

## >>> biomolecular modelling

– from drug discovery to nanotechnology

### >>>market opportunity

Modern **pharmaceutical, food, materials** and **nanotechnology** industries increasingly rely on the rationalization and prediction of molecular structure, stability and function in order to optimize their products, reduce the time and cost of development and increase their success rate.

The methods of **molecular modelling** and **computer simulation** are ideally suited to provide a detailed structural and time-dependent account of the molecular mechanisms behind many physical, chemical and biological phenomena where experimental methods may offer limited insight.

Our research efforts are generally focused on increasing our understanding of the molecular forces that determine the stability and activity of **biomolecules**, the behaviour of polymeric **drug delivery systems**, and the specificity and strength of **drug-protein interactions**.

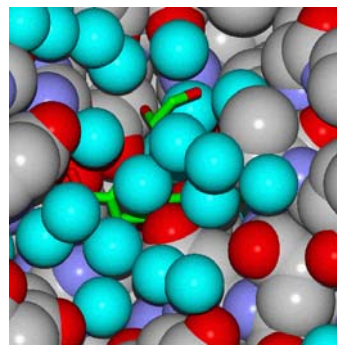
We aim to develop computational algorithms and methods in addition to using currently available software to accelerate programs of drug discovery and delivery. Our in house projects focus on diabetes, cancer and Alzheimer's disease. These developments and their outcomes have great potential for the generation of intellectual property of significant value to the pharmaceutical, biomaterials, nanotechnology and software industries.

### >>> project description

The **Biomolecular Modelling Group (BMMG)** has interests in various areas of research:

- The effect of the solvent and added co-solutes on the solvation forces that dictate the hydrophobic effect, protein stability and **denaturation**, and the stability and properties of **micelles** and **biomembranes**
- The molecular mechanisms of solvent **cryoprotection** and the properties that determine whether a solvent in aqueous mixtures has this behaviour at low temperatures

- The penetration of water into **nanoparticle drug delivery systems**, the mechanism of drug loading and delivery and the influence of polymer composition, pH and ionic strength.
- The implementation of new computational methods to account for the various effects of aqueous solvation in **structure-based drug design**



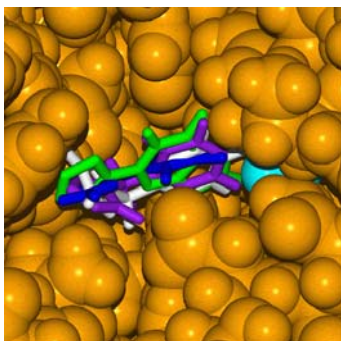
*The crystal structure of a protein of therapeutic interest may reveal the existence of multiple water molecules in the binding site.*

- The rationalisation and prediction of local and large conformational changes in proteins and their effects on the specificity and strength of **drug-protein** and **protein-protein interactions**
- The development, implementation and validation of algorithms for the analysis and classification of the interaction properties of ligand and protein binding sites in proteins
- The application of some of the above methods to a number of protein targets for the **discovery of new drugs** against diseases such as diabetes and cancer.
- The use of proven scaffolds that repeatedly appear in known drugs in **rapid drug discovery** programs to accelerate the identification and optimisation of drug leads for a number of pharmaceutically-important targets.

### >>>capabilities in drug discovery

In terms of our experience and computational resources we possess skills in a wide range of methodologies that are routinely used in connection with various drug discovery programs:

- Protein modelling and simulation
- Small molecule modelling
- Quantum chemical methods
- Structure-based drug design
- Ligand-based drug design
- Ligand-protein docking
- Virtual screening
- ADMET prediction



*The binding of drug molecules to a receptor protein can be predicted using computer methods*

We have broad experience in the use of both academic and commercial software to carry out the above. In addition, our links with the Department of Applied Chemistry and the School of Pharmacy gives us the advantage of having “in-house” medicinal chemistry and drug delivery capabilities.

### >>>capabilities in computer modelling

Our skills in biomolecular modelling and computer simulations are wide ranging:

- Molecular dynamics and Monte Carlo methods
- Forcefield energy calculations
- Free energy methods
- Search and optimisation methods
- Mesoscale modelling
- Computer programming

The Biomolecular Modelling Group has access to various computational resources, including state and national high performance facilities at the Western Australian Interactive Virtual Environments Centre (IVEC) and the Australian Partnerships for Advanced Computing (APAC).

### >>>intellectual property

Our research utilises state-of-the-art computational methods to investigate the hydrophobic effect, micelle-forming molecules, solvation phenomena in protein

denaturation, cryoprotection, drug-receptor binding and drug delivery in nanoparticle systems. Our ultimate goal is to achieve the improved design of micelles, biomembranes, polymers, nanoparticles and drugs. These are highly advanced technological products which can build on Australia’s internationally-recognised drug discovery, bio- and nanotechnology industries.

By providing innovative competitive advantages to the above-mentioned knowledge-based industries we aim to create intellectual property that can lead to the early adoption of technologies in Australia and worldwide.

### >>>progress

We have been conducting and publishing substantial research into the molecular mechanisms of hydrophobic interactions and salting out effects, the solvation properties of non-aqueous solvents, ligand-protein docking, protein-protein interactions, protein flexibility, the role of hydration in drug design, the characterisation of ligand binding sites and the development of rapid drug discovery methods.

In the area of drug discovery, we have contributed to efforts aimed at developing insulin mimetics and p53 inhibitors for the treatment of diabetes and cancer, respectively.

### >>>investment

BMMG is currently seeking partners and investors to assist in the development of cutting edge methods and their applications for drug discovery and delivery, biotechnology and nanotechnology.

### >>>further information

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