



ECO F COVID/FLU A/B Ag



Cepas detectadas

Cepas de Influenza Detectadas

Experimentos foram realizados para confirmar o desempenho de reatividade analítica do ECO F COVID/Flu A/B Ag através de cepas identificadas pelo **Influenza Resource Center (IRC)** e **National Institute for Biological Standards and Control (NIBSC)**.

A reatividade analítica foi demonstrada usando um total de 61 cepas de vírus de influenza compostas de 44 vírus da influenza A e 17 da influenza B. Os resultados do teste obtidos para cada cepa de gripe estão listados abaixo. Outras cepas podem ser detectadas, no entanto, não foram avaliadas neste estudo.

Linhagem Viral	Tipo viral	Subtipo	Limite de detecção (µgHa/mL)
A/Beijing/262/95	A	H1N1	0.0391
A/Brazil/11/78	A	H1N1	0.1563
A/Brisbane/59/2007 (IVR-148) (H1N1)	A	H1N1	0.0101
A/California/7/09 (H1N1) (NYMC-X181)	A	H1N1	0.3516
A/California/7/09 (H1N1)v (NIBRG-121xp) (EggDerived)	A	H1N1	0.0045
A/California/7/09 (H1N1)v (NYMCX-179A) (CellDerived)	A	H1N1	0.0061
A/California/7/2009 (H1N1) Like (A/Brisbane/10/2010-cell derived)	A	H1N1	0.0405
A/California/7/2009 -like(NIB -74)	A	H1N1	0.0142
A/Johannesburg/82/96	A	H1N1	0.1523
A/Michigan/45/2015 (NYMC X-275)	A	H1N1	1.1875
A/New Caledonia/20/99	A	H1N1	0.0508
A/New Caledonia/20/99 (IVR-116)	A	H1N1	1.6250
A/New Caledonia/71/2014 (NYMC-257A) (Egg derived antigen)	A	H1N1	0.0293
A/Puerto Rico/8/34 (H1N1)	A	H1N1	0.0488
A/Singapore/GP1908/2015 (IVR -180)	A	H1N1	0.0391
A/Solomon Islands/3/2006 (H1N1) (IVR-145)	A	H1N1	0.0278
A/Texas/36/91	A	H1N1	0.0273
A/USSR/92/77	A	H1N1	0.0840
A/California/7/2009 (H1N1pdm) (NYMC X-179A)	A	H1N1pdm	1.0938
A/Singapore/1/57 (H2N2)	A	H2N2	0.1758
A/Brisbane/10/2007 -like	A	H3N2	0.0547
A/Hiroshima/52/2005 (H3N2) (IVR-142)	A	H3N2	0.0625
A/Hong Kong/4801/2014(NYMC -263B)	A	H3N2	0.9375
A/Johannesburg/33/94	A	H3N2	0.0332
A/New York/55/2004 (H3N2) (NYMC X-157)	A	H3N2	0.1074
A/South Australia/55/2014 Cell derived	A	H3N2	0.0200
A/Switzerland/9715293/2013 (NIB88)	A	H3N2	0.8594
A/Sydney/5/97	A	H3N2	1.4063
A/Texas/1/77	A	H3N2	0.0898
A/Texas/50/2012 (NYMC X-223)	A	H3N2	0.0361
A/Texas/50/2012 (NYMC X -223A) (Cell derived)	A	H3N2	0.0352
A/Victoria/210/2009 (H3N2) (NYMCX -187)	A	H3N2	0.0352
A/Victoria/361/2011(H3N2) (IVR-165)	A	H3N2	0.6172
A/Wyoming/03/03	A	H3N2	1.5625
A/Equine/Newmarket/1/93	A	H3N8	0.3203
A/Equine/Newmarket/2/93	A	H3N8	4.0000
A/Anhui/ 1/05 (H5N1) IBCDC-RG -6	A	H5N1	0.0483
A/turkey/Turkey/1/2005 (H5N1) NIBRG-23	A	H5N1	0.1563
A/Vietnam/1194/2004 (H5N1) NIBRG-14	A	H5N1	0.0654
A/Duck/Singapore -Q/F119 -3/97	A	H5N3	0.0742
A/mallard/Netherlands/12/00 (H7N3) NIBRG-60	A	H7N3	0.0281
A/Anhui/1/ 2013 (NIBRG -268) (H7N9)	A	H7N9	0.0464
A/chick/Hong Kong/69/1997 (H9N2) NIBRG-91	A	H9N2	0.0205
Influenza Virus Infectious A/Singapore/INF1MH-16-0019/2016	A	H3N2	0.0652

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Linhagem Viral	Tipo viral	Subtipo	Limite de detecção (µgHa/mL)
B/Jiangsu/10/2003	B	-	4.0000
B/Brisbane/60/08	B	-	1.3125
B/Brisbane/60/2008 (NYMC BX-35) (Egg Derived)	B	-	0.3516
B/Brisbane/60/2008 (NYMC BX-35) (Cell Derived)	B	-	0.0664
B/Brisbane/9/2014 (Egg Derived)	B	-	38.6479
B/Florida/4/2006	B	-	0.0439
B/Guangdong/120/2000	B	-	0.0195
B/Harbin/7/94	B	-	0.0273
B/Hubei-Wujiagang/158/2009 (NYMCBX-39)	B	-	0.6875
B/Johannesburg/5/99	B	-	1.1875
B/Malaysia/2506/2004	B	-	0.1953
B/Massachusetts/02/2012	B	-	3.7500
B/Phuket/3073/2013	B	-	1.8750
B/Utah/9/2014 (Cell Derived)	B	-	0.024
B/Wisconsin/1/2010 (Cell Derived)	B	-	0.0278
B/Yamanashi/166/98	B	-	0.1641
B/Colorado/06/2017 -like virus(B/Victoria/2/87/lineage)	B	-	0.3125
B/Jiangsu/10/2003	B	-	4.0000
B/Brisbane/60/08	B	-	1.3125
B/Brisbane/60/2008 (NYMC BX-35) (Egg Derived)	B	-	0.3516
B/Brisbane/60/2008 (NYMC BX-35) (Cell Derived)	B	-	0.0664
B/Brisbane/9/2014 (Egg Derived)	B	-	38.6479
B/Florida/4/2006	B	-	0.0439
B/Guangdong/120/2000	B	-	0.0195

Cepas de COVID (SARS-CoV-2) Detectadas

A análise *in silico* da sequência da proteína N foi realizada com outras linhagens e as novas variantes de SARS-CoV-2, apresentando alta homologia.

Linhagem Viral	No. Acesso	GenBank	Homologia comparado com a Wuhan-Hu-1
Korea/SNU01	MT039890		100%
Wuhan-Hu-1	MN908947.3		100%
HKU-SZ-005b	MN975262.1		100%
USA-AZ1	MN997409.1		100%
USA-WA1	MN985325.1		100%
WU02	MN988669.1		100%
WU01	MN988668.1		100%
USA-CA2	MN994468.1		100%
USA-CA1	MN994467.1		100%
USA-IL1	MN988713.1		99.8%
HKU-SZ-002a	MN938384.1		100%

Variante	Sinônimo	Pais de origem	Homologia comparada com a Wuhan-Hu-1
B.1.1.7 (Alpha)	20B/501Y.V1, 501.V1	Reino Unido	99.52%
B.1.351 (Beta)	501.V2, 20C/501Y.V2	África do Sul	99.76%
B.1.1.248 (Gamma)	20J/501Y.V3, P.1	Brasil	99.28%
B.1.617/B.1 (Delta)	-	Índia	99.52%