**Fig. 1 Source Data. HDX summary table**

|  |  |  |  |
| --- | --- | --- | --- |
| **Data Set** | **SARS-2 HexaPro spike** | **SARS-2** | **SARS-2** |
| **HexaPro spike** | **HexaPro spike** |
| **+ 3A3 IgG** | **+ 3A3 Fab** |
| **HDX reaction details** | 200 mM NaCl, 20 mM Tris | | |
| 0.5 μM S2 | 0.5 μM S2 | 0.5 μM S2 |
| 0.55 μM 3A3 IgG | 0.55 μM 3A3 Fab |
| pHread = 7.6 | | |
| **HDX time course (s)** | 10, 100, 1000, 10000 at 25°C | | |
| **HDX control samples** | Unlabeled S2 | | |
| **Back-exchange (mean %)** | ~40 | | |
| **# of peptides** | 192 | | |
| **Sequence coverage (%)** | 56.3 | | |
| **Average peptide length (aa)/redundancy** | 13/3.34 | | |
| **Replicates (biological or technical)** | 4 (technical) | | |
| **Average standard deviation (Da)** | 0.10 | | |
| **Significance** | Average ΔHDX >0.2 Da, *p*-value<0.01 | | |