Parkinson's Disease Gene and Variant Penetrance Table

Updated: 1-6-23

PD Nexus

Gene	Variant (single unless noted)	Penetrance Data	Citations	Summary Statements for Genetic Counseling (Important to compare risk estimate with lifetime background risk of 3% [typically to age 80 used])
GBA1 (GBA)	ALL	a) 15% by age 80, UK, familial GD cohort b) 29.7% by age 80 (CI: 16-40%), France, familial PD cohort c) 10.9% ± 7.2% by age 85, mostly AJ N370S, familial GD cohort d) 7.7% ± 2.74 by age 80, mostly AJ N370S, familial GD cohort e) 19.4% (CI: 12-28%), Italy, PD kin-cohort	a) McNeil et al, 2012 b) Anheim et al, 2012 c) Rana et al, 2013 d) Alcalay et al, 2014 e) Balestrino et al, 2020	Disease risk depends on age, population, and type of variant (refer to specific variant when available) – range is likely 10% to 30% to age 80.
	N370S and other mild variants	a) 5.9% ± 3.14 by age 80, mostly AJ N370S, familial GD cohort b) OR 2.84 to 4.94 for mild variant carriers*	a) Alcalay et al, 2014 b) Gan-Or et al, 2015	Milder variants, in general, have lower disease risk, compared to severe ones.
	E326K	a) OR 1.97 (CI: 1.57-2.46) b) OR 1.99 (CI: 1.57-2.51), across total populations c) May be lower effect in AJ population, OR 1.07 (CI: 0.39-2.93), AJ PD cohort; additive effect suggested when occurring with another variant	a) Zhang et al, 2018 b) Huang et al, 2019 c) Goldstein et al, 2019	This is likely a low risk factor/susceptibility allele for PD.
	T369M	OR 1.78 (CI: 1.20-2.64), across all populations	a) Zhang et al, 2018	This is likely a low risk factor/susceptibility allele for PD.
	84GG, IVS2+1G>A, L444P *(severe variants)*	OR 9.92 to 21.29 for severe variants*	Gan-Or et al, 2015	Severe variants, in general, have and increased disease risk (lifetime risk of 30% or greater using general population risk of 3%), compared to mild variants.
	Gaucher disease (homozygous or compound heterozygous)	a) 9.1% ± 6.07 by age 80, AJ, N370S homozygous or compound heterozygous) b) approximately 9-12% by age 80, AJ, prevalent genotype N370S, (ICGGRegistry)	a) Alcalay et al, 2014 b) Rosenbloom et al, 2011	PD risk is slightly increased compared to that of single variant carriers.
	Detailed *GBA1* variant-specific information including clinical classification (i.e. mild, severe, risk variant, or unknown) w/ supporting literature can be found at the *GBA1*-PD Browser (developed by Gan-Or and Blauwendraat, 2022) pdgenetics.shinyapps.io/gba1browser			

**Initial review developed for the PDGENEration study*

LRRK2	ALL	Reduced penetrance for common variants	GeneReviews: LRRK2	Disease risk depends on age, population, and type of variant (refer to specific variant when available).
	G2019S	a) 26% (CI: 18–36%) lifetime risk by age 80, AJ, PD kin-cohort b) 42.5% (CI: 26.3-65.8%) to age 80, non-AJ populations, PD kin-cohort Note: There was not a significant difference when comparing to AJ populations	a) Marder et al, 2015 b) Lee et al, 2017	There is approximately a 26% lifetime risk for European populations including AJ.
	R1441C	a) > 90% of carriers developed PD by age 75 years based on multicase PD families b) Lower cumulative incidence compared with other *LRRK2* variants, n=27*, Kaplan-Meier method	a) Haugarvoll et al., 2008 b) Trinh et al, 2014	Numbers are too small to quantify risk but suggestion of lower penetrance compared with other *LRRK2* variants; however, studies show mixed data depending on ascertainment.
	R1441G *(Basque variant)*	a) 83.4% (CI: 41.9-95.3%) by age 80, familial PD cohort b) Lower cumulative incidence compared with other *LRRK2* variants, n= 104, Kaplan-Meier method*	a) Ruiz-Martinez et al,2010 b) Trinh et al, 2014	Suggestion of lower penetrance compared with other *LRRK2* variants, however, studies show mixed results.
	Y1699C, N1437H	Penetrance may be increased compared to other variants, small numbers n=16; n=10, Kaplan-Meier method*	Trinh et al, 2014	Numbers are too small to quantify risk.
	I2020T	Similar cumulative incidence compared with to *LRRK2* G2019S, small numbers n=29, Kaplan-Meier method*	Trinh et al, 2014	Penetrance may be similar to *LRRK2* G2019S based on small numbers.
	R1628P, G2385R	OR 1.83 (CI: 1.57-2.13)*	Zhang et al, 2017	Considered to be risk factors in Asian populations (Chinese and related ancestries)
	Homozygous G2019S	Did not find a gene dosage effect for clinical features	Ishihara et al, 2006	Penetrance risk data limited.
GBA1 + LRRK2	ALL	a) OR 11.79 (CI: 5.23–26.61), AJ PD cohort b) Suggestion of "dominant association" of *LRRK2* on *GBA1* expression	a) Goldstein et al, 2019 b) Omer et al, 2020; Ortega et al, 2021	It is not clear if there is an additive effect for age of onset and penetrance; so far, an additive harmful effect has not been observed for clinical features based on small numbers

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SNCA	A53T and other less common point mutations	a) 85% for A53T variant (Italian family cohort) b) 89.7% or > at age 70 for A53T variant (Italian/Greek family cohorts), Kaplan-Meier method	a) Polymeropoulos et al,1996 b) Papadimitriou et al,2016	Based on small numbers, likely reduced but highly penetrant
	Duplications	a) Incomplete penetrance in Korean andJapanese families although not formally assessed b) 43.8% (Japanese familial cohort) c) Similar cumulative incidence compared with *SNCA* point mutations, n=41, Kaplan-Meier method*	a) Ahn et al, 2008 b) Nishioka et al, 2009 c) Trinh et al, 2014	Based on small numbers, duplications show reduced penetrance - likely moderate to high.
	Triplications	Higher cumulative incidence compared with other *SNCA* variants, n= 15, Kaplan-Meier method*	Trinh et al, 2014	Numbers are too small to quantify but likely higher penetrance compared to duplications and other variants.
VPS35	D620N *(primary variantidentified)*	Cumulative incidence >90% by age 70 (n=61)*	Trinh et al, 2014, GeneReviews: VPS35-Related PD	Numbers are too small to quantify but D620N appears to be of high penetrance.
PRKN	Homozygous or compound heterozygous (in trans) for variant	Follows AR inheritance	GeneReviews: Parkin Type of PD	Close to fully penetrant (age-dependent)
	Heterozygous for one variant	a) May act as a susceptibility allele in some families b) Observed in late-onset, familial PD cases c) Frequency of a heterozygous variant in PDpts vs "healthy" controls: 3.2% vs 3.1% d) Cases and controls were similar for single sequence variants whereas cases had increase in dosage variants. Suggest PRKN haploinsufficiency, esp. a dosage variant is arisk factor e) Copy number variants associated with PD risk in carriers (OR 1.60 and OR	a) Oliveira et al, 2003 b) Foroud et al, 2003 c) Kay et al, 2007 d) Pankratz et al, 2009 e) Huttenlocher et al, 2015 f) Lubbe et al, 2021 g) Zhu et al., 2022	One copy of a variant, especially if it affects dose, may represent a susceptibility factor for PD. However, there is the possibility of a "second-hit" that has not been identified confounding these results. Onset has been observed to be later than typical early-onset is some studies. Research still is ongoing to clarify risk.

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		2.11*), case-control cohort and pooled data f) >1.5 fold increased risk, case-control cohorts, OR 1.65 (CI: 1.36-2.00)*, evidence for greater risk with copy number variants (>2.5 fold) g) Using near complete genotyping for SNPs and CNVs *PRKN* variants were assessed in two large cohorts; notably carriers of one PRKN variant were as likely as non-carriers to have PD or an affected parent suggesting one *PRKN* variant does not increase risk		
PINK1 or DJ1	Homozygous or compound heterozygous (in trans) variant	Follows AR inheritance	GeneReviews: *PINK1* TypeYoung-Onset PD	Close to fully penetrant (age-dependent)
	Heterozygous for one variant	Several studies suggest that variants in these genes could result in PD and represent risk factors.	GeneReviews: *PINK1* Type Young-Onset PD Brooks et al, 2009 Sironi et al, 2013	Risk to heterozygotes is not fully known. May be similar to what is observed for *PRKN* single variants based on published literature. Research is ongoing.

**Data derived from meta-analysis*

AJ = Ashkenazi Jewish; AR = autosomal recessive; CI = confidence interval, 95%; GD = Gaucher disease; OR = odds ratio; PD = Parkinson's disease

Odds ratio to risk ratio (relative risk) calculator: https://clincalc.com/Stats/ConvertOR.aspx
(When the incidence of an outcome is low, <10%, the odds ratio is very similar to the risk ratio.)

These risks may be modified by other factors and should be used within the context of medical and family histories. Some of these variants have only been thoroughly studied in certain populations, often European. Thus, ancestry of the patient should be considered when relevant.

Cited articles:

Ahn, T.-B., Kim, S. Y., Kim, J. Y., Park, S.-S., Lee, D. S., Min, H. J., Kim, Y. K., Kim, S. E., Kim, J.-M., Kim, H.-J., Cho, J., & Jeon, B. S. (2008). Alpha-Synuclein geneduplication is present in sporadic Parkinson disease. *Neurology*, *70*(1), 43–49. https://doi.org/10.1212/01.wnl.0000271080.53272.c7

Alcalay, R. N., Dinur, T., Quinn, T., Sakanaka, K., Levy, O., Waters, C., Fahn, S., Dorovski, T., Chung, W. K., Pauciulo, M., Nichols, W., Rana, H. Q., Balwani, M., Bier,L., Elstein, D., & Zimran, A. (2014). Comparison of Parkinson risk in Ashkenazi Jewish patients with Gaucher disease and GBA heterozygotes. *JAMA Neurology*, *71*(6), 752–757. https://doi.org/10.1001/jamaneurol.2014.313

Anheim, M., Elbaz, A., Lesage, S., Durr, A., Condroyer, C., Viallet, F., Pollak, P., Bonaïti, B., Bonaïti-Pellié, C., Brice, A., & French Parkinson Disease Genetic Group.(2012). Penetrance of Parkinson disease in glucocerebrosidase gene mutation carriers. *Neurology*, *78*(6), 417–420. https://doi.org/10.1212/WNL.0b013e318245f476

Brooks, J., Ding, J., Simon-Sanchez, J., Paisan-Ruiz, C., Singleton, A. B., & Scholz, S. W. (2009). Parkin and PINK1 mutations in early-onset Parkinson's disease: Comprehensive screening in publicly available cases and control. *Journal of Medical Genetics*, *46*(6), 375–381. https://doi.org/10.1136/jmg.2008.063917

Brüggemann, N., & Klein, C. (1993). Parkin Type of Early-Onset Parkinson Disease. In M. P. Adam, H. H. Ardinger, R. A. Pagon, S. E. Wallace, L. J. Bean, K. Stephens, & A. Amemiya (Eds.), *GeneReviews®*. University of Washington, Seattle. http://www.ncbi.nlm.nih.gov/books/NBK1478/

Deutschländer, A., Ross, O. A., & Wszolek, Z. K. (1993). VPS35-Related Parkinson Disease. In M. P. Adam, H. H. Ardinger, R. A. Pagon, S. E. Wallace, L. J. Bean, K.Stephens, & A. Amemiya (Eds.), *GeneReviews®*. University of Washington, Seattle. http://www.ncbi.nlm.nih.gov/books/NBK447258/

Foroud, T., Uniacke, S. K., Liu, L. xian, Pankratz, N., Rudolph, A., Halter, C. A., Shults, C. W., Marder, K. S., Conneally, P. M., & Nichols, W. C. (2003). Heterozygosity for a mutation in the parkin gene leads to later onset Parkinson disease. *Neurology*, *60*(5), 796–801. https://doi.org/10.1212/01.WNL.0000049470.00180.07

Gan-Or, Z., Alcalay, R. N., Makarious, M. B., Scholz, S. W., & Blauwendraat, C. (2019). Classification of GBA Variants and Their Effects in Synucleinopathies. Movement Disorders, 34(10), 1581–1582. https://doi.org/10.1002/mds.27803

Gan-Or, Z., Amshalom, I., Kilarski, L. L., Bar-Shira, A., Gana-Weisz, M., Mirelman, A., Marder, K., Bressman, S., Giladi, N., & Orr-Urtreger, A. (2015). Differential effects of severe vs mild GBA mutations on Parkinson disease. Neurology, 84(9), 880–887. https://doi.org/10.1212/WNL.0000000000001315

Goldstein, O., Gana-Weisz, M., Cohen-Avinoam, D., Shiner, T., Thaler, A., Cedarbaum, J. M., John, S., Lalioti, M., Gurevich, T., Bar-Shira, A., Mirelman, A., Giladi, N., & Orr-Urtreger, A. (2019). Revisiting the non-Gaucher-GBA-E326K carrier state: Is it sufficient to increase Parkinson's disease risk? Molecular Genetics and Metabolism, 128(4), 470–475. https://doi.org/10.1016/j.ymgme.2019.10.001

Gopalai, A., Lim, S., abdul aziz, Z., Lim, soo kun, Tan, L. P., Chong, Y.-B., Tan, C., Puvanarajah, S., Viswanathan, S., Kuppusamy, R., Tan, A., Lim, T., Eow, G.,

Mohamed Ibrahim, N., Li, H., Zhao, Y., & Ahmad-Annuar, A. (2013). Lack of Association between the LRRK2 A419V Variant and Asian Parkinson's Disease. Annals of the Academy of Medicine, Singapore, 42, 237–240.

Huttenlocher, J., Stefansson, H., Steinberg, S., Helgadottir, H. T., Sveinbjörnsdóttir, S., Riess, O., Bauer, P., & Stefansson, K. (2015). Heterozygote carriers for CNVs in PARK2 are at increased risk of Parkinson's disease. Human Molecular Genetics, 24(19), 5637–5643. https://doi.org/10.1093/hmg/ddv277

Haugarvoll K, Rademakers R, Kachergus JM, et al. (2008) LRRK2 R1441C parkinsonism is clinically similar to sporadic Parkinson disease. Neurology. 70(16), 1456–60. doi:10.1212/01.wnl.0000304044.22253.03

Huang, Y., Deng, L., Zhong, Y., & Yi, M. (2018). The Association between E326K of GBA and the Risk of Parkinson's Disease [Review Article]. Parkinson’s Disease. https://doi.org/10.1155/2018/1048084

Ishihara, L., Warren, L., Gibson, R., Amouri, R., Lesage, S., Dürr, A., Tazir, M., Wszolek, Z. K., Uitti, R. J., Nichols, W. C., Griffith, A., Hattori, N., Leppert, D., Watts, R., Zabetian, C. P., Foroud, T. M., Farrer, M. J., Brice, A., Middleton, L., & Hentati, F. (2006). Clinical features of Parkinson disease patients with homozygous leucine-rich repeat kinase 2 G2019S mutations. Archives of Neurology, 63(9), 1250–1254. https://doi.org/10.1001/archneur.63.9.1250

Kay, D. M., Moran, D., Moses, L., Poorkaj, P., Zabetian, C. P., Nutt, J., Factor, S. A., Yu, C.-E., Montimurro, J. S., Keefe, R. G., Schellenberg, G. D., & Payami, H. (2007). Heterozygous parkin point mutations are as common in control subjects as in Parkinson's patients. Annals of Neurology, 61(1), 47–54. https://doi.org/10.1002/ana.21039

Kim, C. Y., & Alcalay, R. N. (2017). Genetic Forms of Parkinson's Disease. Seminars in Neurology, 37(2), 135–146. https://doi.org/10.1055/s-0037-1601567

Klein, C., Lohmann-Hedrich, K., Rogaeva, E., Schlossmacher, M. G., & Lang, A. E. (2007). Deciphering the role of heterozygous mutations in genes associated with parkinsonism. The Lancet Neurology, 6(7), 652–662. https://doi.org/10.1016/S1474-4422(07)70174-6

Lee, A. J., Wang, Y., Alcalay, R. N., Mejia-Santana, H., Saunders-Pullman, R., Bressman, S., Corvol, J.-C., Brice, A., Lesage, S., Mangone, G., Tolosa, E., Pont-Sunyer, C., Vilas, D., Schüle, B., Kausar, F., Foroud, T., Berg, D., Brockmann, K., Goldwurm, S., … Michael J. Fox LRRK2 Cohort Consortium. (2017). Penetrance estimate of LRRK2 p.G2019S mutation in individuals of non-Ashkenazi Jewish ancestry. Movement Disorders: Official Journal of the Movement Disorder Society, 32(10), 1432–1438. https://doi.org/10.1002/mds.27059

Lincoln, S. J., Maraganore, D. M., Lesnick, T. G., Bounds, R., de Andrade, M., Bower, J. H., Hardy, J. A., & Farrer, M. J. (2003). Parkin variants in North American Parkinson's disease: Cases and controls. Movement Disorders: Official Journal of the Movement Disorder Society, 18(11), 1306–1311. https://doi.org/10.1002/mds.10601

Lubbe, S.J., Bustos, B.I., Hu, J., Krainc, D., Joseph, T., Hehir, J., Tan, M., Zhang, W., Escott-Price, V., Williams, N.M., Blauwendraat, C., Singleton, A.B., Morris, H.R., for International Parkinson's Disease Genomics Consortium (IPDGC), 2021. Assessing the relationship between monoallelic PRKN mutations and Parkinson's risk. Hum Mol Genet 30, 78–86. https://doi.org/10.1093/hmg/ddaa273

Marder, K., Wang, Y., Alcalay, R. N., Mejia-Santana, H., Tang, M.-X., Lee, A., Raymond, D., Mirelman, A., Saunders-Pullman, R., Clark, L., Ozelius, L., Orr-Urtreger, A., Giladi, N., Bressman, S., & LRRK2 Ashkenazi Jewish Consortium. (2015). Age-specific penetrance of LRRK2 G2019S in the Michael J. Fox Ashkenazi Jewish LRRK2 Consortium. Neurology, 85(1), 89–95. https://doi.org/10.1212/WNL.0000000000001708

McNeill, A., Duran, R., Hughes, D. A., Mehta, A., & Schapira, A. H. V. (2012). A clinical and family history study of Parkinson's disease in heterozygous glucocerebrosidase mutation carriers. Journal of Neurology, Neurosurgery & Psychiatry, 83(8), 853–854. https://doi.org/10.1136/jnnp-2012-302402

Nishioka, K., Ross, O. A., Ishii, K., Kachergus, J. M., Ishiwata, K., Kitagawa, M., Kono, S., Obi, T., Mizoguchi, K., Inoue, Y., Imai, H., Takanashi, M., Mizuno, Y., Farrer, M. J., & Hattori, N. (2009). Expanding the clinical phenotype of SNCA duplication carriers. Movement Disorders: Official Journal of the Movement Disorder Society, 24(12), 1811–1819. https://doi.org/10.1002/mds.22682

Oliveira, S. A., Scott, W. K., Martin, E. R., Nance, M. A., Watts, R. L., Hubble, J. P., Koller, W. C., Pahwa, R., Stern, M. B., Hiner, B. C., Ondo, W. G., Allen, F. H., Scott, B. L., Goetz, C. G., Small, G. W., Mastaglia, F., Stajich, J. M., Zhang, F., Booze, M. W., … Vance, J. M. (2003). Parkin mutations and susceptibility alleles in late-onset Parkinson's disease. Annals of Neurology, 53(5), 624–629. https://doi.org/10.1002/ana.10524

Pankratz, N., Kissell, D. K., Pauciulo, M. W., Halter, C. A., Rudolph, A., Pfeiffer, R. F., Marder, K. S., Foroud, T., Nichols, W. C., & Parkinson Study Group-PROGENI Investigators. (2009). Parkin dosage mutations have greater pathogenicity in familial PD than simple sequence mutations. Neurology, 73(4), 279–286. https://doi.org/10.1212/WNL.0b013e3181af7a33

Papadimitriou, D., Antonelou, R., Miligkos, M., Maniati, M., Papagiannakis, N., Bostantjopoulou, S., Leonardos, A., Koros, C., Simitsi, A., Papageorgiou, S. G., Kapaki, E., Alcalay, R. N., Papadimitriou, A., Athanassiadou, A., Stamelou, M., & Stefanis, L. (2016). Motor and Nonmotor Features of Carriers of the p.A53T Alpha-Synuclein Mutation: A Longitudinal Study. Movement Disorders: Official Journal of the Movement Disorder Society, 31(8), 1226–1230. https://doi.org/10.1002/mds.26615

Polymeropoulos, M. H., Lavedan, C., Leroy, E., Ide, S. E., Dehejia, A., Dutra, A., Pike, B., Root, H., Rubenstein, J., Boyer, R., Stenroos, E. S., Chandrasekharappa, S., Athanassiadou, A., Papapetropoulos, T., Johnson, W. G., Lazzarini, A. M., Duvoisin, R. C., Iorio, G. D., Golbe, L. I., & Nussbaum, R. L. (1997). Mutation in the α-Synuclein Gene Identified in Families with Parkinson's Disease. Science, 276(5321), 2045–2047. https://doi.org/10.1126/science.276.5321.2045

Rana, H. Q., Balwani, M., Bier, L., & Alcalay, R. N. (2013). Age-specific Parkinson disease risk in GBA mutation carriers: Information for genetic counseling. Genetics in Medicine: Official Journal of the American College of Medical Genetics, 15(2), 146–149. https://doi.org/10.1038/gim.2012.107

Rosenbloom, B., Balwani, M., Bronstein, J. M., Kolodny, E., Sathe, S., Gwosdow, A. R., Taylor, J. S., Cole, J. A., Zimran, A., & Weinreb, N. J. (2011). The incidence of Parkinsonism in patients with type 1 Gaucher disease: Data from the ICGG Gaucher Registry. Blood Cells, Molecules & Diseases, 46(1), 95–102. https://doi.org/10.1016/j.bcmd.2010.10.006

Ruiz-Martínez, J., Gorostidi, A., Ibañez, B., Alzualde, A., Otaegui, D., Moreno, F., López de Munain, A., Bergareche, A., Gómez-Esteban, J. C., & Martí Massó, J. F. (2010). Penetrance in Parkinson's disease related to the LRRK2 R1441G mutation in the Basque country (Spain). Movement Disorders: Official Journal of

the Movement Disorder Society, 25(14), 2340–2345. https://doi.org/10.1002/mds.23278

Saunders-Pullman, R., Raymond, D., & Elango, S. (1993). LRRK2 Parkinson Disease. In M. P. Adam, H. H. Ardinger, R. A. Pagon, S. E. Wallace, L. J. Bean, K. Stephens, & A. Amemiya (Eds.), GeneReviews®. University of Washington, Seattle. http://www.ncbi.nlm.nih.gov/books/NBK1208/

Shu, L., Zhang, Y., Sun, Q., Pan, H., & Tang, B. (2019). A Comprehensive Analysis of Population Differences in LRRK2 Variant Distribution in Parkinson's Disease. Frontiers in Aging Neuroscience, 11, 13. https://doi.org/10.3389/fnagi.2019.00013

Sironi, F., Primignani, P., Ricca, S., Tunesi, S., Zini, M., Tesei, S., Cilia, R., Pezzoli, G., Seia, M., & Goldwurm, S. (2013). DJ1 analysis in a large cohort of Italian early onset Parkinson Disease patients. Neuroscience Letters, 557 Pt B, 165–170. https://doi.org/10.1016/j.neulet.2013.10.048

Trinh, J., Guella, I., & Farrer, M. J. (2014). Disease penetrance of late-onset parkinsonism: A meta-analysis. JAMA Neurology, 71(12), 1535–1539. https://doi.org/10.1001/jamaneurol.2014.1909

Wang, C., Cai, Y., Zheng, Z., Tang, B.-S., Xu, Y., Wang, T., Ma, J., Chen, S.-D., Langston, J. W., Tanner, C. M., Chan, P., & Chinese Parkinson Study Group (CPSG). (2012). Penetrance of LRRK2 G2385R and R1628P is modified by common PD-associated genetic variants. Parkinsonism & Related Disorders, 18(8), 958–963. https://doi.org/10.1016/j.parkreldis.2012.05.003

Zhang, Y., Sun, Q., Yi, M., Zhou, X., Guo, J., Xu, Q., Tang, B., & Yan, X. (2017). Genetic Analysis of LRRK2 R1628P in Parkinson's Disease in Asian Populations. Parkinson's Disease, 2017, 8093124. https://doi.org/10.1155/2017/8093124

Zhu W., Huang X., Yoon E. , et al. (2022) Heterozygous PRKN mutations are common but do not increase the risk of Parkinson's disease, Brain, 145(6), 2077–2091. https://doi.org/10.1093/brain/awab456