

Extended Data Table 2 | M-SL9 conservation across representative IAV vaccine strains recommended by WHO, 2002 to 2022.

Northern hemisphere winter	Vaccine type	H1N1 subtype					H3N2 subtype				
		Vaccine virus strain	M-SL9 sequence*	Qa-1 <sup>b</sup> prediction	HLA-E*01:01 prediction	HLA-E*01:03 prediction	Vaccine virus strain	M-SL9 sequence*	Qa-1 <sup>b</sup> prediction	HLA-E*01:01 prediction	HLA-E*01:03 prediction
2002–2003	egg	A/New Caledonia/20/99 (sH1N1)	MSLLERIPIL	0.17	0.01	0.01	A/Moscow/10/99	MSLLGKTQIL	0.37	0.09	0.09
2003–2004	egg	A/New Caledonia/20/99 (sH1N1)	MSLLERIPIL	0.17	0.01	0.01	A/Moscow/10/99	MSLLGKTQIL	0.37	0.09	0.09
2004–2005	egg	A/New Caledonia/20/99 (sH1N1)	MSLLERIPIL	0.17	0.01	0.01	A/Fujian/411/2002	MSLLGKTQIL	0.37	0.09	0.09
2005–2006	egg	A/New Caledonia/20/99 (sH1N1)	MSLLERIPIL	0.17	0.01	0.01	A/California/7/2004	MSLLGKTQIL	0.37	0.09	0.09
2006–2007	egg	A/New Caledonia/20/99 (sH1N1)	MSLLERIPIL	0.17	0.01	0.01	A/Wisconsin/67/2005	MSLLGKTQIL	0.37	0.09	0.09
2007–2008	egg	A/Solomon Islands/3/2006 (sH1N1)	MYLLERIPIL	0.15	0.02	0.02	A/Wisconsin/67/2005	MSLLGKTQIL	0.37	0.09	0.09
2008–2009	egg	A/Brisbane/59/2007 (sH1N1)	MYLLERIPIL	0.15	0.02	0.02	A/Brisbane/10/2007	MSLLGKTQIL	0.37	0.09	0.09
2009–2010	egg	A/Brisbane/59/2007 (sH1N1)	MYLLERIPIL	0.15	0.02	0.02	A/Brisbane/10/2007	MSLLGKTQIL	0.37	0.09	0.09
2010–2011	egg	A/California/7/2009 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Perth/16/2009	MSLLGKTQIL	0.37	0.09	0.09
2011–2012	egg	A/California/7/2009 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Perth/16/2009	MSLLGKTQIL	0.37	0.09	0.09
2012–2013	egg	A/California/7/2009 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Victoria/361/2011	MSLLGKTQIL	0.37	0.09	0.09
2013–2014	egg	A/California/7/2009 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Victoria/361/2011	MSLLGKTQIL	0.37	0.09	0.09
2014–2015	egg	A/California/7/2009 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Texas/50/2012	MSLLGKTQIL	0.37	0.09	0.09
2015–2016	egg	A/California/7/2009 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Switzerland/9715293/2013	MSLLGKTQIL	0.37	0.09	0.09
2016–2017	egg	A/California/7/2009 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Hong Kong/4801/2014	MSLLGKTQIL	0.37	0.09	0.09
2017–2018	egg	A/Michigan/45/2015 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Hong Kong/4801/2014	MSLLGKTQIL	0.37	0.09	0.09
2018–2019	egg	A/Michigan/45/2015 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Singapore/INFIMH-16-0019/2016	MSLLGKTQIL	0.37	0.09	0.09
2019–2020	egg	A/Brisbane/02/2018 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Kansas/14/2017	MSLLGKTQIL	0.37	0.09	0.09
2020–2021	egg	A/Guangdong-Maonan/SWL1536/2019 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Hong Kong/2671/2019	MSLLGKTQIL	0.37	0.09	0.09
2020–2021	cell culture	A/Hawaii/70/2019 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Hong Kong/45/2019	MSLLGKTQIL	0.37	0.09	0.09
2021–2022	egg	A/Victoria/2570/2019 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Cambodia/e0826360/2020	MSLLGKTQIL	0.37	0.09	0.09
2021–2022	cell culture	A/Wisconsin/588/2019 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Cambodia/e0826360/2020	MSLLGKTQIL	0.37	0.09	0.09
2022–2023	egg	A/Victoria/2570/2019 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Darwin/9/2021	MSLLGKTQIL	0.37	0.09	0.09
2022–2023	cell culture	A/Wisconsin/588/2019 (pdm09)	VSLQERTQIL	0.2	0.03	0.03	A/Darwin/6/2021	MSLLGKTQIL	0.37	0.09	0.09
Reference accession	Reference virus name	M-SL9 sequence*	Qa-1 <sup>b</sup> prediction	HLA-E*01:01 prediction	HLA-E*01:03 prediction						
GenBank AF389121	A/Puerto Rico/8/1934	MSLQGRLLIL	0.39	0.06	0.06						

\*M-SL9 sequences are preceded by a methionine codon (AUG2) shown in blue or a valine codon shown in red.