

**Supporting Information:****Structure-Based Design of Highly Selective and Potent G Protein-Coupled Receptor Kinase 2 Inhibitors Based on Paroxetine**

*Helen V. Waldschmidt<sup>a</sup>, Kristoff T. Homan<sup>b,†</sup>, Marilyn C. Cato<sup>b</sup>, Osvaldo Cruz-Rodríguez<sup>b,c</sup>, Alessandro Cannavo<sup>d</sup>, Michael W. Wilson<sup>e</sup>, Jianliang Song<sup>d</sup>, Joseph Y. Cheung<sup>d</sup>, Walter J. Koch<sup>d</sup>, John J. G. Tesmer<sup>a,b,c</sup>, and Scott D. Larsen \*<sup>a,e</sup>*

<sup>a</sup>Department of Medicinal Chemistry, College of Pharmacy, <sup>b</sup>Departments of Pharmacology and Biological Chemistry, Life Sciences Institute, <sup>c</sup>PhD Program in Chemical Biology, <sup>d</sup>Center for Translational Medicine, Temple University, Philadelphia, Pennsylvania, 19140, <sup>e</sup>Vahlteich Medicinal Chemistry Core, University of Michigan, Ann Arbor, Michigan, 48109

## Table of contents:

Table S1: Crystal Refinement Statistics	S2
Table S2: Mouse cardiomyocyte contractility in response to paroxetine, 2, 14ak, and 14as.	S3
Table S3: Biochemical data for compounds <b>15</b> , <b>16</b> , and <b>17</b>	S3

**Supplementary Table 1.** Crystal Refinement Statistics.

Protein Complex	GRK2-G $\beta\gamma$ <b>·14ak</b>	GRK2-G $\beta\gamma$ <b>·14bd</b>	GRK2-G $\beta\gamma$ <b>·14as</b>
X-ray source	APS 21-ID-G	APS 21-ID-G	APS 21-ID-D
wavelength (Å)	0.9785	0.9786	0.9785
$D_{\min}$ (Å)	50.00-2.60 (2.64-2.60)	50.00-2.15 (2.19-2.15)	30-3.0 (3.04-3.03)
space group	<i>P</i> 2	<i>C</i> 2	<i>C</i> 2
unit cell constants (Å) (°)	$a=113.1, b=62.4, c=102.0$ $\beta=92.8$	$a=194.3, b=71.4, c=111.3$ $\beta=110.5$	$a=189.0, b=74.2, c=123.2$ $\beta=115.5$
unique reflections	39963 (1987)	77337 (3805)	29942 (4657)
$R_{\text{sym}}$ (%)	9.8	16.1	12.9
completeness (%)	85.8	99.0	98.5
$\langle I \rangle / \langle \sigma_I \rangle$	9.2 (0.8)	24.9 (1.4)	12.8 (2.0)
redundancy	2.6 (2.5)	18.3 (11.2)	6.8 (6.8)
refinement resolution (Å)	30.00-2.60 (2.69-2.60)	30.00-2.15 (2.23-2.15)	30.00-3.03 (3.14-3.03)
total reflections used	35989	73370	207836
RMSD bond lengths (Å)	0.011	0.018	0.012
RMSD bond angles (°)	1.53	1.90	1.56
est. coordinate error (Å)	0.360	0.142	0.404
Ramachandran Plot:			
most favored, allowed, outliers (%)	92.5, 5.6, 1.9	95.3, 3.8, 0.9	93.2, 5.3, 1.8
$R_{\text{work}}$	0.2207	0.1821	0.1971
$R_{\text{free}}$	0.2807	0.2275	0.2516
protein atoms	8089	8261	8192
water molecules	43	388	23
inhibitor atoms	34	35	33
average $B$ -factor (Å <sup>2</sup> )	80.2	55.2	105.0
protein	80.3	55.6	105.0
inhibitor	70.2	69.3	123.3
MolProbity score	2.01	1.70	1.74
MolProbity % C $\beta$ deviations	0	0.52	0
MolProbity % bad backbone bonds	0	0.04	0.01
MolProbity % bad backbone angles	0	0.05	0.01
PDB entry	---	---	---

\*Entries in parentheses indicate data in the highest resolution shell

**Supplementary Table 2:** Mouse cardiomyocyte contractility in response to paroxetine, 2, 14ak, and 14as.

	Paroxetine				2				14ak			14as				
Concentration ( $\mu\text{M}$ )	0	0.5	1	10	0	0.1	0.5	1	0	0.5	1	0	0.1	0.5	1	
<b>Baseline before isoproterenol</b>																
MCA (% cell length)	5.0 ± 0.5	4.0 ± 0.3	4.3 ± 0.8	4.2 ± 0.5	4.8 ± 0.5	3.6 ± 0.4	4.2 ± 0.3	4.4 ± 0.5	5.1 ± 1.1	5.1 ± 1.1	5.2 ± 0.6	4.4 ± 0.3	3.3 ± 0.2	3.5 ± 0.4	3.5 ± 0.2	
<b>After isoproterenol</b>																
MCA (% cell length)	12 ± 0.6	14 ± 1	13 ± 0.8	16 ± 0.5*	13 ± 0.5	12 ± 0.7	16 ± 1*	17 ± 1.3*	12 ± 1.3	12 ± 1.1	13 ± 0.9	11 ± 0.9	14 ± 0.7*	18 ± 1.3*	15 ± 1.2*	
% increase	146 ± 16	248 ± 26	262 ± 60	296 ± 45*	178 ± 24	252 ± 27	277 ± 28*	293 ± 35*	198 ± 66	166 ± 38	173 ± 41	161 ± 20	341 ± 33*	433 ± 90*	342 ± 65*	

Values represent the mean ± SEM for 6-8 cardiomyocytes. \*,p<0.05 vs DMSO Control. MCA, maximum contraction amplitude.

**Supplementary Table 3:** Biochemical Data for previously reported compounds **15**, **16**, and **17**.

Compound	GRK2 IC <sub>50</sub> ( $\mu\text{M}$ )	GRK1 IC <sub>50</sub> ( $\mu\text{M}$ )	GRK5 IC <sub>50</sub> ( $\mu\text{M}$ )	PKA IC <sub>50</sub> ( $\mu\text{M}$ )	ROCK1 IC <sub>50</sub> ( $\mu\text{M}$ )
<b>15</b>	0.13±0.03	> 100	> 100	> 100	6.7±8.2
<b>16</b>	0.07±0.01	>100	63±32	>100	5.8±5.5
<b>17</b>	0.15±0.07	3.9±1.0	0.38±0.06	>100	0.01±0.01