initially bound <sup>131</sup>I activity up to 24 h compared to that for <sup>125</sup>I. In SK-N-SHsst2 cells, the specific internalized radioactivity of [<sup>131</sup>I]5 was 2- to 4-fold higher than that of [<sup>125</sup>I]GluTOCA. It was 6- to 7-fold higher than that of [<sup>125</sup>I]7 suggesting that, contrary to observations above, NET may have some role in its uptake (OIBG has no significant affinity to NET). In summary, while [<sup>131</sup>I]MIBG-Octreotate demonstrated higher internalized radioactivity in SK-N-SHsst2 cells *in vitro* compared to [<sup>125</sup>I]Glu-TOCA and [<sup>125</sup>I]OIBG-Octreotate, its uptake was lower than that of [<sup>125</sup>I]MIBG. We plan to modify the linker between MIBG and octreotate in order to facilitate the interaction of this hybrid molecule with both tumor associated targets present on NB cells.

## 116 POSTER Inhibition of p53-MDM2 pathway by novel boronic-chalcones

A. Modzelewska<sup>1</sup>, A. Geetha<sup>2</sup>, M. Ghosh<sup>3</sup>, C. Pettit<sup>1</sup>, N.E. Davidson<sup>1</sup>, T. Holak<sup>3</sup>, P. Huang<sup>2</sup>, S.R. Khan<sup>1</sup>. <sup>1</sup>The Johns Hopkins Medical Institutions, Oncology, Baltimore, USA; <sup>2</sup>The University of Texas M.D. Anderson Cancer Center, Molecular Pathology, Houston, USA; <sup>3</sup>Max Planck Institute for Biochemistry, Biochemistry, Munich, Germany

The p53 tumor-suppressor pathway is inactivated in a majority of human cancers. Although the p53 gene is frequently deleted or mutated in many human malignancies, a substantial percentage of tumors also express intact p53 and overexpression of MDM2 is commonly observed. The oncoprotein MDM2 negatively regulates p53 function by binding to this protein to enhance proteolytic degradation, hence destroying the cell cycle checkpoint and allowing the progression of damaged cells. This P53/MDM2 interaction has been implicated as a possible mechanism for cancer development in several tumors including human sarcomas. Thus disruption of p53-MDM2 interaction with synthetic compounds should stabilize p53 in the nucleus and offer a novel therapeutic potential for cancer therapy. A series of boronic-chalcones have been investigated as possible MDM2 antagonists. The goal of the current studies is to build upon the paradigm of the boronic-chalcone analogs to identify more effective and selective agents can be found. We have successfully designed and synthesized boronic-chalcone derivatives that inhibit growth of human breast and colorectal cancer cell lines with  $IC_{50}$  values from 1 to 5  $\mu$ M. The cytotoxic effect of these compounds was measured by multiple analyses including MTT assay, annexin-V reactivity, and colony formation assay. Both apoptosis analysis and colony formation assay in p53 isogenic cells showed that the p53+/+ colon cancer cells are more sensitive to the active boronic-chalcones than the p53-/- colon cancer cells. We have shown by multidimensional NMR spectroscopy that boronic-chalcone derivatives are MDM2 inhibitors that bind to a subsite of the p53-binding cleft of human MDM2. Structure-activity relationship studies and molecular modeling studies of this new class of compounds are underway. Upon the identification of the most active compounds, these cytotoxic agents will be tested for their potency and selectivity for tumor cells. The lead compounds will then be tested in vivo models of human breast and colon cancer. These studies will serve to identify the best candidate that will subsequently test in clinical trials as treatment for breast and colon cancer.

117 POSTER

Identification of novel cyclin dependent kinase 1/2 inhibitors using fragment based high-throughput X-ray crystallography and structure based drug design

P.G. Wyatt<sup>1</sup>, V. Berdini<sup>2</sup>, M.G. Carr<sup>1</sup>, J.E. Curry<sup>3</sup>, D.J. Davis<sup>3</sup>, M. O'Reilly<sup>4</sup>, G. Saxty<sup>1</sup>, M.S. Squires<sup>3</sup>, A.J. Woodhead<sup>1</sup>, A.J.-A. Woolford<sup>1</sup>. <sup>1</sup>Astex Technology, Medicinal Chemistry, Cambridge, UK; <sup>2</sup>Astex Technology, Computational Chemistry, Cambridge, UK; <sup>3</sup>Astex Technology, Biology, Cambridge, UK; <sup>4</sup>Astex Technology, Protein Structure, Cambridge, UK

The poster describes the use of high-throughput X-ray crystallography and fragment-based drug discovery (Astex's Pyramid<sup>TM</sup> technology) to develop a number of lead series with potent cyclin-dependent kinase 1 and 2 (CDK-1, CDK-2) inhibitory activity and antiproliferative activity against cancer cell lines.

Astex has developed an integrated crystallography-based approach, which allows the detection of high efficiency binding molecular fragments and their subsequent optimization using structure-based drug design into potent novel drug candidates. Soaking apo-crystals of CDK-2 with cocktails of low molecular weight compounds identified a number of start points for chemistry programmes. Optimisation of one of these start points, using X-ray structures of synthesized molecules, allowed the rapid identification of compounds with potent CDK activity. Further improvements in the initial

leads have identified compounds with both potent CDK and single figure nanomolar anti-proliferative activity.

These lead molecules were characterised in a range of cell-based assays, demonstrating their anti-proliferative effect resulted from a specific cell cycle arrest and tumour cell death by apoptosis. The mechanism of action of this inhibition was confirmed by monitoring the phosphorylation of downstream substrates

Furthermore the compounds were shown to exhibit negligible toxicity towards non-proliferating fibroblast cells, and were equipotent in cells lacking p53 or expressing PgP.

The in vivo pharmacokinetic and xenograft activity of this series of compounds will be described in the accompanying poster.

In conclusion using Astex's Pyramid<sup>TM</sup> technology a number of potent CDK1/2 inhibitors have been identified with potent anti-tumour activity.

## 118 POSTER Substituted 7-amino-4-anilino-6-alkoxy-3-quinolinecarbonitriles as Src kinase inhibitors

H. Tsou<sup>1</sup>, E. Overbeek-Klumpers<sup>1</sup>, W. Hallett<sup>1</sup>, J. Golas<sup>2</sup>, F. Boschelli<sup>2</sup>.

Wyeth Research, Chemical and Screening Sciences, Pearl River, NY, USA; Wyeth Research, Oncology, Pearl River, NY, USA

As a prototype for non-receptor tyrosine kinases and proto-oncogenes, Src plays an important role in the signal transduction pathways that regulate several cellular functions such as proliferation, differentiation, migration, and angiogenesis. Activation and over-expression of Src have been implicated in cancer, osteoporosis and stroke. Therefore, inhibition of Src kinase could prove effective in the treatment of these diseases. Earlier, a Wyeth team reported 7-alkoxy, 7-alkenyl, 7-alkynyl, and 7-phenyl-4-anilino-3-quinolinecarbonitriles as potent Src kinase inhibitors. In this paper, we report a series of substituted 7-amino-4-anilino-3-quinolinecarbonitriles. Some of them are low nanomolar inhibitors of Src kinase, and their SAR will be discussed. Methods for introducing substituents with various chain lengths on the 7-amino group will also be presented.

## 119 POSTER

## A novel strategy to inhibit Stat3 for human cancer therapy

 $\underline{\text{N. Jing, Y. Li, W. Sha, W. Xiong, D. Tweardy.}}$  Baylor College of Medicine, Medicine, USA

Background: Stat3 has been suggested as a critical mediator of oncogenic signaling in the development and progression of human cancers and is active in prostate cancers (82%), breast cancers (69%), head and neck cancers (HNSCC) (>90%), nasopharygeal carcinoma (71%) as well as in many other cancers. Several Stat3 regulated genes, such as Bcl-x and Mcl-1, play important roles in cancer progression. Despite a strong rationale for targeting Stat3 for the treatment of human cancers, current chemotherapeutic approaches have not yet incorporated this strategy. We propose a novel strategy to inhibit Stat3, which should be useful in the development of novel cancer therapeutic approaches.

Methods: To design a novel inhibitor of Stat3, we employed several procedures: (1) structure-based drug design and optimization based upon our newly established model of drug/Stat3 complex and a structure-activity relationship (SAR) between inhibitors and Stat3, (2) chemical synthesis,