


Curriculum Vitae

A. Basic Information

NAME (EMAIL)	POSITION	BIRTH	
Chung-Chau, HON chungchau.hon@riken.jp	Team Leader, Division of Genomic Technology, RIKEN, Center for Life Science Technologies, Yokohama, Japan	Male, Age: 38 , Hong Kong	
		PROFILE http://bit.ly/2nC9dQB	

EDUCATION

Institution (Location)	Degree / Position	Year	Subject
The University of Hong Kong (Hong Kong)	Bachelor of Science	1998-2001	Molecular Biotechnology, General Bioinformatics Supervisor: Prof. Frederick Chi-Ching Leung fcleung@hkucc.hku.hk
The University of Hong Kong (Hong Kong)	Master of Philosophy	2001-2003	Molecular Virology Supervisor: Prof. Frederick Chi-Ching Leung fcleung@hkucc.hku.hk
IBM Computational Biology Center (New York, USA)	PhD Internship	2005	Massively parallel molecular dynamics simulations Supervisor: Dr. Ruhong Zhou ruhongz@us.ibm.com
The University of Hong Kong (Hong Kong)	Doctor of Philosophy	2003-2008	Population Genetics of Viruses Supervisor: Prof. Frederick Chi-Ching Leung fcleung@hkucc.hku.hk

RESEARCH EXPERIENCES [Institutions] [Number of Publications]

• Genomics and Transcriptomics

- Mammalian transcriptomes (human and mouse) [RIKEN] [3]
- Unicellular parasite transcriptomes (*Entamoeba*, *Plasmodium*, *Trypanosome* etc) [Institute of Pasteur] [16]
- Evolution and functions of long non-coding RNAs [RIKEN] [1]
- Human diseases variants in non-coding genomic regions [RIKEN] [1]
- Gene model annotations and transcriptome assembly [RIKEN, Institute of Pasteur] [4]
- Synteny and orthology of gene families [Institute of Pasteur] [1]
- Mapping of transcription start sites and polyadenylation sites [RIKEN, Institute of Pasteur] [2]

• Viral Phylogenetics and Population Genetics

- Evolution of influenza viruses, birnaviruses and coronaviruses etc [The University of Hong Kong] [10]
- Molecular clock, selection pressure and coalescent analyses [The University of Hong Kong] [8]
- Large scale phylogeny reconstruction and molecular epidemiology [The University of Hong Kong] [6]
- Recombination and reassortment of RNA viruses [The University of Hong Kong] [4]

• Molecular Virology and Immunology

- Viral receptors of coronaviruses and birnaviruses [The University of Hong Kong] [3]
- Viral apoptosis of coronaviruses and birnaviruses [The University of Hong Kong] [3]
- DNA vaccines against coronaviruses and birnaviruses [The University of Hong Kong] [1]
- Diagnosis for coronaviruses [The University of Hong Kong] [2]

• Massively Parallel Molecular Dynamics Simulations

- Simulations of lysozyme unfolding [IBM Computational Biology Center] [1]

B. Postdoctoral Employment

I. Research Scientist

Genome Information Analysis Team, Division of Genomic Technology,
RIKEN Center for Life Science Technologies (Yokohama, Japan)

2014-2017

- **Topic:** long non-coding RNA
- **Supervisor:** Dr Alistair Forrest; email: forrest@gsc.riken.jp

II. Senior Postdoctoral Fellow

Cellular Biology of Parasitism Unit & Transcriptome and Epigenome Platform of Genopole
Institute of Pasteur (Paris)

2011-2014

- **Topic:** Application of Next Generation Sequencing on Comparative genomics and Transcriptomics of *Entamoeba*;
- **Supervisor:** Dr Nancy Guillen; email: nguillen@pasteur.fr

III. Postdoctoral Fellow

Cellular Biology of Parasitism Unit,
Institute of Pasteur (Paris)

2008-2011

- **Topic:** Genomics of *Entamoeba*;
- **Supervisor:** Dr Nancy Guillen; email: nguillen@pasteur.fr

C. Competitive External Funds

I. Agence Nationale Recherche Genomic Grant 2010

2010-2013

- **Title:** Understating the Pathogenicity of *Entamoeba* Using Comparative Transcriptomics and Phylogenomics
- **Amount:** €641,744 (US\$869,258), in total for 3 years;
- **Role:** Proposal writing, project management, corresponding author, high throughput sequencing data analysis

D. Expertise

Levels: **+++ Proficient**; **++ Intermediate**; **+ Amateur**;

I. Bioinformatics

- High-throughput sequencing data processing, e.g. quality control, mapping (**+++**)
- Analyses of RNA-Seq, ChIP-Seq, CAGE and small RNA-Seq data (**+++**)
- Custom assembly and annotation of transcriptomes (**+++**)
- Gene expression analyses, e.g. differential expression, co-expression network (**+++**)
- Analyses of *cis*-regulatory element, e.g. motif discovery, promoter/enhancer correlation (**+++**)
- Identification and annotation of non-coding RNAs (**+++**)
- System biology, e.g. gene set enrichment, gene regulatory network (**+++**)
- Molecular clock and coalescent analyses (**+++**)
- Large scale phylogeny reconstruction (**+++**)
- Single cell RNA-Seq, e.g. cell type clustering, trajectory inference (**++**)
- Analyses of orthologous and syntenic genes (**++**)

II. Molecular Biology

- Molecular cloning, e.g. expression vector construction (**+++**)
- Molecular diagnosis, e.g. PCR, ELISA (**+++**)
- Mammalian cell culture manipulations, e.g. transfection (**++**)
- Animal handling, e.g. injection, tail bleeding (**++**)

III. Programming

- Perl scripting (**+++**)
- Unix system maintenance (**+++**)
- R scripting (**++**)
- Shell scripting (**++**)
- Python scripting (**+**)

D. Publications (by topics, in chronological order)

I. On Genomics and Transcriptomics

1. **Hon, C.C.**, Ramilowski, J.A., Harshbarger, J., Bertin N., Rackham, O.J., Gough, J., Denisenko, E., Schmeier, S., Poulsen, T.M., Severin, J., Lizio, M., Kawaji, H., Kasukawa, T., Itoh, M., Burroughs, A.M., Noma, S., Djebali, S., Alam, T., Medvedeva, Y.A., Testa, A.C., Lipovich, L., Yip, C.W., Abugessaisa, I., Mendez, M., Hasegawa, A., Tang, D., Lassmann, T., Heutink, P., Babina, M., Wells, C.A., Kojima, S., Nakamura, Y., Suzuki, H., Daub, C.O., de Hoon M.J., Arner, E., Hayashizaki, Y., Carninci, P., Forrest, A.R.
An atlas of human long non-coding RNAs with accurate 5' ends.
Nature (2017) <https://doi.org/10.1038/nature21374>
2. **Hon, C.C.**, Shin, J.W., Carninci, P. and Stubbington, J.T.M.
The Human Cell Atlas: Technical challenges and opportunities.
Briefings in functional genomics (2017) <https://doi.org/10.1093/bfpg/elx029>
3. Rie, D., Abugessaisa, I., Alam, T., Arner, E., Arner, P., Ashoor, H., Åström, G., Babina, M., Bertin, N., Burroughs, M., Daub, C.O., Detmar, M., Deviatiiarov, R., Fort, A., Gebhard, C., Goldowitz, D., Guhl, S., Harshbarger, J., Hasegawa, A., Hashimoto, K., Heutink, P., **Hon, C.C.**, Huang, E., Ishizu, Y., Kasukawa, T., Klinken, P., Lassmann, T., Lecellier, C., Lee, W., Lizio, M., Makeev, V., Mathelier, A., Medvedeva, Y., Mungall, C., Noma, S., Ohshima, M., Persson, H., Roudnický, F., Sætrom, P., Severin, J., W.Shin, J., Tarui, H., Vitting-Seerup, K., Winteringham, L., Yamaguchi, Y., Yasuzawa, K., Wells, C., Summers, K.M., Kawaji, H., Sandelin, A., Rehli, M., consortium, t. FANTOM, Hayashizaki, Y., Carninci, P., Forrest, A.R.R., Hoon, M.J.L. de
The FANTOM5 integrated expression atlas of miRNAs and their promoters.
Nature Biotechnology (2017) <https://doi.org/10.1038/nbt.3947>
4. Weber, C., Koutero, M., Dillies, M.-A., Varet, H., Lopez-Camarillo, C., Coppée, J.Y., **Hon, C.C.**, Guillén, N.
Extensive transcriptome analysis correlates the plasticity of *Entamoeba histolytica* pathogenesis to rapid phenotype changes depending on the environment.
Scientific reports (2016) <https://doi.org/10.1038/srep35852>
5. Gonzalez-Hilarion S, Paulet, D., Lee, K.T., **Hon, C.C.**, Lechat P., Mogensen E, Moyrand F, Proux C, Barboux R, Bussotti G, Hwang J, Coppée JY, Bahn YS, Janbon G.
Intron retention-dependent gene regulation in *Cryptococcus neoformans*.
Scientific reports (2016) <https://doi.org/10.1038/srep32252>
6. Zhang, Q., Siegel, T.N., Martins, R.M., Wang, F., Cao, J., Gao, Q., Cheng, X., Jiang, L., **Hon, C.C.**, Scheidig-Benatar, C., Sakamoto H., Turner L., Jensen A. T. R., Claes A., Guizzetti J, Malmquist N.A, and Scherf A.
Exonuclease-mediated degradation of nascent RNA silences genes linked to severe malaria.
Nature (2014) <https://doi.org/10.1038/nature13468>
7. Hernández-Cuevas, N.A, Weber C, **Hon, C.C.**, Guillen N.
Gene expression profiling in *Entamoeba histolytica* identifies key components in iron uptake and metabolism.
PLoS ONE (2014) <https://doi.org/10.1371/journal.pone.0107102>
8. Reynolds, D., Cliffe, L., Förstner, K., **Hon, C.C.**, Siegel, T and Sabatini, R.
Regulation of Transcription Termination by Glucosylated Hydroxymethyluracil, Base J, in *Leishmania major* and *Trypanosoma brucei*.
Nucleic Acids Research (2014) <https://doi.org/10.1093/nar/gku714>
9. **Hon, C.C.**, Weber, C., Sismeiro, O., Proux, C., Koutero, M., Deloger, M., Das, S., Agrahari, M., Dillies, M.-A., Jagla, B., Coppee, J.Y., Bhattacharya, A. and Guillen, N.
Quantification of stochastic noise of splicing and polyadenylation in *Entamoeba histolytica*.
Nucleic Acids Research (2012) <https://doi.org/10.1093/nar/gks1271>
10. Vasquez, J.-J., **Hon, C.C.**, Vanselow J.T., Schlosser A. and Siegel, T.N.
Comparative ribosome-profiling reveals extensive translational complexity in different *Trypanosoma brucei* life-cycle stages.
Nucleic Acids Research (2013) <https://doi.org/10.1093/nar/gkt1386k>
11. Thibeaux, R., Weber, C., **Hon, C.C.**, Dillies, M.-A., Copee, J.Y., Labruye, E. and Guillen, N.
Identification of the virulence landscape essential for *Entamoeba histolytica* invasion of the human colon.
PLoS Pathogens (2013) <https://doi.org/10.1371/journal.ppat.1003824>
12. Njoya, E.M., Weber, C., Hernandez-Cuevas, N.A., **Hon, C.C.**, Janin, Y, Kamini, M.G, Moundipa, P.F and Guillén, N.
Bioassay-guided fractionation of extracts from *Codiaeum variegatum* against *Entamoeba histolytica* discovers compounds that modify expression of ceramide biosynthesis related genes.
PLoS Neglected Tropical Diseases (2013) <https://doi.org/10.1371/journal.pntd.0002607>
13. **Hon, C.C.**, Weber, C., Koutero, M., Coppée, J.-Y., Deloger, M and Guillen, N.
Surveying *Entamoeba histolytica* transcriptome using massively parallel cDNA sequencing.
In '**Amebiasis: Biology and Pathogenesis of Entamoeba**' (2015) https://doi.org/10.1007/978-4-431-55200-0_7

14. Janbon, G., Ormerod, K. L., Paulet, D., Byrnes, E., Chatterjee, G., Yadav, V., **Hon, C.C.**, A., Cuomo, C. A., Dietrich, F. S., Billmyre, Brunel, F., Bahn Y.-S., Chen, W., Chen, Y., Chow E. W. L., Coppée, J.Y., Floyd-Averette, A., Gaillardin C., Gerik, K. J., Goebels, C., Goldberg, J., Gonzalez-Hilarion S., Gujja, S., Hamlin, J. L., Hsueh, Y.-P., Ianiri, G., Jones, S., Kodira, C. D., Lam, W., Marra, M., Mesner, L. D., Mieczkowski, P.A., Moyrand, F., Nielsen, K., Proux, C., Rossignol, T., Scheinl, J. E., Sun, S., Wood, I. A., Zeng, Q., Neuvéglise, C., Newlon, C. S., Perfect, J. R., Lodge, J. K., Idnurm, A., Stajich, J. E., Kronstad, J. W., Sanya, K., Heitman, J., Fraser, J., Cuomo C. A. and Dietrich F.
The genome sequence of *Cryptococcus neoformans* var. *grubii* reveals complex mechanisms of RNA expression and virulence plasticity.
PLoS Genetics (2013) <https://doi.org/10.1371/journal.pgen.1004261>
15. Siegel, N, **Hon, C.C.**, Zhang, Q., Lopez-Rubio, J.J., Coppée, J.-Y., Sismeiro, O and Scherf, A.
Strand-specific RNA-Seq reveals widespread and developmentally regulated transcription of natural antisense transcripts in *Plasmodium falciparum*.
BMC Genomics (2014) <https://doi.org/10.1186/1471-2164-15-150>
16. Santi-Rocca, J., Smith, S., Weber, C., Pineda, E., **Hon, C.C.**, Saavedra, E., Olivos-García, A., Rousseau, S., Dillies, M.-A., Coppée, J.-Y. and Guillén, N
Endoplasmic reticulum stress-sensing mechanism is activated in *Entamoeba histolytica* upon treatment with nitric oxide
PLoS ONE (2012) <http://dx.doi.org/10.1371/journal.pone.0031777>
17. Marquay Markiewicz, J., Syan, S., **Hon, C.C.**, Weber, C., Faust, D. and Guillen, N.
A proteomic and cellular analysis of uropods in the pathogen *Entamoeba histolytica*.
PLoS Neglected Tropical Diseases (2011) <https://doi.org/10.1371/journal.pntd.0001002>
18. **Hon, C.C.**, Nakada-Tsukui, K., Nozaki, T. and Guillen, N.
Dissecting the actin cytoskeleton of *Entamoeba histolytica* from a genomic perspective.
In '**Anaerobic Parasitic Protozoa: Genomics and Molecular Biology**' <https://books.google.com.hk/books?isbn=1904455611>
19. Yeung, Y.S., Yip, C.W., **Hon, C.C.**, Chow, K.Y.C., Ma, I.C.M., Zeng, F. and Leung, F.C.C.
Transcriptional profiling of Vero E6 cells over-expressing SARS-CoV S2 subunit: insights on viral regulation of apoptosis and proliferation.
Virology (2008) <http://dx.doi.org/10.1016/j.virol.2007.09.016>
20. Wang, Y., Zeng, F., **Hon, C.C.**, Zhang, Y. and Leung, F.C.C.
The mitochondrial genome of the *Basidiomycete* fungus *Pleurotus ostreatus* (oyster mushroom).
FEMS Microbiol Letter (2008) <https://doi.org/10.1111/j.1574-6968.2007.01048.x>
21. Wong, R.T.-Y., **Hon, C.C.**, Zeng, F. and Leung, F.C.C.
Screening of differentially expressed transcripts in infectious bursal disease virus-induced apoptotic chicken embryonic fibroblasts by using cDNA microarrays.
J General Virology (2007) <https://doi.org/10.1099/vir.0.82619-0>
22. Zeng, F., **Hon, C.C.**, Sit, W.-H., Chow, K.Y.-C., Hui, R.K.-H., Law, I.K.-M., Ng, V.W.-L., Yang, X.-T., Leung, F.C.C. and Wan, J.M.-F.
Molecular characterization of *Coriolus versicolor* PSP-induced apoptosis in human promyelotic leukemic HL-60 cells using cDNA microarray.
International Journal Oncology (2005) <https://doi.org/10.3892/ijo.27.2.513>
23. Cheung, K.H., **Hon, C.C.**, and Leung, F.C.C.
Illustration of Enhanced Features of Visual Genome Explorer Beta 2.1 by Comparative Analysis of *Helicobacter pylori* Strains 26695 and J99 Genomes.
In '**Biocomputing: Computer Tools for Biologists**' (2003) <http://www.sigmaaldrich.com/catalog/product/sigma/z703559>
24. **Hon, C.C.**, Chow, Y.C., Zeng, F.Y. and Leung, F.C.C.
Genetic authentication of ginseng and other traditional Chinese medicine.
Acta Pharmacologica Sinica (2003) <https://www.ncbi.nlm.nih.gov/pubmed/12956929>

II. On Viral Phylogenetics and Population Genetics

25. Lam, T.T.-Y., Chong, Y.L., Shi, M., **Hon, C.C.**, Li, J., Martin, D.P., Tang, J.W.-T., Mok, C.-K., Shih, S.-R., Yip, C.W., Jiang, J., Hui, R.K., Pybus, O.G., Holmes, E.C., and Leung, F.C.C.
Systematic phylogenetic analysis of influenza A virus reveals many novel mosaic genome segments.
Infection, Genetics and Evolution (2013) <https://doi.org/10.1016/j.meegid.2013.03.015>
26. Lam, T.T.-Y., **Hon, C.C.**, Lemey, P., Pybus, O.G., Shi, M., Tun, H.M., Li, J., Jiang, J., Holmes, E.C. and Leung, F.C.C.
Phylogenetics of H5N1 avian influenza virus in Indonesia.
Molecular Ecology (2012) <https://doi.org/10.1111/j.1365-294X.2012.05577.x>

27. Shi,M., Lam,T.T.-Y., **Hon, C.C.**, Hui,R.K.-H., Faaberg,K.S., Wennblom,T., Murtaugh,M.P., Stadejek,T. and Leung,F.C.C.
Molecular epidemiology of PRRSV: a phylogenetic perspective.
Virus Research (2010) <https://doi.org/10.1016/j.virusres.2010.08.014>
28. Li,Y., Ge,X., **Hon, C.C.**, Zhang,H., Zhou,P., Zhang,Y., Wu,Y., Wang,L.-F. and Shi,Z.
Prevalence and genetic diversity of adeno-associated viruses in bats from China.
Journal of General Virology (2010) <https://doi.org/10.1099/vir.0.020032-0>
29. Shi,M., Lam,T.T.-Y., **Hon, C.C.**, Murtaugh,M.P., Davies,P.R., Hui,R.K.-H., Li,J., Wong,L.T.-W., Yip,C.W., Jiang,J.-W., and Leung,F.C.C.
Phylogeny-based evolutionary, demographical, and geographical dissection of North American type 2 porcine reproductive and respiratory syndrome viruses.
Journal of Virology (2010) <https://doi.org/10.1128/JVI.02551-09>
30. Yuan,J., **Hon, C.C.**, Li,Y., Wang,D., Xu,G., Zhang,H., Zhou,P., Poon,L.L.M., Lam,T.T.-Y., Leung,F.C.C., and Shi,Z
Intraspecies diversity of SARS-like coronaviruses in *Rhinolophus sinicus* and its implications for the origin of SARS coronaviruses in humans.
Journal of Virology (2010) <https://doi.org/10.1099/vir.0.016378-0>
31. Lam,T.T.-Y., **Hon, C.C.**, and Tang,J.W.
Use of phylogenetics in the molecular epidemiology and evolutionary studies of viral infections.
Critical Reviews in Clinical Laboratory Sciences (2010) <https://doi.org/10.3109/10408361003633318>
32. Yip,C.W., **Hon, C.C.**, Shi,M., Lam,T.T.-Y., Chow,K.Y.-C., Zeng,F. and Leung,F.C.C.
Phylogenetic perspectives on the epidemiology and origins of SARS and SARS-like coronaviruses.
Infection, Genetics and Evolution (2009) <https://doi.org/10.1016/j.meegid.2009.09.015>
33. **Hon, C.C.**, Lam,T.T.-Y., Yip,C.W., Wong,R.T.-Y., Shi,M., Jiang,J., Zeng,F. and Leung,F.C.C.
Phylogenetic evidence for homologous recombination within the family *Birnaviridae*.
Journal of General Virology (2008) <https://doi.org/10.1099/vir.0.2008/004101-0>
34. **Hon, C.C.**, Lam,T.-Y., Shi,Z.-L., Drummond,A.J., Yip,C.W., Zeng,F., Lam,P.-Y. and Leung,F.C.C.
Evidence of the recombinant origin of a bat severe acute respiratory syndrome (SARS)-like coronavirus and its implications on the direct ancestor of SARS coronavirus.
Journal of Virology (2008) <https://doi.org/10.1128/JVI.01926-07>
35. Lam,T.-Y., **Hon, C.C.**, Wang,Z., Hui,R.K.-H., Zeng,F. and Leung,F.C.C.
Evolutionary analyses of European H1N2 swine influenza A virus by placing timestamps on the multiple reassortment events.
Virus Research (2008) <https://doi.org/10.1016/j.virusres.2007.08.012>
36. Lam,T.T.-Y., **Hon, C.C.**, Lam,P.-Y., Yip,C.W., Zeng,F. and Leung,F.C.C.
Comments to the predecessor of human SARS coronavirus in 2003-2004 epidemic.
Veterinary Microbiology (2008) <https://doi.org/10.1016/j.vetmic.2007.08.014>
37. Lam,T.T.-Y., **Hon, C.C.**, Pybus,O.G., Kosakovsky Pong,S.L., Wong,R.T.-Y., Yip,C.W., Zeng,F. and Leung,F.C.C.
Evolutionary and transmission dynamics of reassortant H5N1 influenza virus in Indonesia.
PLoS Pathogen (2008) <https://doi.org/http://dx.doi.org/10.1371/journal.ppat.1000130>
38. Ma,C.M., **Hon, C.C.**, Lam,T.-Y., Li,V.Y.-Y., Wong,C.K.-W., de Oliveira,T. and Leung,F.C.C.
Evidence for recombination in natural populations of porcine circovirus type 2 in Hong Kong and mainland China.
Journal of General Virology (2007) <https://doi.org/10.1099/vir.0.82629-0>
39. **Hon, C.C.**, Lam,T.-Y., Drummond,A., Rambaut,A., Lee,Y.-F., Yip,C.W., Zeng,F., Lam,P.-Y., Ng,P.T.W. and Leung,F.C.C.
Phylogenetic analysis reveals a correlation between the expansion of very virulent infectious bursal disease virus and reassortment of its genome segment B.
Journal of Virology (2006) <https://doi.org/10.1128/JVI.00585-06>
40. Guan,Y., Peiris,J.S.M., Zheng,B., Poon,L.L.M., Chan,K.H., Zeng,F.Y., Chan,C.W.M., Chan,M.N., Chen,J.D., Chow,K.Y.C. **Hon, C.C.**, Hui, K.H., Li, J., Li, V.Y.Y., Wang, Y., Leung, S.W., Yuen, K.Y. and Leung F.C.
Molecular epidemiology of the novel coronavirus that causes severe acute respiratory syndrome.
Lancet (2004) [https://doi.org/http://dx.doi.org/10.1016/S0140-6736\(03\)15259-2](https://doi.org/http://dx.doi.org/10.1016/S0140-6736(03)15259-2)
41. Chow,K.Y.-C., **Hon, C.C.**, Hui,R.K.-H., Wong,R.T.-Y., Yip,C.W., Zeng,F. and Leung,F.C.C.
Molecular advances in severe acute respiratory syndrome-associated coronavirus (SARS-CoV).
Genomics Proteomics Bioinformatics (2003) [https://doi.org/10.1016/S1672-0229\(03\)01031-3](https://doi.org/10.1016/S1672-0229(03)01031-3)
42. Zeng,F.Y., Chan,C.W.M., Chan,M.N., Chen,J.D., Chow,K.Y.C., **Hon, C.C.**, Hui,K.H., Li,J., Li,V.Y.Y., Wang, C.Y. Hui, K.H., Li, J., Li, V.Y.Y., Wang, C.Y., Wang, P.Y., Guan, Y., Zheng, B., Poon, L.L.M., Chan, K.H., Yuen, K.Y., Peiris, J.S.M., and Leung F.C.
The complete genome sequence of severe acute respiratory syndrome coronavirus strain HKU-39849 (HK-39).
Experimental Biology and Medicine (2003) <https://doi.org/10.1177/15353702-0322807-13>

III. On Molecular Virology and Immunology

43. Li,K.K.B., Yip,C.W., **Hon, C.C.**, Lam,C.Y., Zeng,F. and Leung,F.C.C.
Characterisation of animal angiotensin-converting enzyme 2 receptors and use of pseudotyped virus to correlate receptor binding with susceptibility of SARS-CoV infection.
Hong Kong Medical Journal (2012) <https://www.ncbi.nlm.nih.gov/pubmed/22865222>
44. Yip,C.W., **Hon, C.C.**, Zeng,F. and Leung,F.C.C.
Cell culture-adapted IBDV uses endocytosis for entry in DF-1 chicken embryonic fibroblasts.
Virus Research (2012) <https://doi.org/10.1016/j.virusres.2011.12.016>
45. Chow,K.Y., Yeung,Y.S., **Hon, C.C.**, Zeng,F., Law,K.M. and Leung,F.C.
SARS coronavirus and apoptosis.
Hong Kong Medical Journal (2008) <https://www.ncbi.nlm.nih.gov/pubmed/18708667>
46. Yip,C.W., Yeung,Y.S., Ma,C.M., Lam,P.-Y., **Hon, C.C.**, Zeng,F. and Leung,F.C.C.
Demonstration of receptor binding properties of VP2 of very virulent strain infectious bursal disease virus on Vero cells.
Virus Research (2007) <https://doi.org/10.1016/j.virusres.2006.08.001>
47. Yip,C.W., **Hon, C.C.**, Zeng,F., Chow,K.Y.C., Chan,K.H., Peiris,J.S.M. and Leung,F.C.C.
Naturally occurring anti-*Escherichia coli* protein antibodies in the sera of healthy humans cause analytical interference in a recombinant nucleocapsid protein-based enzyme-linked immunosorbent assay for serodiagnosis of severe acute respiratory syndrome.
Clinical Vaccine Immunology (2007) <https://doi.org/10.1128/CVI.00136-06>
48. Zeng,F., **Hon, C.C.**, Yip,C.W., Law,K.M., Yeung,Y.S., Chan,K.H., Malik Peiris,J.S. and Leung,F.C.C.
Quantitative comparison of the efficiency of antibodies against S1 and S2 subunit of SARS coronavirus spike protein in virus neutralization and blocking of receptor binding: implications for the functional roles of S2 subunit.
FEBS Letters (2006) <https://doi.org/10.1016/j.febslet.2006.08.085>
49. Chow,K.Y.C., Yeung,Y.S., **Hon, C.C.**, Zeng,F., Law,K.M. and Leung,F.C.C.
Adenovirus-mediated expression of the C-terminal domain of SARS-CoV spike protein is sufficient to induce apoptosis in Vero E6 cells.
FEBS Letters (2005) <https://doi.org/10.1016/j.febslet.2005.10.065>
50. Yip,C.W., **Hon, C.C.**, Zeng,F., Chow,K.Y.C. and Leung,F.C.C.
Prevalence of non-pneumonic infections with SARS-correlated virus.
Lancet (2004) [https://doi.org/10.1016/S0140-6736\(04\)16311-3](https://doi.org/10.1016/S0140-6736(04)16311-3)
51. Zeng,F., Chow,K.Y.-C., **Hon, C.C.**, Law,K.M., Yip,C.W., Chan,K.H., Peiris,J.S.M. and Leung,F.C.C.
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