

#### a. 2018-2019 (H1N1 HA Northern Hemisphere)

WHO: G V A P L H 70 G K C N I A G W I L G N P E C S L S T A S R S W S Y I V E T S N S D N G T C Y P G D F  
DOM: G V A P L H L G K C N I A G W I L G N P E C S L S T A R R S W S Y I V E T S N S D N G T C Y P G D F  
OUT: G V A P L H L G K C N I A G W I L G N P E C S L S T A R R S W S Y I V E T S N S D N G T C Y P G D F

RBD

The diagram illustrates the S protein structure with the RBD domain highlighted in blue. The mutations are indicated by red boxes: S at position 180, T at position 181, and P at position 200.

The diagram shows the sequence of the SARS-CoV-2 spike protein from residue 220 to 260. The RBD domain is indicated by a bracket above the sequence. The sequence is as follows:

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WHO: D A Y V F V G T S R Y S K K F K P E I A T R P K V R D Q E G R M N Y Y W T L V E P G D K I T F E A T
DOM: D A Y V F V G T S R Y S K K F K P E I A T R P K V R D Q E G R M N Y Y W T L V E P G D K I T F E A T

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**b. 2019-2020 (H1N1 HA Northern Hemisphere)**

WHO:	.62	.137	.207	.299	.315	315
DOM:	G	T	X	A	V	315
DNT:	R	A	S	P	-	315

WHO	:	G	T	X	A	V	315
DOM	:	R	A	S	P	I	315
ONT	:	R	T	Q	P	-	315

C. 2018-2019 (H1N1 HA Northern Hemisphere)

A diagram showing the relationship between WHO scores and 312 scores. The WHO scale has 91 points, the 312 scale has 18 points, and the 312 scale has 200 points. The 312 scale is divided into three segments: 100 points (green), 100 points (blue), and 100 points (orange). The WHO scale is aligned with the 312 scale as follows:

WHO Score	312 Scale Segment	312 Score
0	Green	0
~10	Green	~10
~20	Green	~20
~30	Green	~30
~40	Green	~40
~50	Green	~50
~60	Green	~60
~70	Green	~70
~80	Green	~80
~90	Green	~90
~91	Green	~91
~92	Blue	~92
~93	Blue	~93
~94	Blue	~94
~95	Blue	~95
~96	Blue	~96
~97	Blue	~97
~98	Blue	~98
~99	Blue	~99
~100	Blue	~100
~101	Orange	~101
~102	Orange	~102
~103	Orange	~103
~104	Orange	~104
~105	Orange	~105
~106	Orange	~106
~107	Orange	~107
~108	Orange	~108
~109	Orange	~109
~110	Orange	~110
~111	Orange	~111
~112	Orange	~112
~113	Orange	~113
~114	Orange	~114
~115	Orange	~115
~116	Orange	~116
~117	Orange	~117
~118	Orange	~118
~119	Orange	~119
~120	Orange	~120

WHO:	S	S	S	I	312
DOM:	R	T	P	V	312
ONT:	R	T	S	V	312

d. 2016-2017 (H1N1 HA Northern Hemisphere)

WHO:	A	P	S	D	S	X	P	S	S	T	I	T	A	K	V	P	S	P
DOM:	T	T	S	N	Z	N	S	T	T	T	T	T	E	V	V	T	Z	T
ONT:	T	T	S	N	Z	N	N	S	T	T	T	T	E	V	V	T	Z	T
	-13	100	101	114	179	180	200	202	220	233	273	300	300	338	391	468	516	516

e. 2014-2015 (H1N1 HA Southern Hemisphere)

WHO : .9  
DOOM : .1000  
DONT : .1144  
L : .1314  
P : .1800  
E : .2000  
S : .2024  
T : .2220  
A : .2757  
K : .3000  
I : .3385  
U : .3990  
Z : .4686  
N : .5161  
M : .5161  
O : .5161  
R : .5161

f. 2015-2016 (H3N2 HA Northern Hemisphere)

WHO:	L	I	A	S	G	N	S	K	O	P	R	D		505
DOM:	-	T	A	A	R	S	Y	T	H	H	K	N		505
ONT:	-	-	A	A	R	S	Y	T	H	H	K	N		505

█	13.9 (C); Accessible sidechain area (Å <sup>2</sup> )
█	23.0 (I); 23.5 (V); 25.2 (G)
█	28.7 (F); 29.0 (L); 30.5 (M); 31.5 (A)
█	41.7 (W); 44.2 (S); 46.0 (T); 46.7 (H)
█	53.7 (P)
█	59.1 (Y); 60.9 (D); 62.2 (N)
█	72.3 (E); 74.0 (Q)
█	93.8 (R)
█	110.3 (K)

- X acidic (-)
- X basic (+)
- X polar uncharged
- X hydrophobic nonpolar