Indicator	Red, amber or green status*	Confidence level	Assessment and rationale
Transmissibility between humans	Amber	**Low**	**At least as transmissible as currently circulating variants** Omicron is transmitting rapidly and successfully. Increased transmissibility compared to Delta is biologically plausible with the presence of furin cleavage site and nucleocapsid changes associated in vitro with advantages for replication, as well as extensive changes to the RBD. Structural modelling suggests that the mutations present may increase human ACE2 binding affinity to a much greater extent than that seen for any other variant. Phylogeny suggests a recent emergence. Data from South Africa suggests that Omicron has a pronounced growth advantage there. However, this may be due to transmissibility or immune escape related, or both.
Infection severity			**Insufficient data**
Naturally acquired immunity	Red	**Low**	**Mutations suggestive of reduced protection from natural immunity and limited supporting epidemiological evidence** Based on experience with other variants, laboratory data on individual mutations, and structural modelling, the mutations present are very likely to reduce antibody binding and include changes in all 4 neutralising antibody binding sites in the RBD and also in antigenic sites in the S NTD. T cell epitope data is awaited. Analysis from South Africa suggests a reduction in protection from previous infection, including from recent Delta infection. There is no convalescent sera neutralisation data and no relative risk of reinfection analyses as yet.
Vaccine-derived immunity	Red	**Low**	**Mutations suggestive of reduced protection from vaccine derived immunity, no supporting evidence** The mutations present are likely to reduce antibody binding and include changes in all 4 RBD neutralising antibody binding sites. T cell epitope data is awaited. There is no vaccinee sera neutralisation data and no epidemiological data on vaccine effectiveness.
Therapeutics	Red	**Low**	**Mutations suggestive of reduced effectiveness of a treatment in UK clinical use** The mutations present are likely to reduce the binding of most available therapeutic monoclonal antibodies, based on structural modelling. On the same basis, they are unlikely to affect current small molecule antivirals. However, there is no laboratory or clinical data to support these predictions at present.

* Refer to scale and confidence grading slide.