β -STRAND MIMICRY AS THE BASIS FOR A

UNIVERSAL APPROACH TO PROTEASE

Inhibition

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Abstract

This thesis describes the design, preparation, and testing of a range of protease inhibitors. **Chapter One** introduces the concept of peptidomimetics, and discusses how proteases almost universally bind their ligands in a β -strand conformation. The idea of constraining a compound into a biologically active conformation by the introduction of a ring or bridge is discussed. The technique of ring closing metathesis as a strategy for macrocyclisation is introduced. The chapter also discusses calpain and HIV proteases and their structures and implications in human disease.

Chapter Two surveys the acyclic calpain inhibitors reported in the literature. A series of *N*-heterocyclic peptidic calpain inhibitors were docked *in silico* into an ovine m-calpain homology model using Glide, which revealed that compounds 2.60 - 2.67 all adopted a β -strand conformation upon binding. The modelling revealed low energy conformations of 2.60, 2.61 and 2.66 not in a β -strand geometry. The synthesis and testing of these inhibitors is described, with 2.63 displaying an IC₅₀ of 40 nM against m-calpain in an *in vitro* assay.

Chapter Three describes the design and synthesis of the β -strand mimic macrocycle 3.8, which was prepared using ring closing metathesis. The chapter also describes the design of a number of calpain and HIV protease inhibitors that incorporate 3.8. Each inhibitor is designed to bind and inhibit a specific protease target.

Chapter Four describes the synthesis and testing of a series of macrocyclic calpain and proteasome 20S inhibitors. The preparation of the aldehydes 3.9 and 3.10 by elaboration of the macrocycle 3.8 is described. As well, the preparation of 3.10 from the N-capped 4-fluorosulphonyl diene 4.4 is described. The most potent macrocycle in the series was 3.10, which displays an IC₅₀ against m-calpain of 2000 nM, and an IC₅₀ against the chymotrypsin like activity of proteasome 20S of 2 nM.

Chapter Five describes the synthesis of a series of building blocks, and their use in the attempted preparation of the potential HIV protease inhibitor 3.12a, as well as the successful preparation of the potential HIV protease inhibitors 3.11 and 3.12b. Preliminary studies testing the biological activity of compounds 3.11, 3.12b and 5.21 found that they displayed a percentage inhibition of HIV-1 subtype B protease of 86, 63, and 26%, respectively. The K_i of 3.11 against HIV-1 subtype B protease was also determined to be 62 nM. The activity of 3.11 against HIV-1 protease establishes that the common macrocyclic core 3.8 can be incorporated into inhibitors of both calpain, and HIV-1 protease.

Chapter Six describes the preparation of a key macrocycle by cross-metathesis. The preparation of **6.4** by cross-metathesis of the olefins **6.5** and **6.24** is described, as well as the elaboration of **6.4** to give the macrocycle **6.1**. A systematic study of the cross-metathesis of the olefins **6.5**, **6.6**, **6.23** and **6.24** is described. Their percentage conversion to **6.4** was calculated using high performance liquid chromatography analysis. The highest conversion to **6.4** was found to be 60%, from the cross metathesis of an equimolar mixture of **6.6** and **6.23**.

Chapter Seven describes a multi-gram synthesis of the potent macrocyclic calpain inhibitor **CAT0811**. The key step in the synthesis is the base induced macrocyclisation of the iodopeptide **7.10** to give **7.6**. The macrocycle **7.6** was also prepared by macrolactamisation of the pseudopeptide **7.9**. The synthesis was found to be scalable, affordable and efficient, and removes the need for Grubbs' 2nd generation catalyst (II).

Declaration and Published Works

This work contains no material which has been accepted for the award of any other degree or

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Abbreviations

18-crown-6 1,4,7,10,13,16-hexaoxacyclooctadecane

aq aqueous

AIDS Acquired Immunodeficiency Syndrome

Boc *tert*-butoxycarbonyl

br broad (spectroscopic)

calcd calculated

Cbz benzyloxycarbonyl

CM cross-metathesis

conc concentrated

Cy cyclohexyl

DCM dichloromethane

DDQ 2,3-dichloro-5,6-dicyano-1,4-benzoquinone

DIPEA N,N-diisopropylethylamine

DMF dimethylformamide

DMSO dimethyl sulphoxide

EDC 1-ethyl-3-(3-(dimethylamino)propyl)carbodiimide hydrochloride

equiv equivalent

ESI electrospray ionisation

Et ethyl

FTIR Fourier transform infrared

h hour(s)

HAART highly active antiretroviral therapy

HATU 2-(7-aza-1*H*-benzotriazol-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate

HIV Human Immunodeficiency Virus

HOAt 1-hydroxy-7-azabenzotriazole

HOBt 1-hydroxybenzotriazole

HPLC high-performance liquid chromatography

HRMS high-resolution mass spectrometry

iPA isopropylalcohol

IR infrared

lit. literature value

Me methyl

min minute(s)

mp melting point

Ms methylsulphonyl (mesyl)

MS mass spectrometry

m/z mass-to-charge ratio

NHC *N*-heterocyclic carbene

NMR nuclear magnetic resonance

PB 4-phenylbutyryl-

PDB Protein Data Bank

Ph phenyl

PI protease inhibitor(s)

ppm part(s) per million

Pr propyl

PTC phase transfer catalyst

PTSA p-toulenesulphonic acid

Py pyridine

quant quantitative

RCM ring closing metathesis

ROM ring-opening metathesis

ROMP ring-opening metathesis polymerisation

rt room temperature

SAR structure activity relationship

spec spectrometry

TBAB tetrabutylammonium bromide

TBAI tetrabutylammonium iodide

TCE 1,1,2-trichloroethane

TEA triethylamine

temp temperature

TFA trifluoroacetic acid

THF tetrahydrofuran

TLC thin layer chromatography

Ts para-toluenesulphonyl (tosyl)

UV ultraviolet

v/v volume per unit volume

w/w weight per unit weight