# WES PARKINSON DISEASE DG 3.00

| Gene | Median coverage | % covered >10x | % covered >20x | OMIM disease ID |
|---|---|---|---|---|
| ATP13A2 | 138.1 | 100.0 | 99.5 | 606693 |
| ATP1A3 | 173.5 | 100.0 | 99.9 | 128235 |
| C19orf12 | 122.6 | 100.0 | 99.8 | 614298 |
| CHCHD2 | 76.6 | 98.4 | 83.8 | 616710 |
| CHMP2B | 94.7 | 99.7 | 96.7 | 614696 |
| CSF1R | 125.5 | 99.9 | 99.3 | 221820 |
| DCTN1 | 126.0 | 100.0 | 98.8 | 168605 |
| DNAJC6 | 161.6 | 100.0 | 99.4 | 615528 |
| FBXO7 | 206.2 | 99.8 | 97.9 | 260300 |
| FTL | 144.1 | 98.5 | 89.4 | 606159 |
| GBA | 202.3 | 100.0 | 100.0 | 168600 |
| GCH1 | 80.7 | 99.9 | 95.5 | 128230 |
| GRN | 166.2 | 100.0 | 100.0 | 607485 |
| LRRK2 | 140.9 | 99.7 | 97.8 | 607060 |
| MAPT | 166.5 | 100.0 | 99.5 | 600274 |
| MYORG | 188.1 | 100.0 | 100.0 | 618317 |
| PARK7 | 110.5 | 100.0 | 100.0 | 606324 |
| PDGFB | 121.4 | 100.0 | 99.3 | 615483 |
| PDGFRB | 147.6 | 99.2 | 97.5 | 615007 |
| PINK1 | 91.4 | 90.7 | 86.9 | 605909 |
| PLA2G6 | 112.9 | 92.2 | 90.7 | 612953 |
| POLG | 111.5 | 100.0 | 99.3 | 157640 |
| PRKN | 81.8 | 67.0 | 66.2 | 600116 |
| PRKRA | 175.9 | 100.0 | 99.4 | 612067 |
| PSEN1 | 175.0 | 100.0 | 100.0 | 600274 |

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|---|---|---|---|---|
| SLC20A2 | 121.1 | 100.0 | 99.2 | 213600 |
| SLC30A10 | 168.1 | 100.0 | 100.0 | 613280 |
| SLC39A14 | 109.2 | 100.0 | 99.4 | 617013 |
| SLC6A3 | 147.6 | 100.0 | 100.0 | 613135 |
| SNCA | 98.1 | 79.1 | 79.1 | 605543;168601 |
| TAF1 | 108.9 | 99.8 | 97.7 | 314250 |
| TH | 88.5 | 99.3 | 96.1 | 605407 |
| VPS13C | 132.4 | 99.4 | 96.9 | 616840 |
| VPS35 | 105.3 | 97.3 | 91.3 | 614203 |
| WDR45 | 82.5 | 98.1 | 92.4 | 300894 |
| XPR1 | 152.8 | 100.0 | 99.9 | 616413 |

*Gene symbols used follow HGCN guidelines: Gray KA, Yates B, Seal RL, Wright MW, Bruford EA. Nucleic Acids Res. 2015 Jan;43(Database issue):D1079-85.*
*Median Coverage describes the average number of reads seen across 50 exomes.*
*% Covered 10x describes the percentage of a gene's coding sequence that is covered at least 10x.*
*% Covered 10x describes the percentage of a gene's coding sequence that is covered at least 20x.*
*Genes with Median Coverage and % Covered 10x/20x denoting NC are non-coding genes for which coverage statistics could not be generated.*
*OMIM release used for OMIM disease identifiers and descriptions : October 1st, 2016.*

*Ad 1. "No OMIM phenotype" signifies a gene without a current OMIM association Ad 2. OMIM phenotype descriptions between {} signify risk factors*