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Issue 6

Hypothesis

Supplementary material:

Table 1: PDB accession numbers of hemagglutinin structures for each influenza A subtype used in this study.

Subtype	PDB ID	Isolate	
H1N1	3HTT	Duck	
	1RD8	Human	
H3N3	1MQN	Duck	
	1HGF	Human	
H5N1	1JSN	Human	
	2FK0	Human	

Table 2: The threshold values for similarity determination of 3D structures, based on the Root Mean Square Deviation (RMSD) score.

>12 Completely unrelated 7 Dubious relationship 5 May be structurally related 4 Good structural relationship 2 Closely related 1.5 Very closely related 0.8 Differences are not obvious 0.4 Essentially indistinguishable	RMSD (Å)	Structural Relationship
5 May be structurally related 4 Good structural relationship 2 Closely related 1.5 Very closely related 0.8 Differences are not obvious	>12	Completely unrelated
4 Good structural relationship 2 Closely related 1.5 Very closely related 0.8 Differences are not obvious	7	Dubious relationship
2 Closely related 1.5 Very closely related 0.8 Differences are not obvious	5	May be structurally related
1.5 Very closely related 0.8 Differences are not obvious	4	Good structural relationship
0.8 Differences are not obvious	2	Closely related
	1.5	Very closely related
0.4 Essentially indistinguishable	0.8	Differences are not obvious
	0.4	Essentially indistinguishable