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| **\*Title of studentship** | Computational modelling of viral proteins for improved prediction of virus-host pairs |
| **Value / what is covered?** | Fully funded    100% of UK/EU tuition fees paid and an annual stipend for UK residents only (living expenses), currently at **£15,285** |
| **Awarding body** |  |
| **Number of studentships** | 1 |
| **\*Summary descriptive text / Example of research project** | This is a challenging but exciting opportunity for a motivated PhD candidate to contribute to the development and evaluation of novel approaches for host-virus (incl. phages) prediction. Quick and reliable methods of viral proteins modelling and identification of their potential targets are required to obtain better mechanistic understanding of the receptor recognition and binding processes associated with virus infection and therefore would be of significant benefit to studies of viral biology, ecology and evolution and treatment development. Several methods of viral host prediction have been proposed and developed over years, but the majority of them are based on the use of genomic information. With the recent advancements in protein structure prediction tools (e.g. Alphafold 2), it is becoming possible to incorporate structural information into the algorithms for prediction of host-virus pairs. |
| **\*Supervisor(s)** | Dr Timofey Skvortsov |
| **\*Eligibility / residence Status** |  |
| **Country** | Northern Ireland |
| **\*Start date and duration** | 1 March 2022, 3-4 years |
| **\*Faculty** | MHLS |
| **\*Research centre / School** | Pharmacy |
| **Subject area** | Structural protein biology, protein modelling, bacteriophage biology, computational biology, molecular biology, virology |
| **Candidate requirements / Key skills required for the post** | Applicants should have a 1st or 2.1 honours degree (or equivalent) in a relevant subject; strong scientific computing skills are essential. Relevant subjects include Protein Modelling, Computational Biology, Bioinformatics, Machine Learning, or a closely related discipline. Students who have a 2.2 honours degree and a Master’s degree may also be considered, but the School reserves the right to shortlist for interview only those applicants who have demonstrated high academic attainment to date |
| **\*Deadline for applications** | March/April 2022 |
| **\*How to apply / contacts** | Postgraduate Research applicants must have applied to Queen’s, via the Direct Applications Portal.  <https://dap.qub.ac.uk/portal/user/u_login.php> |
| **Relevant links / more information** | <http://www.qub.ac.uk/schools/SchoolofPharmacy/Research/PostgraduatePositions/>  <http://www.qub.ac.uk/schools/SchoolofPharmacy/Research/> |
| **Keywords for search filters** | Bacteriophage, virus, protein modelling, receptor, Alphafold, Rosettafold, host prediction, bioinformatics, computational biology |
| **Training provided through the research project** | The proposed project is focussed on modelling and analysis of bacteriophage proteins. The successful candidate will have an opportunity to develop their skills in programming, microbial bioinformatics and computational protein structural analysis. |
| **Expected impact activities** | This PhD project will help to improve the methods of viral (incl. phages) host prediction. During the work on the project, the PhD student will be encouraged to engage in a variety of impact activities, disseminate the research project findings through publications in relevant peer-reviewed journals, present the results of the study at conferences (in-person and/or online), and make them accessible to general public through broader channels, such as social media and popular science outlets. |