- Developed 100% by my own
  - Structures via Reasoning - Applying AI to Cryo Electron Microscopy to Reveal Structural Variability
    - developed by **DN Kim**, AJ August, HJ Kvinge, J Evans
    - coded by python3
    - iEdison No. 0685901-22-0060, 32452-E, United States
    - 2022
  - *AutoMicroED* (Semi-automated processing of micro electron diffraction data)
    - coded by python3
    - developed by **Doo Nam Kim**, Samantha Powell, Irina Novikova and James Evans
    - Intellectual Property Services, K1-53, 375-6302, United States
    - 2021
  - *cryo_fit* (Semi-automated MD simulation with cryo-EM data)
    - coded by python2,
    - document
    - developed by **Doo Nam Kim**, Serdal Kirmizialtin, Nigel Moriarty and Karissa Sanbonmatsu
    - United States
    - 2019
  - E_a*MEAD* ver. 2.0 (Activation energy prediction of cytochrome p450 mediated phase I Metabolism with Effective Atomic Descriptors)
    - coded by python2
    - developed by **Doo Nam Kim**, Changjoon Lee, and Kyoung Tai No
    - Registered at Committee for Protection of Computer Software Intellectual Property, South Korea, Registration No.: S-2008-007605 (publicly available to use at Premetabolism)
    - 2008

- Co-developed (my contribution: 20~50%)
  - ProCaliper (functional and structural analysis, visualization, and annotation of proteomic data)
    - developed by Song Feng, Jordan C. Rozum, Hunter S. Ufford, **Doo Nam Kim**, Alexandria K. Im,
    - IP ID No. 33329-E, United States
    - coded by python3
    - 2025
  - GRaph Identification of Proteins in Tomograms (GRIP-Tomo) 2.0
    - developed by Li, Chengxuan; George, August D; Neff, Reece William; **Kim, Doo Nam**; Moser, Trevor H; Baldwin, Katharine T; Firoozfar, Arsam; Evans, James E; Cheung-Wyker, Margaret S
    - coded by python3
    - United States
    - 2025
  - GRaph Identification of Proteins in Tomograms (GRIP-Tomo) 1.0
    - developed by George, August D; **Kim, Doo Nam**; Evans, James E; Cheung-Wyker, Margaret S
    - coded by python3

        - United States
        - 2023
    - PNNL DataHub Superfund Research Project
        - developed by Gosline, S. **Kim, D**; Pande, P; Thomas,D; Truong, L; Hoffman, P; Barton,M; Anderson, L; Thessen,A; Anderson, K; Tanguay, RL; Waters, KM
        - NIH iEdison No. 0685901-20-0023, Grant No. ES016465, United States
        - coded by python3, bash script, docker
        - 2021

- Co-developed (my contribution: ~0.3% ?)
    - *Rosetta*
        - coded by c++
        - developed beta-sandwich protein structural feature identification that stores results to a structured database, debugged many other (~150) co-developers' codes
        - 2012-2016