



|  |  |   |
|--|--|---|
|  | <b>Experiment title: Structural studies on cell-cycle proteins in complex with small molecule inhibitors</b> | <b>Experiment number: LS-1382</b>         |
| <b>Beamline:</b><br>ID14-EH3   | <b>Date of experiment:</b><br>from: 30-04-99 to: 01-05-99  | <b>Date of report:</b><br>23 August, 2000 |
| <b>Shifts:</b><br>1  | <b>Local contact(s):</b><br>Dr. E. Mitchell  | <i>Received at ESRF:</i>                  |
| <b>Names and affiliations of applicants</b> (* indicates experimentalists):<br>Dr. Martin Noble*, Dr. Jane Endicott* and Professor Louise Johnson<br>Laboratory of Molecular Biophysics<br>Rex Richards Building<br>South Parks Road<br>Oxford OX1 3QU, U.K. |  |   |

### Report:

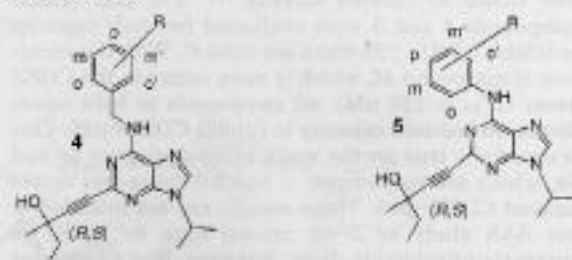
(In collaboration with Dr. M. Legraverend, Centre Universitaire, 91405 Orsay Cedex, France).

(Journal of Medicinal Chemistry **2000** 43 1282-1292)

### **Cyclin-dependent kinase inhibition by New C-2 Alkynylated Purine Derivatives and Molecular Structure of a CDK2-Inhibitor complex**

A new series of 2,6,9-trisubstitued purines, characterized by the presence of a common alkynyl substituent at C-2 and a range of different anilino/benzylamino groups at C-6, were synthesized. These compounds were evaluated for their capacity to inhibit cyclin-dependent kinase activity (CDK1-cyclin B) in vitro. Compounds 4e and 5e (Table 1) exhibited the strongest inhibitory activity with an  $IC_{50}$  of 60 nM. The structure of compound 4b (OL567) in complex with human CDK2 was determined by X-ray crystallography, revealing the molecular basis of inhibition by this molecule. Data collection and refinement statistics are given in Table 2. A Ligplot diagram summarizing the interactions between inhibitor and CDK2 is shown in Figure 1. Subsequent molecular modelling studies allowed us to rationalize the SAR observed for these compounds.

**Table 1.** IC<sub>50</sub> Values against CDK1–Cyclin B for Members of Series 4 and 5



| compd <sup>a</sup>         | R  | IC <sub>50</sub> (nM) |
|----------------------------|--|-----------------------|
| 4a                         | H  | 200                   |
| 4b (OL567)                 | <i>p</i> -OCH <sub>3</sub>                 | 230                   |
| 4c                         | <i>p</i> -OCH <sub>2</sub> CH <sub>3</sub> | 180                   |
| 4d                         | <i>m,p</i> -di-Cl                          | 430                   |
| 4e                         | <i>p</i> -Cl                               | 60                    |
| 4f                         | <i>m,p</i> -OCH <sub>2</sub> O             | 200                   |
| 4g                         | <i>m,p</i> -di-OCH <sub>3</sub>            | 200                   |
| 4h                         | <i>p</i> -N(CH <sub>3</sub> ) <sub>2</sub> | 150                   |
| 5a                         | H  | 400                   |
| 5b                         | <i>p</i> -OCH <sub>3</sub>                 | 200                   |
| 5c                         | <i>p</i> -OCH <sub>2</sub> CH <sub>3</sub> | 200                   |
| 5d                         | <i>m,p</i> -di-Cl                          | 200                   |
| 5e                         | <i>m</i> -Cl                               | 60                    |
| olomoucine                 |  | 7000                  |
| ( <i>R,S</i> )-roscovitine |  | 650                   |

<sup>a</sup> *m* = meta, *p* = para substituents of the phenyl group.

| data collected (space group <i>P</i> 212121)      | CDK2–OL567            |
|---|-----------------------|
| cell dimensions (Å)                               | 53.14, 71.47, 71.91   |
| maximal resolution (Å)                            | 1.80                  |
| observations                                      | 67163                 |
| unique reflections, completeness (%)              | 25001, 95.8           |
| <i>R</i> <sub>merge</sub> <sup>a</sup>            | 0.072                 |
| mean <i>I</i> ( <i>I</i> )                        | 8.4                   |
| protein atoms                                     | 2338                  |
| residues  | 1–35, 44–298          |
| other atoms                                       | 298 water<br>29 OL567 |
| resolution range (Å)                              | 20.00–1.85            |
| <i>R</i> <sub>conv</sub> <sup>b</sup>             | 0.19                  |
| <i>R</i> <sub>free</sub> <sup>c</sup>             | 0.25                  |
| mean protein temperature factors (Å) <sup>2</sup> | 24.0                  |
| mean ligand temperature factors (Å) <sup>2</sup>  | 34.2                  |

**Table 1** IC<sub>50</sub> values against CDK1-Cyclin B  
**Table 2** Data collection statistics for OL567

