

## Antigen Scoring Table

How to read the table: a C100S AA change should return 1 but S100C should return 0.7 (Rows give the source and columns the destination amino acid for each mutation)

	C (Cys)	S (Ser)	T (Thr)	P (Pro)	A (Ala)	G (Gly)	N (Asn)	D (Asp)	E (Glu)	Q (Gln)	H (His)	R (Arg)	K (Lys)	M (Met)	I (Ile)	L (Leu)	V (Val)	F (Phe)	Y (Tyr)	W (Trp)	
C (Cys)	0	1	1.4	1.2	0.8	1	1.4	1.4	1	0.7	1	0.9	1.1	1.3	1.4	0.8	1.5	0.8	0.8	1.4	
S (Ser)	0.7	0	0.5	1.1	0.4	0.6	0.7	0.9	0.8	0.8	0.8	0.8	1	0.9	1	1	0.8	0.8	0.8	1	1.3
T (Thr)	0.9	0.6	0	1.3	0.7	0.9	1.1	1.2	1.2	0.9	1.1	0.9	1.1	1.3	1.2	1	0.8	1	1	1.6	
P (Pro)	0.8	0.7	1	0	0.5	0.7	0.8	1.1	0.8	0.7	0.8	1.1	1.1	1.1	1.2	1	0.6	0.8	0.9	0.9	
A (Ala)	0.7	0.7	0.9	1.1	0	0.7	0.6	1.2	1	0.9	0.9	1	1.1	0.3	1.1	0.9	0.9	0.9	1	1.3	
G (Gly)	1	0.9	1.2	1.4	0.8	0	1.2	1.2	1.2	1	1.1	1.3	1.2	1.2	1.4	1.2	1.2	1.3	1.2	1.3	
N (Asn)	1.1	0.8	0.9	1	0.7	0.7	0	1.2	1.1	0.9	1.1	1.1	1.2	1.1	1.2	1.1	1.1	1.2	1.1	1.4	
D (Asp)	1	1	1.1	1.2	1	1	1.2	0	0.8	1	0.9	1.1	1.2	1.1	0.9	1.1	1.3	1.1	1.1	1.5	
E (Glu)	0.9	0.8	1	1.2	0.4	0.7	1	0.3	0	0.8	0.7	1	0.9	1.2	0.5	0.9	0.8	0.8	0.8	1.4	
Q (Gln)	0.7	0.6	0.8	1.2	0.4	0.7	0.8	1.6	0.6	0	0.7	0.8	0.8	0.4	0.5	0.7	0.1	0.7	0.8	1.3	
H (His)	0.9	0.8	1.2	1.2	0.5	0.8	1.1	1.4	0.9	0.9	0	1	0.9	0.9	1.2	0.8	1.1	0.9	1	1.5	
R (Arg)	1.1	1	1.2	1.4	0.5	1.1	1.6	1.4	1.1	1	1	0	0.9	1.6	1.4	1.1	1.2	1.2	1	1.6	
K (Lys)	0.9	0.7	0.5	1.1	0.1	0.4	0.5	0.5	1	0.6	0.8	0.6	0	0.6	0.4	0.9	0.4	0.8	0.8	1.2	
M (Met)	0.8	0.8	1	1.5	0.8	1.2	0.3	0.7	1	0.7	1	1.4	1.4	0	0.1	0.4	0.8	0.9	0.9	0	
I (Ile)	0.8	1.2	1.2	1.4	0.9	1.3	1.3	1.7	1.2	1.2	1.1	1.4	1.4	1	0	0.6	0.4	0.9	0.9	1.5	
L (Leu)	0.8	1.2	1.3	1.3	0.8	1.2	1.3	1.4	1.2	1.1	1	1.2	1.3	0.8	0.9	0	1	0.8	1	1.3	
V (Val)	0.7	0.9	0.7	1.2	0.7	1	1.4	1.1	1.2	1	1.1	1.2	1.2	0.2	0.3	0.8	0	1.2	1.2	1	
F (Phe)	1.3	1.3	1.1	1.4	1.1	1.5	1.4	1.5	1.6	1.2	1.1	1.4	1.5	1.1	1.3	0.9	1	0	0.9	1.1	
Y (Tyr)	1.4	1.3	1	1.2	0.7	0.8	1.4	1.5	1.3	0.8	1.2	0.8	1.3	0.7	0.9	0.8	1.2	0.8	0	0.9	
W (Trp)	1.4	1.5	1.7	1.6	1.6	1.3	1.4	1.5	1.6	1.6	1.1	1.5	1.6	1.4	1.5	1.3	1.4	0.8	1	0	