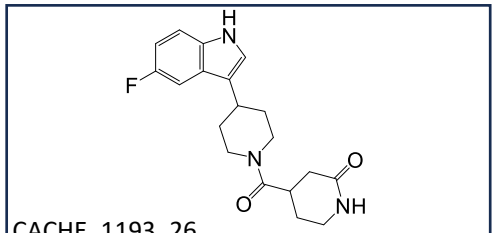
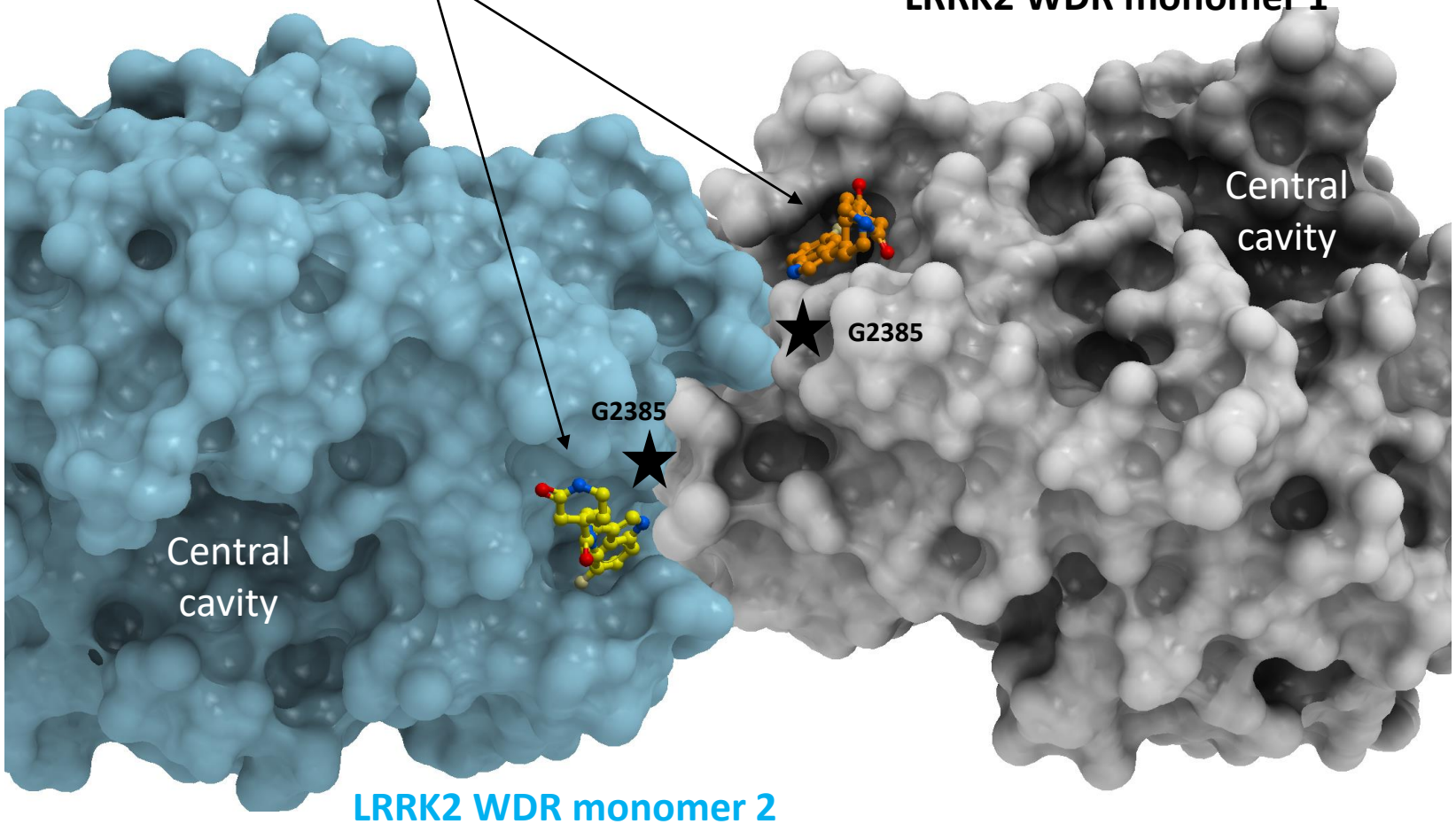


CACHE_1193_26
SPR LRRK2 48µM – 58% binding
SPR NSD2 – NA – 36% binding
100% solub /no agg. at 200 µM
Co-crystallized at unexpected pocket



- Pathogenic, dimerization-defective LRRK2 mutants such as G2385R have enhanced kinase activity
- CACHE_1193_26 occupies a side pocket next to G2385
- CACHE_1193_26 still binds in solution to the G2385R mutant, suggesting a different binding mode in solution.
- Nevertheless, the structure reveals a potential mechanism to stabilize the dimeric form of LRRK2 WDR

Structure solved by Aiping Dong, Hong Zeng and Levon Halebelian, Structural Genomics Consortium