2,CCG025877.1,CCG015560.1,CCG027199.1, CCG009080.1,CCG027198.1,CCG025396.1,CCG008559.1, CCG018287.1,CCG027696.1,CCG010907.1,CCG008748.1, CCG012229.1,CCG010650.1,CCG000708.1,CCG025990.1, CCG024624.1,CCG009543.1,CCG009275.1,CCG004494.1, CCG002947.1,CCG015289.1,CCG010908.1,CCG005716.1, CCG027197.1,CCG022673.1,CCG005886.1,CCG026159.1, CCG027697.1,CCG020442.1,CCG010646.1,CCG017598.1, CCG002852.1,CCG010864.1,CCG024787.1,CCG027695.1,
GO:0044282	small molecule catabolic process	22 of 4104 in the list	33 of 8404 in the genome	1	CCG007203.1,CCG019243.1,CCG010111.1,CCG025521.1, CCG020154.1,CCG000591.1,CCG025108.1,CCG011789.1, CCG006358.1,CCG001082.1,CCG011721.1,CCG006391.1, CCG002231.1,CCG008510.1,CCG005177.1,CCG011722.1, CCG019834.1,CCG018851.1,CCG003063.1,CCG006059.1,
GO:0000096	sulfur amino acid metabolic process	7 of 4104 in the list	8 of 8404 in the genome	1	CCG006994.1,CCG025465.1,CCG018907.1,CCG015568.1, CCG027551.3,CCG015567.1,CCG025636.2
GO:0006302	double-strand break repair	7 of 4104 in the list	8 of 8404 in the genome	1	CCG017444.1,CCG005594.1,CCG005481.1,CCG018472.1, CCG009962.1,CCG004233.1,CCG023155.1
GO:0072528	pyrimidine-containing compound biosynthetic process	15 of 4104 in the list	21 of 8404 in the genome	1	CCG025493.1,CCG018108.1,CCG013610.1,CCG016614.1, CCG004180.1,CCG017995.1,CCG007417.1,CCG021110.1, CCG017175.1,CCG006529.1,CCG023452.1,CCG005938.1, CCG014116.1,CCG010319.1,CCG025940.1

GO:0055086	nucleobase-containing small molecule metabolic process	149 of 4104 in the list	273 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG013000.1, CCG017331.1,CCG013766.1,CCG025989.2,CCG024327.1, CCG015386.1,CCG019020.1,CCG025493.1,CCG026174.1, CCG000016.1,CCG002925.1,CCG023005.1,CCG024375.1, CCG003748.1,CCG009607.1,CCG011006.1,CCG027119.1, CCG025307.1,CCG007993.1,CCG016370.1,CCG006311.1, CCG002917.1,CCG006486.1,CCG025940.1,CCG010944.1, CCG021110.1,CCG010960.2,CCG015746.1,CCG023640.1, CCG025348.1,CCG004191.1,CCG019619.1,CCG004869.1, CCG009080.1,CCG025396.1,CCG028131.1,CCG026953.1, CCG006924.1,CCG021220.1,CCG009165.1,CCG019678.1, CCG003677.1,CCG010460.1,CCG013641.1,CCG015410.1, CCG015289.1,CCG009142.1,CCG003495.1,CCG021411.1, CCG026898.1,CCG001859.1,CCG025131.2,CCG023452.1, CCG014116.1,CCG002852.1,CCG013610.1,CCG010986.1, CCG009518.1,CCG006791.1,CCG007362.1,CCG021152.1, CCG026865.1,CCG023526.2,CCG001285.1,CCG017693.1, CCG007060.1,CCG026047.1,CCG017175.1,CCG006529.1, CCG004309.1,CCG007533.1,CCG008422.1,CCG009243.1, CCG010112.1,CCG007827.1,CCG023963.3,CCG006421.1, CCG013643.1,CCG014434.1,CCG021990.1,CCG002038.1, CCG025027.1,CCG019103.1,CCG000148.1,CCG019629.2, CCG013365.1,CCG005147.1,CCG004988.1,CCG005924.2, CCG006998.1,CCG018108.1,CCG020909.1,CCG004257.1, CCG007532.1,CCG017330.1,CCG007531.1,CCG018447.1, CCG016966.1,CCG016415.1,CCG018820.3,CCG025179.1, CCG000217.1,CCG021934.1,CCG006777.1,CCG014379.1, CCG004308.1,CCG025973.1,CCG004180.1,CCG017995.1, CCG013637.1,CCG026314.1,CCG001440.1,CCG010418.1, CCG016222.1,CCG026852.1,CCG005938.1,CCG009801.1,

GO:0065003	macromolecular complex assembly	94 of 4104 in the list	167 of 8404 in the genome	1	CCG006420.1,CCG013000.1,CCG003361.1,CCG019284.1, CCG008560.1,CCG010136.1,CCG021491.1,CCG010647.1, CCG003310.1,CCG005370.1,CCG009243.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG002696.1, CCG014537.1,CCG010137.1,CCG006421.1,CCG023963.3, CCG005194.1,CCG009461.1,CCG024623.1,CCG025880.1, CCG014836.1,CCG010904.1,CCG024177.1,CCG004481.1, CCG012514.1,CCG027196.1,CCG014772.1,CCG002099.1, CCG026474.1,CCG016370.1,CCG010792.1,CCG025893.1, CCG009637.1,CCG007532.1,CCG010905.1,CCG007531.1, CCG018820.3,CCG026579.1,CCG010909.1,CCG010648.1, CCG017580.1,CCG013637.1,CCG009980.1,CCG010906.1, CCG015968.1,CCG018893.1,CCG010649.1,CCG010138.1, CCG025877.1,CCG010418.1,CCG008892.2,CCG015560.1, CCG027199.1,CCG009080.1,CCG027198.1,CCG025396.1, CCG008559.1,CCG018287.1,CCG027696.1,CCG010907.1, CCG008748.1,CCG012229.1,CCG010650.1,CCG000708.1, CCG025990.1,CCG024624.1,CCG009543.1,CCG009275.1, CCG004494.1,CCG002947.1,CCG015289.1,CCG010908.1, CCG005716.1,CCG007518.1,CCG027197.1,CCG022673.1, CCG005886.1,CCG026159.1,CCG027697.1,CCG020442.1, CCG010646.1,CCG017598.1,CCG002852.1,CCG010864.1,

GO:0060255	regulation of macromolecule metabolic process	277 of 4104 in the list	524 of 8404 in the genome	1	CCG022266.1,CCG008767.3,CCG008741.1,CCG024695.1, CCG003390.1,CCG027427.1,CCG007493.1,CCG021465.1, CCG003175.1,CCG004682.1,CCG023752.1,CCG018321.1, CCG028326.3,CCG013794.1,CCG006134.1,CCG009970.1, CCG016745.1,CCG021436.1,CCG016445.1,CCG012536.1, CCG000659.1,CCG027127.1,CCG018719.1,CCG015425.1, CCG027796.1,CCG022824.1,CCG018533.1,CCG024710.1, CCG022281.1,CCG011465.1,CCG006714.1,CCG020129.1, CCG027186.1,CCG011911.1,CCG000588.1,CCG022045.1, CCG013274.1,CCG028568.1,CCG007647.1,CCG021633.1, CCG012083.1,CCG000562.1,CCG005480.2,CCG017760.1, CCG005486.1,CCG016859.1,CCG020898.1,CCG017591.1, CCG002198.1,CCG021284.1,CCG016924.1,CCG013849.1, CCG000133.1,CCG013224.2,CCG002273.1,CCG001698.1, CCG023777.1,CCG014461.1,CCG026228.2,CCG005487.1, CCG021054.1,CCG016307.1,CCG009805.2,CCG016749.1, CCG028465.1,CCG019250.1,CCG005396.1,CCG025747.1, CCG009823.1,CCG021456.1,CCG014928.1,CCG005168.1, CCG018184.1,CCG018315.1,CCG027580.1,CCG024271.1, CCG025758.1,CCG009458.1,CCG022496.1,CCG015062.1, CCG018164.1,CCG001301.1,CCG023199.2,CCG001431.2, CCG001341.1,CCG022398.1,CCG021521.1,CCG009562.2, CCG010139.1,CCG021940.1,CCG024639.1,CCG015846.1, CCG008833.1,CCG018168.1,CCG014509.1,CCG004783.1, CCG025691.1,CCG018042.1,CCG014463.1,CCG026788.1, CCG020543.1,CCG025549.1,CCG011015.1,CCG027950.1, CCG002045.1,CCG025572.1,CCG004378.1,CCG014243.1, CCG009023.1,CCG018847.1,CCG014323.1,CCG027258.1, CCG008371.1,CCG022947.1,CCG008742.1,CCG011228.1, CCG004762.2,CCG028421.1,CCG003427.1,CCG026259.1,

GO:0051336	regulation of hydrolase activity	32 of 4104 in the list	51 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG022394.1,CCG016027.1,CCG011341.1,CCG019462.1, CCG012519.1,CCG004132.1,CCG017369.1,CCG017560.1, CCG024000.1,CCG025554.1,CCG016965.1,CCG022676.1, CCG013303.1,CCG027878.1,CCG024809.1,CCG009450.1, CCG009024.1,CCG007631.1,CCG015333.1,CCG002971.1, CCG016181.1,CCG013203.1,CCG018776.1,CCG002109.1, CCG021151.1,CCG010260.1,CCG002864.1,CCG005105.1
GO:0071103	DNA conformation change	76 of 4104 in the list	133 of 8404 in the genome	1	CCG016201.1,CCG003361.1,CCG019284.1,CCG008560.1, CCG010136.1,CCG021491.1,CCG010647.1,CCG003310.1, CCG022918.1,CCG013617.1,CCG000433.1,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,CCG026474.1,CCG027183.2, CCG000166.1,CCG025893.1,CCG009637.1,CCG010905.1, CCG026579.1,CCG010909.1,CCG010648.1,CCG011615.1, CCG017580.1,CCG009980.1,CCG010906.1,CCG015968.1, CCG018893.1,CCG010138.1,CCG010649.1,CCG008892.2, CCG025877.1,CCG015560.1,CCG027199.1,CCG027198.1, CCG003438.1,CCG018287.1,CCG008559.1,CCG027696.1, CCG010907.1,CCG012229.1,CCG010650.1,CCG000708.1, CCG025990.1,CCG024624.1,CCG009275.1,CCG004494.1, CCG002947.1,CCG010908.1,CCG005716.1,CCG027197.1, CCG022673.1,CCG026159.1,CCG027697.1,CCG020442.1, CCG010646.1,CCG017598.1,CCG024787.1,CCG027695.1,

GO:1901137	carbohydrate derivative biosynthetic process	76 of 4104 in the list	133 of 8404 in the genome	1	CCG017381.1,CCG018536.1,CCG023617.1,CCG000663.1, CCG006529.1,CCG007766.1,CCG001602.1,CCG025989.2, CCG004806.1,CCG008422.1,CCG024517.1,CCG007330.1, CCG010112.1,CCG004091.1,CCG011531.1,CCG009494.1, CCG025472.1,CCG013643.1,CCG018432.1,CCG022209.1, CCG002038.1,CCG009434.1,CCG014839.1,CCG014579.1, CCG000148.1,CCG013365.1,CCG025889.1,CCG005924.2, CCG024760.1,CCG028332.1,CCG017330.1,CCG019210.1, CCG021110.1,CCG024612.1,CCG021934.1,CCG010700.1, CCG017559.1,CCG017995.1,CCG004180.1,CCG023640.1, CCG013131.1,CCG026370.1,CCG012268.1,CCG025348.1, CCG009928.1,CCG016003.1,CCG019619.1,CCG013999.1, CCG021336.1,CCG007417.1,CCG004440.1,CCG022072.1, CCG007724.1,CCG021610.1,CCG003247.1,CCG010460.1, CCG015410.1,CCG017241.1,CCG025107.1,CCG009142.1, CCG027131.1,CCG026898.1,CCG026812.1,CCG017197.1, CCG013985.1,CCG000552.1,CCG018659.2,CCG014116.1, CCG013610.1,CCG016614.1,CCG028305.1,CCG006221.1,
GO:0035023	regulation of Rho protein signal transduction	23 of 4104 in the list	35 of 8404 in the genome	1	CCG006050.2,CCG026214.1,CCG009980.1,CCG010808.1, CCG009512.1,CCG008035.1,CCG022334.1,CCG008892.2, CCG000596.1,CCG019585.1,CCG012670.1,CCG010849.1, CCG025667.2,CCG003602.1,CCG004884.2,CCG009510.1, CCG018380.1,CCG018015.1,CCG010329.2,CCG021294.1, CCG021483.1,CCG011422.1,CCG001579.1
GO:0006140	regulation of nucleotide metabolic process	33 of 4104 in the list	53 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG022394.1,CCG016027.1,CCG011341.1,CCG019462.1, CCG012519.1,CCG004132.1,CCG028409.1,CCG017369.1, CCG002823.1,CCG000890.1,CCG024000.1,CCG025554.1, CCG016965.1,CCG022676.1,CCG013303.1,CCG027878.1, CCG024809.1,CCG009024.1,CCG007631.1,CCG015333.1, CCG002971.1,CCG016181.1,CCG013203.1,CCG018776.1, CCG002109.1,CCG021151.1,CCG010260.1,CCG002864.1,

GO:0006397	mRNA processing	24 of 4104 in the list	37 of 8404 in the genome	1	CCG017986.1,CCG010912.1,CCG000393.1,CCG026872.2, CCG007177.1,CCG000754.1,CCG028285.1,CCG023511.1, CCG010792.1,CCG004231.1,CCG004927.1,CCG012557.1, CCG004284.1,CCG007636.1,CCG000183.1,CCG025958.1, CCG023686.1,CCG024810.1,CCG001268.1,CCG017408.1, CCG013802.1,CCG003938.1,CCG001395.1,CCG001898.1
GO:0009064	glutamine family amino acid metabolic process	16 of 4104 in the list	23 of 8404 in the genome	1	CCG007203.1,CCG015921.1,CCG001423.1,CCG021923.1, CCG000472.1,CCG023501.1,CCG008860.1,CCG025731.1, CCG017111.1,CCG022773.2,CCG017894.1,CCG002231.1, CCG016220.1,CCG026030.1,CCG025897.1,CCG003871.1
GO:1902589	single-organism organelle organization	48 of 4104 in the list	81 of 8404 in the genome	1	CCG015570.1,CCG018832.1,CCG018647.1,CCG026688.1, CCG006211.1,CCG015784.1,CCG020863.1,CCG026823.1, CCG023682.1,CCG026620.1,CCG019140.1,CCG019356.1, CCG020949.1,CCG027167.1,CCG019028.1,CCG000469.1, CCG012083.1,CCG018326.1,CCG005579.1,CCG001369.2, CCG019029.1,CCG014817.2,CCG003587.1,CCG021448.1, CCG025991.2,CCG020315.1,CCG013028.1,CCG019797.1, CCG027236.1,CCG024028.1,CCG011262.1,CCG009090.1, CCG009641.1,CCG006686.1,CCG016992.2,CCG014318.1, CCG000535.1,CCG022536.3,CCG015398.1,CCG018249.1, CCG021366.1,CCG002137.1,CCG019092.1,CCG024421.3, CCG010538.1,CCG008824.1,CCG010178.1,CCG018646.1

GO:0009141	nucleoside triphosphate metabolic process	84 of 4104 in the list	149 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG004309.1,CCG006529.1, CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1, CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1, CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1, CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1, CCG016370.1,CCG000148.1,CCG019103.1,CCG019629.2, CCG002917.1,CCG006486.1,CCG005924.2,CCG020909.1, CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1, CCG018820.3,CCG021110.1,CCG010960.2,CCG025179.1, CCG021934.1,CCG006777.1,CCG004308.1,CCG025973.1, CCG017995.1,CCG013637.1,CCG023640.1,CCG026314.1, CCG010418.1,CCG025348.1,CCG016222.1,CCG009080.1, CCG004869.1,CCG019619.1,CCG025396.1,CCG026953.1, CCG006924.1,CCG007417.1,CCG021220.1,CCG001066.1, CCG019866.1,CCG019678.1,CCG008748.1,CCG007724.1, CCG013641.1,CCG015410.1,CCG016027.1,CCG015289.1, CCG025107.1,CCG003495.1,CCG021411.1,CCG009142.1, CCG001859.1,CCG026336.1,CCG005886.1,CCG025131.2, CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,
GO:0022402	cell cycle process	10 of 4104 in the list	13 of 8404 in the genome	1	CCG018249.1,CCG016878.1,CCG008308.1,CCG006063.1, CCG001795.1,CCG001794.1,CCG015077.1,CCG000839.1, CCG025057.1,CCG024595.1
GO:0009968	negative regulation of signal transduction	13 of 4104 in the list	18 of 8404 in the genome	1	CCG012573.1,CCG026798.1,CCG024952.1,CCG023484.1, CCG011501.1,CCG019427.1,CCG009446.1,CCG006412.1, CCG001079.1,CCG017498.1,CCG004343.1,CCG021064.1,
GO:0010648	negative regulation of cell communication	13 of 4104 in the list	18 of 8404 in the genome	1	CCG012573.1,CCG026798.1,CCG024952.1,CCG023484.1, CCG011501.1,CCG019427.1,CCG009446.1,CCG006412.1, CCG001079.1,CCG017498.1,CCG004343.1,CCG021064.1,
GO:0023057	negative regulation of signaling	13 of 4104 in the list	18 of 8404 in the genome	1	CCG012573.1,CCG026798.1,CCG024952.1,CCG023484.1, CCG011501.1,CCG019427.1,CCG009446.1,CCG006412.1, CCG001079.1,CCG017498.1,CCG004343.1,CCG021064.1,
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	13 of 4104 in the list	18 of 8404 in the genome	1	CCG028409.1,CCG002823.1,CCG026841.1,CCG025758.1, CCG014461.1,CCG010489.1,CCG000890.1,CCG003390.1, CCG025132.1,CCG018321.1,CCG005898.1,CCG004838.1,

GO:0048585	negative regulation of response to stimulus	13 of 4104 in the list	18 of 8404 in the genome	1	CCG012573.1,CCG026798.1,CCG024952.1,CCG023484.1, CCG011501.1,CCG019427.1,CCG009446.1,CCG006412.1, CCG001079.1,CCG017498.1,CCG004343.1,CCG021064.1,
GO:0051172	negative regulation of nitrogen compound metabolic process	13 of 4104 in the list	18 of 8404 in the genome	1	CCG028409.1,CCG002823.1,CCG026841.1,CCG025758.1, CCG014461.1,CCG010489.1,CCG000890.1,CCG003390.1, CCG025132.1,CCG018321.1,CCG005898.1,CCG004838.1,
GO:0009260	ribonucleotide biosynthetic process	30 of 4104 in the list	48 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG026898.1,CCG026812.1, CCG000148.1,CCG006529.1,CCG025348.1,CCG013365.1, CCG025989.2,CCG019619.1,CCG018659.2,CCG005924.2, CCG008422.1,CCG013610.1,CCG013999.1,CCG021336.1, CCG016614.1,CCG028305.1,CCG010112.1,CCG007417.1, CCG017330.1,CCG006791.1,CCG021110.1,CCG007724.1,
GO:0032318	regulation of Ras GTPase activity	30 of 4104 in the list	48 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG022394.1,CCG016027.1,CCG011341.1,CCG019462.1, CCG012519.1,CCG004132.1,CCG017369.1,CCG024000.1, CCG025554.1,CCG016965.1,CCG022676.1,CCG013303.1, CCG027878.1,CCG024809.1,CCG009024.1,CCG007631.1, CCG015333.1,CCG002971.1,CCG016181.1,CCG013203.1, CCG018776.1,CCG002109.1,CCG021151.1,CCG010260.1,
GO:0046390	ribose phosphate biosynthetic process	30 of 4104 in the list	48 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG026898.1,CCG026812.1, CCG000148.1,CCG006529.1,CCG025348.1,CCG013365.1, CCG025989.2,CCG019619.1,CCG018659.2,CCG005924.2, CCG008422.1,CCG013610.1,CCG013999.1,CCG021336.1, CCG016614.1,CCG028305.1,CCG010112.1,CCG007417.1, CCG017330.1,CCG006791.1,CCG021110.1,CCG007724.1,

GO:0006753	nucleoside phosphate metabolic process	133 of 4104 in the list	244 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG013000.1, CCG013766.1,CCG025989.2,CCG024327.1,CCG015386.1, CCG019020.1,CCG025493.1,CCG026174.1,CCG000016.1, CCG002925.1,CCG023005.1,CCG024375.1,CCG003748.1, CCG009607.1,CCG011006.1,CCG027119.1,CCG025307.1, CCG007993.1,CCG016370.1,CCG006311.1,CCG002917.1, CCG006486.1,CCG010944.1,CCG021110.1,CCG010960.2, CCG015746.1,CCG023640.1,CCG025348.1,CCG004191.1, CCG019619.1,CCG004869.1,CCG009080.1,CCG025396.1, CCG028131.1,CCG026953.1,CCG006924.1,CCG021220.1, CCG019678.1,CCG013641.1,CCG015410.1,CCG015289.1, CCG009142.1,CCG003495.1,CCG021411.1,CCG026898.1, CCG001859.1,CCG025131.2,CCG023452.1,CCG014116.1, CCG002852.1,CCG013610.1,CCG009518.1,CCG006791.1, CCG007362.1,CCG021152.1,CCG026865.1,CCG023526.2, CCG001285.1,CCG017693.1,CCG007060.1,CCG026047.1, CCG006529.1,CCG004309.1,CCG007533.1,CCG008422.1, CCG009243.1,CCG010112.1,CCG023963.3,CCG006421.1, CCG013643.1,CCG014434.1,CCG007827.1,CCG021990.1, CCG002038.1,CCG025027.1,CCG019103.1,CCG000148.1, CCG019629.2,CCG013365.1,CCG005147.1,CCG004988.1, CCG005924.2,CCG006998.1,CCG007532.1,CCG020909.1, CCG017330.1,CCG007531.1,CCG018447.1,CCG016966.1, CCG018820.3,CCG025179.1,CCG000217.1,CCG021934.1, CCG006777.1,CCG014379.1,CCG004308.1,CCG025973.1, CCG004180.1,CCG017995.1,CCG013637.1,CCG026314.1, CCG001440.1,CCG010418.1,CCG016222.1,CCG009084.2, CCG013999.1,CCG021336.1,CCG007417.1,CCG001066.1, CCG019866.1,CCG008748.1,CCG007724.1,CCG022027.1, CCG017295.1,CCG016027.1,CCG025107.1,CCG015747.1,
GO:0001932	regulation of protein phosphorylation	17 of 4104 in the list	25 of 8404 in the genome	1	CCG013849.1,CCG028049.1,CCG017923.1,CCG024695.1, CCG013274.1,CCG012743.1,CCG004783.1,CCG009521.1, CCG009035.1,CCG004682.1,CCG001854.1,CCG020898.1, CCG013794.1,CCG011648.1,CCG026404.1,CCG018184.1,

GO:0031399	regulation of protein modification process	17 of 4104 in the list	25 of 8404 in the genome	1	CCG013849.1,CCG028049.1,CCG017923.1,CCG024695.1, CCG013274.1,CCG012743.1,CCG004783.1,CCG009521.1, CCG009035.1,CCG004682.1,CCG001854.1,CCG020898.1, CCG013794.1,CCG011648.1,CCG026404.1,CCG018184.1,
GO:0043623	cellular protein complex assembly	22 of 4104 in the list	34 of 8404 in the genome	1	CCG006420.1,CCG009543.1,CCG015289.1,CCG013000.1, CCG013637.1,CCG002099.1,CCG016370.1,CCG010418.1, CCG005886.1,CCG005370.1,CCG009080.1,CCG010864.1, CCG002852.1,CCG009243.1,CCG025396.1,CCG007532.1, CCG002696.1,CCG007531.1,CCG018820.3,CCG008748.1,

GO:0009889	regulation of biosynthetic process	266 of 4104 in the list	506 of 8404 in the genome	1	CCG022266.1,CCG008767.3,CCG008741.1,CCG003390.1, CCG027427.1,CCG007493.1,CCG021465.1,CCG003175.1, CCG023752.1,CCG018321.1,CCG028326.3,CCG013794.1, CCG006134.1,CCG009970.1,CCG016745.1,CCG021436.1, CCG016445.1,CCG012536.1,CCG000659.1,CCG027127.1, CCG018719.1,CCG015425.1,CCG027796.1,CCG022824.1, CCG018533.1,CCG024710.1,CCG022281.1,CCG011465.1, CCG006714.1,CCG020129.1,CCG027186.1,CCG011911.1, CCG000588.1,CCG022045.1,CCG013274.1,CCG028568.1, CCG007647.1,CCG021633.1,CCG012083.1,CCG000562.1, CCG005480.2,CCG017760.1,CCG005486.1,CCG016859.1, CCG020898.1,CCG017591.1,CCG002198.1,CCG021284.1, CCG016924.1,CCG000133.1,CCG013224.2,CCG002273.1, CCG001698.1,CCG023777.1,CCG014461.1,CCG026228.2, CCG005487.1,CCG021054.1,CCG016307.1,CCG009805.2, CCG016749.1,CCG028465.1,CCG019250.1,CCG005396.1, CCG025747.1,CCG009823.1,CCG021456.1,CCG014928.1, CCG005168.1,CCG018184.1,CCG018315.1,CCG027580.1, CCG024271.1,CCG025758.1,CCG009458.1,CCG022496.1, CCG015062.1,CCG018164.1,CCG001301.1,CCG023199.2, CCG001431.2,CCG001341.1,CCG022398.1,CCG021521.1, CCG009562.2,CCG010139.1,CCG021940.1,CCG024639.1, CCG015846.1,CCG008833.1,CCG018168.1,CCG014509.1, CCG004783.1,CCG025691.1,CCG018042.1,CCG014463.1, CCG026788.1,CCG020543.1,CCG025549.1,CCG011015.1, CCG027950.1,CCG025572.1,CCG002045.1,CCG004378.1, CCG014243.1,CCG009023.1,CCG018847.1,CCG014323.1, CCG027258.1,CCG008371.1,CCG022947.1,CCG008742.1, CCG011228.1,CCG004762.2,CCG028421.1,CCG003427.1, CCG026259.1,CCG005635.1,CCG020695.1,CCG000593.1,

GO:0010556	regulation of macromolecule biosynthetic process	266 of 4104 in the list	506 of 8404 in the genome	1	CCG022266.1,CCG008767.3,CCG008741.1,CCG003390.1, CCG027427.1,CCG007493.1,CCG021465.1,CCG003175.1, CCG023752.1,CCG018321.1,CCG028326.3,CCG013794.1, CCG006134.1,CCG009970.1,CCG016745.1,CCG021436.1, CCG016445.1,CCG012536.1,CCG000659.1,CCG027127.1, CCG018719.1,CCG015425.1,CCG027796.1,CCG022824.1, CCG018533.1,CCG024710.1,CCG022281.1,CCG011465.1, CCG006714.1,CCG020129.1,CCG027186.1,CCG011911.1, CCG000588.1,CCG022045.1,CCG013274.1,CCG028568.1, CCG007647.1,CCG021633.1,CCG012083.1,CCG000562.1, CCG005480.2,CCG017760.1,CCG005486.1,CCG016859.1, CCG020898.1,CCG017591.1,CCG002198.1,CCG021284.1, CCG016924.1,CCG000133.1,CCG013224.2,CCG002273.1, CCG001698.1,CCG023777.1,CCG014461.1,CCG026228.2, CCG005487.1,CCG021054.1,CCG016307.1,CCG009805.2, CCG016749.1,CCG028465.1,CCG019250.1,CCG005396.1, CCG025747.1,CCG009823.1,CCG021456.1,CCG014928.1, CCG005168.1,CCG018184.1,CCG018315.1,CCG027580.1, CCG024271.1,CCG025758.1,CCG009458.1,CCG022496.1, CCG015062.1,CCG018164.1,CCG001301.1,CCG023199.2, CCG001431.2,CCG001341.1,CCG022398.1,CCG021521.1, CCG009562.2,CCG010139.1,CCG021940.1,CCG024639.1, CCG015846.1,CCG008833.1,CCG018168.1,CCG014509.1, CCG004783.1,CCG025691.1,CCG018042.1,CCG014463.1, CCG026788.1,CCG020543.1,CCG025549.1,CCG011015.1, CCG027950.1,CCG025572.1,CCG002045.1,CCG004378.1, CCG014243.1,CCG009023.1,CCG018847.1,CCG014323.1, CCG027258.1,CCG008371.1,CCG022947.1,CCG008742.1, CCG011228.1,CCG004762.2,CCG028421.1,CCG003427.1, CCG026259.1,CCG005635.1,CCG020695.1,CCG000593.1,

GO:0031326	regulation of cellular biosynthetic process	266 of 4104 in the list	506 of 8404 in the genome	1	CCG022266.1,CCG008767.3,CCG008741.1,CCG003390.1, CCG027427.1,CCG007493.1,CCG021465.1,CCG003175.1, CCG023752.1,CCG018321.1,CCG028326.3,CCG013794.1, CCG006134.1,CCG009970.1,CCG016745.1,CCG021436.1, CCG016445.1,CCG012536.1,CCG000659.1,CCG027127.1, CCG018719.1,CCG015425.1,CCG027796.1,CCG022824.1, CCG018533.1,CCG024710.1,CCG022281.1,CCG011465.1, CCG006714.1,CCG020129.1,CCG027186.1,CCG011911.1, CCG000588.1,CCG022045.1,CCG013274.1,CCG028568.1, CCG007647.1,CCG021633.1,CCG012083.1,CCG000562.1, CCG005480.2,CCG017760.1,CCG005486.1,CCG016859.1, CCG020898.1,CCG017591.1,CCG002198.1,CCG021284.1, CCG016924.1,CCG000133.1,CCG013224.2,CCG002273.1, CCG001698.1,CCG023777.1,CCG014461.1,CCG026228.2, CCG005487.1,CCG021054.1,CCG016307.1,CCG009805.2, CCG016749.1,CCG028465.1,CCG019250.1,CCG005396.1, CCG025747.1,CCG009823.1,CCG021456.1,CCG014928.1, CCG005168.1,CCG018184.1,CCG018315.1,CCG027580.1, CCG024271.1,CCG025758.1,CCG009458.1,CCG022496.1, CCG015062.1,CCG018164.1,CCG001301.1,CCG023199.2, CCG001431.2,CCG001341.1,CCG022398.1,CCG021521.1, CCG009562.2,CCG010139.1,CCG021940.1,CCG024639.1, CCG015846.1,CCG008833.1,CCG018168.1,CCG014509.1, CCG004783.1,CCG025691.1,CCG018042.1,CCG014463.1, CCG026788.1,CCG020543.1,CCG025549.1,CCG011015.1, CCG027950.1,CCG025572.1,CCG002045.1,CCG004378.1, CCG014243.1,CCG009023.1,CCG018847.1,CCG014323.1, CCG027258.1,CCG008371.1,CCG022947.1,CCG008742.1, CCG011228.1,CCG004762.2,CCG028421.1,CCG003427.1, CCG026259.1,CCG005635.1,CCG020695.1,CCG000593.1,

GO:2000112	regulation of cellular macromolecule biosynthetic process	266 of 4104 in the list	506 of 8404 in the genome	1	CCG022266.1,CCG008767.3,CCG008741.1,CCG003390.1, CCG027427.1,CCG007493.1,CCG021465.1,CCG003175.1, CCG023752.1,CCG018321.1,CCG028326.3,CCG013794.1, CCG006134.1,CCG009970.1,CCG016745.1,CCG021436.1, CCG016445.1,CCG012536.1,CCG000659.1,CCG027127.1, CCG018719.1,CCG015425.1,CCG027796.1,CCG022824.1, CCG018533.1,CCG024710.1,CCG022281.1,CCG011465.1, CCG006714.1,CCG020129.1,CCG027186.1,CCG011911.1, CCG000588.1,CCG022045.1,CCG013274.1,CCG028568.1, CCG007647.1,CCG021633.1,CCG012083.1,CCG000562.1, CCG005480.2,CCG017760.1,CCG005486.1,CCG016859.1, CCG020898.1,CCG017591.1,CCG002198.1,CCG021284.1, CCG016924.1,CCG000133.1,CCG013224.2,CCG002273.1, CCG001698.1,CCG023777.1,CCG014461.1,CCG026228.2, CCG005487.1,CCG021054.1,CCG016307.1,CCG009805.2, CCG016749.1,CCG028465.1,CCG019250.1,CCG005396.1, CCG025747.1,CCG009823.1,CCG021456.1,CCG014928.1, CCG005168.1,CCG018184.1,CCG018315.1,CCG027580.1, CCG024271.1,CCG025758.1,CCG009458.1,CCG022496.1, CCG015062.1,CCG018164.1,CCG001301.1,CCG023199.2, CCG001431.2,CCG001341.1,CCG022398.1,CCG021521.1, CCG009562.2,CCG010139.1,CCG021940.1,CCG024639.1, CCG015846.1,CCG008833.1,CCG018168.1,CCG014509.1, CCG004783.1,CCG025691.1,CCG018042.1,CCG014463.1, CCG026788.1,CCG020543.1,CCG025549.1,CCG011015.1, CCG027950.1,CCG025572.1,CCG002045.1,CCG004378.1, CCG014243.1,CCG009023.1,CCG018847.1,CCG014323.1, CCG027258.1,CCG008371.1,CCG022947.1,CCG008742.1, CCG011228.1,CCG004762.2,CCG028421.1,CCG003427.1, CCG026259.1,CCG005635.1,CCG020695.1,CCG000593.1,

GO:0009894	regulation of catabolic process	33 of 4104 in the list	54 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG022394.1,CCG016027.1,CCG011341.1,CCG019462.1, CCG012519.1,CCG004132.1,CCG003824.3,CCG017369.1, CCG024000.1,CCG025554.1,CCG016965.1,CCG022676.1, CCG013303.1,CCG027878.1,CCG024809.1,CCG009024.1, CCG007631.1,CCG023747.3,CCG015333.1,CCG002971.1, CCG016181.1,CCG013203.1,CCG018776.1,CCG002109.1, CCG021151.1,CCG015233.1,CCG010260.1,CCG002864.1,
GO:0009893	positive regulation of metabolic process	8 of 4104 in the list	10 of 8404 in the genome	1	CCG018164.1,CCG026216.1,CCG021944.1,CCG026155.1, CCG023747.3,CCG015233.1,CCG027118.1,CCG003824.3
GO:0031325	positive regulation of cellular metabolic process	8 of 4104 in the list	10 of 8404 in the genome	1	CCG018164.1,CCG026216.1,CCG021944.1,CCG026155.1, CCG023747.3,CCG015233.1,CCG027118.1,CCG003824.3
GO:0009069	serine family amino acid metabolic process	18 of 4104 in the list	27 of 8404 in the genome	1	CCG019954.3,CCG025465.1,CCG010111.1,CCG018907.1, CCG020154.1,CCG022025.2,CCG025636.2,CCG017201.1, CCG025108.1,CCG006994.1,CCG001082.1,CCG028131.1, CCG008510.1,CCG019834.1,CCG015568.1,CCG003063.1,
GO:0042325	regulation of phosphorylation	18 of 4104 in the list	27 of 8404 in the genome	1	CCG013849.1,CCG028049.1,CCG017923.1,CCG024695.1, CCG013274.1,CCG012743.1,CCG004783.1,CCG009521.1, CCG009035.1,CCG004682.1,CCG001854.1,CCG020898.1, CCG013794.1,CCG011162.1,CCG011648.1,CCG026404.1,

GO:0009116	nucleoside metabolic process	102 of 4104 in the list	185 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG017331.1,CCG017175.1, CCG004309.1,CCG006529.1,CCG025989.2,CCG024327.1, CCG007533.1,CCG015386.1,CCG019020.1,CCG009243.1, CCG008422.1,CCG010112.1,CCG009607.1,CCG011006.1, CCG007827.1,CCG014434.1,CCG013643.1,CCG006421.1, CCG023963.3,CCG002038.1,CCG025027.1,CCG016370.1, CCG000148.1,CCG019103.1,CCG019629.2,CCG002917.1, CCG006486.1,CCG005924.2,CCG025940.1,CCG020909.1, CCG007532.1,CCG018447.1,CCG007531.1,CCG016966.1, CCG018820.3,CCG016415.1,CCG021110.1,CCG025179.1, CCG021934.1,CCG006777.1,CCG004308.1,CCG025973.1, CCG017995.1,CCG013637.1,CCG023640.1,CCG026314.1, CCG010418.1,CCG025348.1,CCG019619.1,CCG009080.1, CCG004869.1,CCG009801.1,CCG025396.1,CCG021336.1, CCG013999.1,CCG026953.1,CCG006924.1,CCG007417.1, CCG021220.1,CCG009165.1,CCG001066.1,CCG004440.1, CCG019866.1,CCG019678.1,CCG007724.1,CCG008748.1, CCG003677.1,CCG010460.1,CCG013641.1,CCG015410.1, CCG016027.1,CCG015289.1,CCG025107.1,CCG009142.1, CCG003495.1,CCG021411.1,CCG001859.1,CCG026812.1, CCG026336.1,CCG005886.1,CCG025131.2,CCG016542.1, CCG026154.1,CCG015654.1,CCG018659.2,CCG002852.1, CCG010864.1,CCG013610.1,CCG010986.1,CCG016614.1,

GO:1901657	glycosyl compound metabolic process	102 of 4104 in the list	185 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG017331.1,CCG017175.1, CCG004309.1,CCG006529.1,CCG025989.2,CCG024327.1, CCG007533.1,CCG015386.1,CCG019020.1,CCG009243.1, CCG008422.1,CCG010112.1,CCG009607.1,CCG011006.1, CCG007827.1,CCG014434.1,CCG013643.1,CCG006421.1, CCG023963.3,CCG002038.1,CCG025027.1,CCG016370.1, CCG000148.1,CCG019103.1,CCG019629.2,CCG002917.1, CCG006486.1,CCG005924.2,CCG025940.1,CCG020909.1, CCG007532.1,CCG018447.1,CCG007531.1,CCG016966.1, CCG018820.3,CCG016415.1,CCG021110.1,CCG025179.1, CCG021934.1,CCG006777.1,CCG004308.1,CCG025973.1, CCG017995.1,CCG013637.1,CCG023640.1,CCG026314.1, CCG010418.1,CCG025348.1,CCG019619.1,CCG009080.1, CCG004869.1,CCG009801.1,CCG025396.1,CCG021336.1, CCG013999.1,CCG026953.1,CCG006924.1,CCG007417.1, CCG021220.1,CCG009165.1,CCG001066.1,CCG004440.1, CCG019866.1,CCG019678.1,CCG007724.1,CCG008748.1, CCG003677.1,CCG010460.1,CCG013641.1,CCG015410.1, CCG016027.1,CCG015289.1,CCG025107.1,CCG009142.1, CCG003495.1,CCG021411.1,CCG001859.1,CCG026812.1, CCG026336.1,CCG005886.1,CCG025131.2,CCG016542.1, CCG026154.1,CCG015654.1,CCG018659.2,CCG002852.1, CCG010864.1,CCG013610.1,CCG010986.1,CCG016614.1,
GO:0009152	purine ribonucleotide biosynthetic process	28 of 4104 in the list	45 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG026898.1,CCG026812.1, CCG000148.1,CCG006529.1,CCG025348.1,CCG013365.1, CCG025989.2,CCG019619.1,CCG018659.2,CCG005924.2, CCG008422.1,CCG013999.1,CCG021336.1,CCG028305.1, CCG010112.1,CCG007417.1,CCG017330.1,CCG006791.1, CCG021110.1,CCG007724.1,CCG021934.1,CCG013643.1
GO:0006417	regulation of translation	11 of 4104 in the list	15 of 8404 in the genome	1	CCG003216.1,CCG003765.1,CCG016445.1,CCG005486.1, CCG006714.1,CCG015062.1,CCG026155.1,CCG005487.1, CCG005485.1,CCG023431.1,CCG016835.2

GO:0010608	posttranscriptional regulation of gene expression	11 of 4104 in the list	15 of 8404 in the genome	1	CCG003216.1,CCG003765.1,CCG016445.1,CCG005486.1, CCG006714.1,CCG015062.1,CCG026155.1,CCG005487.1, CCG005485.1,CCG023431.1,CCG016835.2
GO:0006006	glucose metabolic process	23 of 4104 in the list	36 of 8404 in the genome	1	CCG022035.1,CCG020616.1,CCG005588.1,CCG003215.3, CCG028524.1,CCG025307.1,CCG010373.1,CCG007981.1, CCG007023.1,CCG022214.1,CCG012840.1,CCG017278.1, CCG000431.1,CCG004388.1,CCG013339.1,CCG009084.2, CCG019953.1,CCG017200.1,CCG003220.2,CCG006203.1, CCG022453.1,CCG025277.1,CCG003748.1
GO:0071822	protein complex subunit organization	92 of 4104 in the list	166 of 8404 in the genome	1	CCG006420.1,CCG013000.1,CCG003361.1,CCG019284.1, CCG008560.1,CCG010136.1,CCG021491.1,CCG010647.1, CCG003310.1,CCG005370.1,CCG009243.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG002696.1, CCG014537.1,CCG010137.1,CCG006421.1,CCG023963.3, CCG005194.1,CCG009461.1,CCG024623.1,CCG025880.1, CCG014836.1,CCG010904.1,CCG024177.1,CCG004481.1, CCG012514.1,CCG027196.1,CCG014772.1,CCG002099.1, CCG026474.1,CCG016370.1,CCG025893.1,CCG009637.1, CCG007532.1,CCG010905.1,CCG007531.1,CCG018820.3, CCG026579.1,CCG010909.1,CCG010648.1,CCG017580.1, CCG013637.1,CCG009980.1,CCG010906.1,CCG015968.1, CCG018893.1,CCG010649.1,CCG010138.1,CCG010418.1, CCG008892.2,CCG025877.1,CCG015560.1,CCG027199.1, CCG009080.1,CCG027198.1,CCG025396.1,CCG008559.1, CCG018287.1,CCG027696.1,CCG010907.1,CCG008748.1, CCG012229.1,CCG010650.1,CCG000708.1,CCG025990.1, CCG024624.1,CCG009543.1,CCG009275.1,CCG004494.1, CCG002947.1,CCG015289.1,CCG010908.1,CCG005716.1, CCG027197.1,CCG022673.1,CCG005886.1,CCG026159.1, CCG027697.1,CCG020442.1,CCG010646.1,CCG017598.1, CCG002852.1,CCG010864.1,CCG024787.1,CCG027695.1,

GO:0009117	nucleotide metabolic process	126 of 4104 in the list	232 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG026047.1,CCG013766.1, CCG004309.1,CCG006529.1,CCG025989.2,CCG024327.1, CCG015386.1,CCG019020.1,CCG009243.1,CCG008422.1, CCG025493.1,CCG026174.1,CCG000016.1,CCG010112.1, CCG002925.1,CCG023005.1,CCG024375.1,CCG003748.1, CCG009607.1,CCG011006.1,CCG027119.1,CCG007827.1, CCG014434.1,CCG013643.1,CCG006421.1,CCG023963.3, CCG021990.1,CCG002038.1,CCG025027.1,CCG025307.1, CCG007993.1,CCG016370.1,CCG000148.1,CCG019103.1, CCG013365.1,CCG019629.2,CCG006311.1,CCG002917.1, CCG005147.1,CCG006486.1,CCG005924.2,CCG004988.1, CCG006998.1,CCG020909.1,CCG007532.1,CCG018447.1, CCG007531.1,CCG017330.1,CCG016966.1,CCG018820.3, CCG010944.1,CCG021110.1,CCG010960.2,CCG025179.1, CCG021934.1,CCG006777.1,CCG004308.1,CCG014379.1, CCG025973.1,CCG017995.1,CCG004180.1,CCG013637.1, CCG023640.1,CCG001440.1,CCG026314.1,CCG010418.1, CCG025348.1,CCG016222.1,CCG019619.1,CCG004869.1, CCG009080.1,CCG009084.2,CCG025396.1,CCG021336.1, CCG013999.1,CCG026953.1,CCG028131.1,CCG006924.1, CCG007417.1,CCG021220.1,CCG001066.1,CCG019866.1, CCG019678.1,CCG007724.1,CCG008748.1,CCG022027.1, CCG013641.1,CCG015410.1,CCG016027.1,CCG015289.1, CCG025107.1,CCG009142.1,CCG003495.1,CCG021411.1, CCG026898.1,CCG001859.1,CCG026812.1,CCG026336.1, CCG005886.1,CCG025131.2,CCG016542.1,CCG023452.1, CCG026154.1,CCG015654.1,CCG018659.2,CCG014116.1, CCG002852.1,CCG010864.1,CCG001445.1,CCG013610.1,

GO:0006333	chromatin assembly or disassembly	70 of 4104 in the list	124 of 8404 in the genome	1	CCG003361.1,CCG019284.1,CCG008560.1,CCG010136.1, CCG021491.1,CCG010647.1,CCG003310.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG014537.1, CCG010137.1,CCG009461.1,CCG005194.1,CCG024623.1, CCG025880.1,CCG014836.1,CCG010904.1,CCG024177.1, CCG004481.1,CCG012514.1,CCG027196.1,CCG014772.1, CCG026474.1,CCG025893.1,CCG009637.1,CCG010905.1, CCG026579.1,CCG010909.1,CCG010648.1,CCG017580.1, CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1, CCG010138.1,CCG010649.1,CCG018767.1,CCG008892.2, CCG025877.1,CCG015560.1,CCG027199.1,CCG027198.1, CCG018287.1,CCG008559.1,CCG027696.1,CCG010907.1, CCG012229.1,CCG010650.1,CCG000708.1,CCG025990.1, CCG024624.1,CCG009275.1,CCG004494.1,CCG002947.1, CCG010908.1,CCG005716.1,CCG027197.1,CCG022673.1, CCG027697.1,CCG026159.1,CCG020442.1,CCG010646.1, CCG017598.1,CCG024787.1,CCG027695.1,CCG012584.1

GO:0043933	macromolecular complex subunit organization	95 of 4104 in the list	172 of 8404 in the genome	1	CCG006420.1,CCG013000.1,CCG003361.1,CCG019284.1, CCG008560.1,CCG010136.1,CCG021491.1,CCG010647.1, CCG003310.1,CCG005370.1,CCG009243.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG002696.1, CCG014537.1,CCG010137.1,CCG006421.1,CCG023963.3, CCG005194.1,CCG009461.1,CCG024623.1,CCG025880.1, CCG014836.1,CCG010904.1,CCG024177.1,CCG004481.1, CCG012514.1,CCG027196.1,CCG014772.1,CCG002099.1, CCG026474.1,CCG016370.1,CCG010792.1,CCG025893.1, CCG009637.1,CCG007532.1,CCG010905.1,CCG007531.1, CCG018820.3,CCG026579.1,CCG010909.1,CCG010648.1, CCG017580.1,CCG013637.1,CCG009980.1,CCG010906.1, CCG015968.1,CCG018893.1,CCG010649.1,CCG010138.1, CCG025877.1,CCG010418.1,CCG008892.2,CCG015560.1, CCG027199.1,CCG009080.1,CCG027198.1,CCG025396.1, CCG008559.1,CCG018287.1,CCG027696.1,CCG010907.1, CCG008748.1,CCG012229.1,CCG010650.1,CCG000708.1, CCG025990.1,CCG024624.1,CCG009543.1,CCG009275.1, CCG004494.1,CCG002947.1,CCG015289.1,CCG010908.1, CCG005716.1,CCG007518.1,CCG027197.1,CCG022673.1, CCG005886.1,CCG026159.1,CCG027697.1,CCG020442.1, CCG010646.1,CCG017598.1,CCG002852.1,CCG010864.1, CCG024787.1,CCG027695.1,CCG000915.1,CCG012584.1,

GO:0009144	purine nucleoside triphosphate metabolic process	82 of 4104 in the list	147 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG004309.1,CCG006529.1, CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1, CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1, CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1, CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1, CCG016370.1,CCG000148.1,CCG019103.1,CCG019629.2, CCG002917.1,CCG006486.1,CCG005924.2,CCG020909.1, CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1, CCG018820.3,CCG021110.1,CCG025179.1,CCG021934.1, CCG006777.1,CCG004308.1,CCG025973.1,CCG017995.1, CCG013637.1,CCG023640.1,CCG026314.1,CCG010418.1, CCG025348.1,CCG009080.1,CCG004869.1,CCG019619.1, CCG025396.1,CCG026953.1,CCG006924.1,CCG007417.1, CCG021220.1,CCG001066.1,CCG019866.1,CCG019678.1, CCG008748.1,CCG007724.1,CCG013641.1,CCG015410.1, CCG016027.1,CCG015289.1,CCG025107.1,CCG003495.1, CCG021411.1,CCG009142.1,CCG001859.1,CCG026336.1, CCG005886.1,CCG025131.2,CCG016542.1,CCG015654.1, CCG026154.1,CCG002852.1,CCG010864.1,CCG021152.1,

GO:0009199	ribonucleoside triphosphate metabolic process	82 of 4104 in the list	147 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG004309.1,CCG006529.1, CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1, CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1, CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1, CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1, CCG016370.1,CCG000148.1,CCG019103.1,CCG019629.2, CCG002917.1,CCG006486.1,CCG005924.2,CCG020909.1, CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1, CCG018820.3,CCG021110.1,CCG025179.1,CCG021934.1, CCG006777.1,CCG004308.1,CCG025973.1,CCG017995.1, CCG013637.1,CCG023640.1,CCG026314.1,CCG010418.1, CCG025348.1,CCG009080.1,CCG004869.1,CCG019619.1, CCG025396.1,CCG026953.1,CCG006924.1,CCG007417.1, CCG021220.1,CCG001066.1,CCG019866.1,CCG019678.1, CCG008748.1,CCG007724.1,CCG013641.1,CCG015410.1, CCG016027.1,CCG015289.1,CCG025107.1,CCG003495.1, CCG021411.1,CCG009142.1,CCG001859.1,CCG026336.1, CCG005886.1,CCG025131.2,CCG016542.1,CCG015654.1, CCG026154.1,CCG002852.1,CCG010864.1,CCG021152.1,

GO:0009205	purine ribonucleoside triphosphate metabolic process	82 of 4104 in the list	147 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG004309.1,CCG006529.1, CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1, CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1, CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1, CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1, CCG016370.1,CCG000148.1,CCG019103.1,CCG019629.2, CCG002917.1,CCG006486.1,CCG005924.2,CCG020909.1, CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1, CCG018820.3,CCG021110.1,CCG025179.1,CCG021934.1, CCG006777.1,CCG004308.1,CCG025973.1,CCG017995.1, CCG013637.1,CCG023640.1,CCG026314.1,CCG010418.1, CCG025348.1,CCG009080.1,CCG004869.1,CCG019619.1, CCG025396.1,CCG026953.1,CCG006924.1,CCG007417.1, CCG021220.1,CCG001066.1,CCG019866.1,CCG019678.1, CCG008748.1,CCG007724.1,CCG013641.1,CCG015410.1, CCG016027.1,CCG015289.1,CCG025107.1,CCG003495.1, CCG021411.1,CCG009142.1,CCG001859.1,CCG026336.1, CCG005886.1,CCG025131.2,CCG016542.1,CCG015654.1, CCG026154.1,CCG002852.1,CCG010864.1,CCG021152.1,

GO:0005975	carbohydrate metabolic process	175 of 4104 in the list	328 of 8404 in the genome	1	CCG018536.1,CCG022363.1,CCG004122.1,CCG007885.1, CCG007046.2,CCG015677.1,CCG009776.1,CCG001501.1, CCG018730.1,CCG018613.1,CCG023324.1,CCG020504.1, CCG003220.2,CCG022974.1,CCG006203.1,CCG004091.1, CCG004020.1,CCG001355.1,CCG009685.1,CCG000970.1, CCG022453.1,CCG003748.1,CCG009494.1,CCG012558.1, CCG025472.1,CCG025412.1,CCG001038.1,CCG018432.1, CCG010996.1,CCG013485.1,CCG015610.1,CCG025307.1, CCG023374.1,CCG019693.1,CCG016653.1,CCG007771.1, CCG008317.1,CCG023890.1,CCG019874.1,CCG003001.1, CCG019210.1,CCG015235.1,CCG010652.1,CCG010019.1, CCG025277.1,CCG017651.1,CCG003215.3,CCG028548.1, CCG025362.1,CCG002418.1,CCG009596.1,CCG013169.3, CCG025948.4,CCG006042.2,CCG006010.1,CCG002600.1, CCG020739.1,CCG023172.1,CCG008484.1,CCG027416.1, CCG006671.1,CCG025962.1,CCG026284.1,CCG007772.1, CCG027708.4,CCG004165.1,CCG015038.1,CCG002307.1, CCG008663.1,CCG010818.1,CCG013318.1,CCG010414.1, CCG017197.1,CCG013985.1,CCG022214.1,CCG011451.2, CCG012840.1,CCG006213.1,CCG017278.1,CCG024829.1, CCG018423.1,CCG028116.1,CCG017200.1,CCG023757.1, CCG023420.1,CCG006221.1,CCG005177.1,CCG007200.2, CCG028454.1,CCG011996.1,CCG003277.1,CCG025015.2, CCG002599.1,CCG002702.1,CCG015170.1,CCG017381.1, CCG005588.1,CCG023617.1,CCG011547.1,CCG010373.1, CCG008437.1,CCG028547.1,CCG007766.1,CCG001602.1, CCG020802.1,CCG009803.1,CCG027015.1,CCG008287.1, CCG006358.1,CCG020803.1,CCG018480.1,CCG012048.1, CCG019825.2,CCG001590.1,CCG022035.1,CCG013172.1, CCG007045.1,CCG020511.1,CCG023748.1,CCG028524.1,

GO:0009118	regulation of nucleoside metabolic process	30 of 4104 in the list	49 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG022394.1,CCG016027.1,CCG011341.1,CCG019462.1, CCG012519.1,CCG004132.1,CCG017369.1,CCG024000.1, CCG025554.1,CCG016965.1,CCG022676.1,CCG013303.1, CCG027878.1,CCG024809.1,CCG009024.1,CCG007631.1, CCG015333.1,CCG002971.1,CCG016181.1,CCG013203.1, CCG018776.1,CCG002109.1,CCG021151.1,CCG010260.1,
GO:0030811	regulation of nucleotide catabolic process	30 of 4104 in the list	49 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG022394.1,CCG016027.1,CCG011341.1,CCG019462.1, CCG012519.1,CCG004132.1,CCG017369.1,CCG024000.1, CCG025554.1,CCG016965.1,CCG022676.1,CCG013303.1, CCG027878.1,CCG024809.1,CCG009024.1,CCG007631.1, CCG015333.1,CCG002971.1,CCG016181.1,CCG013203.1, CCG018776.1,CCG002109.1,CCG021151.1,CCG010260.1,
GO:0033121	regulation of purine nucleotide catabolic process	30 of 4104 in the list	49 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG022394.1,CCG016027.1,CCG011341.1,CCG019462.1, CCG012519.1,CCG004132.1,CCG017369.1,CCG024000.1, CCG025554.1,CCG016965.1,CCG022676.1,CCG013303.1, CCG027878.1,CCG024809.1,CCG009024.1,CCG007631.1, CCG015333.1,CCG002971.1,CCG016181.1,CCG013203.1, CCG018776.1,CCG002109.1,CCG021151.1,CCG010260.1,
GO:0033124	regulation of GTP catabolic process	30 of 4104 in the list	49 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG022394.1,CCG016027.1,CCG011341.1,CCG019462.1, CCG012519.1,CCG004132.1,CCG017369.1,CCG024000.1, CCG025554.1,CCG016965.1,CCG022676.1,CCG013303.1, CCG027878.1,CCG024809.1,CCG009024.1,CCG007631.1, CCG015333.1,CCG002971.1,CCG016181.1,CCG013203.1, CCG018776.1,CCG002109.1,CCG021151.1,CCG010260.1,
GO:0043087	regulation of GTPase activity	30 of 4104 in the list	49 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG022394.1,CCG016027.1,CCG011341.1,CCG019462.1, CCG012519.1,CCG004132.1,CCG017369.1,CCG024000.1, CCG025554.1,CCG016965.1,CCG022676.1,CCG013303.1, CCG027878.1,CCG024809.1,CCG009024.1,CCG007631.1, CCG015333.1,CCG002971.1,CCG016181.1,CCG013203.1, CCG018776.1,CCG002109.1,CCG021151.1,CCG010260.1,

GO:1900542	regulation of purine nucleotide metabolic process	30 of 4104 in the list	49 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG025433.1, CCG022394.1,CCG016027.1,CCG011341.1,CCG019462.1, CCG012519.1,CCG004132.1,CCG017369.1,CCG024000.1, CCG025554.1,CCG016965.1,CCG022676.1,CCG013303.1, CCG027878.1,CCG024809.1,CCG009024.1,CCG007631.1, CCG015333.1,CCG002971.1,CCG016181.1,CCG013203.1, CCG018776.1,CCG002109.1,CCG021151.1,CCG010260.1,
GO:0006534	cysteine metabolic process	6 of 4104 in the list	7 of 8404 in the genome	1	CCG006994.1,CCG025465.1,CCG018907.1,CCG015568.1, CCG015567.1,CCG025636.2
GO:0005992	trehalose biosynthetic process	4 of 4104 in the list	4 of 8404 in the genome	1	CCG019693.1,CCG014260.1,CCG024762.1,CCG013129.1
GO:0006023	aminoglycan biosynthetic process	4 of 4104 in the list	4 of 8404 in the genome	1	CCG017559.1,CCG024517.1,CCG022072.1,CCG025840.1
GO:0006024	glycosaminoglycan biosynthetic process	4 of 4104 in the list	4 of 8404 in the genome	1	CCG017559.1,CCG024517.1,CCG022072.1,CCG025840.1
GO:0006269	DNA replication, synthesis of RNA primer	4 of 4104 in the list	4 of 8404 in the genome	1	CCG015694.1,CCG009896.1,CCG006164.1,CCG016381.1
GO:0006338	chromatin remodeling	4 of 4104 in the list	4 of 8404 in the genome	1	CCG011675.1,CCG001913.1,CCG027348.1,CCG000575.1
GO:0006405	RNA export from nucleus	4 of 4104 in the list	4 of 8404 in the genome	1	CCG011567.1,CCG017874.1,CCG021221.1,CCG026989.1
GO:0006406	mRNA export from nucleus	4 of 4104 in the list	4 of 8404 in the genome	1	CCG011567.1,CCG017874.1,CCG021221.1,CCG026989.1
GO:0006421	asparaginyl-tRNA aminoacylation	4 of 4104 in the list	4 of 8404 in the genome	1	CCG021774.1,CCG015367.1,CCG010565.1,CCG010321.1
GO:0006458	'de novo' protein folding	4 of 4104 in the list	4 of 8404 in the genome	1	CCG012492.1,CCG007076.1,CCG006921.1,CCG014012.1
GO:0006528	asparagine metabolic process	4 of 4104 in the list	4 of 8404 in the genome	1	CCG006821.1,CCG010174.2,CCG009333.1,CCG024133.1
GO:0006529	asparagine biosynthetic process	4 of 4104 in the list	4 of 8404 in the genome	1	CCG006821.1,CCG010174.2,CCG009333.1,CCG024133.1
GO:0007033	vacuole organization	4 of 4104 in the list	4 of 8404 in the genome	1	CCG019082.1,CCG002366.1,CCG000834.1,CCG013509.1
GO:0007088	regulation of mitosis	4 of 4104 in the list	4 of 8404 in the genome	1	CCG004331.1,CCG002269.1,CCG027068.1,CCG018116.1
GO:0008156	negative regulation of DNA	4 of 4104 in the list	4 of 8404 in the genome	1	CCG018321.1,CCG026841.1,CCG025758.1,CCG014323.1
GO:0009067	aspartate family amino acid biosynthetic process	4 of 4104 in the list	4 of 8404 in the genome	1	CCG006821.1,CCG010174.2,CCG009333.1,CCG024133.1
GO:0010498	proteasomal protein catabolic process	4 of 4104 in the list	4 of 8404 in the genome	1	CCG005241.1,CCG004331.1,CCG027068.1,CCG001769.1
GO:0010628	positive regulation of gene	4 of 4104 in the list	4 of 8404 in the genome	1	CCG018164.1,CCG026216.1,CCG021944.1,CCG027118.1
GO:0030071	regulation of mitotic metaphase/anaphase transition	4 of 4104 in the list	4 of 8404 in the genome	1	CCG004331.1,CCG002269.1,CCG027068.1,CCG018116.1
GO:0031120	snRNA pseudouridine synthesis	4 of 4104 in the list	4 of 8404 in the genome	1	CCG002792.1,CCG000540.1,CCG028653.1,CCG016652.1
GO:0040031	snRNA modification	4 of 4104 in the list	4 of 8404 in the genome	1	CCG002792.1,CCG000540.1,CCG028653.1,CCG016652.1

GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic	4 of 4104 in the list	4 of 8404 in the genome	1	CCG005241.1,CCG004331.1,CCG027068.1,CCG001769.1
GO:0045893	positive regulation of transcription, DNA-templated	4 of 4104 in the list	4 of 8404 in the genome	1	CCG018164.1,CCG026216.1,CCG021944.1,CCG027118.1
GO:0046351	disaccharide biosynthetic process	4 of 4104 in the list	4 of 8404 in the genome	1	CCG019693.1,CCG014260.1,CCG024762.1,CCG013129.1
GO:0051053	negative regulation of DNA metabolic process	4 of 4104 in the list	4 of 8404 in the genome	1	CCG018321.1,CCG026841.1,CCG025758.1,CCG014323.1
GO:0051084	'de novo' posttranslational protein folding	4 of 4104 in the list	4 of 8404 in the genome	1	CCG012492.1,CCG007076.1,CCG006921.1,CCG014012.1
GO:0051085	chaperone mediated protein folding requiring cofactor	4 of 4104 in the list	4 of 8404 in the genome	1	CCG012492.1,CCG007076.1,CCG006921.1,CCG014012.1
GO:0051168	nuclear export	4 of 4104 in the list	4 of 8404 in the genome	1	CCG011567.1,CCG017874.1,CCG021221.1,CCG026989.1
GO:0051302	regulation of cell division	4 of 4104 in the list	4 of 8404 in the genome	1	CCG004331.1,CCG002269.1,CCG027068.1,CCG018116.1
GO:0051783	regulation of nuclear division	4 of 4104 in the list	4 of 8404 in the genome	1	CCG004331.1,CCG002269.1,CCG027068.1,CCG018116.1
GO:0061077	chaperone-mediated protein	4 of 4104 in the list	4 of 8404 in the genome	1	CCG012492.1,CCG007076.1,CCG006921.1,CCG014012.1
GO:1902099	regulation of metaphase/anaphase transition of	4 of 4104 in the list	4 of 8404 in the genome	1	CCG004331.1,CCG002269.1,CCG027068.1,CCG018116.1
GO:0007049	cell cycle	25 of 4104 in the list	40 of 8404 in the genome	1	CCG023588.1,CCG016924.1,CCG019773.1,CCG010140.1, CCG016878.1,CCG022393.1,CCG008308.1,CCG006063.1, CCG004222.1,CCG026841.1,CCG001795.1,CCG026106.1, CCG003424.1,CCG027505.1,CCG027928.1,CCG018249.1, CCG021047.1,CCG001794.1,CCG015077.1,CCG018321.1, CCG004378.1,CCG000839.1,CCG025057.1,CCG024595.1,

GO:0006082	organic acid metabolic process	141 of 4104 in the list	262 of 8404 in the genome	1	CCG010174.2,CCG019078.1,CCG023277.1,CCG014396.1, CCG010191.3,CCG028623.1,CCG009878.1,CCG015950.3, CCG025108.1,CCG016238.1,CCG006391.1,CCG017097.1, CCG019834.1,CCG016220.1,CCG027607.1,CCG025307.1, CCG018907.1,CCG025521.1,CCG001423.1,CCG022025.2, CCG008860.1,CCG006994.1,CCG011722.1,CCG001553.1, CCG003063.1,CCG013063.1,CCG000414.1,CCG019909.1, CCG020877.1,CCG006231.1,CCG008321.1,CCG009244.1, CCG025465.1,CCG020154.1,CCG005204.1,CCG028131.1, CCG011721.1,CCG008510.1,CCG018290.1,CCG022407.1, CCG016315.1,CCG021610.1,CCG027312.1,CCG017543.1, CCG014436.2,CCG006821.1,CCG023315.1,CCG003865.1, CCG009662.1,CCG025439.1,CCG025636.2,CCG017111.1, CCG019545.1,CCG011789.1,CCG022773.2,CCG019330.1, CCG001876.1,CCG002231.1,CCG026570.1,CCG026155.1, CCG015567.1,CCG008388.1,CCG021774.1,CCG015367.1, CCG010111.1,CCG011491.1,CCG012619.1,CCG009333.1, CCG021923.1,CCG006188.1,CCG023501.1,CCG000591.1, CCG027352.3,CCG011135.1,CCG019112.1,CCG013727.1, CCG028092.1,CCG015568.1,CCG019111.1,CCG020441.1, CCG010561.1,CCG026910.1,CCG010321.1,CCG008776.1, CCG022869.1,CCG000138.1,CCG017344.1,CCG027551.3, CCG000472.1,CCG015577.3,CCG018615.3,CCG025731.1, CCG018108.1,CCG026099.1,CCG001082.1,CCG024133.1, CCG026030.1,CCG003751.1,CCG025897.1,CCG002018.1, CCG007203.1,CCG019954.3,CCG015921.1,CCG001811.1, CCG012408.1,CCG020559.1,CCG017708.1,CCG004949.1, CCG005938.1,CCG009084.2,CCG017894.1,CCG013043.1, CCG018289.1,CCG021716.1,CCG021820.1,CCG006570.1, CCG002662.1,CCG006059.1,CCG000352.1,CCG008932.1,

GO:0019752	carboxylic acid metabolic process	141 of 4104 in the list	262 of 8404 in the genome	1	CCG010174.2,CCG019078.1,CCG023277.1,CCG014396.1, CCG010191.3,CCG028623.1,CCG009878.1,CCG015950.3, CCG025108.1,CCG016238.1,CCG006391.1,CCG017097.1, CCG019834.1,CCG016220.1,CCG027607.1,CCG025307.1, CCG018907.1,CCG025521.1,CCG001423.1,CCG022025.2, CCG008860.1,CCG006994.1,CCG011722.1,CCG001553.1, CCG003063.1,CCG013063.1,CCG000414.1,CCG019909.1, CCG020877.1,CCG006231.1,CCG008321.1,CCG009244.1, CCG025465.1,CCG020154.1,CCG005204.1,CCG028131.1, CCG011721.1,CCG008510.1,CCG018290.1,CCG022407.1, CCG016315.1,CCG021610.1,CCG027312.1,CCG017543.1, CCG014436.2,CCG006821.1,CCG023315.1,CCG003865.1, CCG009662.1,CCG025439.1,CCG025636.2,CCG017111.1, CCG019545.1,CCG011789.1,CCG022773.2,CCG019330.1, CCG001876.1,CCG002231.1,CCG026570.1,CCG026155.1, CCG015567.1,CCG008388.1,CCG021774.1,CCG015367.1, CCG010111.1,CCG011491.1,CCG012619.1,CCG009333.1, CCG021923.1,CCG006188.1,CCG023501.1,CCG000591.1, CCG027352.3,CCG011135.1,CCG019112.1,CCG013727.1, CCG028092.1,CCG015568.1,CCG019111.1,CCG020441.1, CCG010561.1,CCG026910.1,CCG010321.1,CCG008776.1, CCG022869.1,CCG000138.1,CCG017344.1,CCG027551.3, CCG000472.1,CCG015577.3,CCG018615.3,CCG025731.1, CCG018108.1,CCG026099.1,CCG001082.1,CCG024133.1, CCG026030.1,CCG003751.1,CCG025897.1,CCG002018.1, CCG007203.1,CCG019954.3,CCG015921.1,CCG001811.1, CCG012408.1,CCG020559.1,CCG017708.1,CCG004949.1, CCG005938.1,CCG009084.2,CCG017894.1,CCG013043.1, CCG018289.1,CCG021716.1,CCG021820.1,CCG006570.1, CCG002662.1,CCG006059.1,CCG000352.1,CCG008932.1,

GO:0043436	oxoacid metabolic process	141 of 4104 in the list	262 of 8404 in the genome	1	CCG010174.2,CCG019078.1,CCG023277.1,CCG014396.1, CCG010191.3,CCG028623.1,CCG009878.1,CCG015950.3, CCG025108.1,CCG016238.1,CCG006391.1,CCG017097.1, CCG019834.1,CCG016220.1,CCG027607.1,CCG025307.1, CCG018907.1,CCG025521.1,CCG001423.1,CCG022025.2, CCG008860.1,CCG006994.1,CCG011722.1,CCG001553.1, CCG003063.1,CCG013063.1,CCG000414.1,CCG019909.1, CCG020877.1,CCG006231.1,CCG008321.1,CCG009244.1, CCG025465.1,CCG020154.1,CCG005204.1,CCG028131.1, CCG011721.1,CCG008510.1,CCG018290.1,CCG022407.1, CCG016315.1,CCG021610.1,CCG027312.1,CCG017543.1, CCG014436.2,CCG006821.1,CCG023315.1,CCG003865.1, CCG009662.1,CCG025439.1,CCG025636.2,CCG017111.1, CCG019545.1,CCG011789.1,CCG022773.2,CCG019330.1, CCG001876.1,CCG002231.1,CCG026570.1,CCG026155.1, CCG015567.1,CCG008388.1,CCG021774.1,CCG015367.1, CCG010111.1,CCG011491.1,CCG012619.1,CCG009333.1, CCG021923.1,CCG006188.1,CCG023501.1,CCG000591.1, CCG027352.3,CCG011135.1,CCG019112.1,CCG013727.1, CCG028092.1,CCG015568.1,CCG019111.1,CCG020441.1, CCG010561.1,CCG026910.1,CCG010321.1,CCG008776.1, CCG022869.1,CCG000138.1,CCG017344.1,CCG027551.3, CCG000472.1,CCG015577.3,CCG018615.3,CCG025731.1, CCG018108.1,CCG026099.1,CCG001082.1,CCG024133.1, CCG026030.1,CCG003751.1,CCG025897.1,CCG002018.1, CCG007203.1,CCG019954.3,CCG015921.1,CCG001811.1, CCG012408.1,CCG020559.1,CCG017708.1,CCG004949.1, CCG005938.1,CCG009084.2,CCG017894.1,CCG013043.1, CCG018289.1,CCG021716.1,CCG021820.1,CCG006570.1, CCG002662.1,CCG006059.1,CCG000352.1,CCG008932.1,
GO:0016054	organic acid catabolic process	20 of 4104 in the list	31 of 8404 in the genome	1	CCG007203.1,CCG019243.1,CCG010111.1,CCG025521.1, CCG020154.1,CCG000591.1,CCG025108.1,CCG011789.1, CCG001082.1,CCG011721.1,CCG006391.1,CCG002231.1, CCG008510.1,CCG011722.1,CCG019834.1,CCG018851.1, CCG003063.1,CCG006059.1,CCG017543.1,CCG008388.1

GO:0046395	carboxylic acid catabolic process	20 of 4104 in the list	31 of 8404 in the genome	1	CCG007203.1,CCG019243.1,CCG010111.1,CCG025521.1, CCG020154.1,CCG000591.1,CCG025108.1,CCG011789.1, CCG001082.1,CCG011721.1,CCG006391.1,CCG002231.1, CCG008510.1,CCG011722.1,CCG019834.1,CCG018851.1, CCG003063.1,CCG006059.1,CCG017543.1,CCG008388.1
GO:0006220	pyrimidine nucleotide metabolic process	12 of 4104 in the list	17 of 8404 in the genome	1	CCG025493.1,CCG013610.1,CCG016614.1,CCG004180.1, CCG017995.1,CCG007417.1,CCG021110.1,CCG010960.2, CCG006529.1,CCG016222.1,CCG023452.1,CCG014116.1
GO:0009084	glutamine family amino acid biosynthetic process	12 of 4104 in the list	17 of 8404 in the genome	1	CCG017111.1,CCG025731.1,CCG007203.1,CCG022773.2, CCG017894.1,CCG002231.1,CCG016220.1,CCG015921.1, CCG001423.1,CCG025897.1,CCG003871.1,CCG008860.1
GO:0009063	cellular amino acid catabolic process	16 of 4104 in the list	24 of 8404 in the genome	1	CCG011789.1,CCG007203.1,CCG025108.1,CCG019243.1, CCG001082.1,CCG011721.1,CCG002231.1,CCG008510.1, CCG011722.1,CCG010111.1,CCG019834.1,CCG003063.1, CCG020154.1,CCG006059.1,CCG008388.1,CCG017543.1
GO:0006323	DNA packaging	69 of 4104 in the list	123 of 8404 in the genome	1	CCG003361.1,CCG019284.1,CCG008560.1,CCG010136.1, CCG021491.1,CCG010647.1,CCG003310.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG014537.1, CCG010137.1,CCG009461.1,CCG005194.1,CCG024623.1, CCG025880.1,CCG014836.1,CCG010904.1,CCG024177.1, CCG004481.1,CCG012514.1,CCG027196.1,CCG014772.1, CCG026474.1,CCG025893.1,CCG009637.1,CCG010905.1, CCG026579.1,CCG010909.1,CCG010648.1,CCG017580.1, CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1, CCG010138.1,CCG010649.1,CCG008892.2,CCG025877.1, CCG015560.1,CCG027199.1,CCG027198.1,CCG018287.1, CCG008559.1,CCG027696.1,CCG010907.1,CCG012229.1, CCG010650.1,CCG000708.1,CCG025990.1,CCG024624.1, CCG009275.1,CCG004494.1,CCG002947.1,CCG010908.1, CCG005716.1,CCG027197.1,CCG022673.1,CCG027697.1, CCG026159.1,CCG020442.1,CCG010646.1,CCG017598.1, CCG024787.1,CCG027695.1,CCG012584.1,CCG008302.1

GO:0006334	nucleosome assembly	69 of 4104 in the list	123 of 8404 in the genome	1	CCG003361.1,CCG019284.1,CCG008560.1,CCG010136.1, CCG021491.1,CCG010647.1,CCG003310.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG014537.1, CCG010137.1,CCG009461.1,CCG005194.1,CCG024623.1, CCG025880.1,CCG014836.1,CCG010904.1,CCG024177.1, CCG004481.1,CCG012514.1,CCG027196.1,CCG014772.1, CCG026474.1,CCG025893.1,CCG009637.1,CCG010905.1, CCG026579.1,CCG010909.1,CCG010648.1,CCG017580.1, CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1, CCG010138.1,CCG010649.1,CCG008892.2,CCG025877.1, CCG015560.1,CCG027199.1,CCG027198.1,CCG018287.1, CCG008559.1,CCG027696.1,CCG010907.1,CCG012229.1, CCG010650.1,CCG000708.1,CCG025990.1,CCG024624.1, CCG009275.1,CCG004494.1,CCG002947.1,CCG010908.1, CCG005716.1,CCG027197.1,CCG022673.1,CCG027697.1, CCG026159.1,CCG020442.1,CCG010646.1,CCG017598.1, CCG024787.1,CCG027695.1,CCG012584.1,CCG008302.1
GO:0031497	chromatin assembly	69 of 4104 in the list	123 of 8404 in the genome	1	CCG003361.1,CCG019284.1,CCG008560.1,CCG010136.1, CCG021491.1,CCG010647.1,CCG003310.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG014537.1, CCG010137.1,CCG009461.1,CCG005194.1,CCG024623.1, CCG025880.1,CCG014836.1,CCG010904.1,CCG024177.1, CCG004481.1,CCG012514.1,CCG027196.1,CCG014772.1, CCG026474.1,CCG025893.1,CCG009637.1,CCG010905.1, CCG026579.1,CCG010909.1,CCG010648.1,CCG017580.1, CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1, CCG010138.1,CCG010649.1,CCG008892.2,CCG025877.1, CCG015560.1,CCG027199.1,CCG027198.1,CCG018287.1, CCG008559.1,CCG027696.1,CCG010907.1,CCG012229.1, CCG010650.1,CCG000708.1,CCG025990.1,CCG024624.1, CCG009275.1,CCG004494.1,CCG002947.1,CCG010908.1, CCG005716.1,CCG027197.1,CCG022673.1,CCG027697.1, CCG026159.1,CCG020442.1,CCG010646.1,CCG017598.1, CCG024787.1,CCG027695.1,CCG012584.1,CCG008302.1

GO:0034728	nucleosome organization	69 of 4104 in the list	123 of 8404 in the genome	1	CCG003361.1,CCG019284.1,CCG008560.1,CCG010136.1, CCG021491.1,CCG010647.1,CCG003310.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG014537.1, CCG010137.1,CCG009461.1,CCG005194.1,CCG024623.1, CCG025880.1,CCG014836.1,CCG010904.1,CCG024177.1, CCG004481.1,CCG012514.1,CCG027196.1,CCG014772.1, CCG026474.1,CCG025893.1,CCG009637.1,CCG010905.1, CCG026579.1,CCG010909.1,CCG010648.1,CCG017580.1, CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1, CCG010138.1,CCG010649.1,CCG008892.2,CCG025877.1, CCG015560.1,CCG027199.1,CCG027198.1,CCG018287.1, CCG008559.1,CCG027696.1,CCG010907.1,CCG012229.1, CCG010650.1,CCG000708.1,CCG025990.1,CCG024624.1, CCG009275.1,CCG004494.1,CCG002947.1,CCG010908.1, CCG005716.1,CCG027197.1,CCG022673.1,CCG027697.1, CCG026159.1,CCG020442.1,CCG010646.1,CCG017598.1, CCG024787.1,CCG027695.1,CCG012584.1,CCG008302.1
GO:0065004	protein-DNA complex assembly	69 of 4104 in the list	123 of 8404 in the genome	1	CCG003361.1,CCG019284.1,CCG008560.1,CCG010136.1, CCG021491.1,CCG010647.1,CCG003310.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG014537.1, CCG010137.1,CCG009461.1,CCG005194.1,CCG024623.1, CCG025880.1,CCG014836.1,CCG010904.1,CCG024177.1, CCG004481.1,CCG012514.1,CCG027196.1,CCG014772.1, CCG026474.1,CCG025893.1,CCG009637.1,CCG010905.1, CCG026579.1,CCG010909.1,CCG010648.1,CCG017580.1, CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1, CCG010138.1,CCG010649.1,CCG008892.2,CCG025877.1, CCG015560.1,CCG027199.1,CCG027198.1,CCG018287.1, CCG008559.1,CCG027696.1,CCG010907.1,CCG012229.1, CCG010650.1,CCG000708.1,CCG025990.1,CCG024624.1, CCG009275.1,CCG004494.1,CCG002947.1,CCG010908.1, CCG005716.1,CCG027197.1,CCG022673.1,CCG027697.1, CCG026159.1,CCG020442.1,CCG010646.1,CCG017598.1, CCG024787.1,CCG027695.1,CCG012584.1,CCG008302.1

GO:0071824	protein-DNA complex subunit organization	69 of 4104 in the list	123 of 8404 in the genome	1	CCG003361.1,CCG019284.1,CCG008560.1,CCG010136.1, CCG021491.1,CCG010647.1,CCG003310.1,CCG013617.1, CCG000433.1,CCG026473.1,CCG012476.1,CCG014537.1, CCG010137.1,CCG009461.1,CCG005194.1,CCG024623.1, CCG025880.1,CCG014836.1,CCG010904.1,CCG024177.1, CCG004481.1,CCG012514.1,CCG027196.1,CCG014772.1, CCG026474.1,CCG025893.1,CCG009637.1,CCG010905.1, CCG026579.1,CCG010909.1,CCG010648.1,CCG017580.1, CCG009980.1,CCG010906.1,CCG015968.1,CCG018893.1, CCG010138.1,CCG010649.1,CCG008892.2,CCG025877.1, CCG015560.1,CCG027199.1,CCG027198.1,CCG018287.1, CCG008559.1,CCG027696.1,CCG010907.1,CCG012229.1, CCG010650.1,CCG000708.1,CCG025990.1,CCG024624.1, CCG009275.1,CCG004494.1,CCG002947.1,CCG010908.1, CCG005716.1,CCG027197.1,CCG022673.1,CCG027697.1, CCG026159.1,CCG020442.1,CCG010646.1,CCG017598.1, CCG024787.1,CCG027695.1,CCG012584.1,CCG008302.1
GO:1901361	organic cyclic compound catabolic process	82 of 4104 in the list	148 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG007060.1, CCG005524.1,CCG013000.1,CCG013766.1,CCG024327.1, CCG015386.1,CCG019020.1,CCG009243.1,CCG020685.1, CCG002925.1,CCG023005.1,CCG024375.1,CCG009607.1, CCG011006.1,CCG027119.1,CCG004448.2,CCG007827.1, CCG014434.1,CCG006421.1,CCG023963.3,CCG021990.1, CCG025027.1,CCG016370.1,CCG019103.1,CCG019629.2, CCG006311.1,CCG002917.1,CCG005147.1,CCG004988.1, CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1, CCG016966.1,CCG018820.3,CCG019674.1,CCG011722.1, CCG025179.1,CCG006777.1,CCG007203.1,CCG025973.1, CCG013637.1,CCG009424.1,CCG001440.1,CCG010418.1, CCG018917.1,CCG009080.1,CCG004869.1,CCG007690.1, CCG025396.1,CCG026953.1,CCG011721.1,CCG006924.1, CCG021220.1,CCG008748.1,CCG006059.1,CCG013641.1, CCG016027.1,CCG015289.1,CCG003495.1,CCG021411.1, CCG001859.1,CCG026336.1,CCG005886.1,CCG009582.1, CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1, CCG002852.1,CCG010864.1,CCG011789.1,CCG001445.1, CCG013765.1,CCG002231.1,CCG007362.1,CCG021152.1,

GO:0006457	protein folding	70 of 4104 in the list	125 of 8404 in the genome	1	CCG021998.1,CCG003491.1,CCG019684.1,CCG023237.1, CCG013640.1,CCG025006.1,CCG021889.1,CCG025005.1, CCG009881.1,CCG000247.1,CCG003605.1,CCG009574.1, CCG012726.1,CCG014012.1,CCG007750.2,CCG011681.1, CCG000413.3,CCG007076.1,CCG015580.1,CCG025714.1, CCG017244.1,CCG012492.1,CCG006264.1,CCG016271.1, CCG020417.1,CCG011874.1,CCG005429.3,CCG026501.1, CCG002446.2,CCG002465.1,CCG005738.1,CCG017448.1, CCG011095.1,CCG005024.1,CCG025028.1,CCG005069.1, CCG028346.1,CCG015268.1,CCG020060.1,CCG023148.1, CCG026694.1,CCG015511.1,CCG015074.1,CCG006921.1, CCG017706.1,CCG002982.1,CCG000546.1,CCG002534.1, CCG022020.1,CCG012166.1,CCG009266.1,CCG011939.1, CCG025031.1,CCG022993.1,CCG023764.1,CCG024791.1, CCG008539.2,CCG024897.1,CCG005780.1,CCG022509.1, CCG027565.1,CCG027653.1,CCG003657.2,CCG007108.1, CCG000444.1,CCG026112.1,CCG003480.1,CCG026959.1
GO:0009725	response to hormone	17 of 4104 in the list	26 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG016745.1,CCG008741.1, CCG017795.1,CCG000659.1,CCG014509.1,CCG027127.1, CCG019520.1,CCG019185.1,CCG022281.1,CCG020586.1, CCG012009.1,CCG010702.1,CCG020224.1,CCG004878.1,
GO:0009755	hormone-mediated signaling pathway	17 of 4104 in the list	26 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG016745.1,CCG008741.1, CCG017795.1,CCG000659.1,CCG014509.1,CCG027127.1, CCG019520.1,CCG019185.1,CCG022281.1,CCG020586.1, CCG012009.1,CCG010702.1,CCG020224.1,CCG004878.1,
GO:0014070	response to organic cyclic compound	17 of 4104 in the list	26 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG016745.1,CCG008741.1, CCG017795.1,CCG000659.1,CCG014509.1,CCG027127.1, CCG019520.1,CCG019185.1,CCG022281.1,CCG020586.1, CCG012009.1,CCG010702.1,CCG020224.1,CCG004878.1,
GO:0032870	cellular response to hormone stimulus	17 of 4104 in the list	26 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG016745.1,CCG008741.1, CCG017795.1,CCG000659.1,CCG014509.1,CCG027127.1, CCG019520.1,CCG019185.1,CCG022281.1,CCG020586.1, CCG012009.1,CCG010702.1,CCG020224.1,CCG004878.1,

GO:0033993	response to lipid	17 of 4104 in the list	26 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG016745.1,CCG008741.1, CCG017795.1,CCG000659.1,CCG014509.1,CCG027127.1, CCG019520.1,CCG019185.1,CCG022281.1,CCG020586.1, CCG012009.1,CCG010702.1,CCG020224.1,CCG004878.1,
GO:0043401	steroid hormone mediated signaling pathway	17 of 4104 in the list	26 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG016745.1,CCG008741.1, CCG017795.1,CCG000659.1,CCG014509.1,CCG027127.1, CCG019520.1,CCG019185.1,CCG022281.1,CCG020586.1, CCG012009.1,CCG010702.1,CCG020224.1,CCG004878.1,
GO:0048545	response to steroid hormone	17 of 4104 in the list	26 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG016745.1,CCG008741.1, CCG017795.1,CCG000659.1,CCG014509.1,CCG027127.1, CCG019520.1,CCG019185.1,CCG022281.1,CCG020586.1, CCG012009.1,CCG010702.1,CCG020224.1,CCG004878.1,
GO:0071383	cellular response to steroid hormone stimulus	17 of 4104 in the list	26 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG016745.1,CCG008741.1, CCG017795.1,CCG000659.1,CCG014509.1,CCG027127.1, CCG019520.1,CCG019185.1,CCG022281.1,CCG020586.1, CCG012009.1,CCG010702.1,CCG020224.1,CCG004878.1,
GO:0071396	cellular response to lipid	17 of 4104 in the list	26 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG016745.1,CCG008741.1, CCG017795.1,CCG000659.1,CCG014509.1,CCG027127.1, CCG019520.1,CCG019185.1,CCG022281.1,CCG020586.1, CCG012009.1,CCG010702.1,CCG020224.1,CCG004878.1,
GO:0071407	cellular response to organic cyclic compound	17 of 4104 in the list	26 of 8404 in the genome	1	CCG024271.1,CCG008742.1,CCG016745.1,CCG008741.1, CCG017795.1,CCG000659.1,CCG014509.1,CCG027127.1, CCG019520.1,CCG019185.1,CCG022281.1,CCG020586.1, CCG012009.1,CCG010702.1,CCG020224.1,CCG004878.1,
GO:0019318	hexose metabolic process	35 of 4104 in the list	59 of 8404 in the genome	1	CCG020616.1,CCG005588.1,CCG003215.3,CCG010373.1, CCG007981.1,CCG008437.1,CCG007046.2,CCG008287.1, CCG000431.1,CCG004388.1,CCG009084.2,CCG019953.1, CCG012740.1,CCG003220.2,CCG006203.1,CCG001355.1, CCG022453.1,CCG003748.1,CCG001038.1,CCG010996.1, CCG022035.1,CCG007045.1,CCG025307.1,CCG028524.1, CCG022214.1,CCG007023.1,CCG012840.1,CCG007771.1, CCG017278.1,CCG013339.1,CCG018423.1,CCG017200.1,

GO:0009119	ribonucleoside metabolic process	93 of 4104 in the list	170 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG004309.1,CCG006529.1, CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1, CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1, CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1, CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1, CCG016370.1,CCG000148.1,CCG019103.1,CCG019629.2, CCG002917.1,CCG006486.1,CCG005924.2,CCG020909.1, CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1, CCG018820.3,CCG021110.1,CCG025179.1,CCG021934.1, CCG006777.1,CCG004308.1,CCG025973.1,CCG017995.1, CCG013637.1,CCG023640.1,CCG026314.1,CCG010418.1, CCG025348.1,CCG009080.1,CCG004869.1,CCG019619.1, CCG025396.1,CCG013999.1,CCG026953.1,CCG021336.1, CCG006924.1,CCG007417.1,CCG021220.1,CCG001066.1, CCG019866.1,CCG004440.1,CCG019678.1,CCG007724.1, CCG008748.1,CCG010460.1,CCG013641.1,CCG015410.1, CCG016027.1,CCG015289.1,CCG025107.1,CCG003495.1, CCG021411.1,CCG009142.1,CCG001859.1,CCG026812.1, CCG026336.1,CCG005886.1,CCG025131.2,CCG016542.1, CCG026154.1,CCG015654.1,CCG018659.2,CCG002852.1, CCG010864.1,CCG013610.1,CCG016614.1,CCG006791.1,

GO:0010468	regulation of gene expression	262 of 4104 in the list	503 of 8404 in the genome	1	CCG022266.1,CCG008767.3,CCG008741.1,CCG003390.1, CCG027427.1,CCG007493.1,CCG021465.1,CCG003175.1, CCG023752.1,CCG028326.3,CCG013794.1,CCG006134.1, CCG009970.1,CCG016745.1,CCG021436.1,CCG016445.1, CCG012536.1,CCG000659.1,CCG027127.1,CCG018719.1, CCG015425.1,CCG027796.1,CCG022824.1,CCG018533.1, CCG024710.1,CCG022281.1,CCG011465.1,CCG006714.1, CCG020129.1,CCG027186.1,CCG000588.1,CCG022045.1, CCG013274.1,CCG028568.1,CCG007647.1,CCG021633.1, CCG012083.1,CCG000562.1,CCG005480.2,CCG017760.1, CCG005486.1,CCG016859.1,CCG020898.1,CCG017591.1, CCG002198.1,CCG021284.1,CCG016924.1,CCG000133.1, CCG013224.2,CCG002273.1,CCG001698.1,CCG023777.1, CCG014461.1,CCG026228.2,CCG005487.1,CCG021054.1, CCG016307.1,CCG009805.2,CCG016749.1,CCG028465.1, CCG019250.1,CCG005396.1,CCG025747.1,CCG009823.1, CCG021456.1,CCG014928.1,CCG005168.1,CCG018184.1, CCG018315.1,CCG027580.1,CCG024271.1,CCG009458.1, CCG022496.1,CCG015062.1,CCG018164.1,CCG001301.1, CCG023199.2,CCG001431.2,CCG001341.1,CCG022398.1, CCG021521.1,CCG009562.2,CCG010139.1,CCG021940.1, CCG024639.1,CCG015846.1,CCG008833.1,CCG018168.1, CCG014509.1,CCG004783.1,CCG025691.1,CCG018042.1, CCG014463.1,CCG026788.1,CCG020543.1,CCG025549.1, CCG011015.1,CCG027950.1,CCG025572.1,CCG002045.1, CCG004378.1,CCG014243.1,CCG009023.1,CCG018847.1, CCG027258.1,CCG008371.1,CCG022947.1,CCG008742.1, CCG011228.1,CCG004762.2,CCG028421.1,CCG003427.1, CCG005635.1,CCG020695.1,CCG000593.1,CCG004151.1, CCG014982.1,CCG000436.1,CCG002199.1,CCG019279.1,
GO:0017148	negative regulation of translation	10 of 4104 in the list	14 of 8404 in the genome	1	CCG003216.1,CCG003765.1,CCG016445.1,CCG005486.1, CCG006714.1,CCG015062.1,CCG005487.1,CCG005485.1, CCG023431.1,CCG016835.2
GO:0009070	serine family amino acid biosynthetic process	7 of 4104 in the list	9 of 8404 in the genome	1	CCG015568.1,CCG028131.1,CCG019954.3,CCG022025.2, CCG015567.1,CCG025636.2,CCG017201.1

GO:1901617	organic hydroxy compound biosynthetic process	7 of 4104 in the list	9 of 8404 in the genome	1	CCG024095.1,CCG014174.1,CCG026536.1,CCG020559.1, CCG023757.1,CCG016653.1,CCG026331.1
GO:0007156	homophilic cell adhesion	20 of 4104 in the list	32 of 8404 in the genome	1	CCG026424.3,CCG022123.1,CCG017729.1,CCG007182.1, CCG016263.1,CCG028158.1,CCG001422.1,CCG000237.1, CCG021360.1,CCG007356.1,CCG000127.1,CCG012634.1, CCG020013.1,CCG007575.1,CCG004542.1,CCG016446.1, CCG027757.1,CCG007117.1,CCG013255.1,CCG013707.1
GO:0016337	cell-cell adhesion	20 of 4104 in the list	32 of 8404 in the genome	1	CCG026424.3,CCG022123.1,CCG017729.1,CCG007182.1, CCG016263.1,CCG028158.1,CCG001422.1,CCG000237.1, CCG021360.1,CCG007356.1,CCG000127.1,CCG012634.1, CCG020013.1,CCG007575.1,CCG004542.1,CCG016446.1, CCG027757.1,CCG007117.1,CCG013255.1,CCG013707.1
GO:0019439	aromatic compound catabolic process	80 of 4104 in the list	146 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG007060.1, CCG005524.1,CCG013000.1,CCG013766.1,CCG024327.1, CCG015386.1,CCG019020.1,CCG009243.1,CCG020685.1, CCG002925.1,CCG023005.1,CCG024375.1,CCG009607.1, CCG011006.1,CCG027119.1,CCG004448.2,CCG007827.1, CCG014434.1,CCG006421.1,CCG023963.3,CCG021990.1, CCG025027.1,CCG016370.1,CCG019103.1,CCG019629.2, CCG006311.1,CCG002917.1,CCG005147.1,CCG004988.1, CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1, CCG016966.1,CCG018820.3,CCG019674.1,CCG011722.1, CCG025179.1,CCG006777.1,CCG025973.1,CCG013637.1, CCG009424.1,CCG001440.1,CCG010418.1,CCG018917.1, CCG009080.1,CCG004869.1,CCG007690.1,CCG025396.1, CCG026953.1,CCG011721.1,CCG006924.1,CCG021220.1, CCG008748.1,CCG006059.1,CCG013641.1,CCG016027.1, CCG015289.1,CCG003495.1,CCG021411.1,CCG001859.1, CCG026336.1,CCG005886.1,CCG009582.1,CCG025131.2, CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1, CCG010864.1,CCG011789.1,CCG001445.1,CCG013765.1,
GO:1901606	alpha-amino acid catabolic process	15 of 4104 in the list	23 of 8404 in the genome	1	CCG011789.1,CCG007203.1,CCG025108.1,CCG001082.1, CCG011721.1,CCG002231.1,CCG008510.1,CCG011722.1, CCG010111.1,CCG019834.1,CCG003063.1,CCG020154.1, CCG006059.1,CCG008388.1,CCG017543.1

GO:0008277	regulation of G-protein coupled receptor protein signaling pathway	11 of 4104 in the list	16 of 8404 in the genome	1	CCG012573.1,CCG026798.1,CCG024952.1,CCG023484.1, CCG011501.1,CCG019427.1,CCG009446.1,CCG006412.1, CCG017498.1,CCG004343.1,CCG015459.1
GO:0023021	termination of signal transduction	11 of 4104 in the list	16 of 8404 in the genome	1	CCG012573.1,CCG026798.1,CCG024952.1,CCG023484.1, CCG011501.1,CCG019427.1,CCG009446.1,CCG006412.1, CCG017498.1,CCG004343.1,CCG015459.1
GO:0032269	negative regulation of cellular protein metabolic process	11 of 4104 in the list	16 of 8404 in the genome	1	CCG003216.1,CCG003765.1,CCG016445.1,CCG005486.1, CCG006714.1,CCG015062.1,CCG005487.1,CCG005485.1, CCG023431.1,CCG016835.2,CCG021794.1
GO:0038032	termination of G-protein coupled receptor signaling pathway	11 of 4104 in the list	16 of 8404 in the genome	1	CCG012573.1,CCG026798.1,CCG024952.1,CCG023484.1, CCG011501.1,CCG019427.1,CCG009446.1,CCG006412.1, CCG017498.1,CCG004343.1,CCG015459.1
GO:0045744	negative regulation of G-protein coupled receptor protein signaling pathway	11 of 4104 in the list	16 of 8404 in the genome	1	CCG012573.1,CCG026798.1,CCG024952.1,CCG023484.1, CCG011501.1,CCG019427.1,CCG009446.1,CCG006412.1, CCG017498.1,CCG004343.1,CCG015459.1
GO:0051248	negative regulation of protein metabolic process	11 of 4104 in the list	16 of 8404 in the genome	1	CCG003216.1,CCG003765.1,CCG016445.1,CCG005486.1, CCG006714.1,CCG015062.1,CCG005487.1,CCG005485.1, CCG023431.1,CCG016835.2,CCG021794.1
GO:0005996	monosaccharide metabolic process	35 of 4104 in the list	60 of 8404 in the genome	1	CCG020616.1,CCG005588.1,CCG003215.3,CCG010373.1, CCG007981.1,CCG008437.1,CCG007046.2,CCG008287.1, CCG000431.1,CCG004388.1,CCG009084.2,CCG019953.1, CCG012740.1,CCG003220.2,CCG006203.1,CCG001355.1, CCG022453.1,CCG003748.1,CCG001038.1,CCG010996.1, CCG022035.1,CCG007045.1,CCG025307.1,CCG028524.1, CCG022214.1,CCG007023.1,CCG012840.1,CCG007771.1, CCG017278.1,CCG013339.1,CCG018423.1,CCG017200.1,
GO:0032313	regulation of Rab GTPase activity	22 of 4104 in the list	36 of 8404 in the genome	1	CCG025433.1,CCG016027.1,CCG011341.1,CCG012519.1, CCG017369.1,CCG024000.1,CCG016965.1,CCG022676.1, CCG013303.1,CCG027878.1,CCG024809.1,CCG009024.1, CCG007631.1,CCG015333.1,CCG002971.1,CCG016181.1, CCG013203.1,CCG018776.1,CCG002109.1,CCG021151.1,

GO:0032483	regulation of Rab protein signal transduction	22 of 4104 in the list	36 of 8404 in the genome	1	CCG025433.1,CCG016027.1,CCG011341.1,CCG012519.1, CCG017369.1,CCG024000.1,CCG016965.1,CCG022676.1, CCG013303.1,CCG027878.1,CCG024809.1,CCG009024.1, CCG007631.1,CCG015333.1,CCG002971.1,CCG016181.1, CCG013203.1,CCG018776.1,CCG002109.1,CCG021151.1,
GO:0046700	heterocycle catabolic process	79 of 4104 in the list	145 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG007060.1, CCG005524.1,CCG013000.1,CCG013766.1,CCG024327.1, CCG015386.1,CCG019020.1,CCG009243.1,CCG020685.1, CCG002925.1,CCG023005.1,CCG024375.1,CCG009607.1, CCG011006.1,CCG027119.1,CCG004448.2,CCG007827.1, CCG014434.1,CCG006421.1,CCG023963.3,CCG021990.1, CCG025027.1,CCG016370.1,CCG019103.1,CCG019629.2, CCG006311.1,CCG002917.1,CCG005147.1,CCG004988.1, CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1, CCG016966.1,CCG018820.3,CCG019674.1,CCG025179.1, CCG006777.1,CCG007203.1,CCG025973.1,CCG013637.1, CCG009424.1,CCG001440.1,CCG010418.1,CCG018917.1, CCG009080.1,CCG004869.1,CCG007690.1,CCG025396.1, CCG026953.1,CCG006924.1,CCG021220.1,CCG008748.1, CCG006059.1,CCG013641.1,CCG016027.1,CCG015289.1, CCG003495.1,CCG021411.1,CCG001859.1,CCG026336.1, CCG005886.1,CCG009582.1,CCG025131.2,CCG016542.1, CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1, CCG001445.1,CCG013765.1,CCG002231.1,CCG007362.1,
GO:0006020	inositol metabolic process	5 of 4104 in the list	6 of 8404 in the genome	1	CCG014174.1,CCG006358.1,CCG023757.1,CCG016653.1, CCG005177.1
GO:0006072	glycerol-3-phosphate metabolic process	5 of 4104 in the list	6 of 8404 in the genome	1	CCG009685.1,CCG000970.1,CCG025146.1,CCG012558.1, CCG014228.2
GO:0006606	protein import into nucleus	5 of 4104 in the list	6 of 8404 in the genome	1	CCG022771.1,CCG017077.1,CCG017078.1,CCG001809.1, CCG011696.1
GO:0034504	protein localization to nucleus	5 of 4104 in the list	6 of 8404 in the genome	1	CCG022771.1,CCG017077.1,CCG017078.1,CCG001809.1, CCG011696.1
GO:0044744	protein targeting to nucleus	5 of 4104 in the list	6 of 8404 in the genome	1	CCG022771.1,CCG017077.1,CCG017078.1,CCG001809.1, CCG011696.1
GO:0051170	nuclear import	5 of 4104 in the list	6 of 8404 in the genome	1	CCG022771.1,CCG017077.1,CCG017078.1,CCG001809.1, CCG011696.1

GO:1902593	single-organism nuclear import	5 of 4104 in the list	6 of 8404 in the genome	1	CCG022771.1,CCG017077.1,CCG017078.1,CCG001809.1, CCG011696.1
GO:1901135	carbohydrate derivative metabolic process	236 of 4104 in the list	455 of 8404 in the genome	1	CCG010077.1,CCG006420.1,CCG017420.1,CCG002549.1, CCG018536.1,CCG013000.1,CCG006912.1,CCG017331.1, CCG000663.1,CCG005809.1,CCG025989.2,CCG024327.1, CCG015386.1,CCG019020.1,CCG020504.1,CCG024517.1, CCG007330.1,CCG004091.1,CCG004020.1,CCG009685.1, CCG000970.1,CCG009607.1,CCG009494.1,CCG011531.1, CCG011006.1,CCG011695.1,CCG012558.1,CCG025472.1, CCG007816.1,CCG005029.1,CCG018432.1,CCG015610.1, CCG020799.1,CCG009434.1,CCG016370.1,CCG006911.1, CCG002917.1,CCG022378.1,CCG006486.1,CCG025940.1, CCG023890.1,CCG019371.1,CCG028332.1,CCG014180.1, CCG019210.1,CCG021110.1,CCG003601.1,CCG010019.1, CCG010960.2,CCG024612.1,CCG017559.1,CCG011972.1, CCG016153.1,CCG023640.1,CCG010728.1,CCG002418.1, CCG013131.1,CCG025948.4,CCG025348.1,CCG019619.1, CCG004869.1,CCG009080.1,CCG012725.1,CCG025396.1, CCG023924.1,CCG026953.1,CCG006924.1,CCG021220.1, CCG009165.1,CCG025962.1,CCG014181.1,CCG019678.1, CCG003677.1,CCG021610.1,CCG010460.1,CCG013641.1, CCG025233.1,CCG015410.1,CCG011257.1,CCG015289.1, CCG009142.1,CCG021411.1,CCG003495.1,CCG026898.1, CCG001859.1,CCG015029.1,CCG017197.1,CCG013985.1, CCG026044.1,CCG025131.2,CCG000552.1,CCG024829.1, CCG015804.1,CCG014116.1,CCG002852.1,CCG013610.1, CCG010986.1,CCG018643.1,CCG023420.1,CCG014228.2, CCG006221.1,CCG010727.1,CCG006791.1,CCG028454.1, CCG021152.1,CCG020663.1,CCG023526.2,CCG011996.1, CCG001285.1,CCG017381.1,CCG017693.1,CCG007060.1, CCG023617.1,CCG017175.1,CCG004309.1,CCG006529.1, CCG017730.1,CCG007766.1,CCG021005.1,CCG001602.1,

GO:0019637	organophosphate metabolic process	180 of 4104 in the list	344 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG019820.1, CCG013000.1,CCG000663.1,CCG013766.1,CCG025989.2, CCG024327.1,CCG024092.1,CCG015386.1,CCG019020.1, CCG012875.1,CCG025493.1,CCG026174.1,CCG000016.1, CCG007330.1,CCG009685.1,CCG000970.1,CCG002925.1, CCG023005.1,CCG024375.1,CCG003748.1,CCG009607.1, CCG011531.1,CCG011006.1,CCG027119.1,CCG012558.1, CCG025307.1,CCG009434.1,CCG007993.1,CCG016370.1, CCG012308.1,CCG006311.1,CCG016653.1,CCG002917.1, CCG006486.1,CCG028332.1,CCG010944.1,CCG006965.1, CCG021110.1,CCG010960.2,CCG016148.1,CCG024612.1, CCG015746.1,CCG023393.1,CCG023640.1,CCG013131.1, CCG025348.1,CCG004191.1,CCG019619.1,CCG004869.1, CCG009080.1,CCG022352.1,CCG025396.1,CCG028131.1, CCG026953.1,CCG006924.1,CCG021220.1,CCG024432.2, CCG019678.1,CCG021610.1,CCG013641.1,CCG025233.1, CCG015410.1,CCG015289.1,CCG009142.1,CCG021411.1, CCG003495.1,CCG026898.1,CCG001859.1,CCG025131.2, CCG000552.1,CCG023452.1,CCG014116.1,CCG002852.1, CCG024903.1,CCG013610.1,CCG023757.1,CCG009518.1, CCG014228.2,CCG006791.1,CCG007362.1,CCG021152.1, CCG023526.2,CCG026865.1,CCG019697.2,CCG001285.1, CCG004532.1,CCG000789.1,CCG017693.1,CCG007060.1, CCG026047.1,CCG006529.1,CCG004309.1,CCG008287.1, CCG004806.1,CCG007533.1,CCG008422.1,CCG009243.1, CCG010112.1,CCG015130.1,CCG007827.1,CCG024155.1, CCG023963.3,CCG006421.1,CCG013643.1,CCG014434.1, CCG021990.1,CCG022209.1,CCG002038.1,CCG024778.1, CCG025027.1,CCG014839.1,CCG000148.1,CCG019103.1, CCG013365.1,CCG019629.2,CCG025889.1,CCG011658.1,

GO:0042278	purine nucleoside metabolic process	88 of 4104 in the list	163 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG004309.1,CCG006529.1, CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1, CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1, CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1, CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1, CCG016370.1,CCG000148.1,CCG019103.1,CCG019629.2, CCG002917.1,CCG006486.1,CCG005924.2,CCG020909.1, CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1, CCG018820.3,CCG021110.1,CCG025179.1,CCG021934.1, CCG006777.1,CCG004308.1,CCG025973.1,CCG017995.1, CCG013637.1,CCG023640.1,CCG026314.1,CCG010418.1, CCG025348.1,CCG009080.1,CCG004869.1,CCG019619.1, CCG025396.1,CCG013999.1,CCG026953.1,CCG021336.1, CCG006924.1,CCG007417.1,CCG021220.1,CCG001066.1, CCG019866.1,CCG019678.1,CCG007724.1,CCG008748.1, CCG013641.1,CCG015410.1,CCG016027.1,CCG015289.1, CCG025107.1,CCG003495.1,CCG021411.1,CCG009142.1, CCG001859.1,CCG026812.1,CCG026336.1,CCG005886.1, CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1, CCG018659.2,CCG002852.1,CCG010864.1,CCG006791.1,

GO:0046128	purine ribonucleoside metabolic process	88 of 4104 in the list	163 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG004309.1,CCG006529.1, CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1, CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1, CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1, CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1, CCG016370.1,CCG000148.1,CCG019103.1,CCG019629.2, CCG002917.1,CCG006486.1,CCG005924.2,CCG020909.1, CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1, CCG018820.3,CCG021110.1,CCG025179.1,CCG021934.1, CCG006777.1,CCG004308.1,CCG025973.1,CCG017995.1, CCG013637.1,CCG023640.1,CCG026314.1,CCG010418.1, CCG025348.1,CCG009080.1,CCG004869.1,CCG019619.1, CCG025396.1,CCG013999.1,CCG026953.1,CCG021336.1, CCG006924.1,CCG007417.1,CCG021220.1,CCG001066.1, CCG019866.1,CCG019678.1,CCG007724.1,CCG008748.1, CCG013641.1,CCG015410.1,CCG016027.1,CCG015289.1, CCG025107.1,CCG003495.1,CCG021411.1,CCG009142.1, CCG001859.1,CCG026812.1,CCG026336.1,CCG005886.1, CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1, CCG018659.2,CCG002852.1,CCG010864.1,CCG006791.1,
GO:0015711	organic anion transport	18 of 4104 in the list	29 of 8404 in the genome	1	CCG024382.1,CCG004637.1,CCG006348.1,CCG016959.1, CCG026667.1,CCG024222.1,CCG027758.1,CCG026707.1, CCG024383.1,CCG005768.1,CCG005769.1,CCG018073.1, CCG020840.1,CCG019407.1,CCG008734.1,CCG010965.1,
GO:0015849	organic acid transport	18 of 4104 in the list	29 of 8404 in the genome	1	CCG024382.1,CCG004637.1,CCG006348.1,CCG016959.1, CCG026667.1,CCG024222.1,CCG027758.1,CCG026707.1, CCG024383.1,CCG005768.1,CCG005769.1,CCG018073.1, CCG020840.1,CCG019407.1,CCG008734.1,CCG010965.1,
GO:0046942	carboxylic acid transport	18 of 4104 in the list	29 of 8404 in the genome	1	CCG024382.1,CCG004637.1,CCG006348.1,CCG016959.1, CCG026667.1,CCG024222.1,CCG027758.1,CCG026707.1, CCG024383.1,CCG005768.1,CCG005769.1,CCG018073.1, CCG020840.1,CCG019407.1,CCG008734.1,CCG010965.1,

GO:0050789	regulation of biological process	687 of 4104 in the list	1363 of 8404 in the genome	1	CCG005254.1,CCG017420.1,CCG027068.1,CCG014340.1, CCG005375.1,CCG022266.1,CCG003824.3,CCG008603.1, CCG008767.3,CCG008741.1,CCG003390.1,CCG000646.1, CCG004595.1,CCG007493.1,CCG026174.1,CCG020785.1, CCG010849.1,CCG002338.1,CCG021465.1,CCG020974.1, CCG002841.1,CCG018321.1,CCG013794.1,CCG010275.1, CCG026360.1,CCG021064.1,CCG006134.1,CCG017266.1, CCG016689.2,CCG020709.1,CCG014466.1,CCG015101.1, CCG012536.1,CCG027127.1,CCG015425.1,CCG027796.1, CCG022824.1,CCG018533.1,CCG024710.1,CCG000526.1, CCG022281.1,CCG027669.1,CCG015967.1,CCG021661.1, CCG022420.1,CCG013308.1,CCG023579.1,CCG006714.1, CCG025026.1,CCG010157.1,CCG011911.1,CCG008685.1, CCG004132.1,CCG000588.1,CCG004548.1,CCG022045.1, CCG004279.1,CCG013274.1,CCG024663.1,CCG028568.1, CCG022676.1,CCG007647.1,CCG004331.1,CCG018494.1, CCG024809.1,CCG012083.1,CCG026953.1,CCG017760.1, CCG018380.1,CCG016859.1,CCG005486.1,CCG017498.1, CCG020898.1,CCG017591.1,CCG023464.1,CCG002198.1, CCG021284.1,CCG001579.1,CCG013641.1,CCG016924.1, CCG000732.1,CCG003317.1,CCG000133.1,CCG003495.1, CCG013224.2,CCG002273.1,CCG007951.1,CCG023777.1, CCG026228.2,CCG005487.1,CCG025131.2,CCG009805.2, CCG028465.1,CCG008444.1,CCG017701.1,CCG009823.1, CCG014712.1,CCG000876.1,CCG021456.1,CCG025057.1, CCG024664.1,CCG015638.1,CCG000789.1,CCG024662.1, CCG026047.1,CCG022496.1,CCG024000.1,CCG008939.1, CCG018164.1,CCG019427.1,CCG001431.2,CCG016760.1, CCG014345.2,CCG021521.1,CCG010139.1,CCG006787.1, CCG028500.2,CCG020654.1,CCG015426.1,CCG008833.1,

GO:0050794	regulation of cellular process	680 of 4104 in the list	1349 of 8404 in the genome	1	CCG005254.1,CCG017420.1,CCG027068.1,CCG014340.1, CCG005375.1,CCG022266.1,CCG003824.3,CCG008603.1, CCG008767.3,CCG008741.1,CCG003390.1,CCG000646.1, CCG004595.1,CCG007493.1,CCG026174.1,CCG020785.1, CCG010849.1,CCG002338.1,CCG021465.1,CCG020974.1, CCG002841.1,CCG018321.1,CCG013794.1,CCG010275.1, CCG026360.1,CCG021064.1,CCG006134.1,CCG017266.1, CCG016689.2,CCG020709.1,CCG014466.1,CCG015101.1, CCG012536.1,CCG027127.1,CCG015425.1,CCG027796.1, CCG022824.1,CCG018533.1,CCG024710.1,CCG000526.1, CCG022281.1,CCG027669.1,CCG015967.1,CCG021661.1, CCG022420.1,CCG013308.1,CCG023579.1,CCG006714.1, CCG025026.1,CCG010157.1,CCG011911.1,CCG008685.1, CCG004132.1,CCG000588.1,CCG004548.1,CCG022045.1, CCG004279.1,CCG013274.1,CCG024663.1,CCG028568.1, CCG022676.1,CCG007647.1,CCG004331.1,CCG018494.1, CCG024809.1,CCG012083.1,CCG026953.1,CCG017760.1, CCG018380.1,CCG016859.1,CCG005486.1,CCG017498.1, CCG020898.1,CCG017591.1,CCG023464.1,CCG002198.1, CCG021284.1,CCG001579.1,CCG013641.1,CCG016924.1, CCG000732.1,CCG003317.1,CCG000133.1,CCG003495.1, CCG013224.2,CCG002273.1,CCG007951.1,CCG023777.1, CCG026228.2,CCG005487.1,CCG025131.2,CCG009805.2, CCG028465.1,CCG008444.1,CCG017701.1,CCG009823.1, CCG014712.1,CCG000876.1,CCG021456.1,CCG025057.1, CCG024664.1,CCG015638.1,CCG000789.1,CCG024662.1, CCG026047.1,CCG022496.1,CCG024000.1,CCG008939.1, CCG018164.1,CCG019427.1,CCG001431.2,CCG016760.1, CCG014345.2,CCG021521.1,CCG010139.1,CCG006787.1, CCG028500.2,CCG020654.1,CCG015426.1,CCG008833.1,

GO:0009259	ribonucleotide metabolic process	93 of 4104 in the list	173 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG004309.1,CCG006529.1, CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1, CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1, CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1, CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1, CCG016370.1,CCG000148.1,CCG019103.1,CCG013365.1, CCG019629.2,CCG002917.1,CCG006486.1,CCG005924.2, CCG020909.1,CCG007532.1,CCG017330.1,CCG007531.1, CCG018447.1,CCG016966.1,CCG018820.3,CCG021110.1, CCG025179.1,CCG021934.1,CCG006777.1,CCG004308.1, CCG025973.1,CCG017995.1,CCG013637.1,CCG023640.1, CCG026314.1,CCG010418.1,CCG025348.1,CCG009080.1, CCG004869.1,CCG019619.1,CCG025396.1,CCG013999.1, CCG026953.1,CCG021336.1,CCG006924.1,CCG007417.1, CCG021220.1,CCG001066.1,CCG019866.1,CCG019678.1, CCG007724.1,CCG008748.1,CCG013641.1,CCG015410.1, CCG016027.1,CCG015289.1,CCG025107.1,CCG003495.1, CCG021411.1,CCG009142.1,CCG026898.1,CCG001859.1, CCG026812.1,CCG026336.1,CCG005886.1,CCG025131.2, CCG016542.1,CCG026154.1,CCG015654.1,CCG018659.2, CCG002852.1,CCG010864.1,CCG013610.1,CCG016614.1,

GO:0019693	ribose phosphate metabolic process	93 of 4104 in the list	173 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG004309.1,CCG006529.1, CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1, CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1, CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1, CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1, CCG016370.1,CCG000148.1,CCG019103.1,CCG013365.1, CCG019629.2,CCG002917.1,CCG006486.1,CCG005924.2, CCG020909.1,CCG007532.1,CCG017330.1,CCG007531.1, CCG018447.1,CCG016966.1,CCG018820.3,CCG021110.1, CCG025179.1,CCG021934.1,CCG006777.1,CCG004308.1, CCG025973.1,CCG017995.1,CCG013637.1,CCG023640.1, CCG026314.1,CCG010418.1,CCG025348.1,CCG009080.1, CCG004869.1,CCG019619.1,CCG025396.1,CCG013999.1, CCG026953.1,CCG021336.1,CCG006924.1,CCG007417.1, CCG021220.1,CCG001066.1,CCG019866.1,CCG019678.1, CCG007724.1,CCG008748.1,CCG013641.1,CCG015410.1, CCG016027.1,CCG015289.1,CCG025107.1,CCG003495.1, CCG021411.1,CCG009142.1,CCG026898.1,CCG001859.1, CCG026812.1,CCG026336.1,CCG005886.1,CCG025131.2, CCG016542.1,CCG026154.1,CCG015654.1,CCG018659.2, CCG002852.1,CCG010864.1,CCG013610.1,CCG016614.1,

GO:0034655	nucleobase-containing compound catabolic process	75 of 4104 in the list	138 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG007060.1, CCG005524.1,CCG013000.1,CCG013766.1,CCG024327.1, CCG015386.1,CCG019020.1,CCG009243.1,CCG020685.1, CCG002925.1,CCG023005.1,CCG024375.1,CCG009607.1, CCG011006.1,CCG027119.1,CCG004448.2,CCG007827.1, CCG014434.1,CCG006421.1,CCG023963.3,CCG021990.1, CCG025027.1,CCG016370.1,CCG019103.1,CCG019629.2, CCG006311.1,CCG002917.1,CCG005147.1,CCG004988.1, CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1, CCG016966.1,CCG018820.3,CCG019674.1,CCG025179.1, CCG006777.1,CCG025973.1,CCG013637.1,CCG001440.1, CCG010418.1,CCG018917.1,CCG009080.1,CCG004869.1, CCG007690.1,CCG025396.1,CCG026953.1,CCG006924.1, CCG021220.1,CCG008748.1,CCG013641.1,CCG016027.1, CCG015289.1,CCG003495.1,CCG021411.1,CCG001859.1, CCG026336.1,CCG005886.1,CCG009582.1,CCG016542.1, CCG025131.2,CCG026154.1,CCG015654.1,CCG002852.1, CCG010864.1,CCG001445.1,CCG013765.1,CCG007362.1,
GO:0044723	single-organism carbohydrate metabolic process	78 of 4104 in the list	144 of 8404 in the genome	1	CCG017381.1,CCG005588.1,CCG018536.1,CCG023617.1, CCG010373.1,CCG008437.1,CCG007046.2,CCG007766.1, CCG001602.1,CCG009803.1,CCG008287.1,CCG006358.1, CCG003220.2,CCG006203.1,CCG004091.1,CCG001355.1, CCG022453.1,CCG003748.1,CCG009494.1,CCG019825.2, CCG025472.1,CCG001038.1,CCG018432.1,CCG022035.1, CCG010996.1,CCG007045.1,CCG028524.1,CCG025307.1, CCG015986.1,CCG007023.1,CCG019693.1,CCG014579.1, CCG016653.1,CCG007771.1,CCG008317.1,CCG022430.1, CCG004760.1,CCG019210.1,CCG025277.1,CCG017651.1, CCG024762.1,CCG010700.1,CCG020616.1,CCG003215.3, CCG022108.2,CCG000331.1,CCG007981.1,CCG012268.1, CCG009928.1,CCG016003.1,CCG008130.1,CCG004388.1, CCG000431.1,CCG009084.2,CCG019953.1,CCG012740.1, CCG014260.1,CCG003247.1,CCG013129.1,CCG027131.1, CCG013318.1,CCG017197.1,CCG013985.1,CCG022214.1, CCG011451.2,CCG012840.1,CCG006213.1,CCG017278.1, CCG013339.1,CCG018423.1,CCG015587.1,CCG017200.1, CCG016373.1,CCG023757.1,CCG006221.1,CCG005177.1,

GO:0006436	tryptophanyl-tRNA aminoacylation	3 of 4104 in the list	3 of 8404 in the genome	1	CCG008321.1,CCG017344.1,CCG026570.1
GO:0006558	L-phenylalanine metabolic process	3 of 4104 in the list	3 of 8404 in the genome	1	CCG011789.1,CCG011721.1,CCG011722.1
GO:0006559	L-phenylalanine catabolic process	3 of 4104 in the list	3 of 8404 in the genome	1	CCG011789.1,CCG011721.1,CCG011722.1
GO:0006564	L-serine biosynthetic process	3 of 4104 in the list	3 of 8404 in the genome	1	CCG019954.3,CCG022025.2,CCG017201.1
GO:0006570	tyrosine metabolic process	3 of 4104 in the list	3 of 8404 in the genome	1	CCG011789.1,CCG011721.1,CCG011722.1
GO:0006637	acyl-CoA metabolic process	3 of 4104 in the list	3 of 8404 in the genome	1	CCG018113.1,CCG013216.1,CCG003683.2
GO:0006729	tetrahydrobiopterin biosynthetic process	3 of 4104 in the list	3 of 8404 in the genome	1	CCG021086.2,CCG023780.2,CCG003173.1
GO:0007179	transforming growth factor beta receptor signaling pathway	3 of 4104 in the list	3 of 8404 in the genome	1	CCG018533.1,CCG022741.1,CCG016307.1
GO:0008612	peptidyl-lysine modification to hypusine	3 of 4104 in the list	3 of 8404 in the genome	1	CCG008932.1,CCG026155.1,CCG013043.1
GO:0009896	positive regulation of catabolic process	3 of 4104 in the list	3 of 8404 in the genome	1	CCG023747.3,CCG015233.1,CCG003824.3
GO:0010506	regulation of autophagy	3 of 4104 in the list	3 of 8404 in the genome	1	CCG023747.3,CCG015233.1,CCG003824.3
GO:0010508	positive regulation of autophagy	3 of 4104 in the list	3 of 8404 in the genome	1	CCG023747.3,CCG015233.1,CCG003824.3
GO:0018205	peptidyl-lysine modification	3 of 4104 in the list	3 of 8404 in the genome	1	CCG008932.1,CCG026155.1,CCG013043.1
GO:0031331	positive regulation of cellular catabolic process	3 of 4104 in the list	3 of 8404 in the genome	1	CCG023747.3,CCG015233.1,CCG003824.3
GO:0035383	thioester metabolic process	3 of 4104 in the list	3 of 8404 in the genome	1	CCG018113.1,CCG013216.1,CCG003683.2
GO:0043244	regulation of protein complex disassembly	3 of 4104 in the list	3 of 8404 in the genome	1	CCG026155.1,CCG025026.1,CCG019102.1
GO:0046146	tetrahydrobiopterin metabolic	3 of 4104 in the list	3 of 8404 in the genome	1	CCG021086.2,CCG023780.2,CCG003173.1
GO:0046439	L-cysteine metabolic process	3 of 4104 in the list	3 of 8404 in the genome	1	CCG006994.1,CCG025465.1,CCG018907.1
GO:0046516	hypusine metabolic process	3 of 4104 in the list	3 of 8404 in the genome	1	CCG008932.1,CCG026155.1,CCG013043.1
GO:0070848	response to growth factor	3 of 4104 in the list	3 of 8404 in the genome	1	CCG018533.1,CCG022741.1,CCG016307.1
GO:0071363	cellular response to growth factor stimulus	3 of 4104 in the list	3 of 8404 in the genome	1	CCG018533.1,CCG022741.1,CCG016307.1
GO:0071559	response to transforming growth factor beta	3 of 4104 in the list	3 of 8404 in the genome	1	CCG018533.1,CCG022741.1,CCG016307.1
GO:0071560	cellular response to transforming growth factor beta stimulus	3 of 4104 in the list	3 of 8404 in the genome	1	CCG018533.1,CCG022741.1,CCG016307.1
GO:1902221	erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic	3 of 4104 in the list	3 of 8404 in the genome	1	CCG011789.1,CCG011721.1,CCG011722.1

GO:1902222	erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic	3 of 4104 in the list	3 of 8404 in the genome	1	CCG011789.1,CCG011721.1,CCG011722.1
GO:0006413	translational initiation	20 of 4104 in the list	33 of 8404 in the genome	1	CCG021940.1,CCG021933.1,CCG004807.1,CCG005622.1, CCG021944.1,CCG018168.1,CCG000368.1,CCG018719.1, CCG018164.1,CCG014819.1,CCG001777.1,CCG027281.1, CCG024529.1,CCG006344.1,CCG014947.2,CCG021521.1, CCG008592.1,CCG026825.1,CCG007705.1,CCG000294.1
GO:0009150	purine ribonucleotide metabolic process	91 of 4104 in the list	170 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG004309.1,CCG006529.1, CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1, CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1, CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1, CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1, CCG016370.1,CCG000148.1,CCG019103.1,CCG013365.1, CCG019629.2,CCG002917.1,CCG006486.1,CCG005924.2, CCG020909.1,CCG007532.1,CCG017330.1,CCG007531.1, CCG018447.1,CCG016966.1,CCG018820.3,CCG021110.1, CCG025179.1,CCG021934.1,CCG006777.1,CCG004308.1, CCG025973.1,CCG017995.1,CCG013637.1,CCG023640.1, CCG026314.1,CCG010418.1,CCG025348.1,CCG009080.1, CCG004869.1,CCG019619.1,CCG025396.1,CCG013999.1, CCG026953.1,CCG021336.1,CCG006924.1,CCG007417.1, CCG021220.1,CCG001066.1,CCG019866.1,CCG019678.1, CCG007724.1,CCG008748.1,CCG013641.1,CCG015410.1, CCG016027.1,CCG015289.1,CCG025107.1,CCG003495.1, CCG021411.1,CCG009142.1,CCG026898.1,CCG001859.1, CCG026812.1,CCG026336.1,CCG005886.1,CCG025131.2, CCG016542.1,CCG026154.1,CCG015654.1,CCG018659.2, CCG002852.1,CCG010864.1,CCG028305.1,CCG006791.1,
GO:0032012	regulation of ARF protein signal transduction	15 of 4104 in the list	24 of 8404 in the genome	1	CCG016454.1,CCG028651.1,CCG021442.1,CCG022083.1, CCG022394.1,CCG021263.1,CCG019462.1,CCG004132.1, CCG022749.1,CCG025470.1,CCG022420.1,CCG010260.1, CCG010157.1,CCG020983.1,CCG025554.1
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	6 of 4104 in the list	8 of 8404 in the genome	1	CCG021110.1,CCG010960.2,CCG006529.1,CCG016222.1, CCG017995.1,CCG007417.1

GO:0009262	deoxyribonucleotide metabolic process	6 of 4104 in the list	8 of 8404 in the genome	1	CCG001445.1,CCG001440.1,CCG010960.2,CCG016222.1, CCG004180.1,CCG014116.1
GO:0042775	mitochondrial ATP synthesis coupled electron transport	6 of 4104 in the list	8 of 8404 in the genome	1	CCG020879.1,CCG006459.1,CCG001649.1,CCG025163.3, CCG024297.1,CCG006864.1
GO:0052646	alditol phosphate metabolic process	6 of 4104 in the list	8 of 8404 in the genome	1	CCG009685.1,CCG000970.1,CCG025146.1,CCG021610.1, CCG012558.1,CCG014228.2
GO:0006221	pyrimidine nucleotide biosynthetic process	10 of 4104 in the list	15 of 8404 in the genome	1	CCG025493.1,CCG013610.1,CCG016614.1,CCG004180.1, CCG017995.1,CCG007417.1,CCG021110.1,CCG006529.1, CCG023452.1,CCG014116.1
GO:0044270	cellular nitrogen compound catabolic process	77 of 4104 in the list	143 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG007060.1, CCG005524.1,CCG013000.1,CCG013766.1,CCG024327.1, CCG015386.1,CCG019020.1,CCG009243.1,CCG020685.1, CCG002925.1,CCG023005.1,CCG024375.1,CCG009607.1, CCG011006.1,CCG027119.1,CCG004448.2,CCG007827.1, CCG014434.1,CCG006421.1,CCG023963.3,CCG021990.1, CCG025027.1,CCG016370.1,CCG019103.1,CCG019629.2, CCG006311.1,CCG002917.1,CCG005147.1,CCG004988.1, CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1, CCG016966.1,CCG018820.3,CCG019674.1,CCG025179.1, CCG006777.1,CCG025973.1,CCG013637.1,CCG009424.1, CCG001440.1,CCG010418.1,CCG018917.1,CCG009080.1, CCG004869.1,CCG007690.1,CCG025396.1,CCG026953.1, CCG006924.1,CCG021220.1,CCG008748.1,CCG006059.1, CCG013641.1,CCG016027.1,CCG015289.1,CCG003495.1, CCG021411.1,CCG001859.1,CCG026336.1,CCG005886.1, CCG009582.1,CCG016542.1,CCG025131.2,CCG026154.1, CCG015654.1,CCG002852.1,CCG010864.1,CCG001445.1, CCG013765.1,CCG007362.1,CCG021152.1,CCG023526.2,

GO:0006355	regulation of transcription, DNA-templated	249 of 4104 in the list	485 of 8404 in the genome	1	CCG019737.1,CCG017812.1,CCG022266.1,CCG015241.1, CCG003291.1,CCG008767.3,CCG001799.1,CCG021944.1, CCG008741.1,CCG017795.1,CCG003390.1,CCG005898.1, CCG018346.1,CCG027427.1,CCG012958.1,CCG007493.1, CCG011229.1,CCG016772.1,CCG021465.1,CCG003175.1, CCG028032.1,CCG001978.1,CCG023752.1,CCG028326.3, CCG013794.1,CCG006134.1,CCG009970.1,CCG011092.1, CCG022741.1,CCG016745.1,CCG021436.1,CCG012536.1, CCG015773.1,CCG000659.1,CCG027127.1,CCG018719.1, CCG015425.1,CCG027796.1,CCG022824.1,CCG012372.1, CCG018533.1,CCG024710.1,CCG022281.1,CCG011465.1, CCG025856.1,CCG020129.1,CCG027186.1,CCG008229.1, CCG018515.1,CCG013077.1,CCG020044.1,CCG000588.1, CCG022045.1,CCG017156.1,CCG012902.1,CCG013274.1, CCG028568.1,CCG024689.1,CCG013879.1,CCG007647.1, CCG021633.1,CCG000587.1,CCG012083.1,CCG000562.1, CCG028528.2,CCG004861.1,CCG014682.1,CCG018068.1, CCG012009.1,CCG005480.2,CCG017760.1,CCG016859.1, CCG020898.1,CCG017591.1,CCG002390.1,CCG002198.1, CCG021284.1,CCG023588.1,CCG016924.1,CCG009894.1, CCG011710.1,CCG000133.1,CCG013224.2,CCG002273.1, CCG002039.1,CCG001698.1,CCG023777.1,CCG014461.1, CCG026228.2,CCG027658.1,CCG021054.1,CCG022286.1, CCG016307.1,CCG022434.1,CCG009805.2,CCG016749.1, CCG012792.1,CCG017524.1,CCG028465.1,CCG002422.1, CCG019250.1,CCG019222.1,CCG005396.1,CCG010702.1, CCG001096.1,CCG025747.1,CCG009823.1,CCG014983.1, CCG021456.1,CCG014928.1,CCG005168.1,CCG018184.1, CCG018315.1,CCG027580.1,CCG010140.1,CCG027118.1, CCG024271.1,CCG024319.1,CCG005895.1,CCG009458.1,

GO:0051252	regulation of RNA metabolic process	249 of 4104 in the list	485 of 8404 in the genome	1	CCG019737.1,CCG017812.1,CCG022266.1,CCG015241.1, CCG003291.1,CCG008767.3,CCG001799.1,CCG021944.1, CCG008741.1,CCG017795.1,CCG003390.1,CCG005898.1, CCG018346.1,CCG027427.1,CCG012958.1,CCG007493.1, CCG011229.1,CCG016772.1,CCG021465.1,CCG003175.1, CCG028032.1,CCG001978.1,CCG023752.1,CCG028326.3, CCG013794.1,CCG006134.1,CCG009970.1,CCG011092.1, CCG022741.1,CCG016745.1,CCG021436.1,CCG012536.1, CCG015773.1,CCG000659.1,CCG027127.1,CCG018719.1, CCG015425.1,CCG027796.1,CCG022824.1,CCG012372.1, CCG018533.1,CCG024710.1,CCG022281.1,CCG011465.1, CCG025856.1,CCG020129.1,CCG027186.1,CCG008229.1, CCG018515.1,CCG013077.1,CCG020044.1,CCG000588.1, CCG022045.1,CCG017156.1,CCG012902.1,CCG013274.1, CCG028568.1,CCG024689.1,CCG013879.1,CCG007647.1, CCG021633.1,CCG000587.1,CCG012083.1,CCG000562.1, CCG028528.2,CCG004861.1,CCG014682.1,CCG018068.1, CCG012009.1,CCG005480.2,CCG017760.1,CCG016859.1, CCG020898.1,CCG017591.1,CCG002390.1,CCG002198.1, CCG021284.1,CCG023588.1,CCG016924.1,CCG009894.1, CCG011710.1,CCG000133.1,CCG013224.2,CCG002273.1, CCG002039.1,CCG001698.1,CCG023777.1,CCG014461.1, CCG026228.2,CCG027658.1,CCG021054.1,CCG022286.1, CCG016307.1,CCG022434.1,CCG009805.2,CCG016749.1, CCG012792.1,CCG017524.1,CCG028465.1,CCG002422.1, CCG019250.1,CCG019222.1,CCG005396.1,CCG010702.1, CCG001096.1,CCG025747.1,CCG009823.1,CCG014983.1, CCG021456.1,CCG014928.1,CCG005168.1,CCG018184.1, CCG018315.1,CCG027580.1,CCG010140.1,CCG027118.1, CCG024271.1,CCG024319.1,CCG005895.1,CCG009458.1,

GO:2001141	regulation of RNA biosynthetic process	249 of 4104 in the list	485 of 8404 in the genome	1	CCG019737.1,CCG017812.1,CCG022266.1,CCG015241.1, CCG003291.1,CCG008767.3,CCG001799.1,CCG021944.1, CCG008741.1,CCG017795.1,CCG003390.1,CCG005898.1, CCG018346.1,CCG027427.1,CCG012958.1,CCG007493.1, CCG011229.1,CCG016772.1,CCG021465.1,CCG003175.1, CCG028032.1,CCG001978.1,CCG023752.1,CCG028326.3, CCG013794.1,CCG006134.1,CCG009970.1,CCG011092.1, CCG022741.1,CCG016745.1,CCG021436.1,CCG012536.1, CCG015773.1,CCG000659.1,CCG027127.1,CCG018719.1, CCG015425.1,CCG027796.1,CCG022824.1,CCG012372.1, CCG018533.1,CCG024710.1,CCG022281.1,CCG011465.1, CCG025856.1,CCG020129.1,CCG027186.1,CCG008229.1, CCG018515.1,CCG013077.1,CCG020044.1,CCG000588.1, CCG022045.1,CCG017156.1,CCG012902.1,CCG013274.1, CCG028568.1,CCG024689.1,CCG013879.1,CCG007647.1, CCG021633.1,CCG000587.1,CCG012083.1,CCG000562.1, CCG028528.2,CCG004861.1,CCG014682.1,CCG018068.1, CCG012009.1,CCG005480.2,CCG017760.1,CCG016859.1, CCG020898.1,CCG017591.1,CCG002390.1,CCG002198.1, CCG021284.1,CCG023588.1,CCG016924.1,CCG009894.1, CCG011710.1,CCG000133.1,CCG013224.2,CCG002273.1, CCG002039.1,CCG001698.1,CCG023777.1,CCG014461.1, CCG026228.2,CCG027658.1,CCG021054.1,CCG022286.1, CCG016307.1,CCG022434.1,CCG009805.2,CCG016749.1, CCG012792.1,CCG017524.1,CCG028465.1,CCG002422.1, CCG019250.1,CCG019222.1,CCG005396.1,CCG010702.1, CCG001096.1,CCG025747.1,CCG009823.1,CCG014983.1, CCG021456.1,CCG014928.1,CCG005168.1,CCG018184.1, CCG018315.1,CCG027580.1,CCG010140.1,CCG027118.1, CCG024271.1,CCG024319.1,CCG005895.1,CCG009458.1,

GO:0044260	cellular macromolecule metabolic process	1189 of 4104 in the list	2388 of 8404 in the genome	1	CCG014531.2,CCG027068.1,CCG014396.1,CCG006549.1, CCG004887.1,CCG026106.1,CCG016952.1,CCG026174.1, CCG004468.1,CCG012726.1,CCG024584.1,CCG001292.1, CCG018432.1,CCG001040.1,CCG017266.1,CCG028198.1, CCG016689.2,CCG025208.1,CCG021479.1,CCG003362.1, CCG019113.1,CCG023381.1,CCG019382.1,CCG019735.1, CCG016094.1,CCG026413.3,CCG023474.1,CCG026871.2, CCG010792.1,CCG012623.1,CCG021616.1,CCG005738.1, CCG013876.1,CCG010905.1,CCG008270.1,CCG024612.1, CCG027636.1,CCG028653.1,CCG004569.1,CCG020286.1, CCG013109.1,CCG006465.1,CCG015074.1,CCG019571.1, CCG008871.1,CCG015694.1,CCG018788.1,CCG006484.1, CCG002982.1,CCG012083.1,CCG026602.1,CCG023686.1, CCG007457.1,CCG021737.1,CCG025990.1,CCG015350.1, CCG021948.1,CCG020651.1,CCG005284.1,CCG004927.1, CCG009805.2,CCG021137.1,CCG022056.1,CCG001876.1, CCG012584.1,CCG015186.1,CCG016327.2,CCG018688.1, CCG024200.1,CCG010624.1,CCG023458.1,CCG027748.1, CCG017001.1,CCG021767.1,CCG003520.1,CCG004926.1, CCG006928.1,CCG017381.1,CCG010912.1,CCG004955.1, CCG007874.3,CCG001704.1,CCG005524.1,CCG013640.1, CCG008404.1,CCG018201.1,CCG010136.1,CCG009574.1, CCG022370.1,CCG010112.1,CCG009038.1,CCG022513.2, CCG007750.2,CCG025707.1,CCG028092.1,CCG020078.1, CCG000209.1,CCG023486.1,CCG001395.1,CCG016557.1, CCG005594.1,CCG024922.1,CCG027000.1,CCG022183.1, CCG006804.1,CCG018168.1,CCG006264.1,CCG019426.1, CCG009394.1,CCG024760.1,CCG011015.1,CCG009177.1, CCG014222.1,CCG008498.1,CCG000612.1,CCG012278.1, CCG008367.1,CCG010797.1,CCG004008.1,CCG010138.1,

GO:0046434	organophosphate catabolic process	68 of 4104 in the list	126 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG007060.1, CCG013000.1,CCG013766.1,CCG024327.1,CCG015386.1, CCG019020.1,CCG009243.1,CCG009685.1,CCG002925.1, CCG023005.1,CCG024375.1,CCG009607.1,CCG011006.1, CCG027119.1,CCG007827.1,CCG014434.1,CCG006421.1, CCG023963.3,CCG021990.1,CCG025027.1,CCG016370.1, CCG019103.1,CCG019629.2,CCG006311.1,CCG002917.1, CCG005147.1,CCG004988.1,CCG020909.1,CCG007532.1, CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3, CCG025179.1,CCG006777.1,CCG025973.1,CCG013637.1, CCG001440.1,CCG010418.1,CCG009080.1,CCG004869.1, CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1, CCG008748.1,CCG013641.1,CCG016027.1,CCG015289.1, CCG003495.1,CCG021411.1,CCG001859.1,CCG026336.1, CCG005886.1,CCG016542.1,CCG025131.2,CCG015654.1, CCG026154.1,CCG002852.1,CCG010864.1,CCG001445.1, CCG013765.1,CCG007362.1,CCG021152.1,CCG023526.2
GO:0006497	protein lipidation	17 of 4104 in the list	28 of 8404 in the genome	1	CCG022209.1,CCG017241.1,CCG025177.1,CCG009434.1, CCG014839.1,CCG000663.1,CCG013131.1,CCG026370.1, CCG025889.1,CCG004806.1,CCG000552.1,CCG022255.1, CCG024760.1,CCG028332.1,CCG007330.1,CCG011531.1,
GO:0042157	lipoprotein metabolic process	17 of 4104 in the list	28 of 8404 in the genome	1	CCG022209.1,CCG017241.1,CCG025177.1,CCG009434.1, CCG014839.1,CCG000663.1,CCG013131.1,CCG026370.1, CCG025889.1,CCG004806.1,CCG000552.1,CCG022255.1, CCG024760.1,CCG028332.1,CCG007330.1,CCG011531.1,
GO:0042158	lipoprotein biosynthetic process	17 of 4104 in the list	28 of 8404 in the genome	1	CCG022209.1,CCG017241.1,CCG025177.1,CCG009434.1, CCG014839.1,CCG000663.1,CCG013131.1,CCG026370.1, CCG025889.1,CCG004806.1,CCG000552.1,CCG022255.1, CCG024760.1,CCG028332.1,CCG007330.1,CCG011531.1,
GO:0071705	nitrogen compound transport	17 of 4104 in the list	28 of 8404 in the genome	1	CCG006348.1,CCG011567.1,CCG005539.1,CCG021221.1, CCG023244.1,CCG026667.1,CCG009454.1,CCG024222.1, CCG005768.1,CCG005769.1,CCG018073.1,CCG020840.1, CCG026989.1,CCG010135.1,CCG019407.1,CCG017874.1,

GO:0055085	transmembrane transport	276 of 4104 in the list	540 of 8404 in the genome	1	CCG005307.1,CCG020245.1,CCG010623.2,CCG021740.1, CCG000585.1,CCG000205.1,CCG001468.1,CCG019285.1, CCG000300.1,CCG003878.1,CCG022794.1,CCG002389.1, CCG017210.1,CCG014382.1,CCG016326.1,CCG023583.1, CCG001379.1,CCG009367.1,CCG025274.1,CCG009530.1, CCG003934.1,CCG017240.1,CCG018883.1,CCG012307.1, CCG025450.1,CCG018133.1,CCG018416.1,CCG014240.1, CCG006525.1,CCG016754.1,CCG026050.1,CCG009208.1, CCG019655.1,CCG009668.1,CCG005330.1,CCG016269.1, CCG009207.1,CCG011830.1,CCG014793.1,CCG016267.1, CCG024222.1,CCG026293.1,CCG018264.1,CCG017477.1, CCG005391.2,CCG018263.1,CCG007597.1,CCG016756.1, CCG015530.1,CCG022587.1,CCG009959.1,CCG016719.1, CCG000983.1,CCG022488.2,CCG001285.1,CCG011829.1, CCG016753.1,CCG008709.1,CCG011252.1,CCG008403.1, CCG008422.1,CCG022802.1,CCG010112.1,CCG020491.1, CCG027154.1,CCG001652.1,CCG016266.1,CCG000080.1, CCG001267.1,CCG026819.1,CCG012195.1,CCG025467.2, CCG011827.1,CCG009811.1,CCG018271.1,CCG010663.1, CCG002135.1,CCG019611.1,CCG000148.1,CCG025510.1, CCG000809.1,CCG021125.1,CCG025611.1,CCG016459.1, CCG021934.1,CCG019890.1,CCG023983.1,CCG012326.1, CCG001585.1,CCG001453.2,CCG006770.1,CCG011634.1, CCG010872.1,CCG022510.1,CCG018753.1,CCG018073.1, CCG016278.1,CCG016956.1,CCG001066.1,CCG019407.1, CCG007691.1,CCG007724.1,CCG027971.1,CCG022511.1, CCG025568.1,CCG006348.1,CCG009368.1,CCG025107.1, CCG018455.1,CCG021273.1,CCG024625.1,CCG017290.1, CCG018265.1,CCG025851.1,CCG010965.1,CCG016268.2, CCG021007.1,CCG015823.1,CCG025989.2,CCG020949.1,

GO:0065007	biological regulation	703 of 4104 in the list	1402 of 8404 in the genome	1	CCG005254.1,CCG017420.1,CCG027068.1,CCG014340.1, CCG005375.1,CCG022266.1,CCG003824.3,CCG008603.1, CCG008767.3,CCG008741.1,CCG003390.1,CCG000646.1, CCG004595.1,CCG007493.1,CCG026174.1,CCG020785.1, CCG010849.1,CCG002338.1,CCG021465.1,CCG003587.1, CCG020974.1,CCG002841.1,CCG018321.1,CCG013794.1, CCG010275.1,CCG026360.1,CCG021064.1,CCG006134.1, CCG017266.1,CCG016689.2,CCG020709.1,CCG014466.1, CCG015101.1,CCG012536.1,CCG027127.1,CCG015425.1, CCG027796.1,CCG022824.1,CCG018533.1,CCG024710.1, CCG000526.1,CCG022281.1,CCG027669.1,CCG015967.1, CCG021661.1,CCG022420.1,CCG013308.1,CCG023579.1, CCG006714.1,CCG025026.1,CCG010157.1,CCG011911.1, CCG008685.1,CCG004132.1,CCG000588.1,CCG004548.1, CCG022045.1,CCG004279.1,CCG013274.1,CCG024663.1, CCG028568.1,CCG022676.1,CCG007647.1,CCG004331.1, CCG018494.1,CCG024809.1,CCG012083.1,CCG026953.1, CCG017760.1,CCG018380.1,CCG016859.1,CCG005486.1, CCG017498.1,CCG020898.1,CCG017591.1,CCG023464.1, CCG002198.1,CCG021284.1,CCG001579.1,CCG013641.1, CCG016924.1,CCG000732.1,CCG003317.1,CCG000133.1, CCG003495.1,CCG013224.2,CCG002273.1,CCG007951.1, CCG023777.1,CCG026228.2,CCG005487.1,CCG025131.2, CCG009805.2,CCG028465.1,CCG008444.1,CCG017701.1, CCG009823.1,CCG014712.1,CCG000876.1,CCG021456.1, CCG025057.1,CCG024664.1,CCG015638.1,CCG000789.1, CCG024662.1,CCG026047.1,CCG022496.1,CCG024000.1, CCG008939.1,CCG018164.1,CCG019427.1,CCG001431.2, CCG016760.1,CCG014345.2,CCG021521.1,CCG010139.1, CCG006787.1,CCG028500.2,CCG020654.1,CCG015426.1,

GO:1901360	organic cyclic compound metabolic process	839 of 4104 in the list	1678 of 8404 in the genome	1	CCG017420.1,CCG027300.1,CCG014396.1,CCG006549.1, CCG026106.1,CCG006357.1,CCG009878.1,CCG024072.1, CCG026174.1,CCG020685.1,CCG013625.1,CCG004468.1, CCG023989.1,CCG016238.1,CCG024584.1,CCG001292.1, CCG016220.1,CCG018321.1,CCG002470.1,CCG005194.1, CCG001040.1,CCG014836.1,CCG025208.1,CCG025307.1, CCG019382.1,CCG016370.1,CCG016094.1,CCG027183.2, CCG023474.1,CCG010792.1,CCG004231.1,CCG012623.1, CCG005053.1,CCG010905.1,CCG011722.1,CCG020471.1, CCG021110.1,CCG010909.1,CCG023129.1,CCG028653.1, CCG021342.1,CCG024326.1,CCG014946.1,CCG020286.1, CCG002735.1,CCG027133.1,CCG021086.2,CCG014280.1, CCG015694.1,CCG013865.1,CCG025396.1,CCG006484.1, CCG026953.1,CCG001461.1,CCG023686.1,CCG004402.1, CCG019678.1,CCG003938.1,CCG023468.1,CCG025990.1, CCG013641.1,CCG015350.1,CCG003495.1,CCG021948.1, CCG011148.1,CCG020651.1,CCG025131.2,CCG005284.1, CCG004927.1,CCG023452.1,CCG009805.2,CCG002852.1, CCG019545.1,CCG003142.1,CCG021137.1,CCG013610.1, CCG001876.1,CCG012584.1,CCG013465.1,CCG009518.1, CCG024200.1,CCG010624.1,CCG002231.1,CCG023125.1, CCG016381.1,CCG011727.1,CCG026865.1,CCG017001.1, CCG024788.1,CCG007263.1,CCG021767.1,CCG004926.1, CCG001285.1,CCG004907.1,CCG010912.1,CCG004955.1, CCG015367.1,CCG003750.1,CCG005524.1,CCG026047.1, CCG011491.1,CCG024857.1,CCG022772.1,CCG010136.1, CCG005501.1,CCG003310.1,CCG026516.1,CCG024570.2, CCG018164.1,CCG013617.1,CCG004224.1,CCG010112.1, CCG022513.2,CCG028092.1,CCG018650.1,CCG000209.1, CCG016760.1,CCG021521.1,CCG007902.1,CCG023486.1,
GO:0006265	DNA topological change	7 of 4104 in the list	10 of 8404 in the genome	1	CCG022918.1,CCG008972.1,CCG027183.2,CCG016201.1, CCG000166.1,CCG011615.1,CCG003438.1
GO:0006479	protein methylation	7 of 4104 in the list	10 of 8404 in the genome	1	CCG025991.2,CCG021449.1,CCG012083.1,CCG001369.2, CCG015398.1,CCG026248.1,CCG025942.1
GO:0008213	protein alkylation	7 of 4104 in the list	10 of 8404 in the genome	1	CCG025991.2,CCG021449.1,CCG012083.1,CCG001369.2, CCG015398.1,CCG026248.1,CCG025942.1

GO:0009132	nucleoside diphosphate metabolic process	7 of 4104 in the list	10 of 8404 in the genome	1	CCG021110.1,CCG006529.1,CCG000217.1,CCG004191.1, CCG017995.1,CCG007417.1,CCG014116.1
GO:0043604	amide biosynthetic process	7 of 4104 in the list	10 of 8404 in the genome	1	CCG006821.1,CCG010174.2,CCG009333.1,CCG002897.1, CCG003865.1,CCG026099.1,CCG024133.1
GO:0044711	single-organism biosynthetic process	162 of 4104 in the list	313 of 8404 in the genome	1	CCG010174.2,CCG017331.1,CCG000663.1,CCG025989.2, CCG024517.1,CCG025493.1,CCG026174.1,CCG000016.1, CCG007330.1,CCG017097.1,CCG016220.1,CCG011531.1, CCG001102.1,CCG005923.1,CCG026536.1,CCG009434.1, CCG007993.1,CCG019693.1,CCG012308.1,CCG001423.1, CCG016653.1,CCG007771.1,CCG022025.2,CCG005053.1, CCG025940.1,CCG008860.1,CCG028332.1,CCG010944.1, CCG006965.1,CCG021110.1,CCG024612.1,CCG019909.1, CCG017559.1,CCG015746.1,CCG009244.1,CCG023640.1, CCG012002.1,CCG013131.1,CCG025348.1,CCG019619.1, CCG022352.1,CCG028131.1,CCG016315.1,CCG021610.1, CCG027312.1,CCG010460.1,CCG006821.1,CCG015410.1, CCG003865.1,CCG009142.1,CCG026898.1,CCG012840.1, CCG017278.1,CCG000552.1,CCG023452.1,CCG025636.2, CCG014116.1,CCG017111.1,CCG013610.1,CCG022773.2, CCG023757.1,CCG009518.1,CCG002231.1,CCG015411.1, CCG006791.1,CCG026155.1,CCG026865.1,CCG015567.1, CCG004532.1,CCG026047.1,CCG017175.1,CCG011491.1, CCG006529.1,CCG009333.1,CCG009803.1,CCG004806.1, CCG007533.1,CCG008422.1,CCG010112.1,CCG015568.1, CCG020441.1,CCG013643.1,CCG024155.1,CCG019263.1, CCG022209.1,CCG002038.1,CCG010561.1,CCG028524.1, CCG014839.1,CCG015986.1,CCG022134.1,CCG000148.1, CCG013365.1,CCG025889.1,CCG005924.2,CCG018615.3, CCG024760.1,CCG025731.1,CCG022430.1,CCG018108.1, CCG026099.1,CCG024133.1,CCG004257.1,CCG017330.1, CCG003751.1,CCG025897.1,CCG006009.1,CCG024762.1, CCG021934.1,CCG014379.1,CCG007203.1,CCG027212.1, CCG019954.3,CCG004180.1,CCG017995.1,CCG000331.1, CCG012408.1,CCG015921.1,CCG026370.1,CCG020559.1,

GO:0009166	nucleotide catabolic process	67 of 4104 in the list	125 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG007060.1, CCG013000.1,CCG013766.1,CCG024327.1,CCG015386.1, CCG019020.1,CCG009243.1,CCG002925.1,CCG023005.1, CCG024375.1,CCG009607.1,CCG011006.1,CCG027119.1, CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3, CCG021990.1,CCG025027.1,CCG016370.1,CCG019103.1, CCG019629.2,CCG006311.1,CCG002917.1,CCG005147.1, CCG004988.1,CCG020909.1,CCG007532.1,CCG007531.1, CCG018447.1,CCG016966.1,CCG018820.3,CCG025179.1, CCG006777.1,CCG025973.1,CCG013637.1,CCG001440.1, CCG010418.1,CCG009080.1,CCG004869.1,CCG025396.1, CCG026953.1,CCG006924.1,CCG021220.1,CCG008748.1, CCG013641.1,CCG016027.1,CCG015289.1,CCG003495.1, CCG021411.1,CCG001859.1,CCG026336.1,CCG005886.1, CCG016542.1,CCG025131.2,CCG015654.1,CCG026154.1, CCG002852.1,CCG010864.1,CCG001445.1,CCG013765.1
GO:1901292	nucleoside phosphate catabolic process	67 of 4104 in the list	125 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG007060.1, CCG013000.1,CCG013766.1,CCG024327.1,CCG015386.1, CCG019020.1,CCG009243.1,CCG002925.1,CCG023005.1, CCG024375.1,CCG009607.1,CCG011006.1,CCG027119.1, CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3, CCG021990.1,CCG025027.1,CCG016370.1,CCG019103.1, CCG019629.2,CCG006311.1,CCG002917.1,CCG005147.1, CCG004988.1,CCG020909.1,CCG007532.1,CCG007531.1, CCG018447.1,CCG016966.1,CCG018820.3,CCG025179.1, CCG006777.1,CCG025973.1,CCG013637.1,CCG001440.1, CCG010418.1,CCG009080.1,CCG004869.1,CCG025396.1, CCG026953.1,CCG006924.1,CCG021220.1,CCG008748.1, CCG013641.1,CCG016027.1,CCG015289.1,CCG003495.1, CCG021411.1,CCG001859.1,CCG026336.1,CCG005886.1, CCG016542.1,CCG025131.2,CCG015654.1,CCG026154.1, CCG002852.1,CCG010864.1,CCG001445.1,CCG013765.1
GO:0006643	membrane lipid metabolic process	21 of 4104 in the list	36 of 8404 in the genome	1	CCG025233.1,CCG021085.1,CCG022209.1,CCG017241.1, CCG009434.1,CCG014839.1,CCG013509.1,CCG000663.1, CCG013131.1,CCG026370.1,CCG025889.1,CCG004806.1, CCG000552.1,CCG024760.1,CCG017994.1,CCG028332.1, CCG007330.1,CCG023779.1,CCG019082.1,CCG011531.1,

GO:0009100	glycoprotein metabolic process	21 of 4104 in the list	36 of 8404 in the genome	1	CCG017381.1,CCG018536.1,CCG023617.1,CCG027131.1, CCG017197.1,CCG013985.1,CCG014579.1,CCG012268.1, CCG007766.1,CCG001602.1,CCG016003.1,CCG009928.1, CCG004091.1,CCG006221.1,CCG019210.1,CCG012164.1, CCG009494.1,CCG003247.1,CCG025472.1,CCG010700.1,
GO:0090407	organophosphate biosynthetic process	76 of 4104 in the list	143 of 8404 in the genome	1	CCG004532.1,CCG026047.1,CCG000663.1,CCG006529.1, CCG025989.2,CCG004806.1,CCG007533.1,CCG008422.1, CCG025493.1,CCG000016.1,CCG026174.1,CCG007330.1, CCG010112.1,CCG011531.1,CCG024155.1,CCG013643.1, CCG022209.1,CCG002038.1,CCG009434.1,CCG014839.1, CCG007993.1,CCG012308.1,CCG000148.1,CCG013365.1, CCG016653.1,CCG025889.1,CCG005924.2,CCG024760.1, CCG028332.1,CCG017330.1,CCG010944.1,CCG006965.1, CCG021110.1,CCG016148.1,CCG024612.1,CCG021934.1, CCG010319.1,CCG014379.1,CCG015746.1,CCG017995.1, CCG004180.1,CCG023640.1,CCG013131.1,CCG026370.1, CCG025348.1,CCG019619.1,CCG022352.1,CCG013999.1, CCG028131.1,CCG021336.1,CCG007417.1,CCG024432.2, CCG007724.1,CCG021610.1,CCG023102.1,CCG017295.1, CCG017241.1,CCG015410.1,CCG025107.1,CCG009142.1, CCG026898.1,CCG015747.1,CCG026812.1,CCG000552.1, CCG023452.1,CCG018659.2,CCG014116.1,CCG013610.1, CCG023757.1,CCG016614.1,CCG028305.1,CCG009518.1
GO:0007155	cell adhesion	51 of 4104 in the list	94 of 8404 in the genome	1	CCG026424.3,CCG022123.1,CCG007182.1,CCG025334.1, CCG016263.1,CCG023740.2,CCG004279.1,CCG001422.1, CCG000237.1,CCG021360.1,CCG007356.1,CCG008089.1, CCG008253.1,CCG007575.1,CCG002875.1,CCG020013.1, CCG015458.1,CCG004542.1,CCG003587.1,CCG006479.1, CCG011199.1,CCG015596.1,CCG007117.1,CCG024898.1, CCG021854.1,CCG013707.1,CCG016035.1,CCG026389.1, CCG019884.1,CCG028452.1,CCG004753.1,CCG020708.1, CCG008075.1,CCG017729.1,CCG015389.1,CCG008431.1, CCG017851.1,CCG000554.1,CCG028158.1,CCG014318.1, CCG011200.2,CCG008251.1,CCG010990.1,CCG000127.1, CCG012634.1,CCG000526.1,CCG021355.1,CCG016446.1, CCG008809.1,CCG027757.1,CCG013255.1

GO:0022610	biological adhesion	51 of 4104 in the list	94 of 8404 in the genome	1	CCG026424.3,CCG022123.1,CCG007182.1,CCG025334.1, CCG016263.1,CCG023740.2,CCG004279.1,CCG001422.1, CCG000237.1,CCG021360.1,CCG007356.1,CCG008089.1, CCG008253.1,CCG007575.1,CCG002875.1,CCG020013.1, CCG015458.1,CCG004542.1,CCG003587.1,CCG006479.1, CCG011199.1,CCG015596.1,CCG007117.1,CCG024898.1, CCG021854.1,CCG013707.1,CCG016035.1,CCG026389.1, CCG019884.1,CCG028452.1,CCG004753.1,CCG020708.1, CCG008075.1,CCG017729.1,CCG015389.1,CCG008431.1, CCG017851.1,CCG000554.1,CCG028158.1,CCG014318.1, CCG011200.2,CCG008251.1,CCG010990.1,CCG000127.1, CCG012634.1,CCG000526.1,CCG021355.1,CCG016446.1, CCG008809.1,CCG027757.1,CCG013255.1
GO:0006790	sulfur compound metabolic process	14 of 4104 in the list	23 of 8404 in the genome	1	CCG006994.1,CCG002897.1,CCG003865.1,CCG026099.1, CCG004535.1,CCG025465.1,CCG018907.1,CCG016955.1, CCG015568.1,CCG003751.1,CCG027551.3,CCG015567.1, CCG025636.2,CCG010319.1
GO:0006904	vesicle docking involved in exocytosis	8 of 4104 in the list	12 of 8404 in the genome	1	CCG002121.1,CCG016860.1,CCG016836.2,CCG002937.1, CCG000631.1,CCG005810.1,CCG016493.2,CCG023051.1
GO:0032312	regulation of ARF GTPase activity	8 of 4104 in the list	12 of 8404 in the genome	1	CCG016454.1,CCG021442.1,CCG022083.1,CCG022394.1, CCG019462.1,CCG010260.1,CCG004132.1,CCG025554.1
GO:0009081	branched-chain amino acid metabolic process	4 of 4104 in the list	5 of 8404 in the genome	1	CCG022407.1,CCG025307.1,CCG025439.1,CCG009084.2
GO:0016571	histone methylation	4 of 4104 in the list	5 of 8404 in the genome	1	CCG025991.2,CCG012083.1,CCG001369.2,CCG015398.1
GO:0034968	histone lysine methylation	4 of 4104 in the list	5 of 8404 in the genome	1	CCG025991.2,CCG012083.1,CCG001369.2,CCG015398.1
GO:0046165	alcohol biosynthetic process	4 of 4104 in the list	5 of 8404 in the genome	1	CCG024095.1,CCG014174.1,CCG023757.1,CCG016653.1

GO:0006807	nitrogen compound metabolic process	982 of 4104 in the list	1973 of 8404 in the genome	1	CCG017420.1,CCG027300.1,CCG014396.1,CCG006549.1, CCG006912.1,CCG026106.1,CCG006357.1,CCG009878.1, CCG024072.1,CCG012875.1,CCG024517.1,CCG025108.1, CCG026174.1,CCG020685.1,CCG013625.1,CCG004468.1, CCG023989.1,CCG016238.1,CCG024584.1,CCG004020.1, CCG001292.1,CCG016220.1,CCG018321.1,CCG002470.1, CCG005194.1,CCG001040.1,CCG014836.1,CCG020799.1, CCG025208.1,CCG025307.1,CCG019382.1,CCG016370.1, CCG016094.1,CCG027183.2,CCG023474.1,CCG010792.1, CCG004231.1,CCG012623.1,CCG022025.2,CCG005053.1, CCG019371.1,CCG010905.1,CCG011722.1,CCG020471.1, CCG021110.1,CCG003063.1,CCG010909.1,CCG023129.1, CCG018110.1,CCG028653.1,CCG021342.1,CCG016153.1, CCG024326.1,CCG014946.1,CCG020286.1,CCG002735.1, CCG027133.1,CCG021086.2,CCG014280.1,CCG015694.1, CCG013865.1,CCG025396.1,CCG006484.1,CCG026953.1, CCG001461.1,CCG023686.1,CCG004402.1,CCG019678.1, CCG003938.1,CCG023468.1,CCG025990.1,CCG013641.1, CCG006821.1,CCG015350.1,CCG003495.1,CCG021948.1, CCG011148.1,CCG020651.1,CCG025131.2,CCG005284.1, CCG004927.1,CCG023452.1,CCG009805.2,CCG002852.1, CCG019545.1,CCG003142.1,CCG021137.1,CCG013610.1, CCG001876.1,CCG012584.1,CCG013465.1,CCG009518.1, CCG024200.1,CCG010624.1,CCG002231.1,CCG023125.1, CCG016381.1,CCG011727.1,CCG028454.1,CCG020663.1, CCG026865.1,CCG017001.1,CCG024788.1,CCG007263.1, CCG021767.1,CCG008388.1,CCG004926.1,CCG001285.1, CCG004907.1,CCG010912.1,CCG004955.1,CCG015367.1, CCG003750.1,CCG005524.1,CCG026047.1,CCG011491.1, CCG024857.1,CCG022772.1,CCG010136.1,CCG009333.1,
GO:0006913	nucleocytoplasmic transport	26 of 4104 in the list	46 of 8404 in the genome	1	CCG013641.1,CCG011567.1,CCG017078.1,CCG003495.1, CCG007060.1,CCG001809.1,CCG011696.1,CCG026336.1, CCG019629.2,CCG016542.1,CCG021221.1,CCG004869.1, CCG015386.1,CCG019020.1,CCG022771.1,CCG020909.1, CCG006924.1,CCG021220.1,CCG018447.1,CCG026989.1, CCG008116.1,CCG021152.1,CCG011006.1,CCG017077.1,

GO:0051169	nuclear transport	26 of 4104 in the list	46 of 8404 in the genome	1	CCG013641.1,CCG011567.1,CCG017078.1,CCG003495.1, CCG007060.1,CCG001809.1,CCG011696.1,CCG026336.1, CCG019629.2,CCG016542.1,CCG021221.1,CCG004869.1, CCG015386.1,CCG019020.1,CCG022771.1,CCG020909.1, CCG006924.1,CCG021220.1,CCG018447.1,CCG026989.1, CCG008116.1,CCG021152.1,CCG011006.1,CCG017077.1,
GO:0016569	covalent chromatin modification	9 of 4104 in the list	14 of 8404 in the genome	1	CCG012083.1,CCG018326.1,CCG001369.2,CCG006686.1, CCG006211.1,CCG020863.1,CCG025991.2,CCG013028.1,
GO:0016570	histone modification	9 of 4104 in the list	14 of 8404 in the genome	1	CCG012083.1,CCG018326.1,CCG001369.2,CCG006686.1, CCG006211.1,CCG020863.1,CCG025991.2,CCG013028.1,

GO:0009056	catabolic process	204 of 4104 in the list	399 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG027068.1, CCG013000.1,CCG013766.1,CCG024327.1,CCG024092.1, CCG015386.1,CCG019020.1,CCG003288.1,CCG025108.1, CCG003220.2,CCG020685.1,CCG022635.1,CCG006203.1, CCG006391.1,CCG004020.1,CCG009685.1,CCG002925.1, CCG019834.1,CCG025387.1,CCG022453.1,CCG023005.1, CCG024375.1,CCG003748.1,CCG009607.1,CCG011006.1, CCG001539.1,CCG027119.1,CCG004448.2,CCG005029.1, CCG012828.1,CCG015610.1,CCG020799.1,CCG025307.1, CCG019113.1,CCG025521.1,CCG016370.1,CCG028595.1, CCG026413.3,CCG006311.1,CCG005441.1,CCG002917.1, CCG023890.1,CCG002974.1,CCG013876.1,CCG002139.1, CCG011722.1,CCG010019.1,CCG025277.1,CCG003063.1, CCG008217.1,CCG003215.3,CCG009424.1,CCG011238.1, CCG002418.1,CCG019571.1,CCG010879.1,CCG020154.1, CCG002366.1,CCG004869.1,CCG009080.1,CCG001877.1, CCG007690.1,CCG004331.1,CCG025396.1,CCG026953.1, CCG008969.2,CCG011721.1,CCG006924.1,CCG021220.1, CCG008510.1,CCG025962.1,CCG013832.1,CCG017543.1, CCG013641.1,CCG015289.1,CCG021411.1,CCG003495.1, CCG001859.1,CCG001769.1,CCG027283.1,CCG022214.1, CCG009582.1,CCG025131.2,CCG021807.1,CCG024829.1, CCG002852.1,CCG011789.1,CCG022742.2,CCG017200.1, CCG023420.1,CCG002231.1,CCG000834.1,CCG027763.1, CCG005177.1,CCG007362.1,CCG021152.1,CCG023526.2, CCG019697.2,CCG011996.1,CCG026612.1,CCG008388.1, CCG003060.1,CCG005588.1,CCG001704.1,CCG007060.1, CCG007080.1,CCG005524.1,CCG001350.1,CCG010373.1, CCG010111.1,CCG019599.1,CCG024974.1,CCG000591.1, CCG009243.1,CCG012628.1,CCG006358.1,CCG016477.1,

GO:0009165	nucleotide biosynthetic process	43 of 4104 in the list	79 of 8404 in the genome	1	CCG014379.1,CCG004180.1,CCG017995.1,CCG023640.1, CCG026047.1,CCG006529.1,CCG025348.1,CCG025989.2, CCG019619.1,CCG008422.1,CCG025493.1,CCG000016.1, CCG026174.1,CCG021336.1,CCG028131.1,CCG013999.1, CCG010112.1,CCG007417.1,CCG007724.1,CCG013643.1, CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG026898.1,CCG026812.1,CCG007993.1,CCG000148.1, CCG013365.1,CCG023452.1,CCG005924.2,CCG018659.2, CCG014116.1,CCG013610.1,CCG016614.1,CCG028305.1, CCG009518.1,CCG004188.3,CCG017330.1,CCG010944.1, CCG006791.1,CCG021110.1,CCG021934.1
GO:0006164	purine nucleotide biosynthetic process	28 of 4104 in the list	50 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1, CCG017995.1,CCG023640.1,CCG026898.1,CCG026812.1, CCG000148.1,CCG006529.1,CCG025348.1,CCG013365.1, CCG025989.2,CCG019619.1,CCG018659.2,CCG005924.2, CCG008422.1,CCG013999.1,CCG021336.1,CCG028305.1, CCG010112.1,CCG007417.1,CCG017330.1,CCG006791.1, CCG021110.1,CCG007724.1,CCG021934.1,CCG013643.1
GO:1901293	nucleoside phosphate biosynthetic process	48 of 4104 in the list	89 of 8404 in the genome	1	CCG014379.1,CCG015746.1,CCG004180.1,CCG017995.1, CCG023640.1,CCG026047.1,CCG006529.1,CCG025348.1, CCG025989.2,CCG019619.1,CCG007533.1,CCG008422.1, CCG025493.1,CCG000016.1,CCG026174.1,CCG021336.1, CCG028131.1,CCG013999.1,CCG010112.1,CCG007417.1, CCG007724.1,CCG013643.1,CCG017295.1,CCG015410.1, CCG002038.1,CCG025107.1,CCG009142.1,CCG026898.1, CCG015747.1,CCG026812.1,CCG007993.1,CCG000148.1, CCG013365.1,CCG023452.1,CCG005924.2,CCG018659.2, CCG014116.1,CCG013610.1,CCG016614.1,CCG028305.1, CCG009518.1,CCG004188.3,CCG017330.1,CCG010944.1, CCG006791.1,CCG021110.1,CCG026865.1,CCG021934.1

GO:1901565	organonitrogen compound catabolic process	90 of 4104 in the list	172 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG007060.1, CCG013000.1,CCG010111.1,CCG024327.1,CCG015386.1, CCG019020.1,CCG009243.1,CCG025108.1,CCG004020.1, CCG016477.1,CCG019834.1,CCG009607.1,CCG011006.1, CCG012048.1,CCG007827.1,CCG014434.1,CCG006421.1, CCG023963.3,CCG005029.1,CCG015610.1,CCG020799.1, CCG025027.1,CCG016370.1,CCG020793.1,CCG019103.1, CCG019629.2,CCG002917.1,CCG023890.1,CCG001082.1, CCG020909.1,CCG007532.1,CCG018447.1,CCG007531.1, CCG016966.1,CCG018820.3,CCG011722.1,CCG010019.1, CCG025179.1,CCG003063.1,CCG006777.1,CCG007203.1, CCG025973.1,CCG013637.1,CCG009424.1,CCG002418.1, CCG010418.1,CCG009080.1,CCG004869.1,CCG020154.1, CCG021117.1,CCG025396.1,CCG026953.1,CCG011721.1, CCG006924.1,CCG021220.1,CCG008510.1,CCG025962.1, CCG008748.1,CCG006059.1,CCG017543.1,CCG013641.1, CCG019243.1,CCG016027.1,CCG015289.1,CCG019470.1, CCG003495.1,CCG021411.1,CCG015907.1,CCG001859.1, CCG026336.1,CCG005886.1,CCG025131.2,CCG016542.1, CCG024829.1,CCG028235.1,CCG015654.1,CCG026154.1, CCG002852.1,CCG010864.1,CCG011789.1,CCG002417.1,

GO:0006725	cellular aromatic compound metabolic process	824 of 4104 in the list	1655 of 8404 in the genome	1	CCG017420.1,CCG027300.1,CCG014396.1,CCG006549.1, CCG026106.1,CCG006357.1,CCG009878.1,CCG024072.1, CCG026174.1,CCG020685.1,CCG013625.1,CCG004468.1, CCG023989.1,CCG016238.1,CCG024584.1,CCG001292.1, CCG018321.1,CCG002470.1,CCG005194.1,CCG001040.1, CCG014836.1,CCG025208.1,CCG025307.1,CCG019382.1, CCG016370.1,CCG016094.1,CCG027183.2,CCG023474.1, CCG010792.1,CCG004231.1,CCG012623.1,CCG005053.1, CCG010905.1,CCG011722.1,CCG020471.1,CCG021110.1, CCG010909.1,CCG023129.1,CCG028653.1,CCG021342.1, CCG024326.1,CCG014946.1,CCG020286.1,CCG002735.1, CCG027133.1,CCG021086.2,CCG014280.1,CCG015694.1, CCG013865.1,CCG025396.1,CCG006484.1,CCG026953.1, CCG001461.1,CCG023686.1,CCG004402.1,CCG019678.1, CCG003938.1,CCG023468.1,CCG025990.1,CCG013641.1, CCG015350.1,CCG003495.1,CCG021948.1,CCG011148.1, CCG020651.1,CCG025131.2,CCG005284.1,CCG004927.1, CCG023452.1,CCG009805.2,CCG002852.1,CCG019545.1, CCG003142.1,CCG021137.1,CCG013610.1,CCG001876.1, CCG012584.1,CCG013465.1,CCG009518.1,CCG024200.1, CCG010624.1,CCG023125.1,CCG016381.1,CCG011727.1, CCG026865.1,CCG017001.1,CCG024788.1,CCG007263.1, CCG021767.1,CCG004926.1,CCG001285.1,CCG004907.1, CCG010912.1,CCG004955.1,CCG015367.1,CCG003750.1, CCG005524.1,CCG026047.1,CCG011491.1,CCG024857.1, CCG022772.1,CCG010136.1,CCG005501.1,CCG003310.1, CCG026516.1,CCG024570.2,CCG018164.1,CCG013617.1, CCG004224.1,CCG010112.1,CCG022513.2,CCG028092.1, CCG018650.1,CCG000209.1,CCG016760.1,CCG021521.1, CCG007902.1,CCG023486.1,CCG024232.1,CCG006133.1,

GO:0046483	heterocycle metabolic process	821 of 4104 in the list	1649 of 8404 in the genome	1	CCG017420.1,CCG027300.1,CCG014396.1,CCG006549.1, CCG026106.1,CCG006357.1,CCG009878.1,CCG024072.1, CCG026174.1,CCG020685.1,CCG013625.1,CCG004468.1, CCG023989.1,CCG016238.1,CCG024584.1,CCG001292.1, CCG016220.1,CCG018321.1,CCG002470.1,CCG005194.1, CCG001040.1,CCG014836.1,CCG025208.1,CCG025307.1, CCG019382.1,CCG016370.1,CCG016094.1,CCG027183.2, CCG023474.1,CCG010792.1,CCG004231.1,CCG012623.1, CCG005053.1,CCG010905.1,CCG020471.1,CCG021110.1, CCG010909.1,CCG023129.1,CCG028653.1,CCG021342.1, CCG024326.1,CCG014946.1,CCG020286.1,CCG002735.1, CCG027133.1,CCG021086.2,CCG014280.1,CCG015694.1, CCG013865.1,CCG025396.1,CCG006484.1,CCG026953.1, CCG001461.1,CCG023686.1,CCG004402.1,CCG019678.1, CCG003938.1,CCG023468.1,CCG025990.1,CCG013641.1, CCG015350.1,CCG003495.1,CCG021948.1,CCG011148.1, CCG020651.1,CCG025131.2,CCG005284.1,CCG004927.1, CCG023452.1,CCG009805.2,CCG002852.1,CCG019545.1, CCG003142.1,CCG021137.1,CCG013610.1,CCG001876.1, CCG012584.1,CCG013465.1,CCG009518.1,CCG024200.1, CCG010624.1,CCG002231.1,CCG023125.1,CCG016381.1, CCG011727.1,CCG026865.1,CCG017001.1,CCG024788.1, CCG007263.1,CCG021767.1,CCG004926.1,CCG001285.1, CCG004907.1,CCG010912.1,CCG004955.1,CCG015367.1, CCG003750.1,CCG005524.1,CCG026047.1,CCG011491.1, CCG024857.1,CCG022772.1,CCG010136.1,CCG005501.1, CCG003310.1,CCG026516.1,CCG024570.2,CCG018164.1, CCG013617.1,CCG004224.1,CCG010112.1,CCG022513.2, CCG028092.1,CCG018650.1,CCG000209.1,CCG016760.1, CCG021521.1,CCG007902.1,CCG023486.1,CCG024232.1,
GO:0006486	protein glycosylation	20 of 4104 in the list	35 of 8404 in the genome	1	CCG017381.1,CCG018536.1,CCG023617.1,CCG027131.1, CCG017197.1,CCG013985.1,CCG014579.1,CCG012268.1, CCG007766.1,CCG001602.1,CCG016003.1,CCG009928.1, CCG004091.1,CCG006221.1,CCG019210.1,CCG009494.1, CCG003247.1,CCG025472.1,CCG010700.1,CCG018432.1

GO:0009101	glycoprotein biosynthetic process	20 of 4104 in the list	35 of 8404 in the genome	1	CCG017381.1,CCG018536.1,CCG023617.1,CCG027131.1, CCG017197.1,CCG013985.1,CCG014579.1,CCG012268.1, CCG007766.1,CCG001602.1,CCG016003.1,CCG009928.1, CCG004091.1,CCG006221.1,CCG019210.1,CCG009494.1, CCG003247.1,CCG025472.1,CCG010700.1,CCG018432.1
GO:0043413	macromolecule glycosylation	20 of 4104 in the list	35 of 8404 in the genome	1	CCG017381.1,CCG018536.1,CCG023617.1,CCG027131.1, CCG017197.1,CCG013985.1,CCG014579.1,CCG012268.1, CCG007766.1,CCG001602.1,CCG016003.1,CCG009928.1, CCG004091.1,CCG006221.1,CCG019210.1,CCG009494.1, CCG003247.1,CCG025472.1,CCG010700.1,CCG018432.1
GO:0005984	disaccharide metabolic process	5 of 4104 in the list	7 of 8404 in the genome	1	CCG019693.1,CCG014260.1,CCG019825.2,CCG024762.1, CCG013129.1
GO:0005991	trehalose metabolic process	5 of 4104 in the list	7 of 8404 in the genome	1	CCG019693.1,CCG014260.1,CCG019825.2,CCG024762.1, CCG013129.1
GO:0007050	cell cycle arrest	5 of 4104 in the list	7 of 8404 in the genome	1	CCG008308.1,CCG006063.1,CCG025057.1,CCG001795.1, CCG001794.1
GO:0009891	positive regulation of biosynthetic process	5 of 4104 in the list	7 of 8404 in the genome	1	CCG018164.1,CCG026216.1,CCG021944.1,CCG026155.1, CCG027118.1
GO:0010557	positive regulation of macromolecule biosynthetic	5 of 4104 in the list	7 of 8404 in the genome	1	CCG018164.1,CCG026216.1,CCG021944.1,CCG026155.1, CCG027118.1
GO:0010604	positive regulation of macromolecule metabolic process	5 of 4104 in the list	7 of 8404 in the genome	1	CCG018164.1,CCG026216.1,CCG021944.1,CCG026155.1, CCG027118.1
GO:0031328	positive regulation of cellular biosynthetic process	5 of 4104 in the list	7 of 8404 in the genome	1	CCG018164.1,CCG026216.1,CCG021944.1,CCG026155.1, CCG027118.1
GO:0032879	regulation of localization	5 of 4104 in the list	7 of 8404 in the genome	1	CCG026240.1,CCG001279.1,CCG013013.1,CCG015389.1, CCG008431.1
GO:0045786	negative regulation of cell cycle	5 of 4104 in the list	7 of 8404 in the genome	1	CCG008308.1,CCG006063.1,CCG025057.1,CCG001795.1, CCG001794.1
GO:0006066	alcohol metabolic process	11 of 4104 in the list	18 of 8404 in the genome	1	CCG012875.1,CCG024095.1,CCG006358.1,CCG023757.1, CCG015949.1,CCG013318.1,CCG005177.1,CCG014174.1, CCG016653.1,CCG008317.1,CCG015587.1

GO:0070085	glycosylation	21 of 4104 in the list	37 of 8404 in the genome	1	CCG017381.1,CCG018536.1,CCG023617.1,CCG027131.1, CCG017197.1,CCG013985.1,CCG014579.1,CCG012268.1, CCG007766.1,CCG001602.1,CCG006213.1,CCG016003.1, CCG009928.1,CCG004091.1,CCG006221.1,CCG019210.1, CCG009494.1,CCG003247.1,CCG025472.1,CCG010700.1,
GO:0030029	actin filament-based process	12 of 4104 in the list	20 of 8404 in the genome	1	CCG000469.1,CCG009090.1,CCG018647.1,CCG005579.1, CCG009641.1,CCG014817.2,CCG021366.1,CCG016992.2, CCG024028.1,CCG019356.1,CCG008834.1,CCG018646.1
GO:0030036	actin cytoskeleton organization	12 of 4104 in the list	20 of 8404 in the genome	1	CCG000469.1,CCG009090.1,CCG018647.1,CCG005579.1, CCG009641.1,CCG014817.2,CCG021366.1,CCG016992.2, CCG024028.1,CCG019356.1,CCG008834.1,CCG018646.1
GO:0006163	purine nucleotide metabolic process	91 of 4104 in the list	175 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1, CCG007060.1,CCG013000.1,CCG004309.1,CCG006529.1, CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1, CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1, CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1, CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1, CCG016370.1,CCG000148.1,CCG019103.1,CCG013365.1, CCG019629.2,CCG002917.1,CCG006486.1,CCG005924.2, CCG020909.1,CCG007532.1,CCG017330.1,CCG007531.1, CCG018447.1,CCG016966.1,CCG018820.3,CCG021110.1, CCG025179.1,CCG021934.1,CCG006777.1,CCG004308.1, CCG025973.1,CCG017995.1,CCG013637.1,CCG023640.1, CCG026314.1,CCG010418.1,CCG025348.1,CCG009080.1, CCG004869.1,CCG019619.1,CCG025396.1,CCG013999.1, CCG026953.1,CCG021336.1,CCG006924.1,CCG007417.1, CCG021220.1,CCG001066.1,CCG019866.1,CCG019678.1, CCG007724.1,CCG008748.1,CCG013641.1,CCG015410.1, CCG016027.1,CCG015289.1,CCG025107.1,CCG003495.1, CCG021411.1,CCG009142.1,CCG026898.1,CCG001859.1, CCG026812.1,CCG026336.1,CCG005886.1,CCG025131.2, CCG016542.1,CCG026154.1,CCG015654.1,CCG018659.2, CCG002852.1,CCG010864.1,CCG028305.1,CCG006791.1,
GO:0006213	pyrimidine nucleoside metabolic process	6 of 4104 in the list	9 of 8404 in the genome	1	CCG021110.1,CCG013610.1,CCG006529.1,CCG016614.1, CCG017995.1,CCG007417.1

GO:0006563	L-serine metabolic process	6 of 4104 in the list	9 of 8404 in the genome	1	CCG015568.1,CCG019954.3,CCG022025.2,CCG015567.1, CCG025636.2,CCG017201.1
GO:0006835	dicarboxylic acid transport	6 of 4104 in the list	9 of 8404 in the genome	1	CCG024382.1,CCG027758.1,CCG013708.1,CCG024383.1, CCG026707.1,CCG016959.1
GO:0009218	pyrimidine ribonucleotide metabolic process	6 of 4104 in the list	9 of 8404 in the genome	1	CCG021110.1,CCG013610.1,CCG006529.1,CCG016614.1, CCG017995.1,CCG007417.1
GO:0009220	pyrimidine ribonucleotide biosynthetic process	6 of 4104 in the list	9 of 8404 in the genome	1	CCG021110.1,CCG013610.1,CCG006529.1,CCG016614.1, CCG017995.1,CCG007417.1
GO:0046131	pyrimidine ribonucleoside metabolic process	6 of 4104 in the list	9 of 8404 in the genome	1	CCG021110.1,CCG013610.1,CCG006529.1,CCG016614.1, CCG017995.1,CCG007417.1
GO:0046132	pyrimidine ribonucleoside biosynthetic process	6 of 4104 in the list	9 of 8404 in the genome	1	CCG021110.1,CCG013610.1,CCG006529.1,CCG016614.1, CCG017995.1,CCG007417.1
GO:0046134	pyrimidine nucleoside biosynthetic process	6 of 4104 in the list	9 of 8404 in the genome	1	CCG021110.1,CCG013610.1,CCG006529.1,CCG016614.1, CCG017995.1,CCG007417.1
GO:1901070	guanosine-containing compound biosynthetic process	6 of 4104 in the list	9 of 8404 in the genome	1	CCG006791.1,CCG021110.1,CCG006529.1,CCG017995.1, CCG007417.1,CCG018659.2

GO:1901575	organic substance catabolic process	193 of 4104 in the list	380 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG027068.1, CCG013000.1,CCG013766.1,CCG024327.1,CCG024092.1, CCG015386.1,CCG019020.1,CCG003288.1,CCG025108.1, CCG003220.2,CCG020685.1,CCG022635.1,CCG006203.1, CCG006391.1,CCG004020.1,CCG009685.1,CCG002925.1, CCG019834.1,CCG025387.1,CCG022453.1,CCG023005.1, CCG024375.1,CCG003748.1,CCG009607.1,CCG011006.1, CCG027119.1,CCG004448.2,CCG005029.1,CCG012828.1, CCG015610.1,CCG020799.1,CCG025307.1,CCG025521.1, CCG016370.1,CCG028595.1,CCG026413.3,CCG006311.1, CCG005441.1,CCG002917.1,CCG023890.1,CCG002974.1, CCG013876.1,CCG011722.1,CCG010019.1,CCG025277.1, CCG003063.1,CCG008217.1,CCG003215.3,CCG009424.1, CCG011238.1,CCG002418.1,CCG019571.1,CCG010879.1, CCG020154.1,CCG004869.1,CCG009080.1,CCG001877.1, CCG007690.1,CCG004331.1,CCG025396.1,CCG026953.1, CCG008969.2,CCG011721.1,CCG006924.1,CCG021220.1, CCG008510.1,CCG025962.1,CCG013832.1,CCG017543.1, CCG013641.1,CCG015289.1,CCG021411.1,CCG003495.1, CCG001859.1,CCG001769.1,CCG027283.1,CCG022214.1, CCG009582.1,CCG025131.2,CCG024829.1,CCG002852.1, CCG011789.1,CCG022742.2,CCG017200.1,CCG023420.1, CCG002231.1,CCG027763.1,CCG005177.1,CCG007362.1, CCG021152.1,CCG023526.2,CCG019697.2,CCG011996.1, CCG026612.1,CCG008388.1,CCG003060.1,CCG005588.1, CCG001704.1,CCG007060.1,CCG007080.1,CCG005524.1, CCG001350.1,CCG010373.1,CCG010111.1,CCG019599.1, CCG000591.1,CCG009243.1,CCG012628.1,CCG006358.1, CCG016477.1,CCG012048.1,CCG007827.1,CCG023963.3, CCG006421.1,CCG014434.1,CCG022035.1,CCG021990.1,
GO:0006032	chitin catabolic process	14 of 4104 in the list	24 of 8404 in the genome	1	CCG021117.1,CCG015610.1,CCG002417.1,CCG023420.1, CCG004020.1,CCG016477.1,CCG002418.1,CCG025962.1, CCG020793.1,CCG010019.1,CCG012048.1,CCG011996.1, CCG024829.1,CCG023890.1

GO:0046348	amino sugar catabolic process	14 of 4104 in the list	24 of 8404 in the genome	1	CCG021117.1,CCG015610.1,CCG002417.1,CCG023420.1, CCG004020.1,CCG016477.1,CCG002418.1,CCG025962.1, CCG020793.1,CCG010019.1,CCG012048.1,CCG011996.1, CCG024829.1,CCG023890.1
GO:1901072	glucosamine-containing compound catabolic process	14 of 4104 in the list	24 of 8404 in the genome	1	CCG021117.1,CCG015610.1,CCG002417.1,CCG023420.1, CCG004020.1,CCG016477.1,CCG002418.1,CCG025962.1, CCG020793.1,CCG010019.1,CCG012048.1,CCG011996.1, CCG024829.1,CCG023890.1
GO:0006820	anion transport	29 of 4104 in the list	53 of 8404 in the genome	1	CCG024382.1,CCG017477.1,CCG004637.1,CCG006348.1, CCG012061.1,CCG027185.1,CCG001279.1,CCG006770.1, CCG023190.1,CCG016959.1,CCG023244.1,CCG026667.1, CCG024222.1,CCG027758.1,CCG005768.1,CCG026707.1, CCG024383.1,CCG005769.1,CCG018073.1,CCG020840.1, CCG008734.1,CCG019407.1,CCG026240.1,CCG013013.1, CCG028221.1,CCG013708.1,CCG010965.1,CCG023191.1,
GO:0000012	single strand break repair	2 of 4104 in the list	2 of 8404 in the genome	1	CCG012803.2,CCG024570.2
GO:0000045	autophagic vacuole assembly	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002366.1,CCG000834.1
GO:0000087	mitotic M phase	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015077.1,CCG000839.1
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	2 of 4104 in the list	2 of 8404 in the genome	1	CCG010489.1,CCG014461.1
GO:0000279	M phase	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015077.1,CCG000839.1
GO:0000724	double-strand break repair via homologous recombination	2 of 4104 in the list	2 of 8404 in the genome	1	CCG017444.1,CCG009962.1
GO:0000725	recombinational repair	2 of 4104 in the list	2 of 8404 in the genome	1	CCG017444.1,CCG009962.1
GO:0000902	cell morphogenesis	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015767.2,CCG006750.1
GO:0000910	cytokinesis	2 of 4104 in the list	2 of 8404 in the genome	1	CCG016878.1,CCG024595.1
GO:0001682	tRNA 5'-leader removal	2 of 4104 in the list	2 of 8404 in the genome	1	CCG004228.1,CCG023129.1
GO:0002526	acute inflammatory response	2 of 4104 in the list	2 of 8404 in the genome	1	CCG024173.1,CCG005170.1
GO:0006044	N-acetylglucosamine metabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025948.4,CCG020504.1
GO:0006084	acetyl-CoA metabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG018113.1,CCG013216.1
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	2 of 4104 in the list	2 of 8404 in the genome	1	CCG006459.1,CCG025163.3
GO:0006189	'de novo' IMP biosynthetic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG028305.1,CCG017330.1
GO:0006266	DNA ligation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG021045.1,CCG006919.1

GO:0006284	base-excision repair	2 of 4104 in the list	2 of 8404 in the genome	1	CCG024792.1,CCG015980.1
GO:0006304	DNA modification	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002946.1,CCG022674.1
GO:0006305	DNA alkylation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002946.1,CCG022674.1
GO:0006306	DNA methylation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002946.1,CCG022674.1
GO:0006379	mRNA cleavage	2 of 4104 in the list	2 of 8404 in the genome	1	CCG023511.1,CCG007636.1
GO:0006383	transcription from RNA polymerase III promoter	2 of 4104 in the list	2 of 8404 in the genome	1	CCG006484.1,CCG017046.2
GO:0006438	valyl-tRNA aminoacylation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG006188.1,CCG016238.1
GO:0006448	regulation of translational	2 of 4104 in the list	2 of 8404 in the genome	1	CCG006714.1,CCG026155.1
GO:0006493	protein O-linked glycosylation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG007766.1,CCG003247.1
GO:0006498	N-terminal protein lipidation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG022255.1,CCG025177.1
GO:0006499	N-terminal protein myristoylation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG022255.1,CCG025177.1
GO:0006562	proline catabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG007203.1,CCG002231.1
GO:0006577	amino-acid betaine metabolic	2 of 4104 in the list	2 of 8404 in the genome	1	CCG020559.1,CCG026331.1
GO:0006578	amino-acid betaine biosynthetic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG020559.1,CCG026331.1
GO:0006672	ceramide metabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG021085.1,CCG023779.1
GO:0006874	cellular calcium ion homeostasis	2 of 4104 in the list	2 of 8404 in the genome	1	CCG026796.1,CCG020400.2
GO:0006906	vesicle fusion	2 of 4104 in the list	2 of 8404 in the genome	1	CCG020315.1,CCG026620.1
GO:0006953	acute-phase response	2 of 4104 in the list	2 of 8404 in the genome	1	CCG024173.1,CCG005170.1
GO:0006954	inflammatory response	2 of 4104 in the list	2 of 8404 in the genome	1	CCG024173.1,CCG005170.1
GO:0007016	cytoskeletal anchoring at plasma membrane	2 of 4104 in the list	2 of 8404 in the genome	1	CCG014318.1,CCG003587.1
GO:0007026	negative regulation of microtubule depolymerization	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:0007040	lysosome organization	2 of 4104 in the list	2 of 8404 in the genome	1	CCG019082.1,CCG013509.1
GO:0008203	cholesterol metabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG024095.1,CCG015949.1
GO:0009065	glutamine family amino acid catabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG007203.1,CCG002231.1
GO:0009200	deoxyribonucleoside triphosphate metabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG010960.2,CCG016222.1
GO:0009211	pyrimidine deoxyribonucleoside triphosphate metabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG010960.2,CCG016222.1
GO:0009225	nucleotide-sugar metabolic	2 of 4104 in the list	2 of 8404 in the genome	1	CCG022027.1,CCG006998.1
GO:0009264	deoxyribonucleotide catabolic	2 of 4104 in the list	2 of 8404 in the genome	1	CCG001445.1,CCG001440.1

GO:0009266	response to temperature stimulus	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002446.2,CCG003657.2
GO:0009267	cellular response to starvation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002366.1,CCG000834.1
GO:0009405	pathogenesis	2 of 4104 in the list	2 of 8404 in the genome	1	CCG012551.1,CCG019159.1
GO:0009408	response to heat	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002446.2,CCG003657.2
GO:0009437	carnitine metabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG020559.1,CCG026331.1
GO:0009991	response to extracellular stimulus	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002366.1,CCG000834.1
GO:0010639	negative regulation of organelle organization	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:0010921	regulation of phosphatase activity	2 of 4104 in the list	2 of 8404 in the genome	1	CCG009450.1,CCG017560.1
GO:0016125	sterol metabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG024095.1,CCG015949.1
GO:0016197	endosomal transport	2 of 4104 in the list	2 of 8404 in the genome	1	CCG017209.1,CCG022927.1
GO:0016236	macroautophagy	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002366.1,CCG000834.1
GO:0016973	poly(A)+ mRNA export from	2 of 4104 in the list	2 of 8404 in the genome	1	CCG017874.1,CCG026989.1
GO:0018377	protein myristoylation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG022255.1,CCG025177.1
GO:0019310	inositol catabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG006358.1,CCG005177.1
GO:0019673	GDP-mannose metabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG022027.1,CCG006998.1
GO:0022403	cell cycle phase	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015077.1,CCG000839.1
GO:0030155	regulation of cell adhesion	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015389.1,CCG008431.1
GO:0030334	regulation of cell migration	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015389.1,CCG008431.1
GO:0030488	tRNA methylation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG004234.1,CCG023156.1
GO:0030518	intracellular steroid hormone receptor signaling pathway	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:0030522	intracellular receptor signaling pathway	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:0031110	regulation of microtubule polymerization or depolymerization	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:0031111	negative regulation of microtubule polymerization or depolymerization	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:0031114	regulation of microtubule depolymerization	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:0031145	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic	2 of 4104 in the list	2 of 8404 in the genome	1	CCG004331.1,CCG027068.1
GO:0031365	N-terminal protein amino acid modification	2 of 4104 in the list	2 of 8404 in the genome	1	CCG022255.1,CCG025177.1

GO:0031667	response to nutrient levels	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002366.1,CCG000834.1
GO:0031668	cellular response to extracellular stimulus	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002366.1,CCG000834.1
GO:0031669	cellular response to nutrient levels	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002366.1,CCG000834.1
GO:0032886	regulation of microtubule-based process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:0032989	cellular component	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015767.2,CCG006750.1
GO:0035075	response to ecdysone	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:0035076	ecdysone receptor-mediated signaling pathway	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:0035303	regulation of dephosphorylation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG009450.1,CCG017560.1
GO:0036314	response to sterol	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:0036315	cellular response to sterol	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:0040012	regulation of locomotion	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015389.1,CCG008431.1
GO:0040029	regulation of gene expression, epigenetic	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002946.1,CCG022674.1
GO:0042147	retrograde transport, endosome to Golgi	2 of 4104 in the list	2 of 8404 in the genome	1	CCG017209.1,CCG022927.1
GO:0042256	mature ribosome assembly	2 of 4104 in the list	2 of 8404 in the genome	1	CCG023663.1,CCG007518.1
GO:0042594	response to starvation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002366.1,CCG000834.1
GO:0043044	ATP-dependent chromatin	2 of 4104 in the list	2 of 8404 in the genome	1	CCG027348.1,CCG000575.1
GO:0043066	negative regulation of apoptotic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG020974.1,CCG004073.1
GO:0043069	negative regulation of programmed cell death	2 of 4104 in the list	2 of 8404 in the genome	1	CCG020974.1,CCG004073.1
GO:0043242	negative regulation of protein complex disassembly	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:0043543	protein acylation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG022255.1,CCG025177.1
GO:0043666	regulation of phosphoprotein phosphatase activity	2 of 4104 in the list	2 of 8404 in the genome	1	CCG009450.1,CCG017560.1
GO:0044275	cellular carbohydrate catabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG006358.1,CCG005177.1
GO:0044728	DNA methylation or demethylation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002946.1,CCG022674.1
GO:0045005	maintenance of fidelity involved in DNA-dependent DNA replication	2 of 4104 in the list	2 of 8404 in the genome	1	CCG018321.1,CCG026841.1

GO:0045116	protein neddylation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG013109.1,CCG007809.1
GO:0045329	carnitine biosynthetic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG020559.1,CCG026331.1
GO:0045995	regulation of embryonic	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015389.1,CCG008431.1
GO:0046080	dUTP metabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG010960.2,CCG016222.1
GO:0046164	alcohol catabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG006358.1,CCG005177.1
GO:0046174	polyol catabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG006358.1,CCG005177.1
GO:0046685	response to arsenic-containing substance	2 of 4104 in the list	2 of 8404 in the genome	1	CCG013113.1,CCG013809.1
GO:0048280	vesicle fusion with Golgi apparatus	2 of 4104 in the list	2 of 8404 in the genome	1	CCG020315.1,CCG026620.1
GO:0048478	replication fork protection	2 of 4104 in the list	2 of 8404 in the genome	1	CCG018321.1,CCG026841.1
GO:0050793	regulation of developmental	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015389.1,CCG008431.1
GO:0051090	regulation of sequence-specific DNA binding transcription factor	2 of 4104 in the list	2 of 8404 in the genome	1	CCG009894.1,CCG004151.1
GO:0051103	DNA ligation involved in DNA	2 of 4104 in the list	2 of 8404 in the genome	1	CCG021045.1,CCG006919.1
GO:0051129	negative regulation of cellular component organization	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:0051239	regulation of multicellular organismal process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015389.1,CCG008431.1
GO:0051270	regulation of cellular component movement	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015389.1,CCG008431.1
GO:0051494	negative regulation of cytoskeleton organization	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:0055074	calcium ion homeostasis	2 of 4104 in the list	2 of 8404 in the genome	1	CCG026796.1,CCG020400.2
GO:0060548	negative regulation of cell death	2 of 4104 in the list	2 of 8404 in the genome	1	CCG020974.1,CCG004073.1
GO:0070507	regulation of microtubule cytoskeleton organization	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:0071390	cellular response to ecdysone	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:0071496	cellular response to external	2 of 4104 in the list	2 of 8404 in the genome	1	CCG002366.1,CCG000834.1
GO:0071722	detoxification of arsenic-containing substance	2 of 4104 in the list	2 of 8404 in the genome	1	CCG013113.1,CCG013809.1
GO:0072503	cellular divalent inorganic cation homeostasis	2 of 4104 in the list	2 of 8404 in the genome	1	CCG026796.1,CCG020400.2
GO:0072507	divalent inorganic cation	2 of 4104 in the list	2 of 8404 in the genome	1	CCG026796.1,CCG020400.2
GO:0090329	regulation of DNA-dependent DNA replication	2 of 4104 in the list	2 of 8404 in the genome	1	CCG018321.1,CCG026841.1

GO:0097305	response to alcohol	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:0097306	cellular response to alcohol	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:1901616	organic hydroxy compound catabolic process	2 of 4104 in the list	2 of 8404 in the genome	1	CCG006358.1,CCG005177.1
GO:1901654	response to ketone	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:1901655	cellular response to ketone	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:1901700	response to oxygen-containing compound	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:1901701	cellular response to oxygen-containing compound	2 of 4104 in the list	2 of 8404 in the genome	1	CCG008741.1,CCG008742.1
GO:1901879	regulation of protein	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:1901880	negative regulation of protein depolymerization	2 of 4104 in the list	2 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:2000026	regulation of multicellular organismal development	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015389.1,CCG008431.1
GO:2000104	negative regulation of DNA-dependent DNA replication	2 of 4104 in the list	2 of 8404 in the genome	1	CCG018321.1,CCG026841.1
GO:2000145	regulation of cell motility	2 of 4104 in the list	2 of 8404 in the genome	1	CCG015389.1,CCG008431.1
GO:0006506	GPI anchor biosynthetic process	15 of 4104 in the list	26 of 8404 in the genome	1	CCG022209.1,CCG017241.1,CCG028332.1,CCG007330.1, CCG009434.1,CCG014839.1,CCG000663.1,CCG013131.1, CCG026370.1,CCG011531.1,CCG024612.1,CCG025889.1, CCG000552.1,CCG004806.1,CCG024760.1
GO:0006661	phosphatidylinositol biosynthetic process	15 of 4104 in the list	26 of 8404 in the genome	1	CCG022209.1,CCG017241.1,CCG028332.1,CCG007330.1, CCG009434.1,CCG014839.1,CCG000663.1,CCG013131.1, CCG026370.1,CCG011531.1,CCG024612.1,CCG025889.1, CCG000552.1,CCG004806.1,CCG024760.1
GO:0009247	glycolipid biosynthetic process	15 of 4104 in the list	26 of 8404 in the genome	1	CCG022209.1,CCG017241.1,CCG028332.1,CCG007330.1, CCG009434.1,CCG014839.1,CCG000663.1,CCG013131.1, CCG026370.1,CCG011531.1,CCG024612.1,CCG025889.1, CCG000552.1,CCG004806.1,CCG024760.1
GO:0046467	membrane lipid biosynthetic process	15 of 4104 in the list	26 of 8404 in the genome	1	CCG022209.1,CCG017241.1,CCG028332.1,CCG007330.1, CCG009434.1,CCG014839.1,CCG000663.1,CCG013131.1, CCG026370.1,CCG011531.1,CCG024612.1,CCG025889.1, CCG000552.1,CCG004806.1,CCG024760.1

GO:0006505	GPI anchor metabolic process	16 of 4104 in the list	28 of 8404 in the genome	1	CCG025233.1,CCG022209.1,CCG017241.1,CCG009434.1, CCG014839.1,CCG000663.1,CCG013131.1,CCG026370.1, CCG025889.1,CCG004806.1,CCG000552.1,CCG024760.1, CCG028332.1,CCG007330.1,CCG011531.1,CCG024612.1
GO:0006664	glycolipid metabolic process	16 of 4104 in the list	28 of 8404 in the genome	1	CCG025233.1,CCG022209.1,CCG017241.1,CCG009434.1, CCG014839.1,CCG000663.1,CCG013131.1,CCG026370.1, CCG025889.1,CCG004806.1,CCG000552.1,CCG024760.1, CCG028332.1,CCG007330.1,CCG011531.1,CCG024612.1
GO:0045017	glycerolipid biosynthetic process	16 of 4104 in the list	28 of 8404 in the genome	1	CCG022209.1,CCG017241.1,CCG009434.1,CCG014839.1, CCG000663.1,CCG013131.1,CCG026370.1,CCG025889.1, CCG004806.1,CCG000552.1,CCG024760.1,CCG028332.1, CCG007330.1,CCG011531.1,CCG021610.1,CCG024612.1
GO:0046474	glycerophospholipid biosynthetic process	16 of 4104 in the list	28 of 8404 in the genome	1	CCG022209.1,CCG017241.1,CCG009434.1,CCG014839.1, CCG000663.1,CCG013131.1,CCG026370.1,CCG025889.1, CCG004806.1,CCG000552.1,CCG024760.1,CCG028332.1, CCG007330.1,CCG011531.1,CCG021610.1,CCG024612.1
GO:0006401	RNA catabolic process	7 of 4104 in the list	11 of 8404 in the genome	1	CCG018917.1,CCG020685.1,CCG005524.1,CCG004448.2, CCG026612.1,CCG019674.1,CCG007690.1
GO:0006801	superoxide metabolic process	7 of 4104 in the list	11 of 8404 in the genome	1	CCG011248.1,CCG008803.1,CCG026431.1,CCG012208.1, CCG017478.1,CCG012209.1,CCG015612.1
GO:0072593	reactive oxygen species metabolic process	7 of 4104 in the list	11 of 8404 in the genome	1	CCG011248.1,CCG008803.1,CCG026431.1,CCG012208.1, CCG017478.1,CCG012209.1,CCG015612.1
GO:0006915	apoptotic process	19 of 4104 in the list	34 of 8404 in the genome	1	CCG010441.1,CCG022871.1,CCG009690.1,CCG009015.1, CCG018585.3,CCG027145.1,CCG021664.1,CCG009582.1, CCG016399.1,CCG022095.1,CCG024631.1,CCG018248.1, CCG009405.1,CCG015407.1,CCG011446.1,CCG003007.1, CCG009823.1,CCG021236.1,CCG000445.1
GO:0008219	cell death	19 of 4104 in the list	34 of 8404 in the genome	1	CCG010441.1,CCG022871.1,CCG009690.1,CCG009015.1, CCG018585.3,CCG027145.1,CCG021664.1,CCG009582.1, CCG016399.1,CCG022095.1,CCG024631.1,CCG018248.1, CCG009405.1,CCG015407.1,CCG011446.1,CCG003007.1, CCG009823.1,CCG021236.1,CCG000445.1

GO:0012501	programmed cell death	19 of 4104 in the list	34 of 8404 in the genome	1	CCG010441.1,CCG022871.1,CCG009690.1,CCG009015.1, CCG018585.3,CCG027145.1,CCG021664.1,CCG009582.1, CCG016399.1,CCG022095.1,CCG024631.1,CCG018248.1, CCG009405.1,CCG015407.1,CCG011446.1,CCG003007.1, CCG009823.1,CCG021236.1,CCG000445.1
GO:0016265	death	19 of 4104 in the list	34 of 8404 in the genome	1	CCG010441.1,CCG022871.1,CCG009690.1,CCG009015.1, CCG018585.3,CCG027145.1,CCG021664.1,CCG009582.1, CCG016399.1,CCG022095.1,CCG024631.1,CCG018248.1, CCG009405.1,CCG015407.1,CCG011446.1,CCG003007.1, CCG009823.1,CCG021236.1,CCG000445.1
GO:0006546	glycine catabolic process	8 of 4104 in the list	13 of 8404 in the genome	1	CCG019834.1,CCG010111.1,CCG025108.1,CCG001082.1, CCG003063.1,CCG020154.1,CCG008510.1,CCG008388.1
GO:0009071	serine family amino acid catabolic process	8 of 4104 in the list	13 of 8404 in the genome	1	CCG019834.1,CCG010111.1,CCG025108.1,CCG001082.1, CCG003063.1,CCG020154.1,CCG008510.1,CCG008388.1
GO:0009112	nucleobase metabolic process	8 of 4104 in the list	13 of 8404 in the genome	1	CCG017175.1,CCG018108.1,CCG016614.1,CCG026852.1, CCG004257.1,CCG005938.1,CCG025940.1,CCG017331.1
GO:0008654	phospholipid biosynthetic process	25 of 4104 in the list	46 of 8404 in the genome	1	CCG004532.1,CCG022209.1,CCG017241.1,CCG009434.1, CCG014839.1,CCG000663.1,CCG013131.1,CCG026370.1, CCG012308.1,CCG016653.1,CCG025889.1,CCG004806.1, CCG000552.1,CCG024760.1,CCG022352.1,CCG028332.1, CCG023757.1,CCG007330.1,CCG006965.1,CCG014174.1, CCG011531.1,CCG024612.1,CCG021610.1,CCG024155.1,

GO:0006139	nucleobase-containing compound metabolic process	790 of 4104 in the list	1595 of 8404 in the genome	1	CCG017420.1,CCG027300.1,CCG014396.1,CCG006549.1, CCG026106.1,CCG006357.1,CCG009878.1,CCG024072.1, CCG026174.1,CCG020685.1,CCG013625.1,CCG004468.1, CCG023989.1,CCG016238.1,CCG024584.1,CCG001292.1, CCG018321.1,CCG002470.1,CCG005194.1,CCG001040.1, CCG014836.1,CCG025208.1,CCG025307.1,CCG019382.1, CCG016370.1,CCG016094.1,CCG027183.2,CCG023474.1, CCG010792.1,CCG004231.1,CCG012623.1,CCG010905.1, CCG020471.1,CCG021110.1,CCG010909.1,CCG023129.1, CCG028653.1,CCG021342.1,CCG024326.1,CCG014946.1, CCG020286.1,CCG002735.1,CCG027133.1,CCG014280.1, CCG015694.1,CCG013865.1,CCG025396.1,CCG006484.1, CCG026953.1,CCG001461.1,CCG023686.1,CCG004402.1, CCG019678.1,CCG003938.1,CCG023468.1,CCG025990.1, CCG013641.1,CCG015350.1,CCG003495.1,CCG021948.1, CCG011148.1,CCG020651.1,CCG025131.2,CCG005284.1, CCG004927.1,CCG023452.1,CCG009805.2,CCG002852.1, CCG019545.1,CCG003142.1,CCG021137.1,CCG013610.1, CCG001876.1,CCG012584.1,CCG013465.1,CCG009518.1, CCG024200.1,CCG010624.1,CCG023125.1,CCG016381.1, CCG011727.1,CCG026865.1,CCG017001.1,CCG024788.1, CCG007263.1,CCG021767.1,CCG004926.1,CCG001285.1, CCG004907.1,CCG010912.1,CCG004955.1,CCG015367.1, CCG003750.1,CCG005524.1,CCG026047.1,CCG024857.1, CCG022772.1,CCG010136.1,CCG005501.1,CCG003310.1, CCG026516.1,CCG024570.2,CCG018164.1,CCG013617.1, CCG004224.1,CCG010112.1,CCG022513.2,CCG028092.1, CCG018650.1,CCG000209.1,CCG016760.1,CCG021521.1, CCG007902.1,CCG023486.1,CCG024232.1,CCG006133.1, CCG001395.1,CCG016557.1,CCG023184.1,CCG021990.1,

GO:0034641	cellular nitrogen compound metabolic process	829 of 4104 in the list	1676 of 8404 in the genome	1	CCG017420.1,CCG027300.1,CCG014396.1,CCG006549.1, CCG026106.1,CCG006357.1,CCG009878.1,CCG024072.1, CCG012875.1,CCG026174.1,CCG020685.1,CCG013625.1, CCG004468.1,CCG023989.1,CCG016238.1,CCG024584.1, CCG001292.1,CCG018321.1,CCG002470.1,CCG005194.1, CCG001040.1,CCG014836.1,CCG025208.1,CCG025307.1, CCG019382.1,CCG016370.1,CCG016094.1,CCG027183.2, CCG023474.1,CCG010792.1,CCG004231.1,CCG012623.1, CCG005053.1,CCG010905.1,CCG020471.1,CCG021110.1, CCG010909.1,CCG023129.1,CCG028653.1,CCG021342.1, CCG024326.1,CCG014946.1,CCG020286.1,CCG002735.1, CCG027133.1,CCG021086.2,CCG014280.1,CCG015694.1, CCG013865.1,CCG025396.1,CCG006484.1,CCG026953.1, CCG001461.1,CCG023686.1,CCG004402.1,CCG019678.1, CCG003938.1,CCG023468.1,CCG025990.1,CCG013641.1, CCG006821.1,CCG015350.1,CCG003495.1,CCG021948.1, CCG011148.1,CCG020651.1,CCG025131.2,CCG005284.1, CCG004927.1,CCG023452.1,CCG009805.2,CCG002852.1, CCG019545.1,CCG003142.1,CCG021137.1,CCG013610.1, CCG001876.1,CCG012584.1,CCG013465.1,CCG009518.1, CCG024200.1,CCG010624.1,CCG023125.1,CCG016381.1, CCG011727.1,CCG026865.1,CCG017001.1,CCG024788.1, CCG007263.1,CCG021767.1,CCG004926.1,CCG001285.1, CCG004907.1,CCG010912.1,CCG004955.1,CCG015367.1, CCG003750.1,CCG005524.1,CCG026047.1,CCG011491.1, CCG024857.1,CCG022772.1,CCG010136.1,CCG009333.1, CCG005501.1,CCG003310.1,CCG026516.1,CCG024570.2, CCG018164.1,CCG013617.1,CCG004224.1,CCG010112.1, CCG022513.2,CCG028092.1,CCG018650.1,CCG000209.1, CCG016760.1,CCG021521.1,CCG007902.1,CCG023486.1,

GO:0008152	metabolic process	2768 of 4104 in the list	5643 of 8404 in the genome	1	CCG014531.2,CCG006922.1,CCG017420.1,CCG027068.1, CCG004122.1,CCG004887.1,CCG002508.1,CCG026106.1, CCG027449.1,CCG000746.1,CCG016952.1,CCG012875.1, CCG025108.1,CCG028016.1,CCG004468.1,CCG023989.1, CCG012726.1,CCG024584.1,CCG004020.1,CCG013059.1, CCG025836.1,CCG012949.1,CCG017266.1,CCG006875.2, CCG011763.1,CCG025208.1,CCG021479.1,CCG003362.1, CCG023381.1,CCG019382.1,CCG016094.1,CCG026413.3, CCG023474.1,CCG017255.1,CCG000948.1,CCG026871.2, CCG010792.1,CCG022025.2,CCG005053.1,CCG021616.1, CCG003767.1,CCG010905.1,CCG008270.1,CCG007696.1, CCG021110.1,CCG009270.1,CCG024612.1,CCG003624.1, CCG028653.1,CCG013109.1,CCG018625.1,CCG006465.1, CCG019571.1,CCG015694.1,CCG018788.1,CCG002982.1, CCG012083.1,CCG023451.1,CCG027190.1,CCG024119.1, CCG023686.1,CCG013641.1,CCG015350.1,CCG021948.1, CCG007467.1,CCG004927.1,CCG024903.1,CCG021137.1, CCG022056.1,CCG013610.1,CCG001876.1,CCG013465.1, CCG018688.1,CCG006456.1,CCG024200.1,CCG008902.1, CCG020663.1,CCG023458.1,CCG025096.1,CCG024708.1, CCG024865.1,CCG004926.1,CCG006928.1,CCG004532.1, CCG000789.1,CCG019844.1,CCG017381.1,CCG010912.1, CCG001704.1,CCG005524.1,CCG024784.1,CCG001289.1, CCG011547.1,CCG013640.1,CCG008404.1,CCG010136.1, CCG027015.1,CCG022370.1,CCG007729.1,CCG020803.1, CCG020179.1,CCG010112.1,CCG022513.2,CCG004986.1, CCG007750.2,CCG027989.1,CCG025707.1,CCG028092.1, CCG019831.2,CCG019825.2,CCG011793.1,CCG001395.1, CCG024155.1,CCG016557.1,CCG007395.1,CCG021990.1, CCG002514.1,CCG027000.1,CCG006804.1,CCG007814.1,
GO:0000097	sulfur amino acid biosynthetic process	3 of 4104 in the list	4 of 8404 in the genome	1	CCG015568.1,CCG015567.1,CCG025636.2
GO:0000394	RNA splicing, via endonucleolytic cleavage and ligation	3 of 4104 in the list	4 of 8404 in the genome	1	CCG000583.2,CCG009393.1,CCG000939.1
GO:0000726	non-recombinational repair	3 of 4104 in the list	4 of 8404 in the genome	1	CCG018472.1,CCG004233.1,CCG023155.1

GO:0006021	inositol biosynthetic process	3 of 4104 in the list	4 of 8404 in the genome	1	CCG014174.1,CCG023757.1,CCG016653.1
GO:0006303	double-strand break repair via nonhomologous end joining	3 of 4104 in the list	4 of 8404 in the genome	1	CCG018472.1,CCG004233.1,CCG023155.1
GO:0006388	tRNA splicing, via endonucleolytic cleavage and ligation	3 of 4104 in the list	4 of 8404 in the genome	1	CCG000583.2,CCG009393.1,CCG000939.1
GO:0006428	isoleucyl-tRNA aminoacylation	3 of 4104 in the list	4 of 8404 in the genome	1	CCG009878.1,CCG006231.1,CCG003528.1
GO:0006433	prolyl-tRNA aminoacylation	3 of 4104 in the list	4 of 8404 in the genome	1	CCG001811.1,CCG002018.1,CCG024526.1
GO:0006434	seryl-tRNA aminoacylation	3 of 4104 in the list	4 of 8404 in the genome	1	CCG019545.1,CCG021716.1,CCG014396.1
GO:0006535	cysteine biosynthetic process from serine	3 of 4104 in the list	4 of 8404 in the genome	1	CCG015568.1,CCG015567.1,CCG025636.2
GO:0006842	tricarboxylic acid transport	3 of 4104 in the list	4 of 8404 in the genome	1	CCG008734.1,CCG004637.1,CCG010965.1
GO:0008616	queuosine biosynthetic process	3 of 4104 in the list	4 of 8404 in the genome	1	CCG027125.1,CCG004440.1,CCG010460.1
GO:0009186	deoxyribonucleoside diphosphate metabolic process	3 of 4104 in the list	4 of 8404 in the genome	1	CCG000217.1,CCG004191.1,CCG014116.1
GO:0009653	anatomical structure morphogenesis	3 of 4104 in the list	4 of 8404 in the genome	1	CCG015767.2,CCG006750.1,CCG028121.1
GO:0010035	response to inorganic substance	3 of 4104 in the list	4 of 8404 in the genome	1	CCG017154.1,CCG026054.2,CCG026055.1
GO:0010038	response to metal ion	3 of 4104 in the list	4 of 8404 in the genome	1	CCG017154.1,CCG026054.2,CCG026055.1
GO:0015746	citrate transport	3 of 4104 in the list	4 of 8404 in the genome	1	CCG008734.1,CCG004637.1,CCG010965.1
GO:0019344	cysteine biosynthetic process	3 of 4104 in the list	4 of 8404 in the genome	1	CCG015568.1,CCG015567.1,CCG025636.2
GO:0030031	cell projection assembly	3 of 4104 in the list	4 of 8404 in the genome	1	CCG018859.3,CCG017033.1,CCG015583.1
GO:0045980	negative regulation of nucleotide metabolic process	3 of 4104 in the list	4 of 8404 in the genome	1	CCG000890.1,CCG028409.1,CCG002823.1
GO:0046116	queuosine metabolic process	3 of 4104 in the list	4 of 8404 in the genome	1	CCG027125.1,CCG004440.1,CCG010460.1
GO:0046173	polyol biosynthetic process	3 of 4104 in the list	4 of 8404 in the genome	1	CCG014174.1,CCG023757.1,CCG016653.1
GO:0046847	filopodium assembly	3 of 4104 in the list	4 of 8404 in the genome	1	CCG018859.3,CCG017033.1,CCG015583.1
GO:0051301	cell division	3 of 4104 in the list	4 of 8404 in the genome	1	CCG018249.1,CCG016878.1,CCG024595.1
GO:0090305	nucleic acid phosphodiester bond hydrolysis	3 of 4104 in the list	4 of 8404 in the genome	1	CCG023511.1,CCG009582.1,CCG007636.1

GO:1901136	carbohydrate derivative catabolic process	77 of 4104 in the list	150 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG007060.1,CCG013000.1,CCG024327.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG004020.1,CCG016477.1,CCG009685.1,CCG009607.1,CCG011006.1,CCG012048.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG005029.1,CCG015610.1,CCG020799.1,CCG025027.1,CCG016370.1,CCG020793.1,CCG019103.1,CCG019629.2,CCG002917.1,CCG023890.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG010019.1,CCG025179.1,CCG006777.1,CCG025973.1,CCG013637.1,CCG002418.1,CCG001440.1,CCG010418.1,CCG009080.1,CCG004869.1,CCG021117.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG025962.1,CCG012164.1,CCG008748.1,CCG013641.1,CCG016027.1,CCG019470.1,CCG015289.1,CCG003495.1,CCG021411.1,CCG015907.1,CCG001859.1,CCG026336.1,CCG005886.1,CCG025131.2,CCG016542.1,CCG024829.1,CCG028235.1,CCG015654.1,CCG026154.1,CCG002852.1,CCG010864.1,CCG001445.1,CCG002417.1,CCG023420.1,CCG021152.1,CCG023526.2,CCG011996.1
GO:1901068	guanosine-containing compound metabolic process	60 of 4104 in the list	116 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG017995.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG006529.1,CCG004869.1,CCG009080.1,CCG024327.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG007417.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG019629.2,CCG005886.1,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG018659.2,CCG010864.1,CCG002852.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG006791.1,CCG021110.1,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:0006366	transcription from RNA polymerase II promoter	14 of 4104 in the list	25 of 8404 in the genome	1	CCG000158.1,CCG017812.1,CCG020286.1,CCG021083.1,CCG023775.1,CCG020044.1,CCG001292.1,CCG011083.1,CCG020129.1,CCG020460.1,CCG025691.1,CCG010175.1,CCG023184.1,CCG026882.1

GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	4 of 4104 in the list	6 of 8404 in the genome	1	CCG020879.1,CCG001649.1,CCG024297.1,CCG006864.1
GO:0006165	nucleoside diphosphate phosphorylation	4 of 4104 in the list	6 of 8404 in the genome	1	CCG021110.1,CCG006529.1,CCG017995.1,CCG007417.1
GO:0006183	GTP biosynthetic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG021110.1,CCG006529.1,CCG017995.1,CCG007417.1
GO:0006228	UTP biosynthetic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG021110.1,CCG006529.1,CCG017995.1,CCG007417.1
GO:0006241	CTP biosynthetic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG021110.1,CCG006529.1,CCG017995.1,CCG007417.1
GO:0006419	alanyl-tRNA aminoacylation	4 of 4104 in the list	6 of 8404 in the genome	1	CCG000138.1,CCG023277.1,CCG008789.1,CCG010191.3
GO:0009074	aromatic amino acid family catabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG011789.1,CCG011721.1,CCG006059.1,CCG011722.1
GO:0009148	pyrimidine nucleoside triphosphate biosynthetic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG021110.1,CCG006529.1,CCG017995.1,CCG007417.1
GO:0009208	pyrimidine ribonucleoside triphosphate metabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG021110.1,CCG006529.1,CCG017995.1,CCG007417.1
GO:0009209	pyrimidine ribonucleoside triphosphate biosynthetic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG021110.1,CCG006529.1,CCG017995.1,CCG007417.1
GO:0009219	pyrimidine deoxyribonucleotide metabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG010960.2,CCG016222.1,CCG004180.1,CCG014116.1
GO:0009312	oligosaccharide biosynthetic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG019693.1,CCG014260.1,CCG024762.1,CCG013129.1
GO:0009394	2'-deoxyribonucleotide metabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG010960.2,CCG016222.1,CCG004180.1,CCG014116.1
GO:0010563	negative regulation of phosphorus metabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG000890.1,CCG028409.1,CCG002823.1,CCG021794.1
GO:0010941	regulation of cell death	4 of 4104 in the list	6 of 8404 in the genome	1	CCG020974.1,CCG007246.2,CCG004073.1,CCG007684.1
GO:0019692	deoxyribose phosphate metabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG010960.2,CCG016222.1,CCG004180.1,CCG014116.1
GO:0042981	regulation of apoptotic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG020974.1,CCG007246.2,CCG004073.1,CCG007684.1
GO:0043067	regulation of programmed cell death	4 of 4104 in the list	6 of 8404 in the genome	1	CCG020974.1,CCG007246.2,CCG004073.1,CCG007684.1
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG018164.1,CCG026216.1,CCG021944.1,CCG027118.1

GO:0045936	negative regulation of phosphate metabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG000890.1,CCG028409.1,CCG002823.1,CCG021794.1
GO:0046036	CTP metabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG021110.1,CCG006529.1,CCG017995.1,CCG007417.1
GO:0046051	UTP metabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG021110.1,CCG006529.1,CCG017995.1,CCG007417.1
GO:0046939	nucleotide phosphorylation	4 of 4104 in the list	6 of 8404 in the genome	1	CCG021110.1,CCG006529.1,CCG017995.1,CCG007417.1
GO:0051173	positive regulation of nitrogen compound metabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG018164.1,CCG026216.1,CCG021944.1,CCG027118.1
GO:0051254	positive regulation of RNA metabolic process	4 of 4104 in the list	6 of 8404 in the genome	1	CCG018164.1,CCG026216.1,CCG021944.1,CCG027118.1
GO:0070925	organelle assembly	4 of 4104 in the list	6 of 8404 in the genome	1	CCG023663.1,CCG002366.1,CCG007518.1,CCG000834.1
GO:0046039	GTP metabolic process	58 of 4104 in the list	113 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG017995.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG006529.1,CCG004869.1,CCG009080.1,CCG024327.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG007417.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG019629.2,CCG005886.1,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021110.1,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:0044283	small molecule biosynthetic process	53 of 4104 in the list	103 of 8404 in the genome	1	CCG007203.1,CCG010174.2,CCG019954.3,CCG009244.1,CCG012408.1,CCG011491.1,CCG015921.1,CCG020559.1,CCG009333.1,CCG028131.1,CCG017894.1,CCG013043.1,CCG017097.1,CCG016220.1,CCG015568.1,CCG016315.1,CCG021610.1,CCG020441.1,CCG027312.1,CCG006821.1,CCG000682.1,CCG008932.1,CCG026536.1,CCG003865.1,CCG002897.1,CCG010561.1,CCG026331.1,CCG001423.1,CCG016653.1,CCG022025.2,CCG025636.2,CCG008860.1,CCG018615.3,CCG017201.1,CCG017111.1,CCG025731.1,CCG015276.2,CCG024095.1,CCG022773.2,CCG026099.1,CCG023757.1,CCG024133.1,CCG002231.1,CCG015943.1,CCG016955.1,CCG014174.1,CCG026155.1,CCG003751.1,CCG025897.1,CCG006009.1,CCG003871.1,CCG015567.1,CCG019909.1

GO:0016053	organic acid biosynthetic process	47 of 4104 in the list	91 of 8404 in the genome	1	CCG007203.1,CCG010174.2,CCG019954.3,CCG009244.1,CCG012408.1,CCG011491.1,CCG015921.1,CCG020559.1,CCG009333.1,CCG028131.1,CCG017894.1,CCG013043.1,CCG017097.1,CCG016220.1,CCG015568.1,CCG016315.1,CCG021610.1,CCG020441.1,CCG027312.1,CCG006821.1,CCG000682.1,CCG008932.1,CCG003865.1,CCG002897.1,CCG010561.1,CCG026331.1,CCG001423.1,CCG022025.2,CCG025636.2,CCG008860.1,CCG018615.3,CCG017201.1,CCG017111.1,CCG025731.1,CCG015276.2,CCG022773.2,CCG026099.1,CCG024133.1,CCG002231.1,CCG015943.1,CCG016955.1,CCG026155.1,CCG025897.1,CCG003751.1,CCG003871.1,CCG015567.1,CCG019909.1
GO:0046394	carboxylic acid biosynthetic process	47 of 4104 in the list	91 of 8404 in the genome	1	CCG007203.1,CCG010174.2,CCG019954.3,CCG009244.1,CCG012408.1,CCG011491.1,CCG015921.1,CCG020559.1,CCG009333.1,CCG028131.1,CCG017894.1,CCG013043.1,CCG017097.1,CCG016220.1,CCG015568.1,CCG016315.1,CCG021610.1,CCG020441.1,CCG027312.1,CCG006821.1,CCG000682.1,CCG008932.1,CCG003865.1,CCG002897.1,CCG010561.1,CCG026331.1,CCG001423.1,CCG022025.2,CCG025636.2,CCG008860.1,CCG018615.3,CCG017201.1,CCG017111.1,CCG025731.1,CCG015276.2,CCG022773.2,CCG026099.1,CCG024133.1,CCG002231.1,CCG015943.1,CCG016955.1,CCG026155.1,CCG025897.1,CCG003751.1,CCG003871.1,CCG015567.1,CCG019909.1
GO:0006402	mRNA catabolic process	5 of 4104 in the list	8 of 8404 in the genome	1	CCG018917.1,CCG005524.1,CCG004448.2,CCG026612.1,CCG007690.1
GO:0006476	protein deacetylation	5 of 4104 in the list	8 of 8404 in the genome	1	CCG022056.1,CCG013028.1,CCG016480.1,CCG000835.1,CCG020863.1
GO:0006665	sphingolipid metabolic process	5 of 4104 in the list	8 of 8404 in the genome	1	CCG021085.1,CCG017994.1,CCG023779.1,CCG019082.1,CCG013509.1
GO:0007160	cell-matrix adhesion	5 of 4104 in the list	8 of 8404 in the genome	1	CCG004279.1,CCG020708.1,CCG000526.1,CCG008809.1,CCG002875.1
GO:0031589	cell-substrate adhesion	5 of 4104 in the list	8 of 8404 in the genome	1	CCG004279.1,CCG020708.1,CCG000526.1,CCG008809.1,CCG002875.1
GO:0035601	protein deacylation	5 of 4104 in the list	8 of 8404 in the genome	1	CCG022056.1,CCG013028.1,CCG016480.1,CCG000835.1,CCG020863.1
GO:0006730	one-carbon metabolic process	6 of 4104 in the list	10 of 8404 in the genome	1	CCG012781.1,CCG008960.1,CCG023355.1,CCG026511.1,CCG023354.1,CCG008959.2

GO:0045892	negative regulation of transcription, DNA-templated	6 of 4104 in the list	10 of 8404 in the genome	1	CCG010489.1,CCG003390.1,CCG025132.1,CCG005898.1,CCG004838.1,CCG014461.1
GO:0051253	negative regulation of RNA metabolic process	6 of 4104 in the list	10 of 8404 in the genome	1	CCG010489.1,CCG003390.1,CCG025132.1,CCG005898.1,CCG004838.1,CCG014461.1
GO:0006720	isoprenoid metabolic process	7 of 4104 in the list	12 of 8404 in the genome	1	CCG003249.1,CCG022134.1,CCG001102.1,CCG005923.1,CCG019035.1,CCG015411.1,CCG012002.1
GO:0008299	isoprenoid biosynthetic process	7 of 4104 in the list	12 of 8404 in the genome	1	CCG003249.1,CCG022134.1,CCG001102.1,CCG005923.1,CCG019035.1,CCG015411.1,CCG012002.1
GO:0009311	oligosaccharide metabolic process	7 of 4104 in the list	12 of 8404 in the genome	1	CCG019693.1,CCG011451.2,CCG014260.1,CCG022108.2,CCG019825.2,CCG024762.1,CCG013129.1
GO:0046112	nucleobase biosynthetic process	7 of 4104 in the list	12 of 8404 in the genome	1	CCG017175.1,CCG018108.1,CCG016614.1,CCG004257.1,CCG005938.1,CCG025940.1,CCG017331.1
GO:0007167	enzyme linked receptor protein signaling pathway	8 of 4104 in the list	14 of 8404 in the genome	1	CCG018533.1,CCG018494.1,CCG022929.1,CCG010631.1,CCG022741.1,CCG016307.1,CCG020978.1,CCG021354.1
GO:0019751	polyol metabolic process	8 of 4104 in the list	14 of 8404 in the genome	1	CCG006358.1,CCG023757.1,CCG013318.1,CCG005177.1,CCG014174.1,CCG016653.1,CCG008317.1,CCG015587.1
GO:0022406	membrane docking	8 of 4104 in the list	14 of 8404 in the genome	1	CCG002121.1,CCG016860.1,CCG016836.2,CCG002937.1,CCG000631.1,CCG005810.1,CCG016493.2,CCG023051.1
GO:0048278	vesicle docking	8 of 4104 in the list	14 of 8404 in the genome	1	CCG002121.1,CCG016860.1,CCG016836.2,CCG002937.1,CCG000631.1,CCG005810.1,CCG016493.2,CCG023051.1
GO:0003333	amino acid transmembrane transport	9 of 4104 in the list	16 of 8404 in the genome	1	CCG026667.1,CCG024222.1,CCG006348.1,CCG005768.1,CCG018073.1,CCG005769.1,CCG020840.1,CCG019407.1,CCG021349.1
GO:0006595	polyamine metabolic process	9 of 4104 in the list	16 of 8404 in the genome	1	CCG022191.1,CCG027282.1,CCG009515.2,CCG002556.1,CCG028391.1,CCG002555.1,CCG016005.1,CCG002883.1,CCG002495.1
GO:0006596	polyamine biosynthetic process	9 of 4104 in the list	16 of 8404 in the genome	1	CCG022191.1,CCG027282.1,CCG009515.2,CCG002556.1,CCG028391.1,CCG002555.1,CCG016005.1,CCG002883.1,CCG002495.1
GO:0006865	amino acid transport	9 of 4104 in the list	16 of 8404 in the genome	1	CCG026667.1,CCG024222.1,CCG006348.1,CCG005768.1,CCG018073.1,CCG005769.1,CCG020840.1,CCG019407.1,CCG021349.1
GO:0009309	amine biosynthetic process	9 of 4104 in the list	16 of 8404 in the genome	1	CCG022191.1,CCG027282.1,CCG009515.2,CCG002556.1,CCG028391.1,CCG002555.1,CCG016005.1,CCG002883.1,CCG002495.1
GO:0016998	cell wall macromolecule catabolic process	9 of 4104 in the list	16 of 8404 in the genome	1	CCG027649.1,CCG019113.1,CCG020388.1,CCG016477.1,CCG016538.1,CCG020793.1,CCG001539.1,CCG021807.1,CCG024974.1
GO:0034637	cellular carbohydrate biosynthetic process	9 of 4104 in the list	16 of 8404 in the genome	1	CCG022430.1,CCG019693.1,CCG014174.1,CCG014260.1,CCG023757.1,CCG016653.1,CCG024762.1,CCG008130.1,CCG013129.1
GO:0042401	cellular biogenic amine biosynthetic process	9 of 4104 in the list	16 of 8404 in the genome	1	CCG022191.1,CCG027282.1,CCG009515.2,CCG002556.1,CCG028391.1,CCG002555.1,CCG016005.1,CCG002883.1,CCG002495.1

GO:0044036	cell wall macromolecule metabolic process	9 of 4104 in the list	16 of 8404 in the genome	1	CCG027649.1,CCG019113.1,CCG020388.1,CCG016477.1,CCG016538.1,CCG020793.1,CCG001539.1,CCG021807.1,CCG024974.1
GO:0071554	cell wall organization or biogenesis	9 of 4104 in the list	16 of 8404 in the genome	1	CCG027649.1,CCG019113.1,CCG020388.1,CCG016477.1,CCG016538.1,CCG020793.1,CCG001539.1,CCG021807.1,CCG024974.1
GO:0002376	immune system process	10 of 4104 in the list	18 of 8404 in the genome	1	CCG027669.1,CCG015967.1,CCG021167.1,CCG027668.1,CCG015966.1,CCG024680.1,CCG001011.2,CCG006124.1,CCG022069.1,CCG027393.1
GO:0006367	transcription initiation from RNA polymerase II promoter	10 of 4104 in the list	18 of 8404 in the genome	1	CCG000158.1,CCG017812.1,CCG020044.1,CCG001292.1,CCG011083.1,CCG020129.1,CCG020460.1,CCG025691.1,CCG010175.1,CCG023184.1
GO:0006952	defense response	10 of 4104 in the list	18 of 8404 in the genome	1	CCG027669.1,CCG015967.1,CCG026732.1,CCG008821.1,CCG005170.1,CCG024173.1,CCG003252.1,CCG027668.1,CCG015966.1,CCG006124.1
GO:0006955	immune response	10 of 4104 in the list	18 of 8404 in the genome	1	CCG027669.1,CCG015967.1,CCG021167.1,CCG027668.1,CCG015966.1,CCG024680.1,CCG001011.2,CCG006124.1,CCG022069.1,CCG027393.1
GO:0018193	peptidyl-amino acid modification	10 of 4104 in the list	18 of 8404 in the genome	1	CCG008932.1,CCG022589.1,CCG008609.1,CCG018536.1,CCG004091.1,CCG009764.1,CCG013043.1,CCG019367.2,CCG026155.1,CCG013914.1

GO:0072521	purine-containing compound metabolic process	95 of 4104 in the list	189 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG017693.1,CCG007060.1,CCG013000.1,CCG017331.1,CCG004309.1,CCG006529.1,CCG025989.2,CCG024327.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG008422.1,CCG010112.1,CCG009607.1,CCG011006.1,CCG007827.1,CCG014434.1,CCG013643.1,CCG006421.1,CCG023963.3,CCG002038.1,CCG025027.1,CCG016370.1,CCG000148.1,CCG019103.1,CCG013365.1,CCG019629.2,CCG002917.1,CCG006486.1,CCG005924.2,CCG020909.1,CCG007532.1,CCG004257.1,CCG018447.1,CCG017330.1,CCG007531.1,CCG016966.1,CCG018820.3,CCG021110.1,CCG025179.1,CCG021934.1,CCG006777.1,CCG004308.1,CCG025973.1,CCG017995.1,CCG013637.1,CCG023640.1,CCG026314.1,CCG010418.1,CCG025348.1,CCG026852.1,CCG009080.1,CCG004869.1,CCG019619.1,CCG025396.1,CCG013999.1,CCG026953.1,CCG021336.1,CCG006924.1,CCG007417.1,CCG021220.1,CCG001066.1,CCG019866.1,CCG019678.1,CCG007724.1,CCG008748.1,CCG013641.1,CCG015410.1,CCG016027.1,CCG015289.1,CCG025107.1,CCG003495.1,CCG021411.1,CCG009142.1,CCG026898.1,CCG001859.1,CCG026812.1,CCG026336.1,CCG005886.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG018659.2,CCG002852.1,CCG010864.1,CCG028305.1,CCG006791.1,CCG016955.1,CCG021152.1,CCG023526.2,CCG001285.1
GO:0006152	purine nucleoside catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1

GO:0006184	GTP catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:0006195	purine nucleotide catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:0009143	nucleoside triphosphate catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1

GO:0009146	purine nucleoside triphosphate catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:0009154	purine ribonucleotide catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:0009164	nucleoside catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1

GO:0009203	ribonucleoside triphosphate catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:0009207	purine ribonucleoside triphosphate catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:0009261	ribonucleotide catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1

GO:0042454	ribonucleoside catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:0046130	purine ribonucleoside catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:0072523	purine-containing compound catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1

GO:1901069	guanosine-containing compound catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:1901658	glycosyl compound catabolic process	54 of 4104 in the list	107 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG013000.1,CCG013637.1,CCG010418.1,CCG004869.1,CCG024327.1,CCG009080.1,CCG015386.1,CCG019020.1,CCG009243.1,CCG025396.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG008748.1,CCG007827.1,CCG014434.1,CCG006421.1,CCG023963.3,CCG013641.1,CCG016027.1,CCG015289.1,CCG025027.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG026336.1,CCG016370.1,CCG019103.1,CCG005886.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG002852.1,CCG010864.1,CCG020909.1,CCG007532.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG018820.3,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1
GO:0006352	DNA-templated transcription, initiation	30 of 4104 in the list	59 of 8404 in the genome	1	CCG024624.1,CCG000158.1,CCG009894.1,CCG017812.1,CCG021940.1,CCG006686.1,CCG006211.1,CCG020044.1,CCG016968.1,CCG027197.1,CCG021944.1,CCG018168.1,CCG010138.1,CCG010647.1,CCG018719.1,CCG025691.1,CCG009805.2,CCG010175.1,CCG004151.1,CCG018164.1,CCG018326.1,CCG027950.1,CCG026473.1,CCG001292.1,CCG011083.1,CCG020129.1,CCG020460.1,CCG021521.1,CCG010650.1,CCG023184.1

GO:0044248	cellular catabolic process	160 of 4104 in the list	324 of 8404 in the genome	1	CCG006420.1,CCG017420.1,CCG002549.1,CCG027068.1,CCG013000.1,CCG013766.1,CCG024327.1,CCG015386.1,CCG019020.1,CCG003288.1,CCG025108.1,CCG020685.1,CCG022635.1,CCG006391.1,CCG002925.1,CCG019834.1,CCG023005.1,CCG024375.1,CCG009607.1,CCG011006.1,CCG001539.1,CCG027119.1,CCG004448.2,CCG012828.1,CCG019113.1,CCG025521.1,CCG016370.1,CCG028595.1,CCG026413.3,CCG006311.1,CCG005441.1,CCG002917.1,CCG002974.1,CCG013876.1,CCG002139.1,CCG011722.1,CCG003063.1,CCG008217.1,CCG009424.1,CCG011238.1,CCG019571.1,CCG010879.1,CCG020154.1,CCG002366.1,CCG004869.1,CCG009080.1,CCG001877.1,CCG007690.1,CCG004331.1,CCG025396.1,CCG026953.1,CCG008969.2,CCG011721.1,CCG006924.1,CCG021220.1,CCG008510.1,CCG013832.1,CCG017543.1,CCG013641.1,CCG015289.1,CCG003495.1,CCG021411.1,CCG001859.1,CCG001769.1,CCG027283.1,CCG009582.1,CCG025131.2,CCG021807.1,CCG002852.1,CCG011789.1,CCG022742.2,CCG002231.1,CCG000834.1,CCG027763.1,CCG007362.1,CCG021152.1,CCG023526.2,CCG026612.1,CCG008388.1,CCG003060.1,CCG007060.1,CCG007080.1,CCG001704.1,CCG005524.1,CCG001350.1,CCG010111.1,CCG019599.1,CCG024974.1,CCG000591.1,CCG009243.1,CCG012628.1,CCG016477.1,CCG007827.1,CCG023963.3,CCG006421.1,CCG014434.1,CCG021825.3,CCG021990.1,CCG013093.1,CCG027000.1,CCG025027.1,CCG001101.1,CCG003809.1,CCG020388.1,CCG020793.1,CCG003858.1,CCG019103.1,CCG026999.1,CCG019629.2,CCG005147.1,CCG004988.1,CCG023684.1,CCG027649.1,CCG001082.1,CCG020909.1,CCG007532.1,CCG014222.1,CCG007531.1,CCG018447.1,CCG016966.1,CCG027945.1,CCG023270.1,CCG001217.1,CCG014393.1,CCG019674.1,CCG018820.3,CCG025179.1,CCG004134.1,CCG006777.1,CCG007203.1,CCG005241.1,CCG025973.1,CCG017376.1,CCG019394.1,CCG013637.1,
GO:0006836	neurotransmitter transport	18 of 4104 in the list	35 of 8404 in the genome	1	CCG005140.1,CCG012096.1,CCG010710.1,CCG026799.1,CCG023060.1,CCG010711.1,CCG023980.1,CCG027718.1,CCG016128.1,CCG026151.1,CCG028141.1,CCG016245.1,CCG009022.2,CCG017641.1,CCG022789.1,CCG008323.1,CCG017552.1,CCG025323.1

GO:0009308	amine metabolic process	12 of 4104 in the list	23 of 8404 in the genome	1	CCG022191.1,CCG012875.1,CCG027282.1,CCG003865.1,CCG009515.2,CCG002556.1,CCG028391.1,CCG002555.1,CCG016005.1,CCG006059.1,CCG002883.1,CCG002495.1
GO:0032446	protein modification by small protein conjugation	12 of 4104 in the list	23 of 8404 in the genome	1	CCG016189.1,CCG019139.1,CCG003060.1,CCG010433.1,CCG020757.1,CCG008557.1,CCG013109.1,CCG006505.1,CCG020230.3,CCG016294.1,CCG022370.1,CCG007809.1
GO:0044106	cellular amine metabolic process	12 of 4104 in the list	23 of 8404 in the genome	1	CCG022191.1,CCG012875.1,CCG027282.1,CCG003865.1,CCG009515.2,CCG002556.1,CCG028391.1,CCG002555.1,CCG016005.1,CCG006059.1,CCG002883.1,CCG002495.1
GO:0070647	protein modification by small protein conjugation or removal	12 of 4104 in the list	23 of 8404 in the genome	1	CCG016189.1,CCG019139.1,CCG003060.1,CCG010433.1,CCG020757.1,CCG008557.1,CCG013109.1,CCG006505.1,CCG020230.3,CCG016294.1,CCG022370.1,CCG007809.1
GO:0006576	cellular biogenic amine metabolic process	11 of 4104 in the list	21 of 8404 in the genome	1	CCG022191.1,CCG012875.1,CCG027282.1,CCG009515.2,CCG002556.1,CCG028391.1,CCG002555.1,CCG016005.1,CCG006059.1,CCG002883.1,CCG002495.1
GO:0006414	translational elongation	9 of 4104 in the list	17 of 8404 in the genome	1	CCG014531.2,CCG005143.1,CCG026280.1,CCG025409.1,CCG026155.1,CCG003684.1,CCG000994.1,CCG027751.1,CCG016511.1
GO:0006544	glycine metabolic process	9 of 4104 in the list	17 of 8404 in the genome	1	CCG025108.1,CCG001082.1,CCG028131.1,CCG008510.1,CCG010111.1,CCG019834.1,CCG003063.1,CCG020154.1,CCG008388.1
GO:0044272	sulfur compound biosynthetic process	9 of 4104 in the list	17 of 8404 in the genome	1	CCG002897.1,CCG003865.1,CCG026099.1,CCG016955.1,CCG015568.1,CCG003751.1,CCG015567.1,CCG010319.1,CCG025636.2
GO:0033013	tetrapyrrole metabolic process	8 of 4104 in the list	15 of 8404 in the genome	1	CCG007610.1,CCG027212.1,CCG018453.1,CCG008609.1,CCG026752.1,CCG021335.1,CCG009424.1,CCG005053.1
GO:0042558	pteridine-containing compound metabolic process	8 of 4104 in the list	15 of 8404 in the genome	1	CCG000682.1,CCG003173.1,CCG010561.1,CCG015943.1,CCG023780.2,CCG011491.1,CCG021086.2,CCG020441.1
GO:0042559	pteridine-containing compound biosynthetic process	8 of 4104 in the list	15 of 8404 in the genome	1	CCG000682.1,CCG003173.1,CCG010561.1,CCG015943.1,CCG023780.2,CCG011491.1,CCG021086.2,CCG020441.1
GO:0051128	regulation of cellular component organization	8 of 4104 in the list	15 of 8404 in the genome	1	CCG028308.1,CCG004331.1,CCG027068.1,CCG025026.1,CCG026155.1,CCG002269.1,CCG019102.1,CCG018116.1
GO:0033014	tetrapyrrole biosynthetic process	7 of 4104 in the list	13 of 8404 in the genome	1	CCG007610.1,CCG027212.1,CCG018453.1,CCG008609.1,CCG026752.1,CCG021335.1,CCG005053.1
GO:0043648	dicarboxylic acid metabolic process	7 of 4104 in the list	13 of 8404 in the genome	1	CCG018290.1,CCG007203.1,CCG019111.1,CCG013063.1,CCG002231.1,CCG019112.1,CCG018289.1
GO:0010629	negative regulation of gene expression	6 of 4104 in the list	11 of 8404 in the genome	1	CCG010489.1,CCG003390.1,CCG025132.1,CCG005898.1,CCG004838.1,CCG014461.1
GO:0019319	hexose biosynthetic process	6 of 4104 in the list	11 of 8404 in the genome	1	CCG012840.1,CCG017278.1,CCG007771.1,CCG028524.1,CCG000431.1,CCG004388.1

GO:0046364	monosaccharide biosynthetic process	6 of 4104 in the list	11 of 8404 in the genome	1	CCG012840.1,CCG017278.1,CCG007771.1,CCG028524.1,CCG000431.1,CCG004388.1
GO:0006012	galactose metabolic process	5 of 4104 in the list	9 of 8404 in the genome	1	CCG010996.1,CCG007046.2,CCG007045.1,CCG018423.1,CCG001038.1
GO:0006094	gluconeogenesis	5 of 4104 in the list	9 of 8404 in the genome	1	CCG012840.1,CCG017278.1,CCG028524.1,CCG000431.1,CCG004388.1
GO:0006108	malate metabolic process	5 of 4104 in the list	9 of 8404 in the genome	1	CCG018290.1,CCG019111.1,CCG013063.1,CCG019112.1,CCG018289.1
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	5 of 4104 in the list	9 of 8404 in the genome	1	CCG018494.1,CCG022929.1,CCG010631.1,CCG020978.1,CCG021354.1
GO:0045087	innate immune response	5 of 4104 in the list	9 of 8404 in the genome	1	CCG027669.1,CCG027668.1,CCG015967.1,CCG015966.1,CCG006124.1
GO:0006013	mannose metabolic process	4 of 4104 in the list	7 of 8404 in the genome	1	CCG012740.1,CCG016373.1,CCG017651.1,CCG007771.1
GO:0006541	glutamine metabolic process	4 of 4104 in the list	7 of 8404 in the genome	1	CCG022773.2,CCG026030.1,CCG021923.1,CCG000472.1
GO:0006635	fatty acid beta-oxidation	4 of 4104 in the list	7 of 8404 in the genome	1	CCG025521.1,CCG018851.1,CCG006391.1,CCG000591.1
GO:0006914	autophagy	4 of 4104 in the list	7 of 8404 in the genome	1	CCG017376.1,CCG002366.1,CCG002139.1,CCG000834.1
GO:0009062	fatty acid catabolic process	4 of 4104 in the list	7 of 8404 in the genome	1	CCG025521.1,CCG018851.1,CCG006391.1,CCG000591.1
GO:0019395	fatty acid oxidation	4 of 4104 in the list	7 of 8404 in the genome	1	CCG025521.1,CCG018851.1,CCG006391.1,CCG000591.1
GO:0034440	lipid oxidation	4 of 4104 in the list	7 of 8404 in the genome	1	CCG025521.1,CCG018851.1,CCG006391.1,CCG000591.1
GO:0044242	cellular lipid catabolic process	4 of 4104 in the list	7 of 8404 in the genome	1	CCG025521.1,CCG018851.1,CCG006391.1,CCG000591.1
GO:0072329	monocarboxylic acid catabolic process	4 of 4104 in the list	7 of 8404 in the genome	1	CCG025521.1,CCG018851.1,CCG006391.1,CCG000591.1
GO:0006431	methionyl-tRNA aminoacylation	3 of 4104 in the list	5 of 8404 in the genome	1	CCG022269.1,CCG001876.1,CCG000414.1
GO:0006525	arginine metabolic process	3 of 4104 in the list	5 of 8404 in the genome	1	CCG025731.1,CCG025897.1,CCG023501.1
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	3 of 4104 in the list	5 of 8404 in the genome	1	CCG018533.1,CCG022741.1,CCG016307.1
GO:0009129	pyrimidine nucleoside monophosphate metabolic process	3 of 4104 in the list	5 of 8404 in the genome	1	CCG013610.1,CCG016614.1,CCG004180.1
GO:0009130	pyrimidine nucleoside monophosphate biosynthetic process	3 of 4104 in the list	5 of 8404 in the genome	1	CCG013610.1,CCG016614.1,CCG004180.1
GO:0009636	response to toxic substance	3 of 4104 in the list	5 of 8404 in the genome	1	CCG013113.1,CCG013809.1,CCG014378.1

GO:0015937	coenzyme A biosynthetic process	3 of 4104 in the list	5 of 8404 in the genome	1	CCG021336.1,CCG013999.1,CCG026812.1
GO:0033866	nucleoside bisphosphate biosynthetic process	3 of 4104 in the list	5 of 8404 in the genome	1	CCG021336.1,CCG013999.1,CCG026812.1
GO:0034030	ribonucleoside bisphosphate biosynthetic process	3 of 4104 in the list	5 of 8404 in the genome	1	CCG021336.1,CCG013999.1,CCG026812.1
GO:0034033	purine nucleoside bisphosphate biosynthetic process	3 of 4104 in the list	5 of 8404 in the genome	1	CCG021336.1,CCG013999.1,CCG026812.1
GO:0043269	regulation of ion transport	3 of 4104 in the list	5 of 8404 in the genome	1	CCG026240.1,CCG001279.1,CCG013013.1
GO:0044070	regulation of anion transport	3 of 4104 in the list	5 of 8404 in the genome	1	CCG026240.1,CCG001279.1,CCG013013.1
GO:0051049	regulation of transport	3 of 4104 in the list	5 of 8404 in the genome	1	CCG026240.1,CCG001279.1,CCG013013.1
GO:0006177	GMP biosynthetic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG006791.1,CCG018659.2
GO:0006188	IMP biosynthetic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG028305.1,CCG017330.1
GO:0006222	UMP biosynthetic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG013610.1,CCG016614.1
GO:0006471	protein ADP-ribosylation	2 of 4104 in the list	3 of 8404 in the genome	1	CCG001602.1,CCG018432.1
GO:0006526	arginine biosynthetic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG025731.1,CCG025897.1
GO:0006573	valine metabolic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG025307.1,CCG009084.2
GO:0006857	oligopeptide transport	2 of 4104 in the list	3 of 8404 in the genome	1	CCG010135.1,CCG005539.1
GO:0007591	molting cycle, chitin-based cuticle	2 of 4104 in the list	3 of 8404 in the genome	1	CCG022367.1,CCG017791.1
GO:0009173	pyrimidine ribonucleoside monophosphate metabolic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG013610.1,CCG016614.1
GO:0009174	pyrimidine ribonucleoside monophosphate biosynthetic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG013610.1,CCG016614.1
GO:0015833	peptide transport	2 of 4104 in the list	3 of 8404 in the genome	1	CCG010135.1,CCG005539.1
GO:0016075	rRNA catabolic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG020685.1,CCG019674.1
GO:0017182	peptidyl-diphthamide metabolic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG022589.1,CCG013914.1
GO:0017183	peptidyl-diphthamide biosynthetic process from peptidyl-histidine	2 of 4104 in the list	3 of 8404 in the genome	1	CCG022589.1,CCG013914.1
GO:0018990	ecdysis, chitin-based cuticle	2 of 4104 in the list	3 of 8404 in the genome	1	CCG022367.1,CCG017791.1
GO:0022404	molting cycle process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG022367.1,CCG017791.1
GO:0034661	ncRNA catabolic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG020685.1,CCG019674.1
GO:0042026	protein refolding	2 of 4104 in the list	3 of 8404 in the genome	1	CCG022020.1,CCG027565.1

GO:0042303	molting cycle	2 of 4104 in the list	3 of 8404 in the genome	1	CCG022367.1,CCG017791.1
GO:0042886	amide transport	2 of 4104 in the list	3 of 8404 in the genome	1	CCG010135.1,CCG005539.1
GO:0046037	GMP metabolic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG006791.1,CCG018659.2
GO:0046040	IMP metabolic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG028305.1,CCG017330.1
GO:0046049	UMP metabolic process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG013610.1,CCG016614.1
GO:0051704	multi-organism process	2 of 4104 in the list	3 of 8404 in the genome	1	CCG012551.1,CCG019159.1
GO:0016051	carbohydrate biosynthetic process	18 of 4104 in the list	36 of 8404 in the genome	1	CCG000331.1,CCG028524.1,CCG015986.1,CCG019693.1,CCG012840.1,CCG016653.1,CCG009803.1,CCG017278.1,CCG007771.1,CCG008130.1,CCG000431.1,CCG004388.1,CCG022430.1,CCG014260.1,CCG023757.1,CCG014174.1,CCG024762.1,CCG013129.1
GO:0072522	purine-containing compound biosynthetic process	31 of 4104 in the list	63 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1,CCG017995.1,CCG023640.1,CCG026898.1,CCG026812.1,CCG017331.1,CCG000148.1,CCG006529.1,CCG025348.1,CCG013365.1,CCG025989.2,CCG019619.1,CCG018659.2,CCG005924.2,CCG008422.1,CCG021336.1,CCG013999.1,CCG028305.1,CCG010112.1,CCG004257.1,CCG007417.1,CCG017330.1,CCG006791.1,CCG021110.1,CCG016955.1,CCG007724.1,CCG021934.1,CCG013643.1
GO:0045454	cell redox homeostasis	29 of 4104 in the list	59 of 8404 in the genome	1	CCG009285.1,CCG009063.1,CCG005375.1,CCG002466.1,CCG006787.1,CCG012993.1,CCG004548.1,CCG028500.2,CCG006600.1,CCG005587.1,CCG012992.1,CCG027430.1,CCG014566.1,CCG020637.1,CCG022471.1,CCG021250.1,CCG001847.1,CCG012678.1,CCG004595.1,CCG005714.1,CCG026500.1,CCG004446.1,CCG013244.3,CCG004445.1,CCG013245.1,CCG008924.1,CCG020472.1,CCG009674.1,CCG027531.2
GO:0042398	cellular modified amino acid biosynthetic process	12 of 4104 in the list	24 of 8404 in the genome	1	CCG000682.1,CCG008932.1,CCG002897.1,CCG026099.1,CCG010561.1,CCG013043.1,CCG015943.1,CCG016955.1,CCG011491.1,CCG026155.1,CCG020441.1,CCG021610.1
GO:0032940	secretion by cell	10 of 4104 in the list	20 of 8404 in the genome	1	CCG016860.1,CCG002374.1,CCG000631.1,CCG008323.1,CCG016493.2,CCG002121.1,CCG002937.1,CCG016836.2,CCG005810.1,CCG023051.1
GO:0046903	secretion	10 of 4104 in the list	20 of 8404 in the genome	1	CCG016860.1,CCG002374.1,CCG000631.1,CCG008323.1,CCG016493.2,CCG002121.1,CCG002937.1,CCG016836.2,CCG005810.1,CCG023051.1
GO:0016042	lipid catabolic process	9 of 4104 in the list	18 of 8404 in the genome	1	CCG025521.1,CCG025387.1,CCG018851.1,CCG019697.2,CCG015351.1,CCG015949.1,CCG006391.1,CCG000591.1,CCG024092.1
GO:0006887	exocytosis	8 of 4104 in the list	16 of 8404 in the genome	1	CCG002121.1,CCG016860.1,CCG016836.2,CCG002937.1,CCG000631.1,CCG005810.1,CCG016493.2,CCG023051.1

GO:0006026	aminoglycan catabolic process	19 of 4104 in the list	39 of 8404 in the genome	1	CCG015610.1,CCG020799.1,CCG019470.1,CCG015907.1,CCG002418.1,CCG020793.1,CCG024829.1,CCG028235.1,CCG023890.1,CCG021117.1,CCG002417.1,CCG023420.1,CCG004020.1,CCG016477.1,CCG025962.1,CCG010019.1,CCG012048.1,CCG011996.1,CCG005029.1
GO:0006816	calcium ion transport	6 of 4104 in the list	12 of 8404 in the genome	1	CCG025568.1,CCG014448.1,CCG027585.1,CCG009808.1,CCG005277.1,CCG011706.1
GO:0007205	protein kinase C-activating G-protein coupled receptor signaling pathway	6 of 4104 in the list	12 of 8404 in the genome	1	CCG008185.1,CCG014837.1,CCG019493.1,CCG017701.1,CCG015807.1,CCG016608.2
GO:0070838	divalent metal ion transport	6 of 4104 in the list	12 of 8404 in the genome	1	CCG025568.1,CCG014448.1,CCG027585.1,CCG009808.1,CCG005277.1,CCG011706.1
GO:0072511	divalent inorganic cation transport	6 of 4104 in the list	12 of 8404 in the genome	1	CCG025568.1,CCG014448.1,CCG027585.1,CCG009808.1,CCG005277.1,CCG011706.1
GO:0072524	pyridine-containing compound metabolic process	6 of 4104 in the list	12 of 8404 in the genome	1	CCG026536.1,CCG003748.1,CCG009518.1,CCG004188.3,CCG025307.1,CCG009084.2

GO:0044765	single-organism transport	437 of 4104 in the list	900 of 8404 in the genome	1	CCG005307.1,CCG020245.1,CCG001809.1,CCG010623.2,CCG003545.1,CCG017209.1,CCG021740.1,CCG004086.1,CCG021738.1,CCG000585.1,CCG000205.1,CCG004026.1,CCG001468.1,CCG019285.1,CCG000300.1,CCG003878.1,CCG027758.1,CCG022794.1,CCG002389.1,CCG017210.1,CCG014382.1,CCG016326.1,CCG013708.1,CCG002766.1,CCG023583.1,CCG003712.1,CCG027184.1,CCG001379.1,CCG005140.1,CCG016860.1,CCG009367.1,CCG017078.1,CCG012061.1,CCG026799.1,CCG011696.1,CCG025274.1,CCG027185.1,CCG009530.1,CCG003934.1,CCG017240.1,CCG005539.1,CCG018883.1,CCG016959.1,CCG012307.1,CCG027368.1,CCG001220.1,CCG019190.1,CCG025450.1,CCG024032.1,CCG018661.1,CCG016654.1,CCG018133.1,CCG008323.1,CCG018416.1,CCG014240.1,CCG006714.1,CCG011862.1,CCG006525.1,CCG016754.1,CCG026050.1,CCG001964.1,CCG009208.1,CCG019655.1,CCG009668.1,CCG010710.1,CCG005330.1,CCG016493.2,CCG007743.1,CCG016269.1,CCG009207.1,CCG019191.1,CCG004573.1,CCG011830.1,CCG012534.1,CCG006588.2,CCG000524.1,CCG014793.1,CCG016267.1,CCG024222.1,CCG006489.1,CCG026293.1,CCG021686.1,CCG019678.1,CCG014000.1,CCG018264.1,CCG024590.1,CCG017477.1,CCG006004.1,CCG005391.2,CCG022168.1,CCG018263.1,CCG007597.1,CCG016756.1,CCG019647.1,CCG015530.1,CCG026151.1,CCG022587.1,CCG009959.1,CCG027182.1,CCG016719.1,CCG013635.1,CCG000983.1,CCG010416.1,CCG002937.1,CCG022488.2,CCG001285.1,CCG011766.1,CCG016753.1,CCG011829.1,CCG005786.1,CCG023060.1,CCG008709.1,CCG011252.1,CCG007954.1,CCG000210.1,CCG008403.1,CCG008422.1,CCG016347.1,CCG022802.1,CCG010112.1,CCG020491.1,CCG014448.1,CCG027154.1,CCG017077.1,CCG001652.1,CCG016266.1,CCG000080.1,CCG001267.1,CCG022137.1,CCG026819.1,CCG012195.1,CCG025467.2,CCG011827.1,CCG009811.1,CCG018271.1,
GO:0006778	porphyrin-containing compound metabolic process	5 of 4104 in the list	10 of 8404 in the genome	1	CCG027212.1,CCG026752.1,CCG021335.1,CCG009424.1,CCG005053.1
GO:0007267	cell-cell signaling	5 of 4104 in the list	10 of 8404 in the genome	1	CCG010339.1,CCG011356.1,CCG026604.1,CCG008323.1,CCG005596.1
GO:0019362	pyridine nucleotide metabolic process	5 of 4104 in the list	10 of 8404 in the genome	1	CCG003748.1,CCG009518.1,CCG004188.3,CCG025307.1,CCG009084.2

GO:0046496	nicotinamide nucleotide metabolic process	5 of 4104 in the list	10 of 8404 in the genome	1	CCG003748.1,CCG009518.1,CCG004188.3,CCG025307.1,CCG009084.2
GO:0048015	phosphatidylinositol-mediated signaling	5 of 4104 in the list	10 of 8404 in the genome	1	CCG000789.1,CCG019820.1,CCG011658.1,CCG023393.1,CCG012959.1
GO:0048017	inositol lipid-mediated signaling	5 of 4104 in the list	10 of 8404 in the genome	1	CCG000789.1,CCG019820.1,CCG011658.1,CCG023393.1,CCG012959.1
GO:0006575	cellular modified amino acid metabolic process	13 of 4104 in the list	27 of 8404 in the genome	1	CCG000682.1,CCG008932.1,CCG002897.1,CCG026099.1,CCG010561.1,CCG013043.1,CCG015943.1,CCG016955.1,CCG011491.1,CCG026155.1,CCG020441.1,CCG021610.1,CCG006059.1
GO:0017038	protein import	13 of 4104 in the list	27 of 8404 in the genome	1	CCG016347.1,CCG022771.1,CCG011766.1,CCG027762.1,CCG017078.1,CCG001809.1,CCG011696.1,CCG027564.1,CCG019797.1,CCG002766.1,CCG017077.1,CCG020949.1,CCG004026.1
GO:0005977	glycogen metabolic process	4 of 4104 in the list	8 of 8404 in the genome	1	CCG022430.1,CCG004760.1,CCG025015.2,CCG008130.1
GO:0006073	cellular glucan metabolic process	4 of 4104 in the list	8 of 8404 in the genome	1	CCG022430.1,CCG004760.1,CCG025015.2,CCG008130.1
GO:0006112	energy reserve metabolic process	4 of 4104 in the list	8 of 8404 in the genome	1	CCG022430.1,CCG004760.1,CCG025015.2,CCG008130.1
GO:0006487	protein N-linked glycosylation	4 of 4104 in the list	8 of 8404 in the genome	1	CCG018536.1,CCG016003.1,CCG004091.1,CCG017197.1
GO:0006779	porphyrin-containing compound biosynthetic process	4 of 4104 in the list	8 of 8404 in the genome	1	CCG027212.1,CCG026752.1,CCG021335.1,CCG005053.1
GO:0044042	glucan metabolic process	4 of 4104 in the list	8 of 8404 in the genome	1	CCG022430.1,CCG004760.1,CCG025015.2,CCG008130.1
GO:0051186	cofactor metabolic process	30 of 4104 in the list	63 of 8404 in the genome	1	CCG000682.1,CCG027212.1,CCG010561.1,CCG026752.1,CCG009424.1,CCG025307.1,CCG003683.2,CCG026812.1,CCG021086.2,CCG011491.1,CCG023780.2,CCG021335.1,CCG005053.1,CCG009084.2,CCG018113.1,CCG003173.1,CCG013999.1,CCG013216.1,CCG021336.1,CCG009518.1,CCG004188.3,CCG015943.1,CCG016955.1,CCG024432.2,CCG003748.1,CCG003751.1,CCG016148.1,CCG006009.1,CCG020441.1,CCG010319.1
GO:0016567	protein ubiquitination	10 of 4104 in the list	21 of 8404 in the genome	1	CCG016189.1,CCG019139.1,CCG003060.1,CCG010433.1,CCG020757.1,CCG008557.1,CCG006505.1,CCG020230.3,CCG016294.1,CCG022370.1

GO:0019725	cellular homeostasis	39 of 4104 in the list	82 of 8404 in the genome	1	CCG009285.1,CCG005375.1,CCG002466.1,CCG012993.1,CCG004548.1,CCG006600.1,CCG026796.1,CCG012992.1,CCG014566.1,CCG008826.1,CCG020637.1,CCG022471.1,CCG012678.1,CCG004595.1,CCG005714.1,CCG004446.1,CCG020472.1,CCG028221.1,CCG012569.1,CCG024590.1,CCG020377.1,CCG009063.1,CCG006787.1,CCG009992.1,CCG028500.2,CCG003104.1,CCG005587.1,CCG027430.1,CCG021250.1,CCG001847.1,CCG026500.1,CCG000302.1,CCG004445.1,CCG013244.3,CCG008924.1,CCG013245.1,CCG020400.2,CCG009674.1,CCG027531.2
GO:0000154	rRNA modification	3 of 4104 in the list	6 of 8404 in the genome	1	CCG019953.1,CCG016274.1,CCG005097.1
GO:0006098	pentose-phosphate shunt	3 of 4104 in the list	6 of 8404 in the genome	1	CCG003748.1,CCG025307.1,CCG009084.2
GO:0006739	NADP metabolic process	3 of 4104 in the list	6 of 8404 in the genome	1	CCG003748.1,CCG025307.1,CCG009084.2
GO:0006740	NADPH regeneration	3 of 4104 in the list	6 of 8404 in the genome	1	CCG003748.1,CCG025307.1,CCG009084.2
GO:0008202	steroid metabolic process	3 of 4104 in the list	6 of 8404 in the genome	1	CCG024095.1,CCG015949.1,CCG011183.1
GO:0022618	ribonucleoprotein complex assembly	3 of 4104 in the list	6 of 8404 in the genome	1	CCG023663.1,CCG010792.1,CCG007518.1
GO:0030030	cell projection organization	3 of 4104 in the list	6 of 8404 in the genome	1	CCG018859.3,CCG017033.1,CCG015583.1
GO:0042168	heme metabolic process	3 of 4104 in the list	6 of 8404 in the genome	1	CCG027212.1,CCG009424.1,CCG005053.1
GO:0071826	ribonucleoprotein complex subunit organization	3 of 4104 in the list	6 of 8404 in the genome	1	CCG023663.1,CCG010792.1,CCG007518.1
GO:0072525	pyridine-containing compound biosynthetic process	3 of 4104 in the list	6 of 8404 in the genome	1	CCG026536.1,CCG009518.1,CCG004188.3
GO:0030203	glycosaminoglycan metabolic process	9 of 4104 in the list	19 of 8404 in the genome	1	CCG017559.1,CCG024517.1,CCG020799.1,CCG019470.1,CCG015907.1,CCG022072.1,CCG025840.1,CCG028235.1,CCG005029.1
GO:0006732	coenzyme metabolic process	25 of 4104 in the list	53 of 8404 in the genome	1	CCG000682.1,CCG010561.1,CCG025307.1,CCG003683.2,CCG026812.1,CCG021086.2,CCG011491.1,CCG023780.2,CCG009084.2,CCG018113.1,CCG003173.1,CCG013999.1,CCG013216.1,CCG021336.1,CCG009518.1,CCG004188.3,CCG015943.1,CCG016955.1,CCG024432.2,CCG003748.1,CCG003751.1,CCG016148.1,CCG006009.1,CCG020441.1,CCG010319.1
GO:0051188	cofactor biosynthetic process	24 of 4104 in the list	51 of 8404 in the genome	1	CCG000682.1,CCG027212.1,CCG010561.1,CCG026752.1,CCG003683.2,CCG026812.1,CCG021086.2,CCG011491.1,CCG023780.2,CCG021335.1,CCG005053.1,CCG003173.1,CCG013999.1,CCG021336.1,CCG009518.1,CCG004188.3,CCG015943.1,CCG016955.1,CCG024432.2,CCG003751.1,CCG016148.1,CCG006009.1,CCG020441.1,CCG010319.1

GO:0042592	homeostatic process	42 of 4104 in the list	89 of 8404 in the genome	1	CCG009285.1,CCG005375.1,CCG002466.1,CCG012993.1,CCG004548.1,CCG006600.1,CCG026796.1,CCG012992.1,CCG014566.1,CCG008826.1,CCG020637.1,CCG022471.1,CCG012678.1,CCG004595.1,CCG005714.1,CCG016162.1,CCG004446.1,CCG016956.1,CCG020472.1,CCG028221.1,CCG012569.1,CCG024590.1,CCG020377.1,CCG009063.1,CCG006787.1,CCG009992.1,CCG028500.2,CCG003104.1,CCG005587.1,CCG027430.1,CCG021250.1,CCG001847.1,CCG026500.1,CCG000302.1,CCG004445.1,CCG013244.3,CCG008924.1,CCG013245.1,CCG020400.2,CCG009674.1,CCG027531.2,CCG023671.2
GO:0005978	glycogen biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG022430.1,CCG008130.1
GO:0006435	threonyl-tRNA aminoacylation	2 of 4104 in the list	4 of 8404 in the genome	1	CCG002662.1,CCG027607.1
GO:0006536	glutamate metabolic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG007203.1,CCG002231.1
GO:0006537	glutamate biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG007203.1,CCG002231.1
GO:0006749	glutathione metabolic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG002897.1,CCG026099.1
GO:0006750	glutathione biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG002897.1,CCG026099.1
GO:0006783	heme biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG027212.1,CCG005053.1
GO:0007229	integrin-mediated signaling pathway	2 of 4104 in the list	4 of 8404 in the genome	1	CCG004279.1,CCG000526.1
GO:0009221	pyrimidine deoxyribonucleotide biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG004180.1,CCG014116.1
GO:0009250	glucan biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG022430.1,CCG008130.1
GO:0009263	deoxyribonucleotide biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG004180.1,CCG014116.1
GO:0009265	2'-deoxyribonucleotide biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG004180.1,CCG014116.1
GO:0009435	NAD biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG009518.1,CCG004188.3
GO:0016050	vesicle organization	2 of 4104 in the list	4 of 8404 in the genome	1	CCG020315.1,CCG026620.1
GO:0016226	iron-sulfur cluster assembly	2 of 4104 in the list	4 of 8404 in the genome	1	CCG003485.1,CCG007395.1
GO:0016575	histone deacetylation	2 of 4104 in the list	4 of 8404 in the genome	1	CCG013028.1,CCG020863.1
GO:0018196	peptidyl-asparagine modification	2 of 4104 in the list	4 of 8404 in the genome	1	CCG018536.1,CCG004091.1
GO:0018279	protein N-linked glycosylation via asparagine	2 of 4104 in the list	4 of 8404 in the genome	1	CCG018536.1,CCG004091.1
GO:0019184	nonribosomal peptide biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG002897.1,CCG026099.1

GO:0019359	nicotinamide nucleotide biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG009518.1,CCG004188.3
GO:0019363	pyridine nucleotide biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG009518.1,CCG004188.3
GO:0019674	NAD metabolic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG009518.1,CCG004188.3
GO:0031163	metallo-sulfur cluster assembly	2 of 4104 in the list	4 of 8404 in the genome	1	CCG003485.1,CCG007395.1
GO:0032784	regulation of DNA-templated transcription, elongation	2 of 4104 in the list	4 of 8404 in the genome	1	CCG014982.1,CCG014983.1
GO:0042255	ribosome assembly	2 of 4104 in the list	4 of 8404 in the genome	1	CCG023663.1,CCG007518.1
GO:0043043	peptide biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG002897.1,CCG026099.1
GO:0043650	dicarboxylic acid biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG007203.1,CCG002231.1
GO:0044801	single-organism membrane fusion	2 of 4104 in the list	4 of 8404 in the genome	1	CCG020315.1,CCG026620.1
GO:0046385	deoxyribose phosphate biosynthetic process	2 of 4104 in the list	4 of 8404 in the genome	1	CCG004180.1,CCG014116.1
GO:0048284	organelle fusion	2 of 4104 in the list	4 of 8404 in the genome	1	CCG020315.1,CCG026620.1
GO:0051205	protein insertion into membrane	2 of 4104 in the list	4 of 8404 in the genome	1	CCG027323.1,CCG007941.1
GO:0051668	localization within membrane	2 of 4104 in the list	4 of 8404 in the genome	1	CCG027323.1,CCG007941.1
GO:0061025	membrane fusion	2 of 4104 in the list	4 of 8404 in the genome	1	CCG020315.1,CCG026620.1
GO:0009108	coenzyme biosynthetic process	20 of 4104 in the list	43 of 8404 in the genome	1	CCG000682.1,CCG010561.1,CCG003683.2,CCG026812.1,CCG021086.2,CCG011491.1,CCG023780.2,CCG003173.1,CCG013999.1,CCG021336.1,CCG009518.1,CCG004188.3,CCG015943.1,CCG016955.1,CCG024432.2,CCG016148.1,CCG003751.1,CCG006009.1,CCG020441.1,CCG010319.1
GO:0044262	cellular carbohydrate metabolic process	20 of 4104 in the list	43 of 8404 in the genome	1	CCG010996.1,CCG005588.1,CCG013318.1,CCG011547.1,CCG019693.1,CCG016653.1,CCG008317.1,CCG008130.1,CCG015587.1,CCG022430.1,CCG004760.1,CCG006358.1,CCG014260.1,CCG023757.1,CCG005177.1,CCG014174.1,CCG019825.2,CCG024762.1,CCG025015.2,CCG013129.1

GO:0035556	intracellular signal transduction	118 of 4104 in the list	248 of 8404 in the genome	1	CCG015638.1,CCG000789.1,CCG017420.1,CCG002549.1,CCG007434.1,CCG019820.1,CCG007060.1,CCG023484.1,CCG026047.1,CCG008603.1,CCG028124.1,CCG022332.1,CCG009446.1,CCG013998.1,CCG024327.1,CCG015386.1,CCG019020.1,CCG013398.1,CCG026174.1,CCG000016.1,CCG017725.1,CCG025387.1,CCG009607.1,CCG011006.1,CCG026360.1,CCG007827.1,CCG014434.1,CCG028477.1,CCG011717.1,CCG025899.1,CCG012573.1,CCG018861.1,CCG016878.1,CCG025027.1,CCG012702.1,CCG022841.1,CCG020709.1,CCG014466.1,CCG008035.1,CCG019420.2,CCG015426.1,CCG007993.1,CCG019103.1,CCG013365.1,CCG019629.2,CCG002917.1,CCG011658.1,CCG018341.1,CCG007335.1,CCG002133.1,CCG002341.1,CCG020909.1,CCG018447.1,CCG016966.1,CCG021661.1,CCG010944.1,CCG012959.1,CCG013308.1,CCG009510.1,CCG018222.1,CCG002413.1,CCG025179.1,CCG019558.1,CCG024595.1,CCG006777.1,CCG010046.1,CCG014379.1,CCG012402.1,CCG007587.1,CCG024840.1,CCG025973.1,CCG002902.1,CCG024952.1,CCG020929.1,CCG014647.1,CCG023393.1,CCG015984.1,CCG009980.1,CCG014506.1,CCG001012.1,CCG016252.1,CCG007830.1,CCG008892.2,CCG003775.1,CCG008152.1,CCG004869.1,CCG017373.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG011087.1,CCG017591.1,CCG024583.1,CCG001579.1,CCG028136.1,CCG013641.1,CCG016027.1,CCG003495.1,CCG021411.1,CCG017127.1,CCG026898.1,CCG001859.1,CCG026336.1,CCG006412.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG014837.1,CCG008652.1,CCG022184.1,CCG028486.1,CCG027309.1,CCG008185.1,CCG021152.1,CCG023526.2,CCG026695.1,CCG016660.1
GO:0033043	regulation of organelle organization	6 of 4104 in the list	13 of 8404 in the genome	1	CCG004331.1,CCG025026.1,CCG002269.1,CCG027068.1,CCG019102.1,CCG018116.1
GO:0016055	Wnt signaling pathway	5 of 4104 in the list	11 of 8404 in the genome	1	CCG015544.1,CCG007152.1,CCG002694.1,CCG025782.1,CCG020733.1
GO:0006662	glycerol ether metabolic process	9 of 4104 in the list	20 of 8404 in the genome	1	CCG026500.1,CCG002466.1,CCG006600.1,CCG012992.1,CCG020472.1,CCG021250.1,CCG020637.1,CCG001847.1,CCG012678.1
GO:0018904	ether metabolic process	9 of 4104 in the list	20 of 8404 in the genome	1	CCG026500.1,CCG002466.1,CCG006600.1,CCG012992.1,CCG020472.1,CCG021250.1,CCG020637.1,CCG001847.1,CCG012678.1
GO:0048869	cellular developmental process	4 of 4104 in the list	9 of 8404 in the genome	1	CCG015767.2,CCG021681.1,CCG006750.1,CCG013272.2

GO:0090304	nucleic acid metabolic process	623 of 4104 in the list	1295 of 8404 in the genome	1	CCG027300.1,CCG014396.1,CCG006549.1,CCG026106.1,CCG006357.1,CCG009878.1,CCG024072.1,CCG020685.1,CCG013625.1,CCG004468.1,CCG016238.1,CCG024584.1,CCG001292.1,CCG018321.1,CCG002470.1,CCG005194.1,CCG001040.1,CCG014836.1,CCG025208.1,CCG019382.1,CCG016094.1,CCG027183.2,CCG023474.1,CCG010792.1,CCG004231.1,CCG012623.1,CCG010905.1,CCG010909.1,CCG023129.1,CCG028653.1,CCG024326.1,CCG014946.1,CCG020286.1,CCG002735.1,CCG027133.1,CCG014280.1,CCG015694.1,CCG013865.1,CCG006484.1,CCG001461.1,CCG023686.1,CCG004402.1,CCG003938.1,CCG023468.1,CCG025990.1,CCG015350.1,CCG021948.1,CCG011148.1,CCG020651.1,CCG005284.1,CCG004927.1,CCG009805.2,CCG019545.1,CCG003142.1,CCG021137.1,CCG001876.1,CCG012584.1,CCG024200.1,CCG010624.1,CCG023125.1,CCG016381.1,CCG011727.1,CCG017001.1,CCG024788.1,CCG007263.1,CCG021767.1,CCG004926.1,CCG004907.1,CCG010912.1,CCG004955.1,CCG015367.1,CCG005524.1,CCG024857.1,CCG022772.1,CCG010136.1,CCG005501.1,CCG003310.1,CCG026516.1,CCG024570.2,CCG018164.1,CCG013617.1,CCG004224.1,CCG022513.2,CCG028092.1,CCG018650.1,CCG000209.1,CCG016760.1,CCG021521.1,CCG007902.1,CCG023486.1,CCG024232.1,CCG006133.1,CCG001395.1,CCG016557.1,CCG023184.1,CCG003153.1,CCG005594.1,CCG027340.1,CCG022183.1,CCG018168.1,CCG018796.1,CCG011015.1,CCG008498.1,CCG000073.1,CCG012278.1,CCG005070.1,CCG001898.1,CCG005241.1,CCG010906.1,CCG008044.1,CCG010797.1,CCG004008.1,CCG010138.1,CCG008916.1,CCG012557.1,CCG013054.1,CCG021716.1,CCG012837.1,CCG012229.1,CCG002662.1,CCG021042.1,CCG023939.1,CCG000929.1,CCG000208.1,CCG007177.1,CCG015312.2,CCG000490.1,CCG027040.1,CCG027197.1,CCG025157.1,CCG028027.1,CCG005269.1,CCG022674.1,CCG003940.1,CCG027695.1,
GO:0006650	glycerophospholipid metabolic process	26 of 4104 in the list	57 of 8404 in the genome	1	CCG000789.1,CCG025233.1,CCG022209.1,CCG017241.1,CCG024778.1,CCG019820.1,CCG023393.1,CCG009434.1,CCG014839.1,CCG000663.1,CCG013131.1,CCG026370.1,CCG011658.1,CCG025889.1,CCG004806.1,CCG000552.1,CCG024760.1,CCG024903.1,CCG012875.1,CCG028332.1,CCG007330.1,CCG012959.1,CCG015130.1,CCG011531.1,CCG024612.1,CCG021610.1

GO:0046486	glycerolipid metabolic process	26 of 4104 in the list	57 of 8404 in the genome	1	CCG000789.1,CCG025233.1,CCG022209.1,CCG017241.1,CCG024778.1,CCG019820.1,CCG023393.1,CCG009434.1,CCG014839.1,CCG000663.1,CCG013131.1,CCG026370.1,CCG011658.1,CCG025889.1,CCG004806.1,CCG000552.1,CCG024760.1,CCG024903.1,CCG012875.1,CCG028332.1,CCG007330.1,CCG012959.1,CCG015130.1,CCG011531.1,CCG024612.1,CCG021610.1
GO:0006818	hydrogen transport	24 of 4104 in the list	53 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1,CCG023640.1,CCG010696.1,CCG000148.1,CCG000585.1,CCG025348.1,CCG003662.1,CCG025989.2,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:0015992	proton transport	24 of 4104 in the list	53 of 8404 in the genome	1	CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1,CCG023640.1,CCG010696.1,CCG000148.1,CCG000585.1,CCG025348.1,CCG003662.1,CCG025989.2,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:0046488	phosphatidylinositol metabolic process	24 of 4104 in the list	53 of 8404 in the genome	1	CCG000789.1,CCG025233.1,CCG022209.1,CCG017241.1,CCG024778.1,CCG019820.1,CCG023393.1,CCG009434.1,CCG014839.1,CCG000663.1,CCG013131.1,CCG026370.1,CCG011658.1,CCG025889.1,CCG004806.1,CCG000552.1,CCG024760.1,CCG024903.1,CCG028332.1,CCG007330.1,CCG012959.1,CCG015130.1,CCG011531.1,CCG024612.1
GO:0006644	phospholipid metabolic process	38 of 4104 in the list	83 of 8404 in the genome	1	CCG004532.1,CCG000789.1,CCG019820.1,CCG023393.1,CCG000663.1,CCG013131.1,CCG026370.1,CCG015351.1,CCG004806.1,CCG024092.1,CCG022352.1,CCG012875.1,CCG007330.1,CCG015130.1,CCG011531.1,CCG021610.1,CCG024155.1,CCG023102.1,CCG025233.1,CCG017241.1,CCG022209.1,CCG024778.1,CCG014839.1,CCG009434.1,CCG012308.1,CCG016653.1,CCG025889.1,CCG011658.1,CCG000552.1,CCG024903.1,CCG024760.1,CCG028332.1,CCG023757.1,CCG012959.1,CCG006965.1,CCG014174.1,CCG019697.2,CCG024612.1
GO:0000042	protein targeting to Golgi	3 of 4104 in the list	7 of 8404 in the genome	1	CCG012550.1,CCG004573.1,CCG028498.1
GO:0000301	retrograde transport, vesicle recycling within Golgi	3 of 4104 in the list	7 of 8404 in the genome	1	CCG012550.1,CCG004573.1,CCG028498.1
GO:0009452	7-methylguanosine RNA capping	3 of 4104 in the list	7 of 8404 in the genome	1	CCG014335.1,CCG007177.1,CCG012557.1

GO:0015936	coenzyme A metabolic process	3 of 4104 in the list	7 of 8404 in the genome	1	CCG021336.1,CCG013999.1,CCG026812.1
GO:0033865	nucleoside bisphosphate metabolic process	3 of 4104 in the list	7 of 8404 in the genome	1	CCG021336.1,CCG013999.1,CCG026812.1
GO:0033875	ribonucleoside bisphosphate metabolic process	3 of 4104 in the list	7 of 8404 in the genome	1	CCG021336.1,CCG013999.1,CCG026812.1
GO:0034032	purine nucleoside bisphosphate metabolic process	3 of 4104 in the list	7 of 8404 in the genome	1	CCG021336.1,CCG013999.1,CCG026812.1
GO:0034067	protein localization to Golgi apparatus	3 of 4104 in the list	7 of 8404 in the genome	1	CCG012550.1,CCG004573.1,CCG028498.1
GO:0036260	RNA capping	3 of 4104 in the list	7 of 8404 in the genome	1	CCG014335.1,CCG007177.1,CCG012557.1
GO:0072600	establishment of protein localization to Golgi	3 of 4104 in the list	7 of 8404 in the genome	1	CCG012550.1,CCG004573.1,CCG028498.1
GO:0006040	amino sugar metabolic process	69 of 4104 in the list	149 of 8404 in the genome	1	CCG010077.1,CCG006912.1,CCG017730.1,CCG005809.1,CCG021005.1,CCG020504.1,CCG007817.1,CCG004020.1,CCG016477.1,CCG012048.1,CCG011695.1,CCG007816.1,CCG015610.1,CCG020165.1,CCG023922.1,CCG007814.1,CCG020793.1,CCG006911.1,CCG022378.1,CCG023890.1,CCG006375.1,CCG026626.1,CCG017079.1,CCG023923.1,CCG019371.1,CCG014180.1,CCG012984.1,CCG003601.1,CCG010019.1,CCG003966.1,CCG014791.1,CCG016153.1,CCG011972.1,CCG015090.1,CCG010728.1,CCG002418.1,CCG019402.1,CCG025948.4,CCG023926.1,CCG017862.1,CCG022227.1,CCG019785.1,CCG001154.1,CCG012725.1,CCG016069.1,CCG021117.1,CCG023924.1,CCG025962.1,CCG014181.1,CCG000044.1,CCG013298.1,CCG023925.1,CCG011257.1,CCG018642.1,CCG015306.1,CCG015029.1,CCG026044.1,CCG007963.1,CCG015804.1,CCG024829.1,CCG018643.1,CCG002417.1,CCG026552.1,CCG023420.1,CCG010727.1,CCG020663.1,CCG028454.1,CCG011996.1,CCG028648.1

GO:1901071	glucosamine-containing compound metabolic process	69 of 4104 in the list	149 of 8404 in the genome	1	CCG010077.1,CCG006912.1,CCG017730.1,CCG005809.1,CCG021005.1,CCG020504.1,CCG007817.1,CCG004020.1,CCG016477.1,CCG012048.1,CCG011695.1,CCG007816.1,CCG015610.1,CCG020165.1,CCG023922.1,CCG007814.1,CCG020793.1,CCG006911.1,CCG022378.1,CCG023890.1,CCG006375.1,CCG026626.1,CCG017079.1,CCG023923.1,CCG019371.1,CCG014180.1,CCG012984.1,CCG003601.1,CCG010019.1,CCG003966.1,CCG014791.1,CCG016153.1,CCG011972.1,CCG015090.1,CCG010728.1,CCG002418.1,CCG019402.1,CCG025948.4,CCG023926.1,CCG017862.1,CCG022227.1,CCG019785.1,CCG001154.1,CCG012725.1,CCG016069.1,CCG021117.1,CCG023924.1,CCG025962.1,CCG014181.1,CCG000044.1,CCG013298.1,CCG023925.1,CCG011257.1,CCG018642.1,CCG015306.1,CCG015029.1,CCG026044.1,CCG007963.1,CCG015804.1,CCG024829.1,CCG018643.1,CCG002417.1,CCG026552.1,CCG023420.1,CCG010727.1,CCG020663.1,CCG028454.1,CCG011996.1,CCG028648.1

GO:0007154	cell communication	332 of 4104 in the list	698 of 8404 in the genome	1	CCG005254.1,CCG010628.1,CCG017420.1,CCG028253.1,CCG014340.1,CCG012989.1,CCG008603.1,CCG008741.1,CCG027955.1,CCG000646.1,CCG019020.1,CCG013398.1,CCG026174.1,CCG020785.1,CCG011006.1,CCG002841.1,CCG010275.1,CCG026360.1,CCG011717.1,CCG017266.1,CCG012573.1,CCG016689.2,CCG016745.1,CCG020709.1,CCG014466.1,CCG007993.1,CCG015101.1,CCG000659.1,CCG009407.1,CCG027127.1,CCG007335.1,CCG018533.1,CCG000647.1,CCG000526.1,CCG022281.1,CCG027669.1,CCG015967.1,CCG008323.1,CCG026537.1,CCG021661.1,CCG010071.1,CCG013308.1,CCG023579.1,CCG009510.1,CCG019717.1,CCG025176.1,CCG000078.1,CCG008685.1,CCG026109.1,CCG024952.1,CCG009980.1,CCG014506.1,CCG016252.1,CCG004279.1,CCG024663.1,CCG003745.1,CCG018494.1,CCG008759.1,CCG026953.1,CCG009427.1,CCG019493.1,CCG017498.1,CCG002520.1,CCG017591.1,CCG023464.1,CCG021284.1,CCG001579.1,CCG028136.1,CCG011437.1,CCG013641.1,CCG000732.1,CCG003317.1,CCG003495.1,CCG017127.1,CCG007951.1,CCG006412.1,CCG025131.2,CCG016307.1,CCG008444.1,CCG017701.1,CCG000515.1,CCG028486.1,CCG000834.1,CCG018859.3,CCG026695.1,CCG014712.1,CCG000876.1,CCG014928.1,CCG024664.1,CCG015638.1,CCG000789.1,CCG024271.1,CCG024662.1,CCG026047.1,CCG020978.1,CCG008939.1,CCG007732.3,CCG005531.1,CCG017725.1,CCG000111.2,CCG014345.2,CCG001759.1,CCG028477.1,CCG025899.1,CCG019881.1,CCG025035.1,CCG000984.1,CCG024639.1,CCG020654.1,CCG015793.1,CCG015426.1,CCG006804.1,CCG023151.1,CCG014509.1,CCG009553.1,CCG021902.1,CCG017033.1,CCG024918.1,CCG023002.1,CCG023662.1,CCG007958.1,CCG015583.1,CCG012959.1,CCG006013.1,CCG017112.1,CCG002413.1,CCG013272.2,CCG024595.1,CCG010046.1,CCG012402.1,CCG008742.1,CCG011228.1,CCG020929.1,CCG014647.1,CCG001012.1,
GO:0006760	folic acid-containing compound metabolic process	5 of 4104 in the list	12 of 8404 in the genome	1	CCG011491.1,CCG000682.1,CCG010561.1,CCG020441.1,CCG015943.1
GO:0009396	folic acid-containing compound biosynthetic process	5 of 4104 in the list	12 of 8404 in the genome	1	CCG011491.1,CCG000682.1,CCG010561.1,CCG020441.1,CCG015943.1

GO:0009058	biosynthetic process	564 of 4104 in the list	1180 of 8404 in the genome	1	CCG014531.2,CCG014396.1,CCG006549.1,CCG013430.1,CCG009878.1,CCG024517.1,CCG026174.1,CCG004468.1,CCG016238.1,CCG001292.1,CCG016220.1,CCG018321.1,CCG013059.1,CCG002470.1,CCG025836.1,CCG025472.1,CCG018432.1,CCG025208.1,CCG026871.2,CCG012623.1,CCG022025.2,CCG005053.1,CCG000944.1,CCG008270.1,CCG021110.1,CCG024612.1,CCG005737.1,CCG024326.1,CCG020286.1,CCG016164.1,CCG016747.1,CCG021086.2,CCG014280.1,CCG008871.1,CCG015694.1,CCG013865.1,CCG018788.1,CCG006484.1,CCG026602.1,CCG006344.1,CCG021737.1,CCG023468.1,CCG006821.1,CCG015350.1,CCG003683.2,CCG021948.1,CCG011148.1,CCG020651.1,CCG012840.1,CCG001163.1,CCG000552.1,CCG023452.1,CCG009805.2,CCG002966.1,CCG019545.1,CCG003142.1,CCG021137.1,CCG013610.1,CCG001876.1,CCG009518.1,CCG024200.1,CCG002231.1,CCG023125.1,CCG016381.1,CCG011727.1,CCG026865.1,CCG027748.1,CCG022788.1,CCG017001.1,CCG000294.1,CCG004926.1,CCG004532.1,CCG017381.1,CCG015367.1,CCG026047.1,CCG024784.1,CCG011491.1,CCG009333.1,CCG005501.1,CCG007766.1,CCG009803.1,CCG018164.1,CCG004224.1,CCG010112.1,CCG028092.1,CCG000209.1,CCG021521.1,CCG007902.1,CCG024232.1,CCG024155.1,CCG007395.1,CCG023184.1,CCG019263.1,CCG010561.1,CCG015986.1,CCG018168.1,CCG000148.1,CCG019426.1,CCG025889.1,CCG018796.1,CCG009394.1,CCG024760.1,CCG026099.1,CCG025038.1,CCG025897.1,CCG006009.1,CCG010319.1,CCG017995.1,CCG008044.1,CCG010797.1,CCG010138.1,CCG026370.1,CCG009928.1,CCG005442.1,CCG008130.1,CCG003249.1,CCG017894.1,CCG007417.1,CCG021716.1,CCG007724.1,CCG002662.1,CCG017295.1,CCG023939.1,CCG008932.1,CCG017241.1,CCG021933.1,CCG026331.1,CCG027131.1,CCG015312.2,CCG015747.1,CCG000490.1,CCG027197.1,CCG025157.1,CCG005269.1,CCG018659.2,

GO:0006886	intracellular protein transport	93 of 4104 in the list	201 of 8404 in the genome	1	CCG026698.1,CCG011766.1,CCG018832.1,CCG003146.1,CCG011408.1,CCG007060.1,CCG001809.1,CCG028124.1,CCG019590.1,CCG027692.1,CCG020949.1,CCG003995.1,CCG015386.1,CCG019020.1,CCG012550.1,CCG002645.1,CCG009428.1,CCG018800.1,CCG024905.1,CCG011813.1,CCG005262.1,CCG020315.1,CCG015568.1,CCG011006.1,CCG017077.1,CCG002766.1,CCG000010.1,CCG000614.1,CCG003531.1,CCG017078.1,CCG011696.1,CCG014307.1,CCG027457.1,CCG019629.2,CCG027257.1,CCG010939.1,CCG007855.1,CCG007283.1,CCG016541.1,CCG020909.1,CCG018447.1,CCG003786.1,CCG006714.1,CCG027473.1,CCG010178.1,CCG006777.1,CCG013984.1,CCG001673.1,CCG001172.1,CCG020280.1,CCG014506.1,CCG018557.1,CCG027564.1,CCG026620.1,CCG015800.2,CCG018217.1,CCG006625.1,CCG003775.1,CCG004573.1,CCG016831.1,CCG004869.1,CCG022771.1,CCG022910.1,CCG023595.1,CCG017373.1,CCG006924.1,CCG028498.1,CCG021220.1,CCG019797.1,CCG006775.1,CCG015087.1,CCG013126.2,CCG013641.1,CCG025233.1,CCG008312.1,CCG003495.1,CCG021377.1,CCG026336.1,CCG027241.1,CCG005195.1,CCG021800.1,CCG016542.1,CCG014226.1,CCG009362.1,CCG020806.1,CCG020634.1,CCG010567.3,CCG025473.1,CCG026947.1,CCG023756.1,CCG021152.1,CCG001481.1,CCG017125.1
GO:0009628	response to abiotic stimulus	8 of 4104 in the list	19 of 8404 in the genome	1	CCG002446.2,CCG009531.1,CCG003657.2,CCG012989.1,CCG012988.1,CCG007317.1,CCG010071.1,CCG017696.1
GO:0006597	spermine biosynthetic process	2 of 4104 in the list	5 of 8404 in the genome	1	CCG009515.2,CCG016005.1
GO:0006694	steroid biosynthetic process	2 of 4104 in the list	5 of 8404 in the genome	1	CCG024095.1,CCG011183.1
GO:0006885	regulation of pH	2 of 4104 in the list	5 of 8404 in the genome	1	CCG023671.2,CCG016956.1
GO:0008215	spermine metabolic process	2 of 4104 in the list	5 of 8404 in the genome	1	CCG009515.2,CCG016005.1
GO:0018202	peptidyl-histidine modification	2 of 4104 in the list	5 of 8404 in the genome	1	CCG022589.1,CCG013914.1
GO:0018342	protein prenylation	2 of 4104 in the list	5 of 8404 in the genome	1	CCG024801.1,CCG023181.1
GO:0018871	1-aminocyclopropane-1-carboxylate metabolic process	2 of 4104 in the list	5 of 8404 in the genome	1	CCG015276.2,CCG016315.1
GO:0035434	copper ion transmembrane transport	2 of 4104 in the list	5 of 8404 in the genome	1	CCG003878.1,CCG000927.1
GO:0042218	1-aminocyclopropane-1-carboxylate biosynthetic process	2 of 4104 in the list	5 of 8404 in the genome	1	CCG015276.2,CCG016315.1

GO:0055067	monovalent inorganic cation homeostasis	2 of 4104 in the list	5 of 8404 in the genome	1	CCG023671.2,CCG016956.1
GO:0097354	prenylation	2 of 4104 in the list	5 of 8404 in the genome	1	CCG024801.1,CCG023181.1
GO:0006891	intra-Golgi vesicle-mediated transport	4 of 4104 in the list	10 of 8404 in the genome	1	CCG012550.1,CCG011862.1,CCG004573.1,CCG028498.1
GO:0006022	aminoglycan metabolic process	76 of 4104 in the list	166 of 8404 in the genome	1	CCG010077.1,CCG006912.1,CCG017730.1,CCG005809.1,CCG021005.1,CCG024517.1,CCG007817.1,CCG004020.1,CCG016477.1,CCG012048.1,CCG011695.1,CCG007816.1,CCG005029.1,CCG015610.1,CCG020799.1,CCG020165.1,CCG023922.1,CCG007814.1,CCG020793.1,CCG006911.1,CCG022378.1,CCG023890.1,CCG006375.1,CCG026626.1,CCG017079.1,CCG023923.1,CCG019371.1,CCG014180.1,CCG012984.1,CCG003601.1,CCG010019.1,CCG003966.1,CCG014791.1,CCG017559.1,CCG016153.1,CCG011972.1,CCG015090.1,CCG010728.1,CCG002418.1,CCG019402.1,CCG023926.1,CCG017862.1,CCG022227.1,CCG019785.1,CCG001154.1,CCG012725.1,CCG016069.1,CCG021117.1,CCG023924.1,CCG025962.1,CCG014181.1,CCG022072.1,CCG000044.1,CCG013298.1,CCG023925.1,CCG019470.1,CCG011257.1,CCG015907.1,CCG018642.1,CCG015306.1,CCG015029.1,CCG026044.1,CCG007963.1,CCG015804.1,CCG024829.1,CCG028235.1,CCG018643.1,CCG002417.1,CCG026552.1,CCG023420.1,CCG010727.1,CCG028454.1,CCG020663.1,CCG011996.1,CCG028648.1,CCG025840.1
GO:0006030	chitin metabolic process	67 of 4104 in the list	147 of 8404 in the genome	1	CCG010077.1,CCG006912.1,CCG017730.1,CCG005809.1,CCG021005.1,CCG007817.1,CCG004020.1,CCG016477.1,CCG012048.1,CCG011695.1,CCG007816.1,CCG015610.1,CCG020165.1,CCG023922.1,CCG007814.1,CCG020793.1,CCG006911.1,CCG022378.1,CCG023890.1,CCG006375.1,CCG026626.1,CCG017079.1,CCG023923.1,CCG019371.1,CCG014180.1,CCG012984.1,CCG010019.1,CCG003601.1,CCG003966.1,CCG014791.1,CCG016153.1,CCG011972.1,CCG015090.1,CCG002418.1,CCG010728.1,CCG019402.1,CCG023926.1,CCG017862.1,CCG022227.1,CCG019785.1,CCG001154.1,CCG012725.1,CCG016069.1,CCG021117.1,CCG023924.1,CCG025962.1,CCG014181.1,CCG013298.1,CCG000044.1,CCG023925.1,CCG011257.1,CCG018642.1,CCG015306.1,CCG015029.1,CCG026044.1,CCG007963.1,CCG015804.1,CCG024829.1,CCG018643.1,CCG002417.1,CCG026552.1,CCG023420.1,CCG010727.1,CCG020663.1,CCG028454.1,CCG011996.1,CCG028648.1

GO:0055065	metal ion homeostasis	10 of 4104 in the list	24 of 8404 in the genome	1	CCG000302.1,CCG016162.1,CCG009992.1,CCG026796.1,CCG003104.1,CCG020400.2,CCG008826.1,CCG024590.1,CCG012569.1,CCG020377.1
GO:0034613	cellular protein localization	97 of 4104 in the list	211 of 8404 in the genome	1	CCG026698.1,CCG011766.1,CCG018832.1,CCG003146.1,CCG011408.1,CCG007060.1,CCG001809.1,CCG028124.1,CCG019590.1,CCG027692.1,CCG020949.1,CCG003995.1,CCG015386.1,CCG019020.1,CCG012550.1,CCG002645.1,CCG009428.1,CCG018800.1,CCG007941.1,CCG024905.1,CCG011813.1,CCG003587.1,CCG005262.1,CCG020315.1,CCG015568.1,CCG011006.1,CCG017077.1,CCG002766.1,CCG000010.1,CCG000614.1,CCG003531.1,CCG017078.1,CCG011696.1,CCG014307.1,CCG027457.1,CCG014318.1,CCG019629.2,CCG027257.1,CCG010939.1,CCG007855.1,CCG007283.1,CCG016541.1,CCG020909.1,CCG018447.1,CCG003786.1,CCG006714.1,CCG027473.1,CCG010178.1,CCG006777.1,CCG013984.1,CCG001673.1,CCG001172.1,CCG020280.1,CCG014506.1,CCG018557.1,CCG027564.1,CCG026620.1,CCG015800.2,CCG018217.1,CCG006625.1,CCG003775.1,CCG004573.1,CCG016831.1,CCG004869.1,CCG022771.1,CCG022910.1,CCG023595.1,CCG017373.1,CCG006924.1,CCG028498.1,CCG021220.1,CCG019797.1,CCG006775.1,CCG015087.1,CCG013126.2,CCG027323.1,CCG013641.1,CCG025233.1,CCG008312.1,CCG003495.1,CCG021377.1,CCG026336.1,CCG027241.1,CCG005195.1,CCG021800.1,CCG016542.1,CCG014226.1,CCG009362.1,CCG020806.1,CCG020634.1,CCG010567.3,CCG025473.1,CCG026947.1,CCG023756.1,CCG021152.1,CCG001481.1,CCG017125.1

GO:0070727	cellular macromolecule localization	97 of 4104 in the list	211 of 8404 in the genome	1	CCG026698.1,CCG011766.1,CCG018832.1,CCG003146.1,CCG011408.1,CCG007060.1,CCG001809.1,CCG028124.1,CCG019590.1,CCG027692.1,CCG020949.1,CCG003995.1,CCG015386.1,CCG019020.1,CCG012550.1,CCG002645.1,CCG009428.1,CCG018800.1,CCG007941.1,CCG024905.1,CCG011813.1,CCG003587.1,CCG005262.1,CCG020315.1,CCG015568.1,CCG011006.1,CCG017077.1,CCG002766.1,CCG000010.1,CCG000614.1,CCG003531.1,CCG017078.1,CCG011696.1,CCG014307.1,CCG027457.1,CCG014318.1,CCG019629.2,CCG027257.1,CCG010939.1,CCG007855.1,CCG007283.1,CCG016541.1,CCG020909.1,CCG018447.1,CCG003786.1,CCG006714.1,CCG027473.1,CCG010178.1,CCG006777.1,CCG013984.1,CCG001673.1,CCG001172.1,CCG020280.1,CCG014506.1,CCG018557.1,CCG027564.1,CCG026620.1,CCG015800.2,CCG018217.1,CCG006625.1,CCG003775.1,CCG004573.1,CCG016831.1,CCG004869.1,CCG022771.1,CCG022910.1,CCG023595.1,CCG017373.1,CCG006924.1,CCG028498.1,CCG021220.1,CCG019797.1,CCG006775.1,CCG015087.1,CCG013126.2,CCG027323.1,CCG013641.1,CCG025233.1,CCG008312.1,CCG003495.1,CCG021377.1,CCG026336.1,CCG027241.1,CCG005195.1,CCG021800.1,CCG016542.1,CCG014226.1,CCG009362.1,CCG020806.1,CCG020634.1,CCG010567.3,CCG025473.1,CCG026947.1,CCG023756.1,CCG021152.1,CCG001481.1,CCG017125.1
GO:0006733	oxidoreduction coenzyme metabolic process	6 of 4104 in the list	15 of 8404 in the genome	1	CCG003748.1,CCG006009.1,CCG009518.1,CCG004188.3,CCG025307.1,CCG009084.2
GO:0006873	cellular ion homeostasis	9 of 4104 in the list	22 of 8404 in the genome	1	CCG000302.1,CCG009992.1,CCG026796.1,CCG003104.1,CCG020400.2,CCG008826.1,CCG024590.1,CCG012569.1,CCG020377.1
GO:0006875	cellular metal ion homeostasis	9 of 4104 in the list	22 of 8404 in the genome	1	CCG000302.1,CCG009992.1,CCG026796.1,CCG003104.1,CCG020400.2,CCG008826.1,CCG024590.1,CCG012569.1,CCG020377.1
GO:0030003	cellular cation homeostasis	9 of 4104 in the list	22 of 8404 in the genome	1	CCG000302.1,CCG009992.1,CCG026796.1,CCG003104.1,CCG020400.2,CCG008826.1,CCG024590.1,CCG012569.1,CCG020377.1
GO:0055082	cellular chemical homeostasis	9 of 4104 in the list	22 of 8404 in the genome	1	CCG000302.1,CCG009992.1,CCG026796.1,CCG003104.1,CCG020400.2,CCG008826.1,CCG024590.1,CCG012569.1,CCG020377.1

GO:0034220	ion transmembrane transport	39 of 4104 in the list	88 of 8404 in the genome	1	CCG006469.1,CCG023640.1,CCG000585.1,CCG009808.1,CCG025348.1,CCG003662.1,CCG025989.2,CCG019619.1,CCG008422.1,CCG024222.1,CCG003878.1,CCG010112.1,CCG005769.1,CCG018073.1,CCG001066.1,CCG019407.1,CCG007724.1,CCG013643.1,CCG006348.1,CCG015410.1,CCG002038.1,CCG025107.1,CCG009142.1,CCG027585.1,CCG000148.1,CCG006486.1,CCG023244.1,CCG005924.2,CCG026667.1,CCG025450.1,CCG005768.1,CCG020840.1,CCG008587.1,CCG000927.1,CCG021934.1,CCG019890.1,CCG021349.1,CCG001285.1,CCG011706.1
GO:0048878	chemical homeostasis	12 of 4104 in the list	29 of 8404 in the genome	1	CCG000302.1,CCG016162.1,CCG009992.1,CCG016956.1,CCG026796.1,CCG003104.1,CCG020400.2,CCG008826.1,CCG024590.1,CCG012569.1,CCG020377.1,CCG023671.2
GO:0050801	ion homeostasis	12 of 4104 in the list	29 of 8404 in the genome	1	CCG000302.1,CCG016162.1,CCG009992.1,CCG016956.1,CCG026796.1,CCG003104.1,CCG020400.2,CCG008826.1,CCG024590.1,CCG012569.1,CCG020377.1,CCG023671.2
GO:0055080	cation homeostasis	12 of 4104 in the list	29 of 8404 in the genome	1	CCG000302.1,CCG016162.1,CCG009992.1,CCG016956.1,CCG026796.1,CCG003104.1,CCG020400.2,CCG008826.1,CCG024590.1,CCG012569.1,CCG020377.1,CCG023671.2
GO:0006071	glycerol metabolic process	3 of 4104 in the list	8 of 8404 in the genome	1	CCG008317.1,CCG013318.1,CCG015587.1
GO:0006144	purine nucleobase metabolic process	3 of 4104 in the list	8 of 8404 in the genome	1	CCG026852.1,CCG004257.1,CCG017331.1
GO:0019400	alditol metabolic process	3 of 4104 in the list	8 of 8404 in the genome	1	CCG008317.1,CCG013318.1,CCG015587.1
GO:0070588	calcium ion transmembrane transport	3 of 4104 in the list	8 of 8404 in the genome	1	CCG027585.1,CCG009808.1,CCG011706.1
GO:0071804	cellular potassium ion transport	3 of 4104 in the list	8 of 8404 in the genome	1	CCG008587.1,CCG006469.1,CCG019890.1
GO:0071805	potassium ion transmembrane transport	3 of 4104 in the list	8 of 8404 in the genome	1	CCG008587.1,CCG006469.1,CCG019890.1
GO:0009605	response to external stimulus	8 of 4104 in the list	20 of 8404 in the genome	1	CCG017696.1,CCG009531.1,CCG012989.1,CCG002366.1,CCG012988.1,CCG007317.1,CCG000834.1,CCG010071.1

GO:0046907	intracellular transport	108 of 4104 in the list	236 of 8404 in the genome	1	CCG026698.1,CCG011766.1,CCG018832.1,CCG003146.1,CCG011408.1,CCG007060.1,CCG001809.1,CCG028124.1,CCG017209.1,CCG019590.1,CCG027692.1,CCG013042.1,CCG020949.1,CCG003995.1,CCG015386.1,CCG019020.1,CCG012550.1,CCG002645.1,CCG009428.1,CCG018800.1,CCG024905.1,CCG011813.1,CCG005262.1,CCG020315.1,CCG002028.1,CCG015568.1,CCG011006.1,CCG017077.1,CCG002766.1,CCG000010.1,CCG000614.1,CCG003531.1,CCG011567.1,CCG017078.1,CCG011696.1,CCG014307.1,CCG027457.1,CCG019629.2,CCG022927.1,CCG027257.1,CCG010939.1,CCG007855.1,CCG007283.1,CCG016541.1,CCG020909.1,CCG018447.1,CCG003786.1,CCG026989.1,CCG027733.1,CCG006714.1,CCG011862.1,CCG027473.1,CCG010178.1,CCG006777.1,CCG013984.1,CCG001673.1,CCG001172.1,CCG020280.1,CCG014506.1,CCG018557.1,CCG027564.1,CCG026620.1,CCG015800.2,CCG018217.1,CCG006625.1,CCG003775.1,CCG004573.1,CCG016831.1,CCG021221.1,CCG004869.1,CCG022771.1,CCG009136.1,CCG022910.1,CCG023595.1,CCG017373.1,CCG006924.1,CCG021220.1,CCG028498.1,CCG023814.2,CCG019797.1,CCG006775.1,CCG015087.1,CCG013126.2,CCG013641.1,CCG025233.1,CCG008312.1,CCG003495.1,CCG021377.1,CCG027241.1,CCG026336.1,CCG005195.1,CCG021800.1,CCG016542.1,CCG014226.1,CCG009362.1,CCG020806.1,CCG020634.1,CCG010567.3,CCG025473.1,CCG007989.1,CCG026947.1,CCG023756.1,CCG008116.1,CCG021152.1,CCG001481.1,CCG017125.1,CCG017141.1,CCG017874.1
GO:0007031	peroxisome organization	5 of 4104 in the list	13 of 8404 in the genome	1	CCG018832.1,CCG019797.1,CCG006223.1,CCG019217.1,CCG010178.1
GO:0009072	aromatic amino acid family metabolic process	5 of 4104 in the list	13 of 8404 in the genome	1	CCG011789.1,CCG011721.1,CCG006059.1,CCG011722.1,CCG014436.2
GO:0042440	pigment metabolic process	5 of 4104 in the list	13 of 8404 in the genome	1	CCG027212.1,CCG004257.1,CCG009424.1,CCG005053.1,CCG017331.1

GO:0051234	establishment of localization	642 of 4104 in the list	1349 of 8404 in the genome	1	CCG005307.1,CCG017420.1,CCG020245.1,CCG024345.1,CCG014880.1,CCG010623.2,CCG003545.1,CCG017209.1,CCG021740.1,CCG004086.1,CCG021738.1,CCG000585.1,CCG003991.1,CCG001468.1,CCG013009.1,CCG019285.1,CCG009428.1,CCG019768.1,CCG022794.1,CCG024905.1,CCG005974.1,CCG013708.1,CCG023583.1,CCG003712.1,CCG017078.1,CCG026799.1,CCG011696.1,CCG009530.1,CCG017240.1,CCG027457.1,CCG027368.1,CCG001220.1,CCG019190.1,CCG018661.1,CCG016654.1,CCG018416.1,CCG014240.1,CCG006714.1,CCG027473.1,CCG026050.1,CCG001964.1,CCG019655.1,CCG009668.1,CCG025596.1,CCG016493.2,CCG009822.1,CCG005191.1,CCG004573.1,CCG011778.1,CCG006588.2,CCG000106.1,CCG014793.1,CCG024222.1,CCG026953.1,CCG006489.1,CCG019678.1,CCG017591.1,CCG018264.1,CCG013641.1,CCG003563.1,CCG017477.1,CCG008236.1,CCG003495.1,CCG005391.2,CCG022168.1,CCG007597.1,CCG016756.1,CCG019647.1,CCG009778.1,CCG015530.1,CCG026151.1,CCG022587.1,CCG020634.1,CCG010567.3,CCG009959.1,CCG027182.1,CCG026422.2,CCG026947.1,CCG016719.1,CCG000983.1,CCG010416.1,CCG009126.1,CCG002937.1,CCG001285.1,CCG016753.1,CCG011252.1,CCG027692.1,CCG008403.1,CCG016347.1,CCG022802.1,CCG010112.1,CCG020491.1,CCG014448.1,CCG005239.1,CCG005919.1,CCG016266.1,CCG022137.1,CCG012195.1,CCG026819.1,CCG025467.2,CCG011827.1,CCG028471.2,CCG002135.1,CCG019611.1,CCG010711.1,CCG000148.1,CCG025510.1,CCG023190.1,CCG022927.1,CCG022219.1,CCG012214.1,CCG027257.1,CCG017641.1,CCG016459.1,CCG016836.2,CCG019890.1,CCG023983.1,CCG020458.1,CCG004308.1,CCG013984.1,CCG026547.1,CCG000631.1,CCG003566.1,CCG006770.1,CCG015800.2,CCG002839.1,CCG022510.1,CCG003775.1,CCG016831.1,CCG021221.1,CCG023595.1,CCG018753.1,CCG018073.1,CCG016956.1,CCG026052.1,

GO:0006810	transport	640 of 4104 in the list	1345 of 8404 in the genome	1	CCG005307.1,CCG017420.1,CCG020245.1,CCG024345.1,CCG014880.1,CCG010623.2,CCG003545.1,CCG017209.1,CCG021740.1,CCG004086.1,CCG021738.1,CCG000585.1,CCG003991.1,CCG001468.1,CCG013009.1,CCG019285.1,CCG009428.1,CCG019768.1,CCG022794.1,CCG024905.1,CCG005974.1,CCG013708.1,CCG023583.1,CCG003712.1,CCG017078.1,CCG026799.1,CCG011696.1,CCG009530.1,CCG017240.1,CCG027457.1,CCG027368.1,CCG001220.1,CCG019190.1,CCG018661.1,CCG016654.1,CCG018416.1,CCG014240.1,CCG006714.1,CCG027473.1,CCG026050.1,CCG001964.1,CCG019655.1,CCG009668.1,CCG025596.1,CCG016493.2,CCG009822.1,CCG005191.1,CCG004573.1,CCG011778.1,CCG006588.2,CCG000106.1,CCG014793.1,CCG024222.1,CCG026953.1,CCG006489.1,CCG019678.1,CCG017591.1,CCG018264.1,CCG013641.1,CCG003563.1,CCG017477.1,CCG008236.1,CCG003495.1,CCG005391.2,CCG022168.1,CCG007597.1,CCG016756.1,CCG019647.1,CCG009778.1,CCG015530.1,CCG026151.1,CCG022587.1,CCG020634.1,CCG010567.3,CCG009959.1,CCG027182.1,CCG026422.2,CCG026947.1,CCG016719.1,CCG000983.1,CCG010416.1,CCG009126.1,CCG002937.1,CCG001285.1,CCG016753.1,CCG011252.1,CCG027692.1,CCG008403.1,CCG016347.1,CCG022802.1,CCG010112.1,CCG020491.1,CCG014448.1,CCG005239.1,CCG005919.1,CCG016266.1,CCG022137.1,CCG012195.1,CCG026819.1,CCG025467.2,CCG011827.1,CCG028471.2,CCG002135.1,CCG019611.1,CCG010711.1,CCG000148.1,CCG025510.1,CCG023190.1,CCG022927.1,CCG022219.1,CCG012214.1,CCG027257.1,CCG017641.1,CCG016459.1,CCG016836.2,CCG019890.1,CCG023983.1,CCG020458.1,CCG004308.1,CCG013984.1,CCG026547.1,CCG000631.1,CCG003566.1,CCG006770.1,CCG015800.2,CCG002839.1,CCG022510.1,CCG003775.1,CCG016831.1,CCG021221.1,CCG023595.1,CCG018753.1,CCG018073.1,CCG016956.1,CCG026052.1,

GO:0051649	establishment of localization in cell	118 of 4104 in the list	258 of 8404 in the genome	1	CCG026698.1, CCG011766.1, CCG018832.1, CCG003146.1, CCG011408.1, CCG007060.1, CCG001809.1, CCG028124.1, CCG017209.1, CCG019590.1, CCG027692.1, CCG013042.1, CCG020949.1, CCG003995.1, CCG015386.1, CCG019020.1, CCG012550.1, CCG002645.1, CCG009428.1, CCG018800.1, CCG024905.1, CCG011813.1, CCG005262.1, CCG020315.1, CCG002028.1, CCG015568.1, CCG011006.1, CCG017077.1, CCG002766.1, CCG000010.1, CCG023051.1, CCG016860.1, CCG000614.1, CCG003531.1, CCG011567.1, CCG017078.1, CCG011696.1, CCG014307.1, CCG027457.1, CCG019629.2, CCG005810.1, CCG022927.1, CCG027257.1, CCG010939.1, CCG007855.1, CCG007283.1, CCG002374.1, CCG016541.1, CCG020909.1, CCG008323.1, CCG018447.1, CCG003786.1, CCG026989.1, CCG027733.1, CCG006714.1, CCG011862.1, CCG016836.2, CCG027473.1, CCG010178.1, CCG006777.1, CCG013984.1, CCG001673.1, CCG001172.1, CCG000631.1, CCG020280.1, CCG014506.1, CCG018557.1, CCG016493.2, CCG026620.1, CCG027564.1, CCG015800.2, CCG018217.1, CCG006625.1, CCG003775.1, CCG004573.1, CCG016831.1, CCG021221.1, CCG004869.1, CCG022771.1, CCG009136.1, CCG022910.1, CCG023595.1, CCG017373.1, CCG006924.1, CCG021220.1, CCG028498.1, CCG023814.2, CCG019797.1, CCG006775.1, CCG015087.1, CCG013126.2, CCG013641.1, CCG025233.1, CCG008312.1, CCG003495.1, CCG021377.1, CCG027241.1, CCG026336.1, CCG002121.1, CCG005195.1, CCG021800.1, CCG016542.1, CCG014226.1, CCG009362.1, CCG020806.1, CCG020634.1, CCG010567.3, CCG025473.1, CCG007989.1, CCG026947.1, CCG023756.1, CCG008116.1, CCG021152.1, CCG001481.1, CCG017125.1, CCG017141.1, CCG002937.1, CCG017874.1

GO:1901576	organic substance biosynthetic process	528 of 4104 in the list	1115 of 8404 in the genome	1	CCG014531.2,CCG014396.1,CCG006549.1,CCG013430.1,CCG009878.1,CCG024517.1,CCG026174.1,CCG004468.1,CCG016238.1,CCG001292.1,CCG016220.1,CCG018321.1,CCG002470.1,CCG025472.1,CCG018432.1,CCG025208.1,CCG026871.2,CCG012623.1,CCG022025.2,CCG005053.1,CCG008270.1,CCG021110.1,CCG024612.1,CCG005737.1,CCG024326.1,CCG020286.1,CCG021086.2,CCG014280.1,CCG008871.1,CCG015694.1,CCG013865.1,CCG018788.1,CCG006484.1,CCG026602.1,CCG006344.1,CCG021737.1,CCG023468.1,CCG006821.1,CCG015350.1,CCG003683.2,CCG021948.1,CCG011148.1,CCG020651.1,CCG012840.1,CCG000552.1,CCG023452.1,CCG009805.2,CCG002966.1,CCG019545.1,CCG003142.1,CCG021137.1,CCG013610.1,CCG001876.1,CCG009518.1,CCG024200.1,CCG002231.1,CCG023125.1,CCG016381.1,CCG011727.1,CCG026865.1,CCG027748.1,CCG017001.1,CCG000294.1,CCG004926.1,CCG004532.1,CCG017381.1,CCG015367.1,CCG026047.1,CCG011491.1,CCG009333.1,CCG005501.1,CCG007766.1,CCG009803.1,CCG018164.1,CCG004224.1,CCG010112.1,CCG028092.1,CCG000209.1,CCG021521.1,CCG007902.1,CCG024232.1,CCG024155.1,CCG023184.1,CCG019263.1,CCG010561.1,CCG015986.1,CCG018168.1,CCG000148.1,CCG019426.1,CCG025889.1,CCG018796.1,CCG009394.1,CCG024760.1,CCG026099.1,CCG025897.1,CCG006009.1,CCG010319.1,CCG017995.1,CCG008044.1,CCG010797.1,CCG010138.1,CCG026370.1,CCG009928.1,CCG005442.1,CCG008130.1,CCG003249.1,CCG017894.1,CCG007417.1,CCG021716.1,CCG007724.1,CCG002662.1,CCG017295.1,CCG023939.1,CCG008932.1,CCG017241.1,CCG021933.1,CCG026331.1,CCG027131.1,CCG015312.2,CCG015747.1,CCG000490.1,CCG027197.1,CCG025157.1,CCG005269.1,CCG018659.2,CCG024529.1,CCG016955.1,CCG015521.1,CCG009141.1,CCG025840.1,CCG003871.1,CCG000158.1,CCG010174.2,CCG006211.1,CCG007710.1,

GO:0044249	cellular biosynthetic process	512 of 4104 in the list	1082 of 8404 in the genome	1	CCG014531.2,CCG018536.1,CCG023277.1,CCG014396.1,CCG006549.1,CCG004807.1,CCG010191.3,CCG017331.1,CCG013430.1,CCG009878.1,CCG010647.1,CCG026882.1,CCG018507.1,CCG026174.1,CCG002354.1,CCG004468.1,CCG016238.1,CCG026473.1,CCG004091.1,CCG001292.1,CCG017097.1,CCG016220.1,CCG018321.1,CCG026825.1,CCG002470.1,CCG003573.1,CCG028505.1,CCG025472.1,CCG025223.1,CCG018432.1,CCG015599.1,CCG004398.1,CCG026536.1,CCG025208.1,CCG012213.2,CCG007993.1,CCG026871.2,CCG016653.1,CCG018719.1,CCG013353.1,CCG012623.1,CCG022025.2,CCG005053.1,CCG025940.1,CCG013914.1,CCG008270.1,CCG019210.1,CCG027115.1,CCG021110.1,CCG018799.1,CCG020129.1,CCG024612.1,CCG005737.1,CCG019909.1,CCG005276.1,CCG024326.1,CCG020877.1,CCG021295.1,CCG009249.1,CCG006231.1,CCG020286.1,CCG014896.1,CCG001863.1,CCG013131.1,CCG021086.2,CCG014280.1,CCG006767.1,CCG019296.1,CCG013065.1,CCG008871.1,CCG014840.1,CCG015694.1,CCG014819.1,CCG013865.1,CCG018788.1,CCG006484.1,CCG010378.2,CCG027114.1,CCG028131.1,CCG026602.1,CCG006344.1,CCG026280.1,CCG024432.2,CCG010510.1,CCG027312.1,CCG021737.1,CCG023468.1,CCG000773.1,CCG006821.1,CCG009119.1,CCG015350.1,CCG003683.2,CCG021948.1,CCG011148.1,CCG020651.1,CCG000552.1,CCG023452.1,CCG009805.2,CCG025636.2,CCG014116.1,CCG002966.1,CCG017111.1,CCG019545.1,CCG003142.1,CCG021137.1,CCG013610.1,CCG019330.1,CCG022773.2,CCG003173.1,CCG001876.1,CCG000915.1,CCG009518.1,CCG015411.1,CCG024200.1,CCG002231.1,CCG023125.1,CCG016381.1,CCG011727.1,CCG028426.1,CCG026865.1,CCG027748.1,CCG017001.1,CCG000294.1,CCG004926.1,CCG004532.1,CCG022191.1,CCG016778.1,CCG017381.1,CCG015367.1,CCG026047.1,CCG007336.1,CCG007155.1,CCG017175.1,CCG007610.1,CCG011491.1,
GO:0046148	pigment biosynthetic process	4 of 4104 in the list	11 of 8404 in the genome	1	CCG027212.1,CCG004257.1,CCG005053.1,CCG017331.1

GO:0051179	localization	645 of 4104 in the list	1360 of 8404 in the genome	1	CCG005307.1,CCG017420.1,CCG020245.1,CCG024345.1,CCG014880.1,CCG010623.2,CCG003545.1,CCG017209.1,CCG021740.1,CCG004086.1,CCG021738.1,CCG000585.1,CCG003991.1,CCG001468.1,CCG013009.1,CCG019285.1,CCG009428.1,CCG019768.1,CCG022794.1,CCG024905.1,CCG005974.1,CCG003587.1,CCG013708.1,CCG023583.1,CCG003712.1,CCG017078.1,CCG026799.1,CCG011696.1,CCG009530.1,CCG017240.1,CCG027457.1,CCG027368.1,CCG001220.1,CCG019190.1,CCG018661.1,CCG016654.1,CCG018416.1,CCG014240.1,CCG006714.1,CCG027473.1,CCG026050.1,CCG001964.1,CCG019655.1,CCG009668.1,CCG025596.1,CCG016493.2,CCG009822.1,CCG005191.1,CCG004573.1,CCG011778.1,CCG006588.2,CCG000106.1,CCG014793.1,CCG024222.1,CCG026953.1,CCG006489.1,CCG019678.1,CCG017591.1,CCG018264.1,CCG013641.1,CCG003563.1,CCG017477.1,CCG008236.1,CCG003495.1,CCG005391.2,CCG022168.1,CCG007597.1,CCG016756.1,CCG019647.1,CCG009778.1,CCG015530.1,CCG026151.1,CCG022587.1,CCG020634.1,CCG010567.3,CCG009959.1,CCG027182.1,CCG026422.2,CCG026947.1,CCG016719.1,CCG000983.1,CCG010416.1,CCG009126.1,CCG002937.1,CCG001285.1,CCG016753.1,CCG011252.1,CCG027692.1,CCG008403.1,CCG016347.1,CCG022802.1,CCG010112.1,CCG020491.1,CCG014448.1,CCG005239.1,CCG005919.1,CCG016266.1,CCG022137.1,CCG012195.1,CCG026819.1,CCG025467.2,CCG011827.1,CCG028471.2,CCG002135.1,CCG019611.1,CCG010711.1,CCG000148.1,CCG025510.1,CCG023190.1,CCG022927.1,CCG022219.1,CCG012214.1,CCG027257.1,CCG017641.1,CCG016459.1,CCG016836.2,CCG019890.1,CCG023983.1,CCG020458.1,CCG004308.1,CCG013984.1,CCG026547.1,CCG000631.1,CCG003566.1,CCG006770.1,CCG015800.2,CCG002839.1,CCG022510.1,CCG003775.1,CCG016831.1,CCG021221.1,CCG023595.1,CCG018753.1,CCG018073.1,CCG016956.1,

GO:0051641	cellular localization	122 of 4104 in the list	268 of 8404 in the genome	1	CCG026698.1,CCG011766.1,CCG018832.1,CCG003146.1,CCG011408.1,CCG007060.1,CCG001809.1,CCG028124.1,CCG017209.1,CCG019590.1,CCG027692.1,CCG013042.1,CCG020949.1,CCG003995.1,CCG015386.1,CCG019020.1,CCG012550.1,CCG002645.1,CCG009428.1,CCG018800.1,CCG007941.1,CCG024905.1,CCG011813.1,CCG003587.1,CCG005262.1,CCG020315.1,CCG002028.1,CCG015568.1,CCG011006.1,CCG017077.1,CCG002766.1,CCG000010.1,CCG023051.1,CCG016860.1,CCG000614.1,CCG003531.1,CCG011567.1,CCG017078.1,CCG011696.1,CCG014307.1,CCG027457.1,CCG014318.1,CCG019629.2,CCG005810.1,CCG022927.1,CCG027257.1,CCG010939.1,CCG007855.1,CCG007283.1,CCG002374.1,CCG016541.1,CCG020909.1,CCG008323.1,CCG018447.1,CCG003786.1,CCG026989.1,CCG027733.1,CCG006714.1,CCG011862.1,CCG016836.2,CCG027473.1,CCG010178.1,CCG006777.1,CCG013984.1,CCG001673.1,CCG001172.1,CCG000631.1,CCG020280.1,CCG014506.1,CCG018557.1,CCG016493.2,CCG026620.1,CCG027564.1,CCG015800.2,CCG018217.1,CCG006625.1,CCG003775.1,CCG004573.1,CCG016831.1,CCG021221.1,CCG004869.1,CCG022771.1,CCG009136.1,CCG022910.1,CCG023595.1,CCG017373.1,CCG006924.1,CCG021220.1,CCG028498.1,CCG023814.2,CCG019797.1,CCG006775.1,CCG015087.1,CCG013126.2,CCG027323.1,CCG013641.1,CCG025233.1,CCG008312.1,CCG003495.1,CCG021377.1,CCG027241.1,CCG026336.1,CCG002121.1,CCG005195.1,CCG021800.1,CCG016542.1,CCG014226.1,CCG009362.1,CCG020806.1,CCG020634.1,CCG010567.3,CCG025473.1,CCG007989.1,CCG026947.1,CCG023756.1,CCG008116.1,CCG021152.1,CCG001481.1,CCG017125.1,CCG017141.1,CCG002937.1,CCG017874.1

GO:0007165	signal transduction	307 of 4104 in the list	657 of 8404 in the genome	1	CCG005254.1,CCG010628.1,CCG017420.1,CCG028253.1,CCG014340.1,CCG012989.1,CCG008603.1,CCG008741.1,CCG000646.1,CCG019020.1,CCG013398.1,CCG026174.1,CCG020785.1,CCG011006.1,CCG002841.1,CCG010275.1,CCG026360.1,CCG011717.1,CCG017266.1,CCG012573.1,CCG016689.2,CCG016745.1,CCG020709.1,CCG014466.1,CCG007993.1,CCG015101.1,CCG000659.1,CCG027127.1,CCG007335.1,CCG018533.1,CCG000647.1,CCG000526.1,CCG022281.1,CCG027669.1,CCG015967.1,CCG026537.1,CCG021661.1,CCG010071.1,CCG013308.1,CCG023579.1,CCG009510.1,CCG019717.1,CCG025176.1,CCG000078.1,CCG008685.1,CCG026109.1,CCG024952.1,CCG009980.1,CCG014506.1,CCG016252.1,CCG004279.1,CCG024663.1,CCG003745.1,CCG018494.1,CCG008759.1,CCG026953.1,CCG009427.1,CCG019493.1,CCG002520.1,CCG017591.1,CCG023464.1,CCG021284.1,CCG001579.1,CCG028136.1,CCG013641.1,CCG000732.1,CCG003317.1,CCG003495.1,CCG017127.1,CCG007951.1,CCG006412.1,CCG025131.2,CCG016307.1,CCG008444.1,CCG017701.1,CCG028486.1,CCG018859.3,CCG026695.1,CCG014712.1,CCG000876.1,CCG014928.1,CCG024664.1,CCG015638.1,CCG000789.1,CCG024271.1,CCG024662.1,CCG026047.1,CCG020978.1,CCG008939.1,CCG005531.1,CCG017725.1,CCG000111.2,CCG014345.2,CCG001759.1,CCG028477.1,CCG025899.1,CCG019881.1,CCG025035.1,CCG000984.1,CCG024639.1,CCG020654.1,CCG015426.1,CCG023151.1,CCG014509.1,CCG009553.1,CCG021902.1,CCG017033.1,CCG024918.1,CCG023002.1,CCG023662.1,CCG007958.1,CCG015583.1,CCG012959.1,CCG006013.1,CCG017112.1,CCG002413.1,CCG013272.2,CCG024595.1,CCG010046.1,CCG012402.1,CCG008742.1,CCG011228.1,CCG020929.1,CCG014647.1,CCG001012.1,CCG017696.1,CCG016883.1,CCG022929.1,CCG007830.1,CCG003775.1,CCG008152.1,CCG018930.1,CCG007702.1,CCG025036.1,CCG027014.1,
GO:0006370	7-methylguanosine mRNA capping	2 of 4104 in the list	6 of 8404 in the genome	1	CCG007177.1,CCG012557.1
GO:0032507	maintenance of protein location in cell	2 of 4104 in the list	6 of 8404 in the genome	1	CCG014318.1,CCG003587.1
GO:0045185	maintenance of protein location	2 of 4104 in the list	6 of 8404 in the genome	1	CCG014318.1,CCG003587.1
GO:0046836	glycolipid transport	2 of 4104 in the list	6 of 8404 in the genome	1	CCG013408.2,CCG024032.1

GO:0051235	maintenance of location	2 of 4104 in the list	6 of 8404 in the genome	1	CCG014318.1,CCG003587.1
GO:0051651	maintenance of location in cell	2 of 4104 in the list	6 of 8404 in the genome	1	CCG014318.1,CCG003587.1
GO:1901264	carbohydrate derivative transport	2 of 4104 in the list	6 of 8404 in the genome	1	CCG013408.2,CCG024032.1
GO:0016482	cytoplasmic transport	42 of 4104 in the list	97 of 8404 in the genome	1	CCG018832.1,CCG007060.1,CCG001809.1,CCG015800.2,CCG018217.1,CCG013042.1,CCG004573.1,CCG020949.1,CCG021221.1,CCG004869.1,CCG015386.1,CCG019020.1,CCG012550.1,CCG022771.1,CCG006924.1,CCG021220.1,CCG028498.1,CCG019797.1,CCG011006.1,CCG015087.1,CCG017077.1,CCG000010.1,CCG013641.1,CCG000614.1,CCG011567.1,CCG003495.1,CCG017078.1,CCG011696.1,CCG026336.1,CCG019629.2,CCG016542.1,CCG020806.1,CCG007989.1,CCG020909.1,CCG018447.1,CCG026989.1,CCG008116.1,CCG006714.1,CCG021152.1,CCG010178.1,CCG017874.1,CCG006777.1
GO:0007601	visual perception	8 of 4104 in the list	21 of 8404 in the genome	1	CCG017696.1,CCG009531.1,CCG012989.1,CCG012988.1,CCG018930.1,CCG004238.1,CCG007317.1,CCG010071.1
GO:0043603	cellular amide metabolic process	8 of 4104 in the list	21 of 8404 in the genome	1	CCG006821.1,CCG010174.2,CCG002897.1,CCG003865.1,CCG026099.1,CCG024133.1,CCG003192.1,CCG009333.1
GO:0050953	sensory perception of light stimulus	8 of 4104 in the list	21 of 8404 in the genome	1	CCG017696.1,CCG009531.1,CCG012989.1,CCG012988.1,CCG018930.1,CCG004238.1,CCG007317.1,CCG010071.1

GO:0006811	ion transport	175 of 4104 in the list	381 of 8404 in the genome	1	CCG007640.1,CCG000855.1,CCG010623.2,CCG003545.1,CCG015823.1,CCG021740.1,CCG004086.1,CCG021738.1,CCG000585.1,CCG006587.2,CCG008826.1,CCG025989.2,CCG000300.1,CCG003878.1,CCG027758.1,CCG005277.1,CCG000723.1,CCG009481.1,CCG016326.1,CCG013708.1,CCG000118.1,CCG003712.1,CCG027184.1,CCG020377.1,CCG009367.1,CCG012061.1,CCG027185.1,CCG015647.1,CCG006486.1,CCG016959.1,CCG026667.1,CCG019190.1,CCG025450.1,CCG018661.1,CCG016654.1,CCG018133.1,CCG020840.1,CCG023314.1,CCG014240.1,CCG016661.1,CCG026050.1,CCG001964.1,CCG021349.1,CCG007906.1,CCG004637.1,CCG014710.1,CCG023640.1,CCG007743.1,CCG026796.1,CCG022916.1,CCG009808.1,CCG025348.1,CCG019191.1,CCG003662.1,CCG012534.1,CCG019619.1,CCG006588.2,CCG014951.1,CCG024222.1,CCG014156.1,CCG024383.1,CCG001145.1,CCG005769.1,CCG021686.1,CCG014158.1,CCG015914.1,CCG026240.1,CCG023153.3,CCG019678.1,CCG012705.1,CCG026363.1,CCG014000.1,CCG027756.1,CCG023191.1,CCG024590.1,CCG017477.1,CCG006004.1,CCG015410.1,CCG009142.1,CCG022168.1,CCG014949.1,CCG019647.1,CCG014950.1,CCG005768.1,CCG027182.1,CCG016864.1,CCG013635.1,CCG008734.1,CCG000983.1,CCG010416.1,CCG023530.2,CCG000927.1,CCG001285.1,CCG017693.1,CCG001584.1,CCG013634.1,CCG007954.1,CCG024132.1,CCG004309.1,CCG008422.1,CCG015612.1,CCG009327.1,CCG003867.1,CCG010112.1,CCG016350.1,CCG000272.1,CCG007334.1,CCG014448.1,CCG018801.1,CCG027154.1,CCG028221.1,CCG010222.1,CCG005496.1,CCG013643.1,CCG015646.1,CCG002038.1,CCG022137.1,CCG025467.2,CCG009992.1,CCG025964.1,CCG027585.1,CCG001279.1,CCG000148.1,CCG023190.1,CCG025510.1,CCG005924.2,CCG025632.1,CCG000302.1,CCG008587.1,CCG002559.1,CCG015653.1,CCG015384.1,CCG027498.1,CCG021934.1,CCG019890.1,

GO:0023052	signaling	312 of 4104 in the list	669 of 8404 in the genome	1	CCG005254.1,CCG010628.1,CCG017420.1,CCG028253.1,CCG014340.1,CCG012989.1,CCG008603.1,CCG008741.1,CCG000646.1,CCG019020.1,CCG013398.1,CCG026174.1,CCG020785.1,CCG011006.1,CCG002841.1,CCG010275.1,CCG026360.1,CCG011717.1,CCG017266.1,CCG012573.1,CCG016689.2,CCG016745.1,CCG020709.1,CCG014466.1,CCG007993.1,CCG015101.1,CCG000659.1,CCG027127.1,CCG007335.1,CCG018533.1,CCG000647.1,CCG000526.1,CCG022281.1,CCG027669.1,CCG015967.1,CCG008323.1,CCG026537.1,CCG021661.1,CCG010071.1,CCG013308.1,CCG023579.1,CCG009510.1,CCG019717.1,CCG025176.1,CCG000078.1,CCG008685.1,CCG026109.1,CCG024952.1,CCG009980.1,CCG014506.1,CCG016252.1,CCG004279.1,CCG024663.1,CCG003745.1,CCG018494.1,CCG008759.1,CCG026953.1,CCG009427.1,CCG019493.1,CCG002520.1,CCG017591.1,CCG023464.1,CCG021284.1,CCG001579.1,CCG028136.1,CCG013641.1,CCG000732.1,CCG003317.1,CCG003495.1,CCG017127.1,CCG007951.1,CCG006412.1,CCG025131.2,CCG016307.1,CCG008444.1,CCG017701.1,CCG028486.1,CCG018859.3,CCG026695.1,CCG014712.1,CCG000876.1,CCG014928.1,CCG024664.1,CCG015638.1,CCG000789.1,CCG024271.1,CCG024662.1,CCG026047.1,CCG020978.1,CCG008939.1,CCG005531.1,CCG017725.1,CCG000111.2,CCG014345.2,CCG001759.1,CCG028477.1,CCG025899.1,CCG019881.1,CCG025035.1,CCG000984.1,CCG024639.1,CCG020654.1,CCG015426.1,CCG023151.1,CCG014509.1,CCG009553.1,CCG021902.1,CCG017033.1,CCG024918.1,CCG023002.1,CCG023662.1,CCG007958.1,CCG015583.1,CCG012959.1,CCG006013.1,CCG017112.1,CCG002413.1,CCG013272.2,CCG024595.1,CCG010046.1,CCG012402.1,CCG008742.1,CCG011228.1,CCG020929.1,CCG014647.1,CCG001012.1,CCG017696.1,CCG016883.1,CCG022929.1,CCG007830.1,CCG003775.1,CCG008152.1,CCG018930.1,CCG005596.1,CCG007702.1,

GO:0044700	single organism signaling	312 of 4104 in the list	669 of 8404 in the genome	1	CCG005254.1,CCG010628.1,CCG017420.1,CCG028253.1,CCG014340.1,CCG012989.1,CCG008603.1,CCG008741.1,CCG000646.1,CCG019020.1,CCG013398.1,CCG026174.1,CCG020785.1,CCG011006.1,CCG002841.1,CCG010275.1,CCG026360.1,CCG011717.1,CCG017266.1,CCG012573.1,CCG016689.2,CCG016745.1,CCG020709.1,CCG014466.1,CCG007993.1,CCG015101.1,CCG000659.1,CCG027127.1,CCG007335.1,CCG018533.1,CCG000647.1,CCG000526.1,CCG022281.1,CCG027669.1,CCG015967.1,CCG008323.1,CCG026537.1,CCG021661.1,CCG010071.1,CCG013308.1,CCG023579.1,CCG009510.1,CCG019717.1,CCG025176.1,CCG000078.1,CCG008685.1,CCG026109.1,CCG024952.1,CCG009980.1,CCG014506.1,CCG016252.1,CCG004279.1,CCG024663.1,CCG003745.1,CCG018494.1,CCG008759.1,CCG026953.1,CCG009427.1,CCG019493.1,CCG002520.1,CCG017591.1,CCG023464.1,CCG021284.1,CCG001579.1,CCG028136.1,CCG013641.1,CCG000732.1,CCG003317.1,CCG003495.1,CCG017127.1,CCG007951.1,CCG006412.1,CCG025131.2,CCG016307.1,CCG008444.1,CCG017701.1,CCG028486.1,CCG018859.3,CCG026695.1,CCG014712.1,CCG000876.1,CCG014928.1,CCG024664.1,CCG015638.1,CCG000789.1,CCG024271.1,CCG024662.1,CCG026047.1,CCG020978.1,CCG008939.1,CCG005531.1,CCG017725.1,CCG000111.2,CCG014345.2,CCG001759.1,CCG028477.1,CCG025899.1,CCG019881.1,CCG025035.1,CCG000984.1,CCG024639.1,CCG020654.1,CCG015426.1,CCG023151.1,CCG014509.1,CCG009553.1,CCG021902.1,CCG017033.1,CCG024918.1,CCG023002.1,CCG023662.1,CCG007958.1,CCG015583.1,CCG012959.1,CCG006013.1,CCG017112.1,CCG002413.1,CCG013272.2,CCG024595.1,CCG010046.1,CCG012402.1,CCG008742.1,CCG011228.1,CCG020929.1,CCG014647.1,CCG001012.1,CCG017696.1,CCG016883.1,CCG022929.1,CCG007830.1,CCG003775.1,CCG008152.1,CCG018930.1,CCG005596.1,CCG007702.1,
GO:0006888	ER to Golgi vesicle-mediated transport	5 of 4104 in the list	14 of 8404 in the genome	1	CCG015800.2,CCG015087.1,CCG007989.1,CCG013042.1,CCG000010.1
GO:0009611	response to wounding	7 of 4104 in the list	19 of 8404 in the genome	1	CCG004753.1,CCG024173.1,CCG015596.1,CCG008075.1,CCG015458.1,CCG005170.1,CCG016035.1

GO:0065008	regulation of biological quality	45 of 4104 in the list	105 of 8404 in the genome	1	CCG009285.1,CCG005375.1,CCG002466.1,CCG012993.1,CCG004548.1,CCG006600.1,CCG026796.1,CCG012992.1,CCG014566.1,CCG008826.1,CCG020637.1,CCG022471.1,CCG012678.1,CCG004595.1,CCG005714.1,CCG016162.1,CCG004446.1,CCG016956.1,CCG003587.1,CCG020472.1,CCG028221.1,CCG012569.1,CCG024590.1,CCG020377.1,CCG009063.1,CCG006787.1,CCG009992.1,CCG028500.2,CCG003104.1,CCG005587.1,CCG027430.1,CCG014318.1,CCG021250.1,CCG001847.1,CCG026500.1,CCG000302.1,CCG004445.1,CCG013244.3,CCG008323.1,CCG008924.1,CCG013245.1,CCG020400.2,CCG009674.1,CCG027531.2,CCG023671.2
GO:0048193	Golgi vesicle transport	11 of 4104 in the list	29 of 8404 in the genome	1	CCG012550.1,CCG007989.1,CCG028498.1,CCG026620.1,CCG011862.1,CCG020315.1,CCG015087.1,CCG015800.2,CCG000010.1,CCG013042.1,CCG004573.1
GO:0007602	phototransduction	6 of 4104 in the list	17 of 8404 in the genome	1	CCG017696.1,CCG009531.1,CCG012989.1,CCG012988.1,CCG007317.1,CCG010071.1
GO:0009314	response to radiation	6 of 4104 in the list	17 of 8404 in the genome	1	CCG017696.1,CCG009531.1,CCG012989.1,CCG012988.1,CCG007317.1,CCG010071.1
GO:0009416	response to light stimulus	6 of 4104 in the list	17 of 8404 in the genome	1	CCG017696.1,CCG009531.1,CCG012989.1,CCG012988.1,CCG007317.1,CCG010071.1
GO:0009581	detection of external stimulus	6 of 4104 in the list	17 of 8404 in the genome	1	CCG017696.1,CCG009531.1,CCG012989.1,CCG012988.1,CCG007317.1,CCG010071.1
GO:0009582	detection of abiotic stimulus	6 of 4104 in the list	17 of 8404 in the genome	1	CCG017696.1,CCG009531.1,CCG012989.1,CCG012988.1,CCG007317.1,CCG010071.1
GO:0009583	detection of light stimulus	6 of 4104 in the list	17 of 8404 in the genome	1	CCG017696.1,CCG009531.1,CCG012989.1,CCG012988.1,CCG007317.1,CCG010071.1
GO:0051606	detection of stimulus	6 of 4104 in the list	17 of 8404 in the genome	1	CCG017696.1,CCG009531.1,CCG012989.1,CCG012988.1,CCG007317.1,CCG010071.1
GO:0005976	polysaccharide metabolic process	4 of 4104 in the list	12 of 8404 in the genome	1	CCG022430.1,CCG004760.1,CCG025015.2,CCG008130.1
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	4 of 4104 in the list	12 of 8404 in the genome	1	CCG006714.1,CCG018217.1,CCG000614.1,CCG020806.1
GO:0007218	neuropeptide signaling pathway	4 of 4104 in the list	12 of 8404 in the genome	1	CCG009427.1,CCG022427.1,CCG022367.1,CCG017791.1
GO:0044264	cellular polysaccharide metabolic process	4 of 4104 in the list	12 of 8404 in the genome	1	CCG022430.1,CCG004760.1,CCG025015.2,CCG008130.1
GO:0045047	protein targeting to ER	4 of 4104 in the list	12 of 8404 in the genome	1	CCG006714.1,CCG018217.1,CCG000614.1,CCG020806.1

GO:0072599	establishment of protein localization to endoplasmic reticulum	4 of 4104 in the list	12 of 8404 in the genome	1	CCG006714.1,CCG018217.1,CCG000614.1,CCG020806.1
GO:0009187	cyclic nucleotide metabolic process	8 of 4104 in the list	22 of 8404 in the genome	1	CCG007993.1,CCG014379.1,CCG026174.1,CCG000016.1,CCG013365.1,CCG026047.1,CCG026898.1,CCG010944.1
GO:0009190	cyclic nucleotide biosynthetic process	8 of 4104 in the list	22 of 8404 in the genome	1	CCG007993.1,CCG014379.1,CCG026174.1,CCG000016.1,CCG013365.1,CCG026047.1,CCG026898.1,CCG010944.1
GO:0055076	transition metal ion homeostasis	8 of 4104 in the list	22 of 8404 in the genome	1	CCG000302.1,CCG016162.1,CCG009992.1,CCG003104.1,CCG008826.1,CCG024590.1,CCG012569.1,CCG020377.1
GO:0030258	lipid modification	13 of 4104 in the list	34 of 8404 in the genome	1	CCG000789.1,CCG024778.1,CCG019820.1,CCG006391.1,CCG023393.1,CCG012959.1,CCG015130.1,CCG025521.1,CCG018851.1,CCG006213.1,CCG011658.1,CCG000591.1,CCG024903.1
GO:0008610	lipid biosynthetic process	44 of 4104 in the list	104 of 8404 in the genome	1	CCG004532.1,CCG009244.1,CCG012002.1,CCG000663.1,CCG013131.1,CCG012408.1,CCG026370.1,CCG004806.1,CCG022352.1,CCG003249.1,CCG007330.1,CCG017097.1,CCG011531.1,CCG001102.1,CCG005923.1,CCG021610.1,CCG027312.1,CCG024155.1,CCG023102.1,CCG019263.1,CCG017241.1,CCG022209.1,CCG011183.1,CCG019857.1,CCG014839.1,CCG009434.1,CCG022134.1,CCG012308.1,CCG016653.1,CCG025889.1,CCG000552.1,CCG018615.3,CCG024760.1,CCG024095.1,CCG028332.1,CCG023757.1,CCG019035.1,CCG015411.1,CCG006965.1,CCG014174.1,CCG003751.1,CCG024612.1,CCG019909.1,CCG020408.1
GO:0000270	peptidoglycan metabolic process	5 of 4104 in the list	15 of 8404 in the genome	1	CCG020799.1,CCG019470.1,CCG015907.1,CCG028235.1,CCG005029.1
GO:0006027	glycosaminoglycan catabolic process	5 of 4104 in the list	15 of 8404 in the genome	1	CCG020799.1,CCG019470.1,CCG015907.1,CCG028235.1,CCG005029.1
GO:0009253	peptidoglycan catabolic process	5 of 4104 in the list	15 of 8404 in the genome	1	CCG020799.1,CCG019470.1,CCG015907.1,CCG028235.1,CCG005029.1
GO:0015698	inorganic anion transport	5 of 4104 in the list	15 of 8404 in the genome	1	CCG017477.1,CCG006770.1,CCG028221.1,CCG023244.1,CCG027185.1
GO:0006879	cellular iron ion homeostasis	7 of 4104 in the list	20 of 8404 in the genome	1	CCG003104.1,CCG000302.1,CCG008826.1,CCG009992.1,CCG012569.1,CCG024590.1,CCG020377.1
GO:0046916	cellular transition metal ion homeostasis	7 of 4104 in the list	20 of 8404 in the genome	1	CCG003104.1,CCG000302.1,CCG008826.1,CCG009992.1,CCG012569.1,CCG024590.1,CCG020377.1
GO:0055072	iron ion homeostasis	7 of 4104 in the list	20 of 8404 in the genome	1	CCG003104.1,CCG000302.1,CCG008826.1,CCG009992.1,CCG012569.1,CCG024590.1,CCG020377.1

GO:0009113	purine nucleobase biosynthetic process	2 of 4104 in the list	7 of 8404 in the genome	1	CCG004257.1,CCG017331.1
GO:0022411	cellular component disassembly	2 of 4104 in the list	7 of 8404 in the genome	1	CCG000915.1,CCG009582.1
GO:0030154	cell differentiation	2 of 4104 in the list	7 of 8404 in the genome	1	CCG021681.1,CCG013272.2
GO:0006813	potassium ion transport	21 of 4104 in the list	53 of 8404 in the genome	1	CCG004308.1,CCG006469.1,CCG017693.1,CCG026314.1,CCG004309.1,CCG019647.1,CCG019191.1,CCG006587.2,CCG006588.2,CCG019190.1,CCG000991.1,CCG014156.1,CCG027182.1,CCG016864.1,CCG008587.1,CCG002559.1,CCG023530.2,CCG001964.1,CCG014000.1,CCG019890.1,CCG027184.1
GO:0016192	vesicle-mediated transport	46 of 4104 in the list	109 of 8404 in the genome	1	CCG026698.1,CCG013984.1,CCG013024.1,CCG000631.1,CCG020280.1,CCG016493.2,CCG026620.1,CCG017209.1,CCG027692.1,CCG015800.2,CCG013042.1,CCG004573.1,CCG016831.1,CCG012550.1,CCG028498.1,CCG011813.1,CCG020315.1,CCG015568.1,CCG015087.1,CCG000010.1,CCG013126.2,CCG023051.1,CCG016860.1,CCG023276.2,CCG008236.1,CCG016306.1,CCG027457.1,CCG002121.1,CCG022927.1,CCG021800.1,CCG005810.1,CCG014226.1,CCG008788.2,CCG027257.1,CCG010559.1,CCG020634.1,CCG025473.1,CCG007989.1,CCG007283.1,CCG026422.2,CCG026947.1,CCG023756.1,CCG011862.1,CCG016836.2,CCG027473.1,CCG002937.1
GO:0006821	chloride transport	3 of 4104 in the list	10 of 8404 in the genome	1	CCG017477.1,CCG006770.1,CCG028221.1

GO:0071702	organic substance transport	163 of 4104 in the list	362 of 8404 in the genome	1	CCG017420.1,CCG018832.1,CCG002549.1,CCG003146.1,CCG011408.1,CCG027762.1,CCG001809.1,CCG028124.1,CCG020949.1,CCG004026.1,CCG003995.1,CCG015386.1,CCG019020.1,CCG012550.1,CCG002645.1,CCG009428.1,CCG027758.1,CCG024905.1,CCG011338.1,CCG009607.1,CCG011006.1,CCG013708.1,CCG002766.1,CCG000614.1,CCG011567.1,CCG017078.1,CCG011696.1,CCG014307.1,CCG005539.1,CCG027457.1,CCG002917.1,CCG016959.1,CCG027368.1,CCG001220.1,CCG026667.1,CCG010939.1,CCG007855.1,CCG011858.1,CCG024032.1,CCG016541.1,CCG020840.1,CCG003786.1,CCG006714.1,CCG027473.1,CCG021349.1,CCG016673.1,CCG001673.1,CCG004637.1,CCG009082.1,CCG014506.1,CCG018557.1,CCG016493.2,CCG026744.1,CCG027564.1,CCG006625.1,CCG025309.1,CCG004573.1,CCG004869.1,CCG000524.1,CCG013408.2,CCG022771.1,CCG022910.1,CCG024222.1,CCG024383.1,CCG026953.1,CCG017373.1,CCG006489.1,CCG006924.1,CCG005769.1,CCG021220.1,CCG017591.1,CCG017137.1,CCG013641.1,CCG025233.1,CCG021411.1,CCG003495.1,CCG001859.1,CCG027241.1,CCG005195.1,CCG014226.1,CCG020806.1,CCG020634.1,CCG010567.3,CCG005768.1,CCG026947.1,CCG023756.1,CCG008734.1,CCG021152.1,CCG017125.1,CCG023526.2,CCG026698.1,CCG011766.1,CCG005786.1,CCG007060.1,CCG023877.1,CCG019590.1,CCG027692.1,CCG000210.1,CCG001221.1,CCG017612.1,CCG016347.1,CCG018800.1,CCG017725.1,CCG011813.1,CCG005262.1,CCG020315.1,CCG015568.1,CCG000010.1,CCG017077.1,CCG007827.1,CCG014434.1,CCG003531.1,CCG025027.1,CCG003334.1,CCG023190.1,CCG019103.1,CCG019629.2,CCG027257.1,CCG007283.1,CCG002374.1,CCG020909.1,CCG018447.1,CCG016966.1,CCG026989.1,CCG010178.1,CCG006777.1,CCG013984.1,CCG001172.1,CCG020280.1,CCG020929.1,CCG026620.1,CCG015800.2,CCG018217.1,CCG003775.1,CCG016831.1,
GO:0006605	protein targeting	19 of 4104 in the list	49 of 8404 in the genome	1	CCG011766.1,CCG018832.1,CCG000614.1,CCG017078.1,CCG001809.1,CCG011696.1,CCG027564.1,CCG018217.1,CCG004573.1,CCG020949.1,CCG020806.1,CCG022771.1,CCG012550.1,CCG028498.1,CCG006714.1,CCG019797.1,CCG017077.1,CCG002766.1,CCG010178.1
GO:0006612	protein targeting to membrane	4 of 4104 in the list	13 of 8404 in the genome	1	CCG006714.1,CCG018217.1,CCG000614.1,CCG020806.1

GO:0006613	cotranslational protein targeting to membrane	4 of 4104 in the list	13 of 8404 in the genome	1	CCG006714.1,CCG018217.1,CCG000614.1,CCG020806.1
GO:0006511	ubiquitin-dependent protein catabolic process	48 of 4104 in the list	115 of 8404 in the genome	1	CCG005241.1,CCG003060.1,CCG008217.1,CCG027068.1,CCG001704.1,CCG007080.1,CCG019394.1,CCG001350.1,CCG010600.1,CCG011238.1,CCG007937.2,CCG019571.1,CCG019599.1,CCG010879.1,CCG001877.1,CCG012628.1,CCG003288.1,CCG004331.1,CCG028137.1,CCG008969.2,CCG022635.1,CCG009737.1,CCG002938.1,CCG024679.1,CCG012828.1,CCG021825.3,CCG001101.1,CCG013093.1,CCG027000.1,CCG003809.1,CCG001769.1,CCG027283.1,CCG003858.1,CCG026413.3,CCG026999.1,CCG028595.1,CCG005441.1,CCG023684.1,CCG022742.2,CCG002974.1,CCG014222.1,CCG013876.1,CCG027945.1,CCG027763.1,CCG001217.1,CCG014393.1,CCG004134.1,CCG019932.1
GO:0019941	modification-dependent protein catabolic process	48 of 4104 in the list	115 of 8404 in the genome	1	CCG005241.1,CCG003060.1,CCG008217.1,CCG027068.1,CCG001704.1,CCG007080.1,CCG019394.1,CCG001350.1,CCG010600.1,CCG011238.1,CCG007937.2,CCG019571.1,CCG019599.1,CCG010879.1,CCG001877.1,CCG012628.1,CCG003288.1,CCG004331.1,CCG028137.1,CCG008969.2,CCG022635.1,CCG009737.1,CCG002938.1,CCG024679.1,CCG012828.1,CCG021825.3,CCG001101.1,CCG013093.1,CCG027000.1,CCG003809.1,CCG001769.1,CCG027283.1,CCG003858.1,CCG026413.3,CCG026999.1,CCG028595.1,CCG005441.1,CCG023684.1,CCG022742.2,CCG002974.1,CCG014222.1,CCG013876.1,CCG027945.1,CCG027763.1,CCG001217.1,CCG014393.1,CCG004134.1,CCG019932.1
GO:0043632	modification-dependent macromolecule catabolic process	48 of 4104 in the list	115 of 8404 in the genome	1	CCG005241.1,CCG003060.1,CCG008217.1,CCG027068.1,CCG001704.1,CCG007080.1,CCG019394.1,CCG001350.1,CCG010600.1,CCG011238.1,CCG007937.2,CCG019571.1,CCG019599.1,CCG010879.1,CCG001877.1,CCG012628.1,CCG003288.1,CCG004331.1,CCG028137.1,CCG008969.2,CCG022635.1,CCG009737.1,CCG002938.1,CCG024679.1,CCG012828.1,CCG021825.3,CCG001101.1,CCG013093.1,CCG027000.1,CCG003809.1,CCG001769.1,CCG027283.1,CCG003858.1,CCG026413.3,CCG026999.1,CCG028595.1,CCG005441.1,CCG023684.1,CCG022742.2,CCG002974.1,CCG014222.1,CCG013876.1,CCG027945.1,CCG027763.1,CCG001217.1,CCG014393.1,CCG004134.1,CCG019932.1

GO:0009057	macromolecule catabolic process	78 of 4104 in the list	181 of 8404 in the genome	1	CCG003060.1,CCG027068.1,CCG001704.1,CCG007080.1,CCG005524.1,CCG001350.1,CCG019599.1,CCG012628.1,CCG003288.1,CCG020685.1,CCG022635.1,CCG004020.1,CCG016477.1,CCG012048.1,CCG004448.2,CCG005029.1,CCG012828.1,CCG021825.3,CCG015610.1,CCG020799.1,CCG001101.1,CCG027000.1,CCG013093.1,CCG003809.1,CCG003858.1,CCG020793.1,CCG028595.1,CCG026999.1,CCG026413.3,CCG005441.1,CCG023684.1,CCG023890.1,CCG002974.1,CCG014222.1,CCG013876.1,CCG027945.1,CCG019674.1,CCG014393.1,CCG001217.1,CCG023270.1,CCG010019.1,CCG004134.1,CCG005241.1,CCG008217.1,CCG019394.1,CCG010600.1,CCG002418.1,CCG011238.1,CCG007937.2,CCG019571.1,CCG018917.1,CCG010879.1,CCG001877.1,CCG007690.1,CCG004331.1,CCG021117.1,CCG028137.1,CCG008969.2,CCG025962.1,CCG013832.1,CCG012164.1,CCG009737.1,CCG002938.1,CCG024679.1,CCG019470.1,CCG015907.1,CCG001769.1,CCG027283.1,CCG009582.1,CCG024829.1,CCG028235.1,CCG022742.2,CCG002417.1,CCG023420.1,CCG027763.1,CCG011996.1,CCG026612.1,CCG019932.1
GO:0040007	growth	9 of 4104 in the list	26 of 8404 in the genome	1	CCG004753.1,CCG008075.1,CCG015458.1,CCG020988.1,CCG007219.1,CCG015596.1,CCG007821.1,CCG002448.1,CCG016035.1
GO:0072594	establishment of protein localization to organelle	16 of 4104 in the list	43 of 8404 in the genome	1	CCG018832.1,CCG000614.1,CCG017078.1,CCG001809.1,CCG011696.1,CCG018217.1,CCG004573.1,CCG020949.1,CCG020806.1,CCG022771.1,CCG012550.1,CCG028498.1,CCG006714.1,CCG019797.1,CCG017077.1,CCG010178.1

GO:0044255	cellular lipid metabolic process	63 of 4104 in the list	149 of 8404 in the genome	1	CCG004532.1,CCG000789.1,CCG021085.1,CCG019820.1,CCG009244.1,CCG023393.1,CCG012002.1,CCG013509.1,CCG000663.1,CCG013131.1,CCG012408.1,CCG026370.1,CCG015351.1,CCG004806.1,CCG000591.1,CCG024092.1,CCG022352.1,CCG003249.1,CCG012875.1,CCG007330.1,CCG019082.1,CCG006391.1,CCG017097.1,CCG015130.1,CCG011531.1,CCG001102.1,CCG005923.1,CCG021610.1,CCG027312.1,CCG024155.1,CCG023102.1,CCG025233.1,CCG022209.1,CCG017241.1,CCG024778.1,CCG009434.1,CCG014839.1,CCG025521.1,CCG022134.1,CCG012308.1,CCG006213.1,CCG016653.1,CCG025889.1,CCG011658.1,CCG000552.1,CCG018615.3,CCG024903.1,CCG024760.1,CCG017994.1,CCG028332.1,CCG023757.1,CCG023779.1,CCG019035.1,CCG015411.1,CCG012959.1,CCG006965.1,CCG025552.1,CCG018851.1,CCG014174.1,CCG019697.2,CCG003751.1,CCG024612.1,CCG019909.1

GO:0044238	primary metabolic process	2012 of 4104 in the list	4200 of 8404 in the genome	1	CCG014531.2,CCG006922.1,CCG017420.1,CCG027068.1,CCG014396.1,CCG004122.1,CCG006549.1,CCG007885.1,CCG004887.1,CCG006912.1,CCG026106.1,CCG016952.1,CCG012875.1,CCG025108.1,CCG028016.1,CCG026174.1,CCG004468.1,CCG023989.1,CCG012726.1,CCG019308.1,CCG024584.1,CCG004020.1,CCG001292.1,CCG018432.1,CCG001040.1,CCG017266.1,CCG006875.2,CCG028198.1,CCG011763.1,CCG005616.1,CCG016689.2,CCG025208.1,CCG021479.1,CCG003362.1,CCG002634.1,CCG023381.1,CCG019382.1,CCG019735.1,CCG020956.1,CCG017289.1,CCG016094.1,CCG026413.3,CCG023474.1,CCG017255.1,CCG026871.2,CCG010792.1,CCG012623.1,CCG022025.2,CCG021616.1,CCG019874.1,CCG003767.1,CCG005738.1,CCG013876.1,CCG010905.1,CCG008270.1,CCG021110.1,CCG010246.1,CCG024612.1,CCG027636.1,CCG003624.1,CCG028653.1,CCG004569.1,CCG020286.1,CCG013109.1,CCG006465.1,CCG015074.1,CCG019571.1,CCG008871.1,CCG015694.1,CCG018788.1,CCG006484.1,CCG002982.1,CCG012083.1,CCG026953.1,CCG026602.1,CCG023686.1,CCG019678.1,CCG007457.1,CCG021737.1,CCG025990.1,CCG013641.1,CCG027708.4,CCG028590.1,CCG015350.1,CCG021948.1,CCG018585.3,CCG020651.1,CCG007467.1,CCG012840.1,CCG014385.1,CCG005284.1,CCG004927.1,CCG009805.2,CCG005089.1,CCG024903.1,CCG021137.1,CCG022056.1,CCG013610.1,CCG001876.1,CCG012584.1,CCG015186.1,CCG012023.1,CCG013465.1,CCG016327.2,CCG018688.1,CCG024200.1,CCG010624.1,CCG002231.1,CCG003608.1,CCG012957.1,CCG023502.1,CCG028454.1,CCG023458.1,CCG027748.1,CCG017001.1,CCG021767.1,CCG003520.1,CCG024865.1,CCG004926.1,CCG006928.1,CCG004532.1,CCG000789.1,CCG017381.1,CCG005588.1,CCG010912.1,CCG004955.1,CCG007874.3,CCG001704.1,CCG005524.1,CCG001289.1,CCG011547.1,CCG013640.1,CCG008404.1,CCG018201.1,CCG010136.1,
GO:0048856	anatomical structure development	8 of 4104 in the list	24 of 8404 in the genome	1	CCG015767.2,CCG004753.1,CCG006750.1,CCG028121.1,CCG015596.1,CCG008075.1,CCG015458.1,CCG016035.1
GO:0000271	polysaccharide biosynthetic process	2 of 4104 in the list	8 of 8404 in the genome	1	CCG022430.1,CCG008130.1
GO:0006182	cGMP biosynthetic process	2 of 4104 in the list	8 of 8404 in the genome	1	CCG013365.1,CCG026898.1
GO:0006825	copper ion transport	2 of 4104 in the list	8 of 8404 in the genome	1	CCG003878.1,CCG000927.1

GO:0033692	cellular polysaccharide biosynthetic process	2 of 4104 in the list	8 of 8404 in the genome	1	CCG022430.1,CCG008130.1
GO:0042180	cellular ketone metabolic process	2 of 4104 in the list	8 of 8404 in the genome	1	CCG006009.1,CCG006059.1
GO:0046068	cGMP metabolic process	2 of 4104 in the list	8 of 8404 in the genome	1	CCG013365.1,CCG026898.1
GO:0052652	cyclic purine nucleotide metabolic process	2 of 4104 in the list	8 of 8404 in the genome	1	CCG013365.1,CCG026898.1
GO:0006869	lipid transport	10 of 4104 in the list	29 of 8404 in the genome	1	CCG027368.1,CCG001220.1,CCG013408.2,CCG011858.1,CCG024032.1,CCG006489.1,CCG005786.1,CCG011338.1,CCG000524.1,CCG001221.1
GO:0010876	lipid localization	10 of 4104 in the list	29 of 8404 in the genome	1	CCG027368.1,CCG001220.1,CCG013408.2,CCG011858.1,CCG024032.1,CCG006489.1,CCG005786.1,CCG011338.1,CCG000524.1,CCG001221.1
GO:0006625	protein targeting to peroxisome	3 of 4104 in the list	11 of 8404 in the genome	1	CCG018832.1,CCG019797.1,CCG010178.1
GO:0043574	peroxisomal transport	3 of 4104 in the list	11 of 8404 in the genome	1	CCG018832.1,CCG019797.1,CCG010178.1
GO:0072662	protein localization to peroxisome	3 of 4104 in the list	11 of 8404 in the genome	1	CCG018832.1,CCG019797.1,CCG010178.1
GO:0072663	establishment of protein localization to peroxisome	3 of 4104 in the list	11 of 8404 in the genome	1	CCG018832.1,CCG019797.1,CCG010178.1
GO:0007264	small GTPase mediated signal transduction	54 of 4104 in the list	130 of 8404 in the genome	1	CCG010046.1,CCG017420.1,CCG002549.1,CCG025973.1,CCG007060.1,CCG020929.1,CCG009980.1,CCG014506.1,CCG016252.1,CCG028124.1,CCG008892.2,CCG003775.1,CCG008152.1,CCG004869.1,CCG024327.1,CCG015386.1,CCG019020.1,CCG026953.1,CCG017373.1,CCG017725.1,CCG006924.1,CCG021220.1,CCG009607.1,CCG011006.1,CCG017591.1,CCG007827.1,CCG014434.1,CCG028136.1,CCG013641.1,CCG016027.1,CCG021411.1,CCG003495.1,CCG025027.1,CCG022841.1,CCG017127.1,CCG001859.1,CCG014466.1,CCG026336.1,CCG019103.1,CCG019629.2,CCG002917.1,CCG025131.2,CCG016542.1,CCG026154.1,CCG015654.1,CCG020909.1,CCG022184.1,CCG018447.1,CCG016966.1,CCG018222.1,CCG021152.1,CCG023526.2,CCG025179.1,CCG006777.1

GO:0044265	cellular macromolecule catabolic process	59 of 4104 in the list	142 of 8404 in the genome	1	CCG005241.1,CCG003060.1,CCG008217.1,CCG027068.1,CCG001704.1,CCG007080.1,CCG019394.1,CCG005524.1,CCG001350.1,CCG010600.1,CCG011238.1,CCG007937.2,CCG018917.1,CCG019571.1,CCG019599.1,CCG010879.1,CCG001877.1,CCG007690.1,CCG012628.1,CCG003288.1,CCG004331.1,CCG028137.1,CCG020685.1,CCG008969.2,CCG022635.1,CCG013832.1,CCG012164.1,CCG009737.1,CCG002938.1,CCG024679.1,CCG004448.2,CCG012828.1,CCG021825.3,CCG001101.1,CCG013093.1,CCG027000.1,CCG003809.1,CCG001769.1,CCG027283.1,CCG003858.1,CCG028595.1,CCG026999.1,CCG026413.3,CCG005441.1,CCG009582.1,CCG023684.1,CCG022742.2,CCG002974.1,CCG014222.1,CCG013876.1,CCG027945.1,CCG019674.1,CCG023270.1,CCG027763.1,CCG001217.1,CCG014393.1,CCG004134.1,CCG026612.1,CCG019932.1

GO:0009059	macromolecule biosynthetic process	369 of 4104 in the list	806 of 8404 in the genome	1	CCG014531.2,CCG018536.1,CCG023277.1,CCG014396.1,CCG006549.1,CCG004807.1,CCG010191.3,CCG013430.1,CCG009878.1,CCG010647.1,CCG026882.1,CCG024517.1,CCG018507.1,CCG002354.1,CCG004468.1,CCG016238.1,CCG026473.1,CCG004091.1,CCG001292.1,CCG009653.1,CCG018321.1,CCG026825.1,CCG002470.1,CCG003573.1,CCG028505.1,CCG025472.1,CCG025223.1,CCG018432.1,CCG015599.1,CCG004398.1,CCG025208.1,CCG012213.2,CCG026871.2,CCG018719.1,CCG013353.1,CCG012623.1,CCG008270.1,CCG019210.1,CCG027115.1,CCG018799.1,CCG020129.1,CCG024612.1,CCG005737.1,CCG005276.1,CCG024326.1,CCG020877.1,CCG021295.1,CCG009249.1,CCG006231.1,CCG020286.1,CCG014896.1,CCG001863.1,CCG013131.1,CCG014280.1,CCG006767.1,CCG019296.1,CCG013065.1,CCG008871.1,CCG014840.1,CCG015694.1,CCG014819.1,CCG013865.1,CCG018788.1,CCG006484.1,CCG010378.2,CCG027114.1,CCG026602.1,CCG006344.1,CCG026280.1,CCG010510.1,CCG021737.1,CCG023468.1,CCG000773.1,CCG009119.1,CCG015350.1,CCG021948.1,CCG011148.1,CCG020651.1,CCG000552.1,CCG009805.2,CCG002966.1,CCG019545.1,CCG003142.1,CCG021137.1,CCG019330.1,CCG001876.1,CCG000915.1,CCG024200.1,CCG023125.1,CCG016381.1,CCG011727.1,CCG028426.1,CCG027748.1,CCG017001.1,CCG000294.1,CCG004926.1,CCG016778.1,CCG017381.1,CCG015367.1,CCG007336.1,CCG007155.1,CCG005501.1,CCG007766.1,CCG000368.1,CCG004806.1,CCG004534.1,CCG003471.1,CCG018164.1,CCG004224.1,CCG010112.1,CCG019398.1,CCG011135.1,CCG006876.1,CCG028092.1,CCG027407.4,CCG000209.1,CCG026258.1,CCG021521.1,CCG007902.1,CCG024232.1,CCG023184.1,CCG022209.1,CCG021940.1,CCG013174.1,CCG014839.1,CCG018168.1,CCG014579.1,CCG017344.1,CCG019426.1,CCG004332.1,CCG025889.1,CCG018796.1,CCG025691.1,CCG009394.1,CCG027401.1,
GO:0006826	iron ion transport	5 of 4104 in the list	17 of 8404 in the genome	1	CCG000302.1,CCG008826.1,CCG009992.1,CCG024590.1,CCG020377.1
GO:0009888	tissue development	5 of 4104 in the list	17 of 8404 in the genome	1	CCG004753.1,CCG015596.1,CCG008075.1,CCG015458.1,CCG016035.1
GO:0031099	regeneration	5 of 4104 in the list	17 of 8404 in the genome	1	CCG004753.1,CCG015596.1,CCG008075.1,CCG015458.1,CCG016035.1

GO:0042060	wound healing	5 of 4104 in the list	17 of 8404 in the genome	1	CCG004753.1,CCG015596.1,CCG008075.1,CCG015458.1,CCG016035.1
GO:0042246	tissue regeneration	5 of 4104 in the list	17 of 8404 in the genome	1	CCG004753.1,CCG015596.1,CCG008075.1,CCG015458.1,CCG016035.1
GO:0071704	organic substance metabolic process	2131 of 4104 in the list	4451 of 8404 in the genome	1	CCG014531.2,CCG006922.1,CCG017420.1,CCG027068.1,CCG004122.1,CCG004887.1,CCG026106.1,CCG016952.1,CCG012875.1,CCG025108.1,CCG028016.1,CCG004468.1,CCG023989.1,CCG012726.1,CCG024584.1,CCG004020.1,CCG017266.1,CCG006875.2,CCG011763.1,CCG025208.1,CCG021479.1,CCG003362.1,CCG023381.1,CCG019382.1,CCG016094.1,CCG026413.3,CCG023474.1,CCG017255.1,CCG026871.2,CCG010792.1,CCG022025.2,CCG005053.1,CCG021616.1,CCG003767.1,CCG010905.1,CCG008270.1,CCG021110.1,CCG024612.1,CCG003624.1,CCG028653.1,CCG013109.1,CCG006465.1,CCG019571.1,CCG015694.1,CCG018788.1,CCG002982.1,CCG012083.1,CCG023686.1,CCG013641.1,CCG015350.1,CCG021948.1,CCG007467.1,CCG004927.1,CCG024903.1,CCG021137.1,CCG022056.1,CCG013610.1,CCG001876.1,CCG013465.1,CCG018688.1,CCG024200.1,CCG020663.1,CCG023458.1,CCG024865.1,CCG004926.1,CCG006928.1,CCG004532.1,CCG000789.1,CCG017381.1,CCG010912.1,CCG001704.1,CCG005524.1,CCG001289.1,CCG011547.1,CCG013640.1,CCG008404.1,CCG010136.1,CCG027015.1,CCG022370.1,CCG020803.1,CCG020179.1,CCG010112.1,CCG022513.2,CCG004986.1,CCG007750.2,CCG027989.1,CCG025707.1,CCG028092.1,CCG019831.2,CCG019825.2,CCG001395.1,CCG024155.1,CCG016557.1,CCG021990.1,CCG027000.1,CCG006804.1,CCG007814.1,CCG006264.1,CCG015896.1,CCG024760.1,CCG011015.1,CCG010865.1,CCG014222.1,CCG012959.1,CCG000612.1,CCG025897.1,CCG004308.1,CCG002466.1,CCG001440.1,CCG006921.1,CCG009928.1,CCG012666.1,CCG014982.1,CCG017894.1,CCG007724.1,CCG024070.1,CCG012229.1,CCG024679.1,CCG013298.1,CCG012843.1,CCG015312.2,CCG000490.1,CCG005269.1,CCG022674.1,CCG021250.1,CCG003940.1,CCG018211.1,CCG003657.2,CCG021641.1,CCG025552.1,CCG028648.1,CCG013199.1,CCG003981.1,CCG021354.1,CCG010174.2,
GO:0046834	lipid phosphorylation	8 of 4104 in the list	25 of 8404 in the genome	1	CCG000789.1,CCG024778.1,CCG019820.1,CCG023393.1,CCG012959.1,CCG015130.1,CCG011658.1,CCG024903.1

GO:0046854	phosphatidylinositol phosphorylation	8 of 4104 in the list	25 of 8404 in the genome	1	CCG000789.1,CCG024778.1,CCG019820.1,CCG023393.1,CCG012959.1,CCG015130.1,CCG011658.1,CCG024903.1
GO:0006412	translation	150 of 4104 in the list	343 of 8404 in the genome	1	CCG014531.2,CCG023277.1,CCG014396.1,CCG004807.1,CCG010191.3,CCG013430.1,CCG021944.1,CCG009878.1,CCG003437.1,CCG004909.1,CCG015950.3,CCG026048.1,CCG002354.1,CCG016238.1,CCG007396.1,CCG026825.1,CCG016378.1,CCG003573.1,CCG025223.1,CCG027607.1,CCG007854.1,CCG008753.1,CCG019944.1,CCG026871.2,CCG018719.1,CCG008270.1,CCG008592.1,CCG000414.1,CCG005737.1,CCG011972.1,CCG020877.1,CCG009249.1,CCG006231.1,CCG008321.1,CCG014896.1,CCG001863.1,CCG002890.1,CCG022229.1,CCG008871.1,CCG007059.1,CCG014819.1,CCG018788.1,CCG005204.1,CCG026602.1,CCG006344.1,CCG027913.1,CCG026280.1,CCG016285.1,CCG003684.1,CCG021737.1,CCG000773.1,CCG023315.1,CCG005622.1,CCG002966.1,CCG019545.1,CCG019330.1,CCG001876.1,CCG000915.1,CCG026570.1,CCG001013.1,CCG011256.1,CCG026155.1,CCG027748.1,CCG007047.1,CCG000294.1,CCG016778.1,CCG021774.1,CCG008569.1,CCG015367.1,CCG027724.1,CCG007256.1,CCG000368.1,CCG006188.1,CCG004104.1,CCG027352.3,CCG003471.1,CCG018164.1,CCG016139.1,CCG010112.1,CCG011135.1,CCG019398.1,CCG013727.1,CCG028092.1,CCG006876.1,CCG021521.1,CCG024781.1,CCG005143.1,CCG021940.1,CCG009349.1,CCG003809.1,CCG010321.1,CCG011345.1,CCG018168.1,CCG019426.1,CCG000138.1,CCG017344.1,CCG008581.1,CCG009394.1,CCG015577.3,CCG002544.1,CCG002644.1,CCG024813.1,CCG016699.1,CCG002018.1,CCG002680.1,CCG006336.1,CCG013870.1,CCG014051.1,CCG005443.1,CCG001811.1,CCG021917.1,CCG004949.1,CCG005442.1,CCG027751.1,CCG003710.1,CCG027281.1,CCG013833.1,CCG020899.1,CCG002408.1,CCG021716.1,CCG014947.2,CCG007705.1,CCG021820.1,CCG020268.1,CCG002238.1,CCG017334.1,CCG000994.1,CCG006570.1,CCG002662.1,CCG016511.1,CCG000352.1,CCG025107.1,CCG021933.1,CCG003528.1,CCG025409.1,
GO:0051493	regulation of cytoskeleton organization	2 of 4104 in the list	9 of 8404 in the genome	1	CCG025026.1,CCG019102.1
GO:0072657	protein localization to membrane	7 of 4104 in the list	23 of 8404 in the genome	1	CCG027323.1,CCG006714.1,CCG018217.1,CCG000614.1,CCG007941.1,CCG020949.1,CCG020806.1

GO:0090150	establishment of protein localization to membrane	7 of 4104 in the list	23 of 8404 in the genome	1	CCG027323.1,CCG006714.1,CCG018217.1,CCG000614.1,CCG007941.1,CCG020949.1,CCG020806.1
GO:0034645	cellular macromolecule biosynthetic process	364 of 4104 in the list	800 of 8404 in the genome	1	CCG014531.2,CCG018536.1,CCG023277.1,CCG014396.1,CCG006549.1,CCG004807.1,CCG010191.3,CCG013430.1,CCG009878.1,CCG010647.1,CCG026882.1,CCG018507.1,CCG002354.1,CCG004468.1,CCG016238.1,CCG026473.1,CCG004091.1,CCG001292.1,CCG018321.1,CCG026825.1,CCG002470.1,CCG003573.1,CCG028505.1,CCG025472.1,CCG025223.1,CCG018432.1,CCG015599.1,CCG004398.1,CCG025208.1,CCG012213.2,CCG026871.2,CCG018719.1,CCG013353.1,CCG012623.1,CCG008270.1,CCG019210.1,CCG027115.1,CCG018799.1,CCG020129.1,CCG024612.1,CCG005737.1,CCG005276.1,CCG024326.1,CCG020877.1,CCG021295.1,CCG009249.1,CCG006231.1,CCG020286.1,CCG014896.1,CCG001863.1,CCG013131.1,CCG014280.1,CCG006767.1,CCG019296.1,CCG013065.1,CCG008871.1,CCG014840.1,CCG015694.1,CCG014819.1,CCG013865.1,CCG018788.1,CCG006484.1,CCG010378.2,CCG027114.1,CCG026602.1,CCG006344.1,CCG026280.1,CCG010510.1,CCG021737.1,CCG023468.1,CCG000773.1,CCG009119.1,CCG015350.1,CCG021948.1,CCG011148.1,CCG020651.1,CCG000552.1,CCG009805.2,CCG002966.1,CCG019545.1,CCG003142.1,CCG021137.1,CCG019330.1,CCG001876.1,CCG000915.1,CCG024200.1,CCG023125.1,CCG016381.1,CCG011727.1,CCG028426.1,CCG027748.1,CCG017001.1,CCG000294.1,CCG004926.1,CCG016778.1,CCG017381.1,CCG015367.1,CCG007336.1,CCG007155.1,CCG005501.1,CCG007766.1,CCG000368.1,CCG004806.1,CCG004534.1,CCG003471.1,CCG018164.1,CCG004224.1,CCG010112.1,CCG019398.1,CCG011135.1,CCG006876.1,CCG028092.1,CCG027407.4,CCG000209.1,CCG026258.1,CCG021521.1,CCG007902.1,CCG024232.1,CCG023184.1,CCG022209.1,CCG021940.1,CCG013174.1,CCG014839.1,CCG018168.1,CCG014579.1,CCG017344.1,CCG019426.1,CCG004332.1,CCG025889.1,CCG018796.1,CCG025691.1,CCG009394.1,CCG027401.1,CCG002644.1,CCG024760.1,

GO:0019538	protein metabolic process	957 of 4104 in the list	2040 of 8404 in the genome	1	CCG011990.4,CCG014531.2,CCG006922.1,CCG027068.1,CCG014396.1,CCG004887.1,CCG006912.1,CCG013430.1,CCG009878.1,CCG002687.2,CCG016952.1,CCG028016.1,CCG026174.1,CCG016238.1,CCG012726.1,CCG019308.1,CCG025472.1,CCG018432.1,CCG017266.1,CCG006875.2,CCG028198.1,CCG016689.2,CCG021479.1,CCG003362.1,CCG026300.1,CCG002634.1,CCG023381.1,CCG019735.1,CCG017289.1,CCG026413.3,CCG016271.1,CCG026871.2,CCG012077.1,CCG008381.1,CCG021616.1,CCG016336.1,CCG026069.1,CCG025069.2,CCG003767.1,CCG005738.1,CCG013876.1,CCG008270.1,CCG024294.1,CCG008301.1,CCG017984.1,CCG024612.1,CCG005737.1,CCG027636.1,CCG003624.1,CCG026212.1,CCG004569.1,CCG024139.1,CCG008040.1,CCG002156.2,CCG013109.1,CCG020562.1,CCG011238.1,CCG011949.1,CCG005125.1,CCG006465.1,CCG015074.1,CCG027940.1,CCG004212.1,CCG003248.1,CCG019571.1,CCG008871.1,CCG004331.1,CCG018788.1,CCG018494.1,CCG002982.1,CCG012083.1,CCG001311.1,CCG026602.1,CCG006344.1,CCG016480.1,CCG022996.1,CCG022627.1,CCG001214.1,CCG007457.1,CCG021737.1,CCG012332.1,CCG026384.1,CCG022225.1,CCG028590.1,CCG002957.1,CCG024897.1,CCG017570.1,CCG018585.3,CCG007467.1,CCG008341.1,CCG014385.1,CCG003203.1,CCG000552.1,CCG013119.1,CCG022994.1,CCG005089.1,CCG002966.1,CCG019545.1,CCG022056.1,CCG001876.1,CCG007823.1,CCG015186.1,CCG012023.1,CCG016327.2,CCG018688.1,CCG003608.1,CCG012957.1,CCG023502.1,CCG023458.1,CCG027748.1,CCG027943.1,CCG006666.1,CCG000294.1,CCG003520.1,CCG024865.1,CCG006928.1,CCG016738.2,CCG017381.1,CCG003554.1,CCG018968.1,CCG007874.3,CCG001704.1,CCG027993.1,CCG015367.1,CCG001289.1,CCG013640.1,CCG008404.1,CCG008099.1,CCG018201.1,CCG005501.1,CCG007766.1,CCG006174.1,CCG021179.1,CCG001108.1,CCG009574.1,
GO:0044802	single-organism membrane organization	9 of 4104 in the list	29 of 8404 in the genome	1	CCG027323.1,CCG000614.1,CCG007941.1,CCG026620.1,CCG006714.1,CCG020315.1,CCG018217.1,CCG020949.1,CCG020806.1
GO:0061024	membrane organization	9 of 4104 in the list	29 of 8404 in the genome	1	CCG027323.1,CCG000614.1,CCG007941.1,CCG026620.1,CCG006714.1,CCG020315.1,CCG018217.1,CCG020949.1,CCG020806.1

GO:0072330	monocarboxylic acid biosynthetic process	12 of 4104 in the list	37 of 8404 in the genome	1	CCG015276.2,CCG003865.1,CCG026331.1,CCG009244.1,CCG017097.1,CCG012408.1,CCG020559.1,CCG003751.1,CCG016315.1,CCG027312.1,CCG019909.1,CCG018615.3
GO:1902582	single-organism intracellular transport	32 of 4104 in the list	85 of 8404 in the genome	1	CCG011766.1,CCG018832.1,CCG001809.1,CCG026620.1,CCG027564.1,CCG017209.1,CCG015800.2,CCG018217.1,CCG013042.1,CCG004573.1,CCG020949.1,CCG012550.1,CCG022771.1,CCG028498.1,CCG023814.2,CCG020315.1,CCG019797.1,CCG015087.1,CCG017077.1,CCG000010.1,CCG002766.1,CCG000614.1,CCG017078.1,CCG011696.1,CCG022927.1,CCG020806.1,CCG007989.1,CCG026989.1,CCG011862.1,CCG006714.1,CCG010178.1,CCG017874.1
GO:0033365	protein localization to organelle	16 of 4104 in the list	47 of 8404 in the genome	1	CCG018832.1,CCG000614.1,CCG017078.1,CCG001809.1,CCG011696.1,CCG018217.1,CCG004573.1,CCG020949.1,CCG020806.1,CCG022771.1,CCG012550.1,CCG028498.1,CCG006714.1,CCG019797.1,CCG017077.1,CCG010178.1
GO:0070972	protein localization to endoplasmic reticulum	4 of 4104 in the list	16 of 8404 in the genome	1	CCG006714.1,CCG018217.1,CCG000614.1,CCG020806.1
GO:0030163	protein catabolic process	51 of 4104 in the list	129 of 8404 in the genome	1	CCG005241.1,CCG003060.1,CCG008217.1,CCG027068.1,CCG001704.1,CCG007080.1,CCG019394.1,CCG001350.1,CCG010600.1,CCG011238.1,CCG007937.2,CCG019571.1,CCG019599.1,CCG010879.1,CCG001877.1,CCG012628.1,CCG003288.1,CCG004331.1,CCG028137.1,CCG008969.2,CCG022635.1,CCG013832.1,CCG012164.1,CCG009737.1,CCG002938.1,CCG024679.1,CCG012828.1,CCG021825.3,CCG001101.1,CCG013093.1,CCG027000.1,CCG003809.1,CCG001769.1,CCG027283.1,CCG003858.1,CCG026413.3,CCG026999.1,CCG028595.1,CCG005441.1,CCG023684.1,CCG022742.2,CCG002974.1,CCG014222.1,CCG013876.1,CCG027945.1,CCG023270.1,CCG027763.1,CCG001217.1,CCG014393.1,CCG004134.1,CCG019932.1
GO:0006897	endocytosis	2 of 4104 in the list	10 of 8404 in the genome	1	CCG007283.1,CCG021800.1
GO:0048589	developmental growth	5 of 4104 in the list	19 of 8404 in the genome	1	CCG004753.1,CCG015596.1,CCG008075.1,CCG015458.1,CCG016035.1

GO:0044257	cellular protein catabolic process	50 of 4104 in the list	128 of 8404 in the genome	1	CCG005241.1,CCG003060.1,CCG008217.1,CCG027068.1,CCG001704.1,CCG007080.1,CCG019394.1,CCG001350.1,CCG010600.1,CCG011238.1,CCG007937.2,CCG019571.1,CCG019599.1,CCG010879.1,CCG001877.1,CCG012628.1,CCG003288.1,CCG004331.1,CCG028137.1,CCG008969.2,CCG022635.1,CCG013832.1,CCG009737.1,CCG002938.1,CCG024679.1,CCG012828.1,CCG021825.3,CCG001101.1,CCG013093.1,CCG027000.1,CCG003809.1,CCG001769.1,CCG027283.1,CCG003858.1,CCG026413.3,CCG026999.1,CCG028595.1,CCG005441.1,CCG023684.1,CCG022742.2,CCG002974.1,CCG014222.1,CCG013876.1,CCG027945.1,CCG023270.1,CCG027763.1,CCG001217.1,CCG014393.1,CCG004134.1,CCG019932.1
GO:0051603	proteolysis involved in cellular protein catabolic process	50 of 4104 in the list	128 of 8404 in the genome	1	CCG005241.1,CCG003060.1,CCG008217.1,CCG027068.1,CCG001704.1,CCG007080.1,CCG019394.1,CCG001350.1,CCG010600.1,CCG011238.1,CCG007937.2,CCG019571.1,CCG019599.1,CCG010879.1,CCG001877.1,CCG012628.1,CCG003288.1,CCG004331.1,CCG028137.1,CCG008969.2,CCG022635.1,CCG013832.1,CCG009737.1,CCG002938.1,CCG024679.1,CCG012828.1,CCG021825.3,CCG001101.1,CCG013093.1,CCG027000.1,CCG003809.1,CCG001769.1,CCG027283.1,CCG003858.1,CCG026413.3,CCG026999.1,CCG028595.1,CCG005441.1,CCG023684.1,CCG022742.2,CCG002974.1,CCG014222.1,CCG013876.1,CCG027945.1,CCG023270.1,CCG027763.1,CCG001217.1,CCG014393.1,CCG004134.1,CCG019932.1
GO:0000041	transition metal ion transport	7 of 4104 in the list	25 of 8404 in the genome	1	CCG000302.1,CCG003878.1,CCG000927.1,CCG008826.1,CCG009992.1,CCG024590.1,CCG020377.1

GO:0045184	establishment of protein localization	124 of 4104 in the list	293 of 8404 in the genome	1	CCG026698.1,CCG011766.1,CCG017420.1,CCG018832.1,CCG002549.1,CCG003146.1,CCG011408.1,CCG027762.1,CCG007060.1,CCG001809.1,CCG023877.1,CCG028124.1,CCG019590.1,CCG027692.1,CCG020949.1,CCG004026.1,CCG003995.1,CCG015386.1,CCG017612.1,CCG019020.1,CCG012550.1,CCG002645.1,CCG016347.1,CCG009428.1,CCG018800.1,CCG017725.1,CCG007941.1,CCG024905.1,CCG011813.1,CCG005262.1,CCG020315.1,CCG015568.1,CCG009607.1,CCG011006.1,CCG017077.1,CCG000010.1,CCG002766.1,CCG007827.1,CCG014434.1,CCG000614.1,CCG003531.1,CCG025027.1,CCG017078.1,CCG003334.1,CCG011696.1,CCG014307.1,CCG027457.1,CCG019103.1,CCG019629.2,CCG002917.1,CCG027257.1,CCG010939.1,CCG007855.1,CCG007283.1,CCG002374.1,CCG016541.1,CCG020909.1,CCG018447.1,CCG003786.1,CCG016966.1,CCG006714.1,CCG027473.1,CCG010178.1,CCG006777.1,CCG013984.1,CCG001673.1,CCG001172.1,CCG020280.1,CCG020929.1,CCG014506.1,CCG018557.1,CCG016493.2,CCG026744.1,CCG026620.1,CCG027564.1,CCG015800.2,CCG018217.1,CCG006625.1,CCG003775.1,CCG004573.1,CCG016831.1,CCG004869.1,CCG022771.1,CCG022910.1,CCG023595.1,CCG017373.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG028498.1,CCG005427.1,CCG019797.1,CCG006775.1,CCG015087.1,CCG017591.1,CCG017137.1,CCG013126.2,CCG027323.1,CCG013641.1,CCG025233.1,CCG016027.1,CCG008312.1,CCG003495.1,CCG021411.1,CCG001859.1,CCG021377.1,CCG027241.1,CCG026336.1,CCG005195.1,CCG021800.1,CCG016542.1,CCG014226.1,CCG009362.1,CCG015654.1,CCG020806.1,CCG020634.1,CCG010567.3,CCG025473.1,CCG026947.1,CCG023756.1,CCG021152.1,CCG001481.1,CCG017125.1,CCG023526.2

GO:0015031	protein transport	122 of 4104 in the list	289 of 8404 in the genome	1	CCG026698.1,CCG011766.1,CCG017420.1,CCG018832.1,CCG002549.1,CCG003146.1,CCG011408.1,CCG027762.1,CCG007060.1,CCG001809.1,CCG023877.1,CCG028124.1,CCG019590.1,CCG027692.1,CCG020949.1,CCG004026.1,CCG003995.1,CCG015386.1,CCG017612.1,CCG019020.1,CCG012550.1,CCG002645.1,CCG016347.1,CCG009428.1,CCG018800.1,CCG017725.1,CCG024905.1,CCG011813.1,CCG005262.1,CCG020315.1,CCG015568.1,CCG009607.1,CCG011006.1,CCG017077.1,CCG000010.1,CCG002766.1,CCG007827.1,CCG014434.1,CCG000614.1,CCG003531.1,CCG025027.1,CCG017078.1,CCG003334.1,CCG011696.1,CCG014307.1,CCG027457.1,CCG019103.1,CCG019629.2,CCG002917.1,CCG027257.1,CCG010939.1,CCG007855.1,CCG007283.1,CCG002374.1,CCG016541.1,CCG020909.1,CCG018447.1,CCG003786.1,CCG016966.1,CCG006714.1,CCG027473.1,CCG010178.1,CCG006777.1,CCG013984.1,CCG001673.1,CCG001172.1,CCG020280.1,CCG020929.1,CCG014506.1,CCG018557.1,CCG016493.2,CCG026744.1,CCG026620.1,CCG027564.1,CCG015800.2,CCG018217.1,CCG006625.1,CCG003775.1,CCG004573.1,CCG016831.1,CCG004869.1,CCG022771.1,CCG022910.1,CCG023595.1,CCG017373.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG028498.1,CCG005427.1,CCG019797.1,CCG006775.1,CCG015087.1,CCG017591.1,CCG017137.1,CCG013126.2,CCG013641.1,CCG025233.1,CCG016027.1,CCG008312.1,CCG003495.1,CCG021411.1,CCG001859.1,CCG021377.1,CCG027241.1,CCG026336.1,CCG005195.1,CCG021800.1,CCG016542.1,CCG014226.1,CCG009362.1,CCG015654.1,CCG020806.1,CCG020634.1,CCG010567.3,CCG025473.1,CCG026947.1,CCG023756.1,CCG021152.1,CCG001481.1,CCG017125.1,CCG023526.2
GO:0006839	mitochondrial transport	2 of 4104 in the list	11 of 8404 in the genome	1	CCG020949.1,CCG023814.2
GO:0016485	protein processing	2 of 4104 in the list	11 of 8404 in the genome	1	CCG020032.1,CCG003192.1
GO:0051604	protein maturation	2 of 4104 in the list	11 of 8404 in the genome	1	CCG020032.1,CCG003192.1
GO:1902578	single-organism localization	10 of 4104 in the list	34 of 8404 in the genome	1	CCG027323.1,CCG018832.1,CCG000614.1,CCG007941.1,CCG006714.1,CCG019797.1,CCG018217.1,CCG010178.1,CCG020949.1,CCG020806.1
GO:1902580	single-organism cellular localization	10 of 4104 in the list	34 of 8404 in the genome	1	CCG027323.1,CCG018832.1,CCG000614.1,CCG007941.1,CCG006714.1,CCG019797.1,CCG018217.1,CCG010178.1,CCG020949.1,CCG020806.1

GO:0006629	lipid metabolic process	126 of 4104 in the list	301 of 8404 in the genome	1	CCG004532.1, CCG010367.1, CCG000789.1, CCG020241.1, CCG009157.1, CCG019820.1, CCG009504.1, CCG008603.1, CCG017935.1, CCG000663.1, CCG004083.1, CCG008690.1, CCG000349.1, CCG004806.1, CCG014925.1, CCG000591.1, CCG020242.1, CCG018048.1, CCG021029.1, CCG024092.1, CCG021640.1, CCG012875.1, CCG007330.1, CCG016997.1, CCG006391.1, CCG009159.1, CCG025600.1, CCG017097.1, CCG015130.1, CCG025387.1, CCG011531.1, CCG001102.1, CCG005923.1, CCG020420.1, CCG024155.1, CCG021030.1, CCG011763.1, CCG019263.1, CCG005616.1, CCG028180.2, CCG022209.1, CCG024778.1, CCG015949.1, CCG009434.1, CCG014839.1, CCG001894.1, CCG023285.1, CCG025521.1, CCG012308.1, CCG022134.1, CCG017255.1, CCG016653.1, CCG003801.1, CCG011658.1, CCG025889.1, CCG024760.1, CCG018615.3, CCG008910.1, CCG028332.1, CCG023779.1, CCG012959.1, CCG006965.1, CCG010246.1, CCG026559.1, CCG003751.1, CCG024612.1, CCG001497.1, CCG019909.1, CCG025477.1, CCG000346.1, CCG004106.1, CCG021085.1, CCG009244.1, CCG014647.1, CCG023393.1, CCG008281.1, CCG001012.1, CCG013509.1, CCG012002.1, CCG013131.1, CCG012408.1, CCG023284.1, CCG026370.1, CCG015351.1, CCG011850.1, CCG013805.1, CCG014364.1, CCG022352.1, CCG001433.1, CCG003249.1, CCG000673.1, CCG024453.1, CCG019082.1, CCG008479.1, CCG025476.1, CCG020243.1, CCG021378.1, CCG021610.1, CCG027312.1, CCG001665.1, CCG023102.1, CCG005542.1, CCG009158.1, CCG025233.1, CCG017241.1, CCG000402.1, CCG011183.1, CCG019857.1, CCG006213.1, CCG000552.1, CCG017257.1, CCG024903.1, CCG024095.1, CCG017994.1, CCG023757.1, CCG017100.1, CCG019035.1, CCG015411.1, CCG015213.1, CCG023643.1, CCG025552.1, CCG018851.1, CCG014174.1, CCG019697.2, CCG026695.1, CCG020408.1

GO:0008104	protein localization	126 of 4104 in the list	302 of 8404 in the genome	1	CCG026698.1,CCG011766.1,CCG017420.1,CCG018832.1,CCG002549.1,CCG003146.1,CCG011408.1,CCG027762.1,CCG007060.1,CCG001809.1,CCG023877.1,CCG028124.1,CCG019590.1,CCG027692.1,CCG020949.1,CCG004026.1,CCG003995.1,CCG015386.1,CCG017612.1,CCG019020.1,CCG012550.1,CCG002645.1,CCG016347.1,CCG009428.1,CCG018800.1,CCG017725.1,CCG007941.1,CCG024905.1,CCG011813.1,CCG003587.1,CCG005262.1,CCG020315.1,CCG015568.1,CCG009607.1,CCG011006.1,CCG017077.1,CCG000010.1,CCG002766.1,CCG007827.1,CCG014434.1,CCG000614.1,CCG003531.1,CCG025027.1,CCG017078.1,CCG003334.1,CCG011696.1,CCG014307.1,CCG027457.1,CCG014318.1,CCG019103.1,CCG019629.2,CCG002917.1,CCG027257.1,CCG010939.1,CCG007855.1,CCG007283.1,CCG002374.1,CCG016541.1,CCG020909.1,CCG018447.1,CCG003786.1,CCG016966.1,CCG006714.1,CCG027473.1,CCG010178.1,CCG006777.1,CCG013984.1,CCG001673.1,CCG001172.1,CCG020280.1,CCG020929.1,CCG014506.1,CCG018557.1,CCG016493.2,CCG026744.1,CCG026620.1,CCG027564.1,CCG015800.2,CCG018217.1,CCG006625.1,CCG003775.1,CCG004573.1,CCG016831.1,CCG004869.1,CCG022771.1,CCG022910.1,CCG023595.1,CCG017373.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG028498.1,CCG005427.1,CCG019797.1,CCG006775.1,CCG015087.1,CCG017591.1,CCG017137.1,CCG013126.2,CCG027323.1,CCG013641.1,CCG025233.1,CCG016027.1,CCG008312.1,CCG003495.1,CCG021411.1,CCG001859.1,CCG021377.1,CCG027241.1,CCG026336.1,CCG005195.1,CCG021800.1,CCG016542.1,CCG014226.1,CCG009362.1,CCG015654.1,CCG020806.1,CCG020634.1,CCG010567.3,CCG025473.1,CCG026947.1,CCG023756.1,CCG021152.1,CCG001481.1,CCG017125.1,CCG023526.2
GO:0006631	fatty acid metabolic process	12 of 4104 in the list	40 of 8404 in the genome	1	CCG009244.1,CCG006391.1,CCG017097.1,CCG025521.1,CCG012408.1,CCG025552.1,CCG018851.1,CCG003751.1,CCG027312.1,CCG000591.1,CCG019909.1,CCG018615.3

GO:0006812	cation transport	107 of 4104 in the list	260 of 8404 in the genome	1	CCG000855.1,CCG017693.1,CCG010623.2,CCG003545.1,CCG015823.1,CCG021740.1,CCG007954.1,CCG004086.1,CCG000585.1,CCG004309.1,CCG006587.2,CCG008826.1,CCG025989.2,CCG009327.1,CCG015612.1,CCG008422.1,CCG003867.1,CCG000300.1,CCG003878.1,CCG010112.1,CCG005277.1,CCG016350.1,CCG009481.1,CCG014448.1,CCG007334.1,CCG027154.1,CCG003712.1,CCG013643.1,CCG005496.1,CCG010222.1,CCG027184.1,CCG020377.1,CCG002038.1,CCG009367.1,CCG025467.2,CCG009992.1,CCG025964.1,CCG027585.1,CCG000148.1,CCG006486.1,CCG005924.2,CCG019190.1,CCG000302.1,CCG025450.1,CCG016654.1,CCG018133.1,CCG023314.1,CCG002559.1,CCG008587.1,CCG015653.1,CCG016661.1,CCG026050.1,CCG001964.1,CCG021934.1,CCG019890.1,CCG023983.1,CCG007906.1,CCG004308.1,CCG006469.1,CCG000299.1,CCG023640.1,CCG026314.1,CCG009808.1,CCG025348.1,CCG017627.1,CCG019191.1,CCG003662.1,CCG012534.1,CCG019619.1,CCG006588.2,CCG014951.1,CCG000991.1,CCG014156.1,CCG016278.1,CCG026052.1,CCG023674.1,CCG016956.1,CCG001066.1,CCG015914.1,CCG019866.1,CCG019678.1,CCG007724.1,CCG012705.1,CCG014000.1,CCG027756.1,CCG024590.1,CCG025568.1,CCG006004.1,CCG015410.1,CCG025107.1,CCG009142.1,CCG010696.1,CCG019647.1,CCG014949.1,CCG027974.2,CCG017290.1,CCG023244.1,CCG014950.1,CCG003289.1,CCG027182.1,CCG016864.1,CCG000983.1,CCG023530.2,CCG000927.1,CCG023671.2,CCG011706.1,CCG001285.1
GO:0006518	peptide metabolic process	3 of 4104 in the list	15 of 8404 in the genome	1	CCG003192.1,CCG002897.1,CCG026099.1
GO:0032787	monocarboxylic acid metabolic process	17 of 4104 in the list	53 of 8404 in the genome	1	CCG003865.1,CCG026331.1,CCG009244.1,CCG025521.1,CCG012408.1,CCG020559.1,CCG000591.1,CCG018615.3,CCG015276.2,CCG006391.1,CCG017097.1,CCG018851.1,CCG025552.1,CCG003751.1,CCG016315.1,CCG027312.1,CCG019909.1

GO:0033036	macromolecule localization	141 of 4104 in the list	336 of 8404 in the genome	1	CCG017420.1,CCG018832.1,CCG002549.1,CCG003146.1,CCG011408.1,CCG027762.1,CCG001809.1,CCG028124.1,CCG020949.1,CCG004026.1,CCG003995.1,CCG015386.1,CCG019020.1,CCG012550.1,CCG002645.1,CCG009428.1,CCG007941.1,CCG024905.1,CCG003587.1,CCG011338.1,CCG009607.1,CCG011006.1,CCG002766.1,CCG000614.1,CCG011567.1,CCG017078.1,CCG011696.1,CCG014307.1,CCG027457.1,CCG014318.1,CCG002917.1,CCG027368.1,CCG001220.1,CCG010939.1,CCG007855.1,CCG011858.1,CCG024032.1,CCG016541.1,CCG003786.1,CCG006714.1,CCG027473.1,CCG001673.1,CCG014506.1,CCG018557.1,CCG016493.2,CCG026744.1,CCG027564.1,CCG006625.1,CCG004573.1,CCG004869.1,CCG000524.1,CCG013408.2,CCG022771.1,CCG022910.1,CCG017373.1,CCG006489.1,CCG026953.1,CCG006924.1,CCG021220.1,CCG017591.1,CCG017137.1,CCG013641.1,CCG025233.1,CCG003495.1,CCG021411.1,CCG001859.1,CCG027241.1,CCG005195.1,CCG014226.1,CCG020806.1,CCG020634.1,CCG010567.3,CCG026947.1,CCG023756.1,CCG021152.1,CCG017125.1,CCG023526.2,CCG026698.1,CCG011766.1,CCG005786.1,CCG007060.1,CCG023877.1,CCG019590.1,CCG027692.1,CCG001221.1,CCG017612.1,CCG016347.1,CCG018800.1,CCG017725.1,CCG011813.1,CCG005262.1,CCG020315.1,CCG015568.1,CCG000010.1,CCG017077.1,CCG007827.1,CCG014434.1,CCG003531.1,CCG025027.1,CCG003334.1,CCG019103.1,CCG019629.2,CCG027257.1,CCG007283.1,CCG002374.1,CCG020909.1,CCG018447.1,CCG016966.1,CCG026989.1,CCG010178.1,CCG006777.1,CCG013984.1,CCG001172.1,CCG020280.1,CCG020929.1,CCG026620.1,CCG018217.1,CCG015800.2,CCG003775.1,CCG016831.1,CCG021221.1,CCG023595.1,CCG009454.1,CCG028498.1,CCG019797.1,CCG005427.1,CCG015087.1,CCG006775.1,CCG013126.2,CCG027323.1,CCG016027.1,CCG008312.1,CCG026336.1,CCG021377.1,CCG021800.1,

GO:0007186	G-protein coupled receptor signaling pathway	65 of 4104 in the list	167 of 8404 in the genome	1	CCG015280.1,CCG012989.1,CCG024662.1,CCG017791.1,CCG009446.1,CCG007135.1,CCG008939.1,CCG011644.1,CCG014844.1,CCG003170.1,CCG020785.1,CCG018200.1,CCG014345.2,CCG002841.1,CCG012684.1,CCG004396.1,CCG019881.1,CCG025035.1,CCG022367.1,CCG012573.1,CCG000984.1,CCG026921.1,CCG019646.1,CCG023151.1,CCG009553.1,CCG000077.1,CCG016608.2,CCG023002.1,CCG023662.1,CCG010071.1,CCG015807.1,CCG008526.1,CCG000078.1,CCG009531.1,CCG024952.1,CCG026109.1,CCG017696.1,CCG024663.1,CCG018930.1,CCG024066.1,CCG025036.1,CCG027014.1,CCG007317.1,CCG020590.1,CCG011297.1,CCG009427.1,CCG020659.1,CCG019493.1,CCG013608.1,CCG000732.1,CCG008755.1,CCG007951.1,CCG027921.1,CCG025238.1,CCG006412.1,CCG014837.1,CCG021862.1,CCG017701.1,CCG012988.1,CCG004238.1,CCG008185.1,CCG022427.1,CCG019721.1,CCG008360.1,CCG024664.1
GO:0015988	energy coupled proton transmembrane transport, against electrochemical gradient	10 of 4104 in the list	36 of 8404 in the genome	1	CCG025450.1,CCG001066.1,CCG000585.1,CCG007724.1,CCG006486.1,CCG003662.1,CCG021934.1,CCG019619.1,CCG001285.1,CCG008422.1
GO:0015991	ATP hydrolysis coupled proton transport	10 of 4104 in the list	36 of 8404 in the genome	1	CCG025450.1,CCG001066.1,CCG000585.1,CCG007724.1,CCG006486.1,CCG003662.1,CCG021934.1,CCG019619.1,CCG001285.1,CCG008422.1

GO:0015672	monovalent inorganic cation transport	68 of 4104 in the list	175 of 8404 in the genome	1	CCG017693.1,CCG007954.1,CCG004086.1,CCG000585.1,CCG004309.1,CCG006587.2,CCG025989.2,CCG008422.1,CCG003867.1,CCG000300.1,CCG010112.1,CCG016350.1,CCG003712.1,CCG013643.1,CCG005496.1,CCG010222.1,CCG027184.1,CCG002038.1,CCG025964.1,CCG000148.1,CCG006486.1,CCG005924.2,CCG019190.1,CCG025450.1,CCG016654.1,CCG023314.1,CCG002559.1,CCG008587.1,CCG015653.1,CCG001964.1,CCG021934.1,CCG019890.1,CCG004308.1,CCG006469.1,CCG000299.1,CCG023640.1,CCG026314.1,CCG025348.1,CCG019191.1,CCG012534.1,CCG003662.1,CCG006588.2,CCG019619.1,CCG000991.1,CCG014951.1,CCG014156.1,CCG016956.1,CCG001066.1,CCG015914.1,CCG007724.1,CCG019678.1,CCG014000.1,CCG027756.1,CCG006004.1,CCG015410.1,CCG025107.1,CCG009142.1,CCG010696.1,CCG014949.1,CCG019647.1,CCG023244.1,CCG014950.1,CCG003289.1,CCG027182.1,CCG016864.1,CCG023530.2,CCG001285.1,CCG023671.2
GO:0006633	fatty acid biosynthetic process	7 of 4104 in the list	28 of 8404 in the genome	1	CCG012408.1,CCG003751.1,CCG027312.1,CCG009244.1,CCG019909.1,CCG017097.1,CCG018615.3
GO:0006814	sodium ion transport	24 of 4104 in the list	72 of 8404 in the genome	1	CCG004308.1,CCG006004.1,CCG017693.1,CCG000299.1,CCG025964.1,CCG026314.1,CCG007954.1,CCG004086.1,CCG004309.1,CCG014949.1,CCG014950.1,CCG014951.1,CCG003289.1,CCG000300.1,CCG016654.1,CCG023314.1,CCG016350.1,CCG016956.1,CCG015914.1,CCG015653.1,CCG027756.1,CCG010222.1,CCG005496.1,CCG023671.2

GO:0007166	cell surface receptor signaling pathway	83 of 4104 in the list	210 of 8404 in the genome	1	CCG015280.1,CCG012989.1,CCG024662.1,CCG020978.1,CCG017791.1,CCG009446.1,CCG007135.1,CCG008939.1,CCG011644.1,CCG014844.1,CCG007152.1,CCG003170.1,CCG020785.1,CCG002694.1,CCG018200.1,CCG014345.2,CCG002841.1,CCG012684.1,CCG004396.1,CCG019881.1,CCG025035.1,CCG022367.1,CCG012573.1,CCG010631.1,CCG000984.1,CCG022741.1,CCG026921.1,CCG019646.1,CCG023151.1,CCG000077.1,CCG009553.1,CCG016608.2,CCG024918.1,CCG018533.1,CCG023002.1,CCG023662.1,CCG000526.1,CCG010071.1,CCG013272.2,CCG015807.1,CCG008526.1,CCG000078.1,CCG009531.1,CCG026109.1,CCG024952.1,CCG004279.1,CCG022929.1,CCG017696.1,CCG024663.1,CCG018930.1,CCG024066.1,CCG025036.1,CCG018494.1,CCG015544.1,CCG027014.1,CCG020590.1,CCG007317.1,CCG020733.1,CCG011297.1,CCG009427.1,CCG020659.1,CCG019493.1,CCG025782.1,CCG013608.1,CCG000732.1,CCG008755.1,CCG007951.1,CCG027921.1,CCG025238.1,CCG006412.1,CCG016307.1,CCG014837.1,CCG008444.1,CCG021862.1,CCG017701.1,CCG012988.1,CCG004238.1,CCG008185.1,CCG022427.1,CCG019721.1,CCG008360.1,CCG024664.1,CCG021354.1

GO:0043170	macromolecule metabolic process	1608 of 4104 in the list	3426 of 8404 in the genome	1	CCG014531.2,CCG006922.1,CCG027068.1,CCG014396.1,CCG006549.1,CCG004887.1,CCG006912.1,CCG026106.1,CCG016952.1,CCG028016.1,CCG026174.1,CCG004468.1,CCG012726.1,CCG019308.1,CCG024584.1,CCG004020.1,CCG001292.1,CCG018432.1,CCG001040.1,CCG017266.1,CCG006875.2,CCG028198.1,CCG016689.2,CCG025208.1,CCG021479.1,CCG003362.1,CCG019113.1,CCG002634.1,CCG023381.1,CCG019382.1,CCG019735.1,CCG017289.1,CCG016094.1,CCG026413.3,CCG023474.1,CCG026871.2,CCG010792.1,CCG012623.1,CCG021616.1,CCG003767.1,CCG005738.1,CCG013876.1,CCG010905.1,CCG008270.1,CCG024612.1,CCG027636.1,CCG028653.1,CCG003624.1,CCG004569.1,CCG020286.1,CCG013109.1,CCG006465.1,CCG015074.1,CCG019571.1,CCG008871.1,CCG015694.1,CCG018788.1,CCG006484.1,CCG002982.1,CCG012083.1,CCG026602.1,CCG023686.1,CCG007457.1,CCG021737.1,CCG025990.1,CCG028590.1,CCG015350.1,CCG021948.1,CCG018585.3,CCG020651.1,CCG007467.1,CCG014385.1,CCG005284.1,CCG004927.1,CCG009805.2,CCG005089.1,CCG021137.1,CCG022056.1,CCG001876.1,CCG012584.1,CCG015186.1,CCG012023.1,CCG016327.2,CCG018688.1,CCG024200.1,CCG010624.1,CCG003608.1,CCG012957.1,CCG023502.1,CCG028454.1,CCG020663.1,CCG023458.1,CCG027748.1,CCG017001.1,CCG021767.1,CCG003520.1,CCG024865.1,CCG004926.1,CCG006928.1,CCG017381.1,CCG010912.1,CCG004955.1,CCG007874.3,CCG001704.1,CCG005524.1,CCG001289.1,CCG013640.1,CCG008404.1,CCG018201.1,CCG010136.1,CCG006174.1,CCG009574.1,CCG022370.1,CCG020179.1,CCG010112.1,CCG009038.1,CCG022513.2,CCG004986.1,CCG007750.2,CCG027989.1,CCG025707.1,CCG028092.1,CCG020078.1,CCG019831.2,CCG000209.1,CCG023486.1,CCG001395.1,CCG016557.1,CCG005594.1,CCG024922.1,CCG027000.1,CCG022871.1,CCG022183.1,CCG006804.1,CCG018168.1,
GO:0032502	developmental process	19 of 4104 in the list	61 of 8404 in the genome	1	CCG015767.2,CCG004753.1,CCG006750.1,CCG000133.1,CCG008075.1,CCG028595.1,CCG017777.1,CCG021681.1,CCG012835.1,CCG028121.1,CCG007152.1,CCG002694.1,CCG015458.1,CCG027945.1,CCG027763.1,CCG019427.1,CCG015596.1,CCG013272.2,CCG016035.1

GO:0007275	multicellular organismal development	10 of 4104 in the list	38 of 8404 in the genome	1	CCG012835.1,CCG007152.1,CCG028121.1,CCG000133.1,CCG002694.1,CCG027945.1,CCG019427.1,CCG027763.1,CCG028595.1,CCG013272.2
GO:0044743	intracellular protein transmembrane import	2 of 4104 in the list	14 of 8404 in the genome	1	CCG019797.1,CCG020949.1
GO:0065002	intracellular protein transmembrane transport	2 of 4104 in the list	14 of 8404 in the genome	1	CCG019797.1,CCG020949.1
GO:0071806	protein transmembrane transport	2 of 4104 in the list	14 of 8404 in the genome	1	CCG019797.1,CCG020949.1
GO:0044767	single-organism developmental process	18 of 4104 in the list	60 of 8404 in the genome	1	CCG015767.2,CCG004753.1,CCG006750.1,CCG000133.1,CCG008075.1,CCG028595.1,CCG021681.1,CCG012835.1,CCG028121.1,CCG007152.1,CCG002694.1,CCG015458.1,CCG027945.1,CCG027763.1,CCG019427.1,CCG015596.1,CCG013272.2,CCG016035.1
GO:0030001	metal ion transport	63 of 4104 in the list	169 of 8404 in the genome	1	CCG004308.1,CCG006469.1,CCG017693.1,CCG000299.1,CCG010623.2,CCG015823.1,CCG026314.1,CCG007954.1,CCG004086.1,CCG009808.1,CCG004309.1,CCG019191.1,CCG006587.2,CCG008826.1,CCG006588.2,CCG015612.1,CCG014951.1,CCG000991.1,CCG000300.1,CCG003878.1,CCG014156.1,CCG005277.1,CCG016956.1,CCG016350.1,CCG015914.1,CCG014448.1,CCG027154.1,CCG019866.1,CCG012705.1,CCG014000.1,CCG027756.1,CCG005496.1,CCG010222.1,CCG024590.1,CCG027184.1,CCG020377.1,CCG025568.1,CCG006004.1,CCG009992.1,CCG025964.1,CCG027585.1,CCG014949.1,CCG019647.1,CCG027974.2,CCG017290.1,CCG014950.1,CCG003289.1,CCG019190.1,CCG000302.1,CCG027182.1,CCG016654.1,CCG018133.1,CCG016864.1,CCG023314.1,CCG002559.1,CCG008587.1,CCG015653.1,CCG023530.2,CCG000927.1,CCG001964.1,CCG019890.1,CCG023671.2,CCG011706.1

GO:0006260	DNA replication	101 of 4104 in the list	267 of 8404 in the genome	1	CCG025352.1,CCG016237.1,CCG026841.1,CCG006549.1,CCG007336.1,CCG000823.1,CCG007710.1,CCG005501.1,CCG003161.1,CCG011912.1,CCG004534.1,CCG027067.1,CCG004468.1,CCG022811.1,CCG013631.1,CCG015711.1,CCG027407.4,CCG020871.1,CCG026258.1,CCG018321.1,CCG007902.1,CCG001000.1,CCG028505.1,CCG024232.1,CCG008719.1,CCG006164.1,CCG015599.1,CCG004398.1,CCG025208.1,CCG012213.2,CCG004012.2,CCG003904.1,CCG025658.1,CCG004332.1,CCG018649.1,CCG022990.1,CCG013353.1,CCG004719.1,CCG012623.1,CCG003402.1,CCG020652.1,CCG006968.1,CCG015929.1,CCG008126.1,CCG025541.1,CCG018799.1,CCG022735.1,CCG022792.1,CCG005276.1,CCG024326.1,CCG021295.1,CCG013722.1,CCG018583.1,CCG017380.1,CCG008044.1,CCG014280.1,CCG013065.1,CCG019446.1,CCG015694.1,CCG021949.1,CCG013865.1,CCG000738.1,CCG010378.2,CCG027114.1,CCG011366.1,CCG018660.1,CCG007741.1,CCG009140.1,CCG022475.1,CCG014486.1,CCG023468.1,CCG013993.1,CCG023939.1,CCG002942.1,CCG009119.1,CCG007611.1,CCG020869.1,CCG015350.1,CCG015312.2,CCG022311.1,CCG025283.1,CCG000490.1,CCG000950.1,CCG021948.1,CCG011148.1,CCG005269.1,CCG020651.1,CCG028222.1,CCG013917.1,CCG003231.1,CCG021137.1,CCG016381.1,CCG017550.1,CCG011727.1,CCG016576.1,CCG009896.1,CCG022428.1,CCG028426.1,CCG017001.1,CCG009141.1,CCG023633.1
GO:0050909	sensory perception of taste	3 of 4104 in the list	38 of 8404 in the genome	1	CCG004249.1,CCG003558.1,CCG008512.1
GO:0007600	sensory perception	15 of 4104 in the list	152 of 8404 in the genome	1	CCG009531.1,CCG012989.1,CCG012988.1,CCG006802.1,CCG004238.1,CCG007317.1,CCG011758.1,CCG010071.1,CCG020881.1,CCG017696.1,CCG004249.1,CCG017217.3,CCG003558.1,CCG018930.1,CCG008512.1
GO:0003008	system process	16 of 4104 in the list	159 of 8404 in the genome	1	CCG009531.1,CCG012989.1,CCG012988.1,CCG006802.1,CCG008323.1,CCG004238.1,CCG007317.1,CCG011758.1,CCG010071.1,CCG020881.1,CCG017696.1,CCG004249.1,CCG017217.3,CCG003558.1,CCG018930.1,CCG008512.1
GO:0050877	neurological system process	16 of 4104 in the list	159 of 8404 in the genome	1	CCG009531.1,CCG012989.1,CCG012988.1,CCG006802.1,CCG008323.1,CCG004238.1,CCG007317.1,CCG011758.1,CCG010071.1,CCG020881.1,CCG017696.1,CCG004249.1,CCG017217.3,CCG003558.1,CCG018930.1,CCG008512.1
GO:0007608	sensory perception of smell	4 of 4104 in the list	93 of 8404 in the genome	1	CCG020881.1,CCG017217.3,CCG006802.1,CCG011758.1

GO:0032501	multicellular organismal process	28 of 4104 in the list	200 of 8404 in the genome	1	CCG022367.1,CCG009531.1,CCG000133.1,CCG012989.1,CCG006802.1,CCG017791.1,CCG011758.1,CCG017696.1,CCG028595.1,CCG004249.1,CCG017217.3,CCG018930.1,CCG008512.1,CCG012835.1,CCG007152.1,CCG028121.1,CCG002694.1,CCG012988.1,CCG008323.1,CCG007317.1,CCG004238.1,CCG027945.1,CCG010071.1,CCG027763.1,CCG019427.1,CCG020881.1,CCG013272.2,CCG003558.1
GO:0007606	sensory perception of chemical stimulus	7 of 4104 in the list	131 of 8404 in the genome	1	CCG020881.1,CCG004249.1,CCG017217.3,CCG003558.1,CCG006802.1,CCG008512.1,CCG011758.1
GO:0044707	single-multicellular organism process	28 of 4104 in the list	198 of 8404 in the genome	1	CCG022367.1,CCG009531.1,CCG000133.1,CCG012989.1,CCG006802.1,CCG017791.1,CCG011758.1,CCG017696.1,CCG028595.1,CCG004249.1,CCG017217.3,CCG018930.1,CCG008512.1,CCG012835.1,CCG007152.1,CCG028121.1,CCG002694.1,CCG012988.1,CCG008323.1,CCG007317.1,CCG004238.1,CCG027945.1,CCG010071.1,CCG027763.1,CCG019427.1,CCG020881.1,CCG013272.2,CCG003558.1
GO:0006278	RNA-dependent DNA replication	36 of 4104 in the list	196 of 8404 in the genome	1	CCG005276.1,CCG008044.1,CCG007710.1,CCG013065.1,CCG005501.1,CCG019446.1,CCG003161.1,CCG004534.1,CCG013865.1,CCG027114.1,CCG004468.1,CCG022811.1,CCG013631.1,CCG007741.1,CCG027407.4,CCG022475.1,CCG007902.1,CCG001000.1,CCG004398.1,CCG009119.1,CCG015350.1,CCG012213.2,CCG025283.1,CCG022311.1,CCG025658.1,CCG018649.1,CCG004719.1,CCG022990.1,CCG003231.1,CCG021137.1,CCG006968.1,CCG011727.1,CCG028426.1,CCG025541.1,CCG017001.1,CCG022792.1

GO:0015074	DNA integration	66 of 4104 in the list	411 of 8404 in the genome	1	CCG022500.1,CCG004270.1,CCG013652.1,CCG004907.1,CCG021260.1,CCG015393.1,CCG023142.2,CCG003161.1,CCG003594.1,CCG017166.1,CCG015376.3,CCG020953.1,CCG022513.2,CCG017734.1,CCG016179.1,CCG024584.1,CCG001361.1,CCG002202.2,CCG006237.1,CCG023486.1,CCG000451.1,CCG014696.1,CCG009549.1,CCG019642.1,CCG021364.1,CCG008496.1,CCG026464.1,CCG010287.1,CCG009575.1,CCG022113.1,CCG026493.1,CCG027703.1,CCG000073.1,CCG004412.1,CCG005275.1,CCG007916.1,CCG008752.1,CCG006020.1,CCG011776.1,CCG012401.1,CCG013397.1,CCG026312.2,CCG013065.1,CCG021639.1,CCG009173.1,CCG013159.1,CCG007708.1,CCG016872.1,CCG010915.1,CCG003137.1,CCG013054.1,CCG011001.1,CCG022961.1,CCG012980.1,CCG000208.1,CCG020016.1,CCG025283.1,CCG022228.1,CCG015137.1,CCG007181.1,CCG009265.1,CCG013381.1,CCG017001.1,CCG013525.1,CCG014484.1,CCG021767.1

GO:0006259	DNA metabolic process	342 of 4104 in the list	912 of 8404 in the genome	1	CCG027300.1,CCG006606.1,CCG006549.1,CCG003361.1,CCG026106.1,CCG010647.1,CCG013625.1,CCG004468.1,CCG020953.1,CCG026473.1,CCG024584.1,CCG002202.2,CCG018321.1,CCG006237.1,CCG028505.1,CCG005194.1,CCG015599.1,CCG004398.1,CCG014836.1,CCG000213.1,CCG024177.1,CCG025208.1,CCG012514.1,CCG027196.1,CCG012213.2,CCG016094.1,CCG027183.2,CCG023474.1,CCG000166.1,CCG010287.1,CCG013353.1,CCG012623.1,CCG004515.1,CCG019692.1,CCG010905.1,CCG004078.1,CCG018799.1,CCG010909.1,CCG005275.1,CCG005276.1,CCG024326.1,CCG021295.1,CCG017580.1,CCG009980.1,CCG011776.1,CCG027133.1,CCG010649.1,CCG014280.1,CCG013065.1,CCG015560.1,CCG003438.1,CCG010116.1,CCG015694.1,CCG013865.1,CCG010378.2,CCG027114.1,CCG008559.1,CCG027696.1,CCG011001.1,CCG004402.1,CCG023468.1,CCG025990.1,CCG012980.1,CCG000805.1,CCG009119.1,CCG004494.1,CCG002364.1,CCG015350.1,CCG020016.1,CCG016903.1,CCG021948.1,CCG011148.1,CCG022673.1,CCG020651.1,CCG026159.1,CCG009582.1,CCG005284.1,CCG021137.1,CCG012584.1,CCG016381.1,CCG011727.1,CCG028426.1,CCG017001.1,CCG024788.1,CCG007263.1,CCG021767.1,CCG004907.1,CCG021045.1,CCG021759.1,CCG007336.1,CCG022772.1,CCG010136.1,CCG022628.1,CCG005501.1,CCG003310.1,CCG024570.2,CCG004534.1,CCG013617.1,CCG022513.2,CCG018650.1,CCG010137.1,CCG027407.4,CCG001361.1,CCG026258.1,CCG007902.1,CCG023486.1,CCG024232.1,CCG006133.1,CCG009461.1,CCG005594.1,CCG014772.1,CCG008816.1,CCG024804.1,CCG008496.1,CCG026464.1,CCG004332.1,CCG011015.1,CCG026493.1,CCG008498.1,CCG027703.1,CCG008126.1,CCG000073.1,CCG005070.1,CCG005241.1,CCG013722.1,CCG008752.1,CCG010906.1,CCG008044.1,CCG017906.1,CCG010138.1,CCG026312.2,CCG021639.1,CCG013159.1,CCG010915.1,CCG013054.1,

GO:0006508	proteolysis	393 of 4104 in the list	1011 of 8404 in the genome	1	CCG011990.4,CCG006922.1,CCG027068.1,CCG005931.1,CCG023235.1,CCG006912.1,CCG015867.1,CCG025135.1,CCG028016.1,CCG001867.2,CCG022635.1,CCG019308.1,CCG009900.1,CCG006875.2,CCG013184.1,CCG002634.1,CCG007993.1,CCG017289.1,CCG026413.3,CCG006911.1,CCG013012.1,CCG027145.1,CCG001168.1,CCG024631.1,CCG021509.1,CCG016336.1,CCG025122.1,CCG005323.1,CCG026069.1,CCG025069.2,CCG003767.1,CCG013876.1,CCG024294.1,CCG014686.1,CCG003624.1,CCG007116.1,CCG019415.1,CCG016105.1,CCG005930.1,CCG020562.1,CCG011238.1,CCG009690.1,CCG005125.1,CCG027940.1,CCG019571.1,CCG000812.1,CCG000602.1,CCG023576.1,CCG001877.1,CCG004331.1,CCG017233.1,CCG027114.1,CCG019188.1,CCG022996.1,CCG015897.1,CCG001214.1,CCG002163.1,CCG017549.1,CCG026384.1,CCG022225.1,CCG017305.1,CCG028590.1,CCG001921.1,CCG023196.1,CCG008004.1,CCG017570.1,CCG018585.3,CCG007467.1,CCG008341.1,CCG000320.1,CCG014385.1,CCG003203.1,CCG012955.1,CCG022226.1,CCG013119.1,CCG022994.1,CCG005089.1,CCG022742.2,CCG012191.1,CCG007823.1,CCG019323.1,CCG012023.1,CCG024254.1,CCG003608.1,CCG012957.1,CCG023502.1,CCG027763.1,CCG010001.1,CCG003421.1,CCG000785.1,CCG009382.1,CCG006666.1,CCG024865.1,CCG003060.1,CCG004293.1,CCG013182.1,CCG024659.1,CCG018098.1,CCG018968.1,CCG011044.1,CCG001704.1,CCG027993.1,CCG001350.1,CCG001289.1,CCG018206.1,CCG008099.1,CCG015991.1,CCG005501.1,CCG019599.1,CCG006174.1,CCG004919.1,CCG020179.1,CCG025915.1,CCG014045.1,CCG021356.1,CCG004986.1,CCG027989.1,CCG015543.1,CCG019831.2,CCG003007.1,CCG020231.1,CCG002834.1,CCG019643.1,CCG021825.3,CCG011426.1,CCG027000.1,CCG022871.1,CCG010842.1,CCG025503.1,CCG002386.1,CCG015896.1,CCG015844.1,CCG016863.1,CCG005200.1,CCG023684.1,