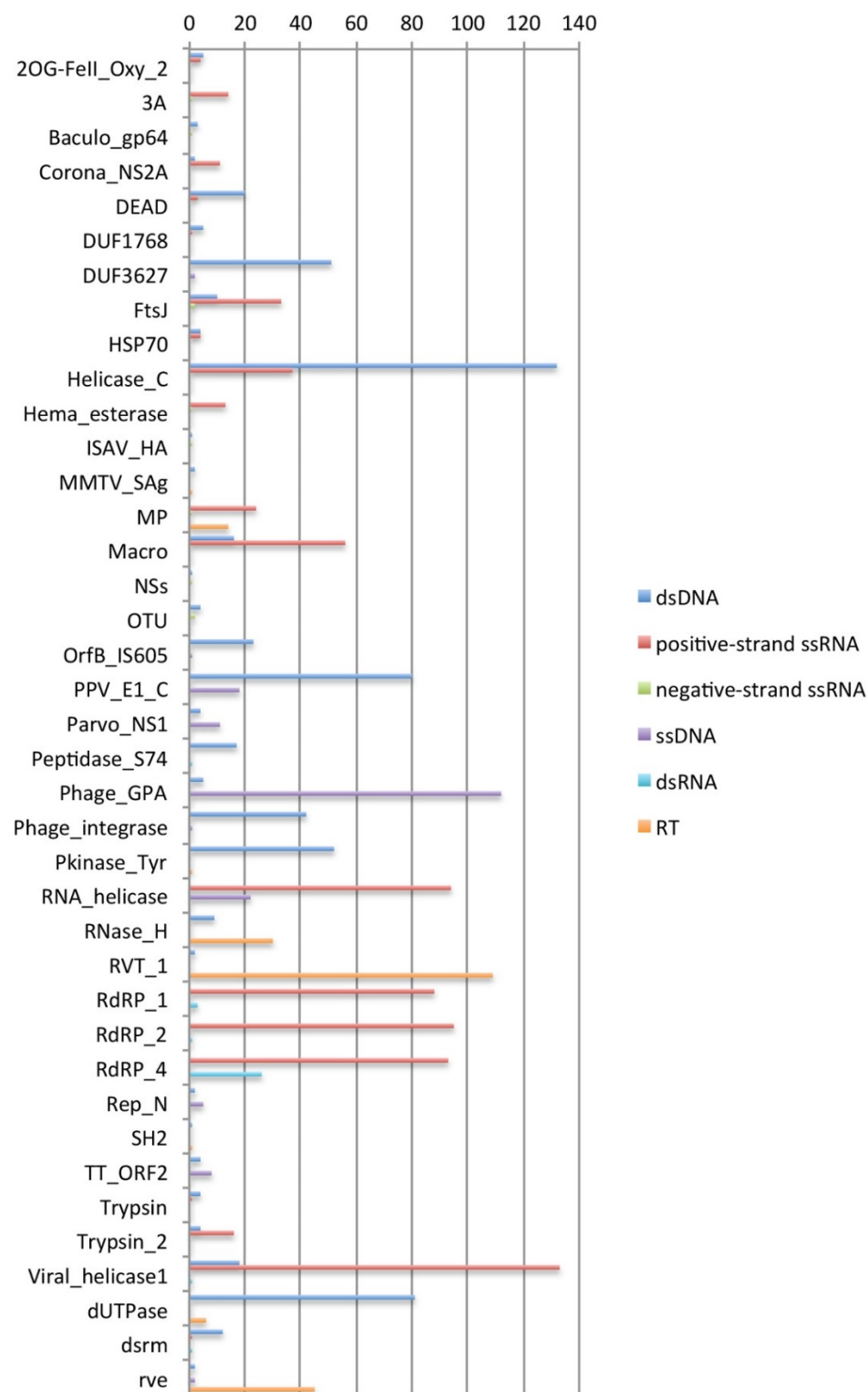


Sequence and Structure Analysis of Distantly-Related Viruses Reveals Extensive Gene Transfer between Viruses and Hosts and among Viruses



(A)

Figure S1. Cont.

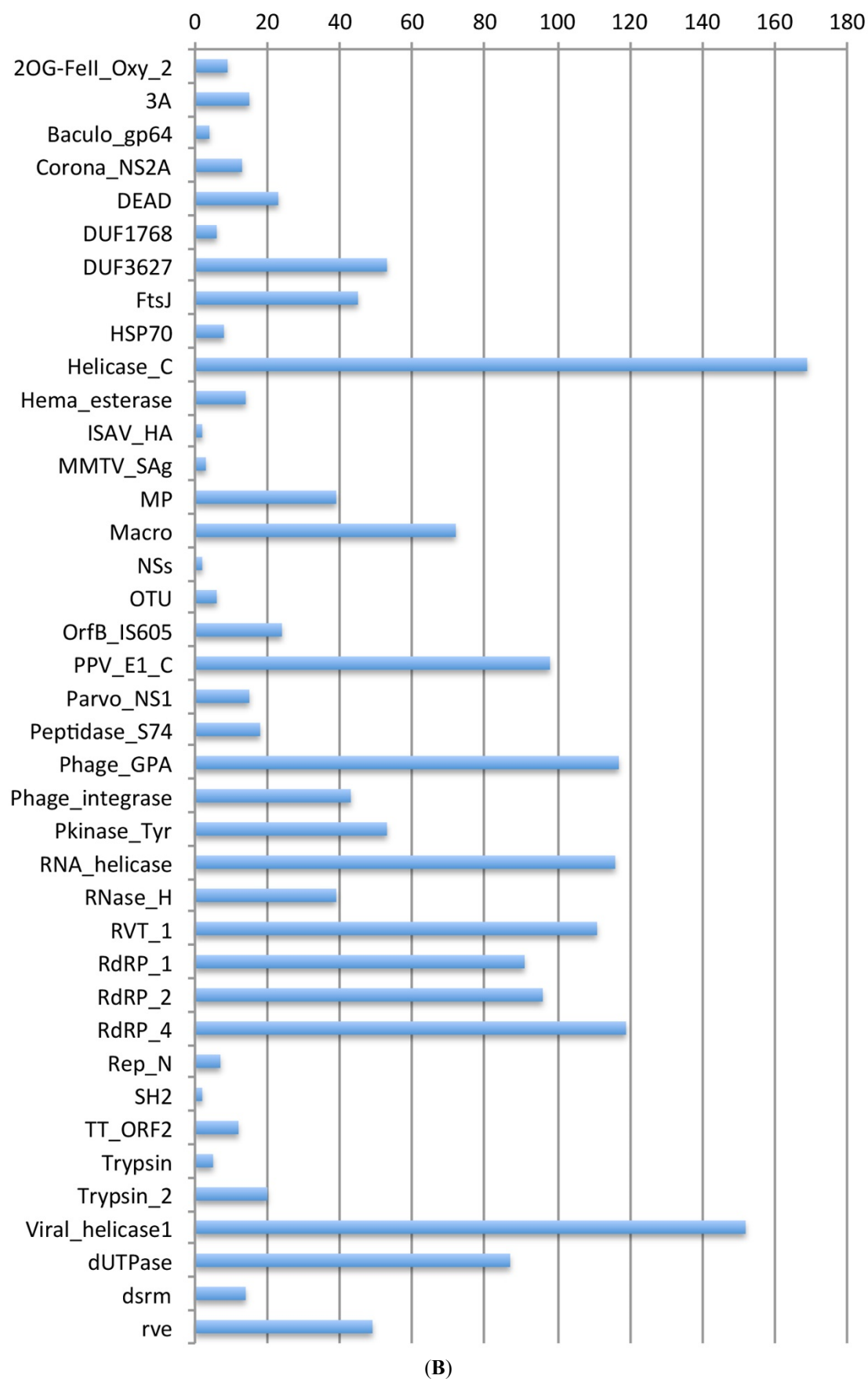


Figure S1. The distribution of proteins from viruses with different genome types (A), and the number of hits within viral reference proteome (B) of protein families identified in the HMMer [1] search.

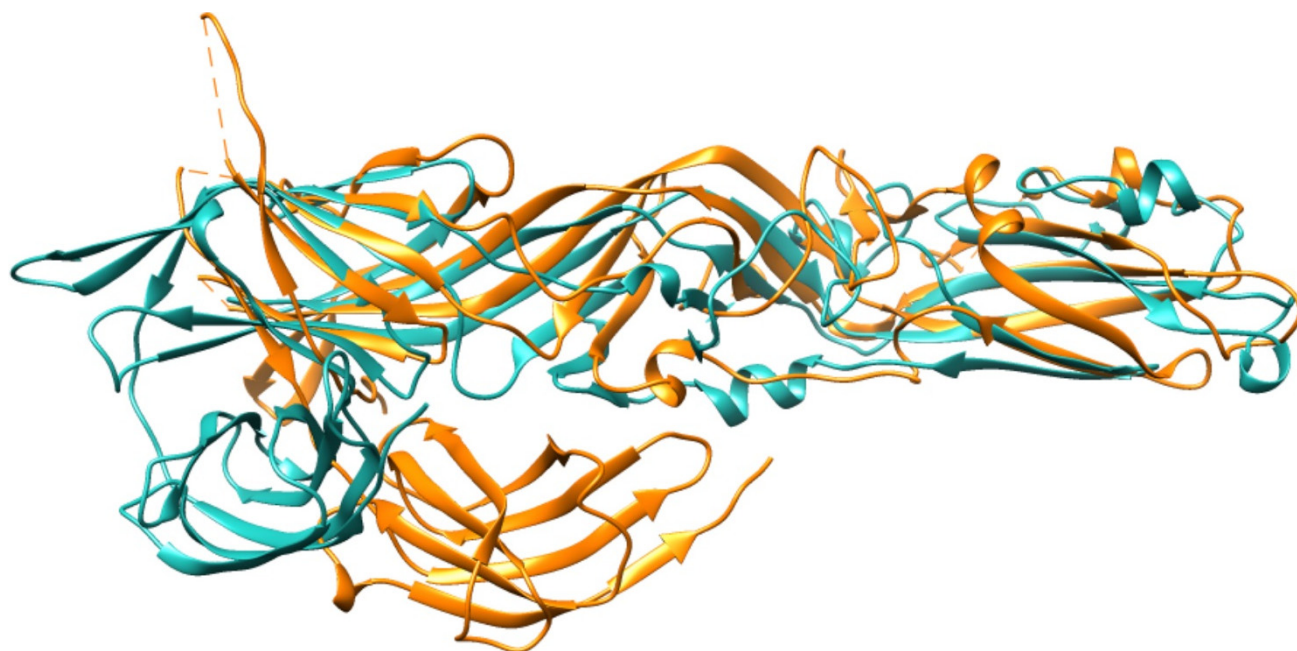


Figure S2. Structural superposition between the envelope glycoprotein of Rift Valley fever virus (4HJ1A, cyan) and EFF-1 of *Caenorhabditis elegans* (4OJDH, orange).

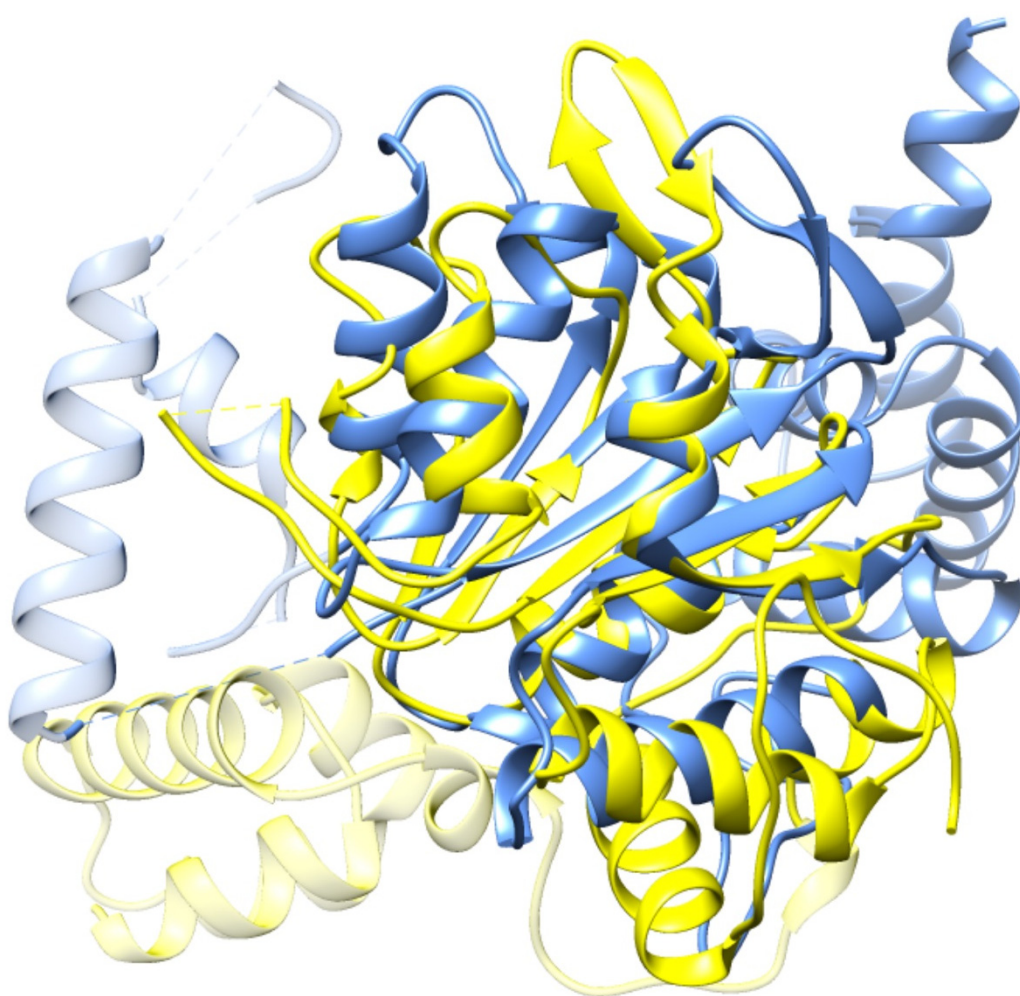


Figure S3. Structural superposition between the Adeno-associated virus-2 helicase (1U0JA, yellow) and the human Tip49b ATPase (3UK6E, light blue).

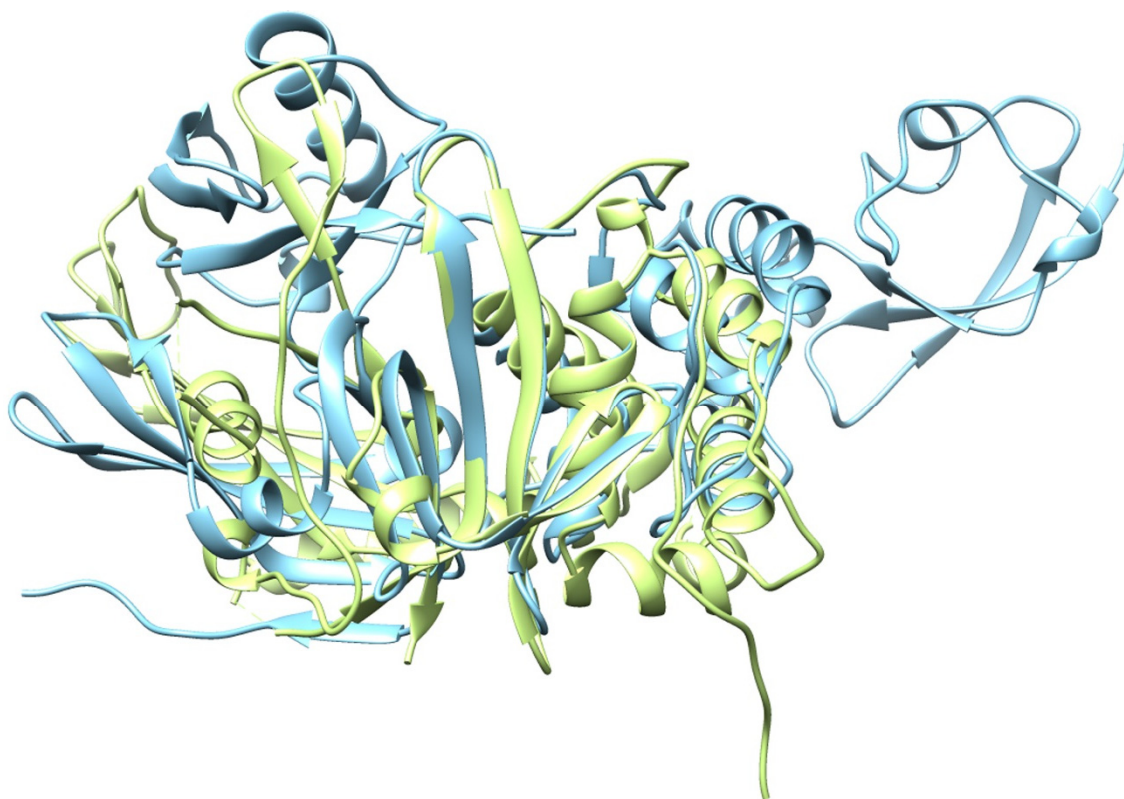


Figure S4. Structural superposition between the papain-like protease of SARS Coronavirus, positive-strand ssRNA (4M0WA, cyan) and the human ubiquitin carboxyl-terminal hydrolase 21 (2Y5BA, green).

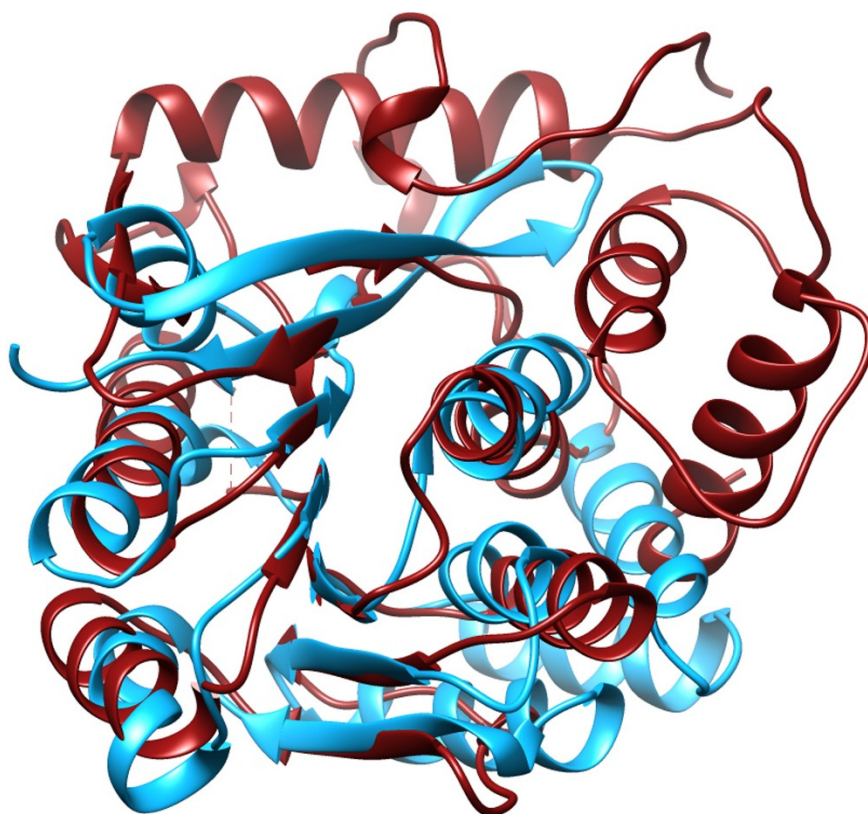


Figure S5. Structural superposition between VP39 of Vaccinia virus, dsDNA (3MAGA, dark red) and human catechol-O-methyltransferase (4PYIA, cyan).

Table S2. Pfam families comprising proteins from viruses with different genome type identified with HMMer [1].

	dsDNA	Positive-Strand ssRNA	Negative-Strand ssRNA	ssDNA	dsRNA	RT
2OG-FeII_Oxy_2	5	4	0	0	0	0
3A	0	14	1	0	0	0
Baculo_gp64	3	0	1	0	0	0
Corona_NS2A	2	11	0	0	0	0
DEAD	20	3	0	0	0	0
DUF1768	5	1	0	0	0	0
DUF3627	51	0	0	2	0	0
FtsJ	10	33	2	0	0	0
HSP70	4	4	0	0	0	0
Helicase_C	132	37	0	0	0	0
Hema_esterase	0	13	1	0	0	0
ISAV_HA	1	0	1	0	0	0
MMTV_SAg	2	0	0	0	0	1
MP	0	24	1	0	0	14
Macro	16	56	0	0	0	0
NSs	1	0	1	0	0	0
OTU	4	0	2	0	0	0
OrfB_IS605	23	0	0	1	0	0
PPV_E1_C	80	0	0	18	0	0
Parvo_NS1	4	0	0	11	0	0
Peptidase_S74	17	0	0	0	1	0
Phage_GPA	5	0	0	112	0	0
Phage_integrase	42	0	0	1	0	0
Pkinase_Tyr	52	0	0	0	0	1
RNA_helicase	0	94	0	22	0	0
RNase_H	9	0	0	0	0	30
RVT_1	2	0	0	0	0	109
RdRP_1	0	88	0	0	3	0
RdRP_2	0	95	0	0	1	0
RdRP_4	0	93	0	0	26	0
Rep_N	2	0	0	5	0	0
SH2	1	0	0	0	0	1
TT_ORF2	4	0	0	8	0	0
Trypsin	4	1	0	0	0	0
Trypsin_2	4	16	0	0	0	0
Viral_helicase1	18	133	0	0	1	0
dUTPase	81	0	0	0	0	6
dsrm	12	1	0	0	1	0
rve	2	0	0	2	0	45

References

1. Finn, R.; Clements, J.; Eddy, S. HMMER web server: Interactive sequence similarity searching. *Nucleic Acids Res.* **2011**, *39*, W29–W37.

© 2015 by the authors; licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution license (<http://creativecommons.org/licenses/by/4.0/>).