# Selected Latent Variable-Enriched Pathways

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Pathway Name | P-value | Term Size | Query Size | Intersection Size | Precision | Recall | Latent Node |
| regulation of nervous system development | 0.0236186136151001 | 457 | 16 | 5 | 0.3125 | 0.0109409190371991 | 7 |
| DNA integration | 0.0287922088818914 | 10 | 15 | 2 | 0.1333333333333333 | 0.2 | 9 |
| Glucagon signaling pathway | 0.0134641808035551 | 107 | 10 | 3 | 0.3 | 0.02803738317757 | 18 |
| Cushing syndrome | 0.0499569897009377 | 153 | 11 | 3 | 0.2727272727272727 | 0.0196078431372549 | 19 |
| Vibrio cholerae infection | 0.0246555455325596 | 50 | 6 | 2 | 0.3333333333333333 | 0.04 | 20 |
| Golgi lumen acidification | 0.0370534161963728 | 13 | 13 | 2 | 0.1538461538461538 | 0.1538461538461538 | 20 |
| Cushing syndrome | 0.0499569897009377 | 153 | 11 | 3 | 0.2727272727272727 | 0.0196078431372549 | 23 |
| tRNA metabolic process | 0.0414263692639973 | 210 | 18 | 4 | 0.2222222222222222 | 0.019047619047619 | 25 |
| ECM-receptor interaction | 0.010145054293642 | 89 | 11 | 3 | 0.2727272727272727 | 0.0337078651685393 | 31 |
| Glyoxylate and dicarboxylate metabolism | 0.012188180777088 | 30 | 7 | 2 | 0.2857142857142857 | 0.0666666666666666 | 34 |
| cellular response to 2,3,7,8-tetrachlorodibenzodioxine | 0.0038484693649248 | 4 | 15 | 2 | 0.1333333333333333 | 0.5 | 41 |
| response to 2,3,7,8-tetrachlorodibenzodioxine | 0.0179299300313183 | 8 | 15 | 2 | 0.1333333333333333 | 0.25 | 41 |
| Base excision repair | 0.0263601360727707 | 44 | 7 | 2 | 0.2857142857142857 | 0.0454545454545454 | 42 |
| RNA degradation | 0.0412133286559642 | 79 | 5 | 2 | 0.4 | 0.0253164556962025 | 43 |
| neuromuscular junction development | 0.0215300187657582 | 54 | 19 | 3 | 0.1578947368421052 | 0.0555555555555555 | 47 |
| regulation of response to external stimulus | 0.0390732084249658 | 1082 | 19 | 7 | 0.3684210526315789 | 0.0064695009242144 | 47 |