



**Supplementary Figure 1: Quality of AlphaFold-predicted structures.**

(A-O) AlphaFold-predicted structures colored in predicted local distance difference test scores (pLDDT; left) as well as heatmaps of predicted aligned error (PAE; right). (A) FMN\_Bind<sub>2</sub>; (B) DUF2271; (C) Flavodoxin\_4; (D) FMN\_Reductase; (E) Flavodoxin\_4 DL; (F) FMN\_Reductase LT; (G) Nqr/Rnf-Like; (H) DUF4405; (I) MsrQ; (J) FezC; (K) 3xFMN\_Bind<sub>1</sub>; (L) 2xFMN\_Bind<sub>1</sub>; (M) 3xFMN\_Bind<sub>1</sub>; (N) 5xFMN\_Bind<sub>1</sub>; (O) 8xFMN\_Bind<sub>1</sub>; (P) 6xFMN\_Bind<sub>2</sub>.