Fig. 3

```
<dock_design>
 <TASKOPERATIONS>
  <InitializeFromCommandline name=IFC/> # use the information in the args file to supplement this XML
   <IncludeCurrent name=IC/> # includes the rotamers in the input structure (may not want to use)
   <RestrictDesignToProteinDNAInterface name= DnaInt base_only =1 z_cutoff =6.0 dna_defs =Z.409.GUA/> # make the target site substitution of interest (chainID.crystalposition.type) and designate the sphere of residues surrounding it that are designable and packable
     <OperateOnCertainResidues name=AUTOprot> # works with the DnaInt operation to enable residues to be chosen for design and packing if they are marked as AUTO
    <AddBehaviorRLT behavior=AUTO/>
    <ResidueHasProperty property=PROTEIN/>
   </OperateOnCertainResidues>
  </TASKOPERATIONS>
  <SCOREFXNS>
   <DNA weights=optimizedenergyfxn/> # energy function for design evaluation, this file must be put in the directory (ie, rosetta_database/scoring/weights/optimizedenergyfxn.wts)
 </SCOREFXNS>
 <FILTERS>
   <FalseFilter name=falsefilter/> # RosettaScripts has the ability to only output designs that pass a designated filter. This functionality is not being used here.
 </FILTERS>
 <MOVERS>
    <DnaInterfacePacker name=DnaPack scorefxn=DNA task_operations=IFC,IC,AUTOprot,DnaInt/>
  </MOVERS>
  <PROTOCOLS>
   <Add mover_name=DnaPack/>
  </PROTOCOLS>
</dock_design>
```