drug binding affinity in terms of the inhibitory constant ($K_i$) was calculated every time the drug molecule was moved. After repeating this procedure for all of the drugs for each protein, the 20 drugs with the lowest $K_i$ values were considered high-affinity drug candidates. Further details of the molecular dynamics simulation and docking protocols are available elsewhere.\textsuperscript{3}

**Results.** We predicted 20 multitarget drugs that showed high affinity across 2 or more proteins (FIGURE). Four are drugs approved by the US Food and Drug Administration for treatment of diseases other than malaria: KN62 (targeting 3 proteins), protoporphyrin IX, phthalylsulfathiazole, and sulfaphenazole (targeting 2 proteins each). The other 16 are experimental, each targeting up to 6 proteins. The best drugs in terms of multitarget functionality were STI-16 ($K_i$ values were considered high-affinity drug candidates. Further details of the molecular dynamics simulation and docking protocols are available elsewhere.\textsuperscript{3}

**Conclusions.** Promising vaccines targeting multiple *Plasmodium* proteins have been evaluated.\textsuperscript{9,10} In a similar fashion, we propose designing new antimalarial drugs that simultaneously target multiple *Plasmodium* proteins. Our computational drug screening protocol provides evidence for 20 approved or experimental drugs that bind strongly to 13 *Plasmodium* proteins. We recommend that these drug candidates be experimentally tested for inhibition of *Plasmodium* growth and used as a starting point for further design of a high-efficacy multitarget antimalarial drug.

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