**Structural insight into guanylyl cyclase receptor hijacking of the kinase–Hsp90 regulatory mechanism**

Nathanael A Caveney1,\*, Naotaka Tsutsumi1,2,3, K Christopher Garcia1,2,\*

1Departments of Molecular and Cellular Physiology and Structural Biology, Stanford University School of Medicine, Stanford, CA 94305, USA

2Howard Hughes Medical Institute, Stanford University School of Medicine, Stanford, CA 94305, USA

3Present address: Graduate School of Medicine, Dentistry and Pharmaceutical Sciences, Okayama University, Okayama, Japan.

\*Correspondence: ncaveney@stanford.edu, kcgarcia@stanford.edu

Material availability: The plasmids used in this study are described below and available from KCG (kcgarcia@stanford.edu) by request.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Reagent type (species) or resource** | **Designation** | **Source or reference** | **Identifiers** | **Additional information** |
| Recombinant DNA reagent | pD649-GCN4-TM-GC-C\_ICD (plasmid) | This paper |  | See: Methods - Cloning and protein expression |

>pD649-GCN4-TM-GC-C\_ICD

ATGAAGACTATAATCGCCCTCTCCTACATATTTTGCTTGGTGTTTGCCGACTACAAGGACGACGATGATAAAGGGTCTCTGGAAGTCCTTTTCCAGGGGCCCGGTAGAATGAAGCAACTCGAAGACAAAGTCGAGGAGCTTCTCTCTAAAAACTATCATCTCGAGAATGAAGTGGCCCGCCTGAAAAAACTCGTTGGCGAACGGAAGTTGCCAAATGATATAACCGGACGCGGACCACAAATTCTTATGATAGCTGTCTTTACACTTACAGGGGCTGTGGTGCTCCTGCTGTTGGTAGCGCTCCTCATGCTTCGAAAATACAGAAAGGATTATGAGCTCCGGCAGAAGAAATGGAGTCACATTCCTCCGGAAAACATTTTTCCTCTCGAGACAAACGAGACGAACCACGTATCCCTGAAAATCGACGACGACAAAAGACGAGATACCATCCAGCGATTGCGCCAGTGTAAATACGATAAGAAAAGAGTAATCCTCAAAGATTTGAAGCATAACGATGGCAATTTCACCGAGAAACAGAAGATTGAGCTGAATAAACTCTTGCAAATTGACTATTATAATTTGACCAAGTTTTACGGGACGGTCAAGTTGGACACGATGATATTTGGGGTGATAGAATATTGTGAACGCGGTAGTCTCAGAGAAGTCCTGAATGACACGATATCCTATCCCGATGGCACCTTTATGGACTGGGAATTCAAGATTAGCGTACTGTACGATATCGCCAAAGGAATGTCATATCTCCATAGTAGCAAAACCGAGGTTCACGGTCGCTTGAAATCAACCAATTGTGTCGTAGATAGTCGCATGGTCGTGAAGATTACTGATTTTGGATGTAATTCCATATTGCCGCCCAAAAAAGACTTGTGGACCGCTCCAGAACACCTTAGGCAGGCCAACATAAGTCAAAAGGGGGACGTTTACTCCTATGGTATTATAGCACAAGAAATTATCCTCCGAAAGGAAACATTTTATACCTTGTCTTGTCGAGACAGGAACGAAAAAATTTTTCGGGTGGAGAATTCCAATGGGATGAAACCATTTAGACCCGACCTCTTTCTGGAGACAGCTGAGGAGAAAGAGCTTGAAGTTTATTTGCTGGTGAAAAACTGTTGGGAAGAGGATCCGGAAAAACGGCCCGACTTTAAGAAGATTGAGACAACCTTGGCAAAAATATTCGGGTTGTTCCATGACCAGAAGAATGAAAGCTACATGGACACATTGATTAGGAGGTTGCAACTGTACTCACGGAACCTGGAGCACCTTGTCGAGGAGAGAACGCAGTTGTATAAGGCAGAAAGGGACCGAGCAGACAGACTGAATTTTATGCTCCTCCCCAGACTGGTTGTAAAAAGCCTGAAAGAAAAAGGCTTCGTGGAGCCTGAGCTGTATGAGGAAGTGACAATATACTTCTCCGACATAGTTGGTTTCACCACTATATGCAAATATTCTACACCCATGGAGGTCGTTGATATGCTCAACGATATATACAAGTCCTTTGACCATATCGTCGATCACCATGACGTATACAAAGTGGAGACCATCGGTGACGCATACATGGTGGCGAGCGGCCTGCCTAAAAGAAACGGTAACCGACATGCGATAGACATTGCTAAAATGGCTCTGGAGATCCTTAGTTTCATGGGCACGTTCGAACTGGAGCATCTCCCAGGCCTGCCTATCTGGATTCGAATAGGTGTGCATTCCGGGCCTTGCGCGGCCGGAGTGGTTGGTATCAAGATGCCGAGATACTGTCTCTTTGGAGACACAGTTAACACCGCCTCACGCATGGAGTCTACCGGGTTGCCGCTCCGCATTCATGTAAGTGGGTCTACGATAGCGATCTTGAAACGGACAGAGTGCCAATTTCTTTACGAAGTACGCGGAGAAACATATCTCAAGGGTCGGGGTAATGAGACCACTTATTGGCTCACGGGGATGAAGGATCAGAAGTTCAATCTGCCCACTCCCCCGACCGTTGAGAACCAGCAGAGACTGCAAGCGGAATTTTCAGATATGATCGCGAACTCTCTGCAGAAGCGGCAAGCGGCTGGGATTCGCTCCCAAAAGCCTAGACGCGTTGCGTCCTATAAGAAGGGTACCTTGGAGTACTTGCAGCTGAATACAACGGACAAAGAATCAACATATTTCGCGGCAGCGCTCGAGGTACTTTTCCAAGGCCCAGGAGCTGCTGAGGATCAGGTCGATCCTCGCCTTATCGACGGCAAACACCATCATCACCATCACCACCACtaaGGATCCGTTACCCGGTAAGCCAATCGGGTATACACGGTCGTCATACTGCAGACAGGGTTCTTCTACTTTGCAAGATAGTCTTGAGTAGTAAAATAAATAGATAGAGAAAATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAATTGCATCACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTAATTCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCTGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCAGCACGTGTTGACAATTAATCATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAACCATGACCGAGTACAAGCCCACGGTGCGCCTCGCCACCCGCGACGACGTCCCCAGGGCCGTACGCACCCTCGCCGCCGCGTTCGCCGACTACCCCGCCACGCGCCACACCGTCGATCCGGACCGCCACATCGAGCGGGTCACCGAGCTGCAAGAACTCTTCCTCACGCGCGTCGGGCTCGACATCGGCAAGGTGTGGGTCGCGGACGACGGCGCCGCGGTGGCGGTCTGGACCACGCCGGAGAGCGTCGAAGCGGGGGCGGTGTTCGCCGAGATCGGCCCGCGCATGGCCGAGTTGAGCGGTTCCCGGCTGGCCGCGCAGCAACAGATGGAAGGCCTCCTGGCGCCGCACCGGCCCAAGGAGCCCGCGTGGTTCCTGGCCACCGTCGGCGTCTCGCCCGACCACCAGGGCAAGGGTCTGGGCAGCGCCGTCGTGCTCCCCGGAGTGGAGGCGGCCGAGCGCGCCGGGGTGCCCGCCTTCCTGGAGACATCCGCGCCCCGCAACCTCCCCTTCTACGAGCGGCTCGGCTTCACCGTCACCGCCGACGTCGAGGTGCCCGAAGGACCGCGCACCTGGTGCATGACCCGCAAGCCCGGTGCCTGACACGTGCTACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGTATACCGTCGACCTCTAGCTAGAGCTTGGCGTAATCATGGTCATTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGCGCTGCGATGATACCGCGAGAACCACGCTCACCGGCTCCGGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATCGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATATTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTCAGTGTTACAACCAATTAACCAATTCTGAACATTATCGCGAGCCCATTTATACCTGAATATGGCTCATAACACCCCTTGCTCATGACCAAAATCCCTTAACGTGAGTTACGCGCGCGTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGCCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGGCGAGAGTAGGGAACTGCCAGGCATCAAACTAAGCAGAAGGCCCCTGACGGATGGCCTTTTTGCGTTTCTACAAACTCTTTCTGTGTTGTAAAACGACGGCCAGTCTTAAGCTCGGGCCCCCTGGGCGGTTCTGATAACGAGTAATCGTTAATCCGCAAATAACGTAAAAACCCGCTTCGGCGGGTTTTTTTATGGGGGGAGTTTAGGGAAAGAGCATTTGTCAGAATATTTAAGGGCGCCTGTCACTTTGCTTGATATATGAGAATTATTTAACCTTATAAATGAGAAAAAAGCAACGCACTTTAAATAAGATACGTTGCTTTTTCGATTGATGAACACCTATAATTAAACTATTCATCTATTATTTATGATTTTTTGTATATACAATATTTCTAGTTTGTTAAAGAGAATTAAGAAAATAAATCTCGAAAATAATAAAGGGAAAATCAGTTTTTGATATCAAAATTATACATGTCAACGATAATACAAAATATAATACAAACTATAAGATGTTATCAGTATTTATTATCATTTAGAATAAATTTTGTGTCGCCCTTAATTGTGAGCGGATAACAATTACGAGCTTCATGCACAGTGGCGTTGACTCAATATTGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAATATTGGCTATTGGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAATATGACCGCCATGTTGGCATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACCCCCTTGGCTTCGTTAGAACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTATAGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACTGCACCTCGGTTCTATCGAAAACGCGCCTGCTAGCGCCACC