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Pox-AbDab: the orthopoxvirus antibody database

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In August 2024, the World Health Organization declared the mpox orthopoxvirus to be a Public Health Emergency of International Concern for the second time in three years, emphasising the need for continued studies into its microbiology and potential therapeutic interventions. Here, we presented the Orthopoxvirus Antibody Database (Pox-AbDab), a repository of data on antibodies known to bind or neutralise viruses from the same genus as mpox (https://opig.stats.ox.ac.uk/webapps/poxabdab). Beyond standardising and centralising the data, we highlighted challenges in translating knowledge across orthopoxviruses, such as the absence of a function-based nomenclature for virion surface antigens. We also performed an exploratory analysis of the known orthopoxvirus-binding antibody landscape, highlighting their aggregate molecular properties, cross-binding/cross-neutralisation profiles, evidence for immunodominance or immune escape from their epitopes, and gaps in coverage to help orient future research.

Systematic review: Code available at: https://opig.stats.ox.ac.uk/webapps/poxabdab.

KEYWORDS

antibody, antigen, epitopes, mpox, neutralising, sequence, structure

Introduction

Mpox is a zoonotic viral disease caused by the monkeypox virus (MPXV), a species of orthopoxvirus first identified in monkey populations in 1958 (1). Mpox infection and transmission in humans have been documented since the 1970s, associated with sudden but relatively localised outbreaks throughout the continent of Africa, containable with standard epidemic response measures (2).

However, a sudden and rapid spread of mpox in May 2022 to all six World Health Organization (WHO) global regions resulted in the first declaration of an mpox outbreak as a "Public Health Emergency of International Concern" (PHEIC). In summer 2024, a genetically divergent mpox upsurge in the Democratic Republic of the Congo spread intercontinentally and led to its second declaration as a PHEIC by the WHO. By 27 July 2025[1], 48,862 lab-confirmed cases have been reported across Africa since 2022, of which

28,953 have been reported since 2025. Together, the pattern of more frequent explosive viral spread, PHEIC declarations, and viral genetic divergence stress the ongoing threat of poxviruses and the need for preparedness measures.

During the COVID-19 pandemic, we compiled and released the Coronavirus Antibody Database (CoV-AbDab) containing coupled molecular and phenotypic data on antibodies and nanobodies that can bind to at least one betacoronavirus (3). Researchers have continually leveraged this centralised information to profile natural antiviral immune responses, assess the impact of vaccination on response shaping, make predictions on potential trajectories of viral escape, and guide the design of monoclonals, bispecifics, or cocktails as prophylactics/therapeutics (e.g. 4–6). An analogous database of antibodies that can bind or neutralise orthopoxviruses would help orient similar investigations from the emergence of any future mpox outbreak. However, while CoV-AbDab provides a helpful template for the design of an antiviral antibody database, substantial adaptations to the data structure are required to account for orthopoxvirus molecular biology.

Orthopoxviruses belong to the genera of poxviruses and contain four species that are pathogenic for humans: variola virus (VARV), vaccinia virus (VACV), cowpox virus (CPXV), and MPXV (7). Unlike single-stranded RNA betacoronaviruses, poxviruses are double-stranded DNA viruses. The central region of the genome is highly conserved and encodes proteins involved in replication and assembly (8), while the flanking regions are variable between virus species and related to host–pathogen interactions (7). For instance, these regions of the left and right termini encode proteins that distinguish MPXV clade I (which caused the 2024 outbreak) from clade II (which caused the 2022 outbreak) (9, 10). Missing and truncated genes between the two clades result in distinct epidemiological features (11, 12); clade I has a higher morbidity/mortality rate and exhibits greater human-to-human transmission compared to clade II (9).

In contrast to betacoronaviruses, which only use a single virion type, the orthopoxviruses have two types of infectious virions, which enable replication and maturation in the cytoplasm of host cells: the extracellular enveloped virus (EEV) and the intracellular mature virus (MV). The MV is the most abundant and important for inter-host transmission (13). Cell lysis allows MVs to be present outside the cell and infect new hosts by direct fusion with cell membranes (14). Additional packing of intracellular MVs in the cytoplasm results in intracellular enveloped viruses (IEVs) that are secreted as EEVs through cell-associated enveloped virus (CEV) (15). Therefore, EEVs have an additional membrane that needs to be disrupted prior to cell entry and is important for intra-host transmission (16, 17).

Further complexity is added by MV and EEV bearing distinct sets of surface proteins. More than 20 surface proteins have been identified for orthopoxviruses, with the majority located on the MV (18). At least four (A26, A27, D8, and H3) are associated with surface attachment, and 11 (A16, A21, A28, F9, G3, G9, H2, J5, L1, L5, and O3) form the entry fusion complex (EFC) (see Supplementary Table S1).

Of these proteins only a subset—MV proteins A27 (attachment), D8 (attachment), F9 (EFC), H3 (attachment), and L1 (EFC), and EEV proteins A33 and B5 (both involved in viral spread)—are considered immunodominant for the B-cell response (19), although other proteins have been shown to elicit some form of antibody response (20, 21). The complement system (22) is often essential for the neutralising activity of these antibodies (23–26), another distinction from anti-coronavirus antibodies, which typically neutralise *via* direct inhibition of spike to ACE-2 (3).

Here, we presented the Orthopoxvirus Antibody Database (Pox-AbDab), a freely accessible repository that centralises sequence, structural, and functional data on antibodies against orthopoxviruses. We showed how Pox-AbDab can reveal knowledge gaps and contribute molecular context to debates around the most effective health protection strategies against orthopoxviruses and the pressures driving their antigenic drift.

Results

Pox-AbDab stores sequence, structural, and functional data of antibodies against orthopoxviruses

As a first step to building Pox-AbDab, we explored to what extent existing resources contain variable region (Fv) sequences of antibodies that engage orthopoxviruses. We previously built PLAbDab (27) and PLAbDab-nano (28), which respectively scrape all antibody and nanobody sequences deposited in GenBank and provide a tag to all common antigens mentioned in their source literature. By searching for a variety of orthopoxvirus-related keywords (see Methods) and reading the studies to verify specificity to an orthopoxvirus, we were able to retrieve 160 antibodies from PLAbDab. Alternative publicly available database searches revealed 22 relevant entries in the Immune Epitope Database (IEDB) (29). Combined, this search resulted in 175 unique entries, which we added to Pox-AbDab. To further extend our database, we developed queries to identify orthopoxvirus-related papers (see Methods) and manually mined these to determine whether variable region sequence information is provided. The data curation process is visualised in Supplementary Figure S1.

We were able to retrieve a further 133 entries; as of June 2025, Pox-AbDab contains 308 antibodies or nanobodies (264 and 44, respectively) that bind at least one of the four most studied orthopoxviruses that can infect humans (Supplementary Figure S2A).

All the data in Pox-AbDab are available through a web application, hosted at https://opig.stats.ox.ac.uk/webapps/poxabdab. This can be searched by antibody properties (construct, species origin, available epitope information, and V- and J-genes), by antigen properties (virus species or strain, and cellular location), or for particular binding, neutralisation, or protection profiles (see Supplementary Figure S3). The result page table contains all columns previously compiled for CoV-AbDab, but is extended with immunological information on the epitope, and notes on the importance of the complement system are provided. We included the latter, as complement activation has been shown to be essential for antibody neutralisation when targeting specific antigens (23–26). A table with sequence similarity scores for antigen proteins

stored in Pox-AbDab is hosted on the main page to help users find all entries relevant to their research question. The complete database can be downloaded for offline analysis.

Pox-AbDab highlights research biases and limitations in sequence and structural data availability

Antibodies in Pox-AbDab are mainly derived from human repertoire B cells (Figure 1A). For 62% of the database entries, full sequence information is available (Figure 1B), and focus has recently shifted from VACV- to MPXV-specific antibodies (Figure 1C). This aligns with general orthopoxvirus literature following the PHEIC declarations and the long-standing use of VACV as a model virus (30). The data are primarily curated from a relatively small set of sources, each reporting a sizeable batch of antibodies or nanobodies (Figure 1C). A crystal structure is only available for 15 antibodies (Supplementary Figure S2D), and while data on target binding are available for all antibodies, *in vitro* neutralisation is only studied in 185 antibodies and *in vivo* protection in 33. All data can be downloaded from our Pox-AbDab web application (Figure 1D) and further general statistical breakdowns of the data are available in Supplementary Figure S2.

Pox-AbDab antibodies target most immunodominant antigens, but gaps exist in function-essential antigens

We next investigated the coverage of orthopoxvirus antigens in Pox-AbDab. While the antigens of coronaviruses have function-

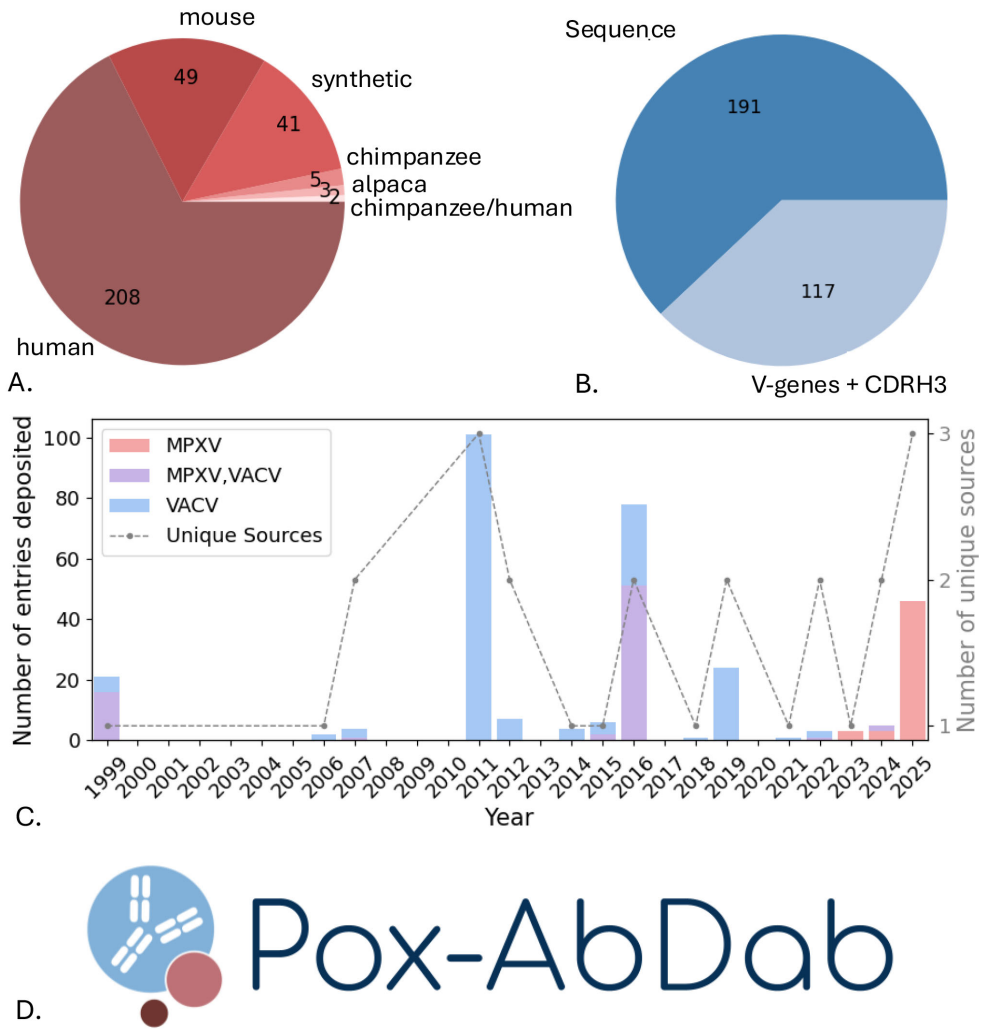

FIGURE 1
Pox-AbDab database content and web application. **(A)** Species origins of antibodies stored in Pox-AbDab. Most antibodies are derived from humans. **(B)** Available sequence information of antibodies stored in Pox-AbDab. For 62% of the entries, full sequence information is available. **(C)** Deposited antibodies stored in Pox-AbDab and their sources per year. Model virus VACV is historically most studied, while recent shifts to MPXV are observed. **(D)** We released Pox-AbDab as a freely available web application (https://opig.stats.ox.ac.uk/webapps/poxabdab). VACV, vaccinia virus; MPXV, monkeypox virus.

related names, such as spike protein, nucleocapsid protein, and membrane protein, orthopoxvirus antigens are named according to their gene position in the genome. They are frequently labelled according to a nomenclature inspired by the genome of the VACV Copenhagen strain prior to the era of whole-genome sequencing. In this scheme, proteins are annotated with a *Hin*dIII restriction endonuclease DNA fragment letter followed by an Open Reading Frame number (7). As it is solely based on genome organisation, this nomenclature can lead to common orthopoxvirus antigens that have the same function being assigned different names. This is even the case among strains of the same virus; for example, orthologs of VACV antigen B5 are labelled B6 in the Bangladesh-1975 strain of VARV and B7 in the India-1967 strain. Some papers replace the virus-specific nomenclature with a label that maps the antigen to an orthologous protein in VACV.

For consistency, we labelled antigens in Pox-AbDab with the annotation supplied in the source paper. For the purposes of this analysis, we additionally highlighted orthologous proteins across orthopoxviruses by colour (Figure 2). For example, the same colour was used to identify orthologs named after the VACV protein [e.g. VACV A33 and VARV A33(o)], while a slightly lighter shade of the same colour was used when an antigen was given a virus-specific name (e.g. VARV A36).

Figure 2 shows that Pox-AbDab antibodies target a variety of antigens and, as most entries in the database derive from human B cells, highlights the wide immunogenic response to orthopoxvirus infections or vaccinations. The VACV proteins H3, D8, B5, A33, A27, and L1, which have previously been characterised as immunodominant (19, 31), are correspondingly part of the most abundant proteins in Pox-AbDab. However, antibodies binding other antigens with essential viral functions are scarce or completely lacking (see Supplementary Table S1). For example, no public antibody is known to bind to proteins A13 and A17, which are important for assembly of mature virions (18, 32), and to proteins G3, G9, H2, J5, L5, and O3, which are involved in fusion with cell membranes and cell entry (18).

Orthopox cross-reactivity is common but not universal across Pox-AbDab antibodies

Orthopoxvirus genomes display over 90% nucleotide identity to one another (7, 33). This is, for example, considerably higher than the similarity between SARS-CoV and SARS-CoV-2 (79.6%) (34) and would imply an even greater potential for antibody cross-reactivity across orthopoxviruses than across betacoronaviruses.

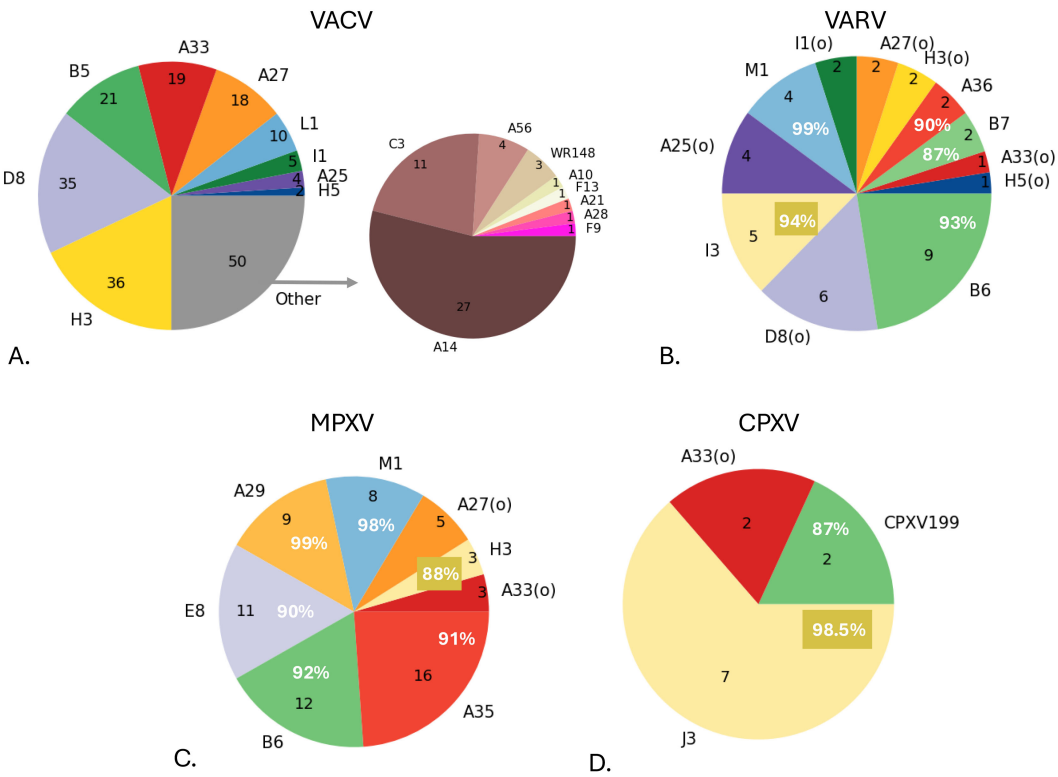

FIGURE 2
Antigen coverage for antibodies in Pox-AbDab. The number of antibodies against various antigens in VACV **(A)**, VARV **(B)**, MPXV **(C)**, and CPXV **(D)**. Antigens are shown according to their labelling in Pox-AbDab and coloured based on studied homology. Most VACV proteins are labelled according to the Copenhagen strain, while orthologs in the other viruses can be labelled according to the VACV ortholog [indicated with "(o)"] or their own naming scheme. The former is assigned the identical colour used for VACV; the latter is assigned a slightly lighter shade of that colour and includes the sequence identity score to VACV (in white). The sequence similarity scores were determined based on the GenBank IDs OP868847.1 (VACV), DQ441428.1 and DQ437581.1 (B6-only) (VARV), HM172544.1 (MPXV), and AF482758.2 (CPXV199) and X94355.2 (J3) (CPXV). VACV, vaccinia virus; VARV, variola virus; MPXV, monkeypox virus; CPXV, cowpox virus.

Binding and neutralisation assays from the source literature (mainly directed to VACV) show that many Pox-AbDab antibodies do indeed exhibit cross-reactivity to several orthopoxviruses (Figures 3A, B). However, despite these high levels of homology across orthopoxviruses, antibody cross-reactivity is by no means guaranteed. For instance, Pox-AbDab antibodies binding to VACV are also found to bind MPXV in 77% of the tested cases. For cross-neutralisation, this statistic drops to just 44% (Figures 3C, D), which may suggest that mpox-specific vaccination approaches offer a benefit over the current vaccinia-based vaccinations suggested to protect against MPXV in terms of inducing robust mpox immunity. The lack of cross-neutralisation to VACV and MPXV is observed in antibodies raised against MPXV antigens and VACV antigens (21). An activated complement system was required for effective neutralisation by at least 45 antibodies in Pox-AbDab (Supplementary Figure S2F); the requirement for efficient recruitment of other components of the immune system may add complexity to neutralisation potential beyond the capacity to cross-bind.

Structural data in Pox-AbDab reveal the potential for immune evasion

Antibodies can impart a natural selection pressure on viruses to mutate so as to evade the protective immune response of their hosts. Such immune evasion is particularly evident in betacoronaviruses, where even early SARS-CoV-2 strains contained mutations that interrupted binding to common human antibody epitope clusters (35). Orthopoxvirus antigens generally show high sequence similarity between species and strains, but it remains unclear whether the variation that does exist is driven by immune escape (e.g. from the vaccinia vaccine), driven by another pressure, or simply reflects genetic drift.

We analysed the binding footprints of the human antibodies structurally characterised in Pox-AbDab, exploring how conserved these binding residues are across orthopoxviruses (Table 1). This revealed a mixed picture dependent on the surface antigen targeted. The epitopes of seven human antibodies against A27, L1, and M1 were entirely conserved across the orthopoxvirus orthologs, even in binding footprints spanning 22 residues. However, eight human antibodies against A33, B6, and D8 targeted sites that vary in sequence across the examined orthopoxviruses. For instance, the D8 epitope footprint for the antibody in 5USH is only 75% conserved. Some positions differ markedly in amino acid chemistry (e.g. the A33 epitope residue 168 in crystal structure 4M1G is negatively charged in VACV, CPXV, and VARV, but positively charged in MPXV). Vaccine development and therapeutic design could incorporate these potentials by focusing on antigens with less evidence of immune evasion.

As a further case study, we analysed Borealpox (BRPV), the most recent orthopoxvirus known to infect humans (36). Borealpox is not yet included in Pox-AbDab, as currently no sequences of antibodies against BRPV have been reported in the literature. Here, we considered its B6 ortholog. Borealpox B6(o) displays relatively low sequence identity to VACV B5 (58%), and yet, despite this divergence, its AlphaFold3 (37) model retains the same overall fold as the crystallised fragment of MPXV B6 and VACV B5, suggesting functional conservation (Figure 4A). We then considered where the non-conserved residues lie in relation to the antigen-binding site of antibody hMB668 (38), an mpox-reactive clone derived from a vaccinia-vaccinated individual (Figure 4B). Across the 15-residue epitope, just five residues are conserved between MPXV and BRPV, or between VACV and BRPV (Figure 4C).

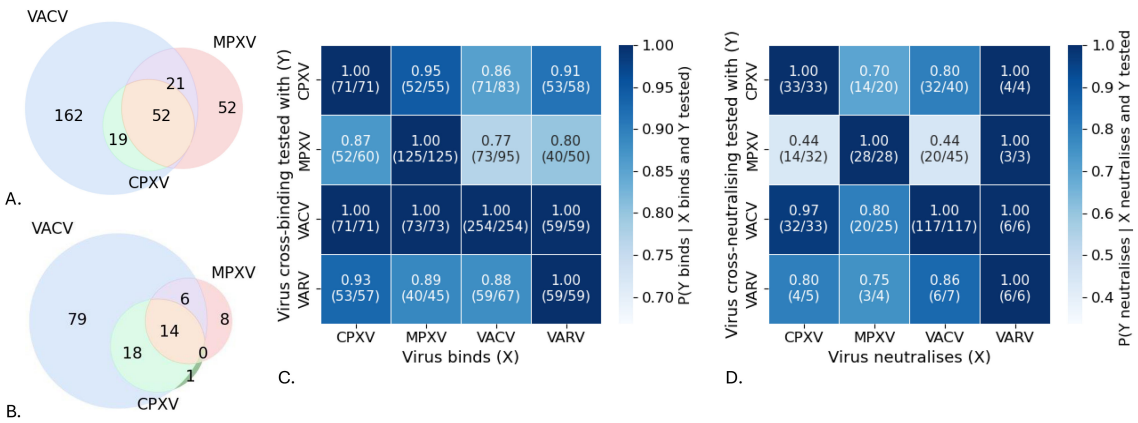

FIGURE 3
Cross-binding and cross-reactivity between orthopoxviruses. The number of cross-binding **(A)** and cross-neutralisation **(B)** antibodies in Pox-AbDab against VACV, MPXV, and CPXV. Fraction of cross-binding **(C)** and cross-neutralisation **(D)** of antibodies in Pox-AbDab. The number of antibodies considered is shown in brackets. While all antibodies binding to VARV, MPXV, and CPXV tested against VACV bind VACV as well, not all VACV-targeting antibodies cross-bind to the other viruses, and cross-neutralisation is even rarer. VACV, vaccinia virus; MPXV, monkeypox virus; CPXV, cowpox virus.

TABLE 1 Epitopes for the 15 antibodies in Pox-AbDab with solved crystal structures.

Antigen	Antibody (PDB ID)	Number of interface residues	Conservation				
			Position	VACV	MPXV	CPXV	VARV
A27	5EOQ	9	–				
A27	5EOR	9	–				
A33	4LQF	12	118	**L**	S	L	L
			120	**S**	E	S	S
			172	**S**	E	S	T
A33	4LU5	13	117	**Q**	K	Q	Q
			118	**L**	S	L	L
A33	4M1G	16	168	**D**	K	E	E
B6	8XS3	16	54	**Q**	S	S	S
D8	4ETQ	20	176	**H**	H	N	H
			205	**L**	S	S	L
D8	5USH	20	2	**P**	P	P	S
			18	**N**	D	D	N
			19	**A**	A	T	A
			118	**V**	A	V	V
			232	**D**	D	N	D
D8	5USL	19	146	**T**	M	T	T
			149	**P**	P	Q	P
D8	6B9J	20	143	**S**	S	S	T
			146	**T**	M	T	T
			149	**P**	P	Q	P
			205	**L**	S	S	L
L1	2I9L	11	–				
L1	4U6H	13	–				
M1	8ZU9	10	–				
M1	8ZUA	13	–				
M1	9J7Y	22	–				

Any non-conserved residues in the binding footprint across the four orthopoxvirus species are shown. Virus sequence definitions: VACV (OP868847.1), MPXV (HM172544.1), CPXV (AF482758.2), and VARV (DQ441428.1). The residue in the epitope of the solved crystal structure is shown in bold. Antigens are labelled according to the VACV Copenhagen nomenclature. VACV, vaccinia virus; MPXV, monkeypox virus; CPXV, cowpox virus; VARV, variola virus; PDB ID, Protein Data Bank identifier.

Genetic profiling of human Pox-AbDab antibodies currently offers little evidence for which clones are immunodominant

Finally, we assessed the sequence diversity and antigen-binding convergence of antibodies in Pox-AbDab.

Antibodies in Pox-AbDab span a full range of germline and CDR3 sequence length usages as observed in natural sequences (see Supplementary Figures S4-S6). The germline-likeliness of these antibodies was explored by comparing the 130 human antibody sequences in Pox-AbDab against a set of natural human naive B-cell receptor repertoires from the Observed Antibody Space (OAS) (39, 40) database using the KA-Search tool (41) (Methods, Figure 5), looking for the most sequence-identical match. This revealed that the human orthopoxvirus antibodies in Pox-AbDab antibodies, on average, lie some distance away from the naive baseline repertoire. As a reference, we also assessed the proximity of a random sample of 130 human B cell-derived coronavirus-binding antibodies from CoV-AbDab (3) (Figure 5). While the Pox-AbDab clones had a median closest chain identity of 86% (heavy chain) and 94% (light chain), the CoV-AbDab clones were closer to the naive repertoire with 92% (heavy chain) and 97% (light chain). We obtained

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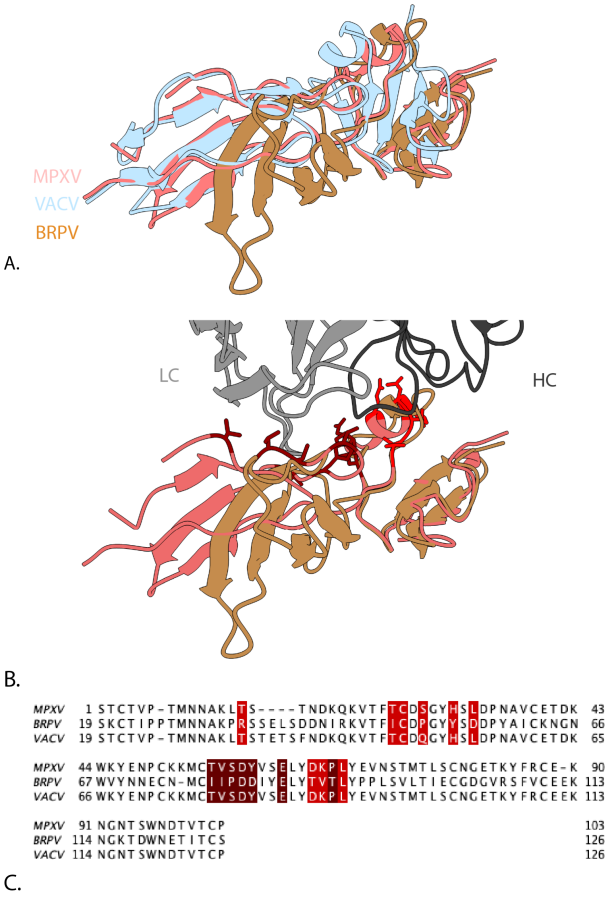

FIGURE 4
The crystal structure of antibody hMB668 (named D68 in the PDB) bound to mpox B6(o) (Protein Data Bank identifier 8XS3.). **(A)** The MPXV B6 protein from 8XS3 (light red) aligned to AlphaFold3 predictions of VACV B5 (light blue) and the BRPV. ortholog (orange). **(B)** Residues on MPXV B6 interacting with antibody hMB668 (grey) shown in dark red (heavy chain) and red (light chain). **(C)** Sequence alignment between MPXV B6, BRPV B6(o), and VACV B5 with the interacting residues highlighted (heavy chain footprint in dark red and light chain footprint in red). MPXV, monkeypox virus; VACV, vaccinia virus; BRPV, Borealpox.

comparable results when we compared them to all B-cell receptors in OAS (Supplementary Figure S7).

We surveyed the Pox-AbDab clones for evidence of response convergence. We first applied clonotyping, which groups antibodies by usage of the same heavy chain V/J genes that bear length-matched and highly similar CDRH3 loop sequences. We obtained multi-occupancy clusters that comprised a total of 62 antibodies; however, all antibodies within the same cluster were derived from the same source, and although the libraries contained pooled blood from many individuals, these clones could derive from the same donor.

It has been frequently observed that antigen-specific antibodies with similar Fv loop shapes tend to engage the same epitope (42). We therefore applied SPACE2, a method for 3D modelling and clustering of antibodies with high Fv structural homology. The 147 antibodies in Pox-AbDab with complete VH and VL sequences clustered into 16 multi-occupancy clusters (119 clusters in total); when allowing clustering between antibodies with length-dissimilar Complementary-determining regions (CDRs), this grew to 19 multi-occupancy clusters. Again, all clusters contained only antibodies reported from the same source. Overall, this indicates that Pox-AbDab cannot yet confidently tell us which clones are immunodominant upon orthopoxvirus infection or vaccination.

Discussion

Pox-AbDab currently stores 308 antibodies binding to at least one of the orthopoxvirus species VACV, VARV, MPXV, and CPXV. For context, this represents roughly three times more data than could be scraped from the literature on betacoronavirus binders prior to the SARS-CoV-2 pandemic (3). New data are continually emerging (e.g. Yefet et al. (43), whose sequence and structural data should be released after peer review), and we will continuously capture these through routine maintenance.

Poxvirus binding and heavy chain clone data are available for every entry, and where possible, we added neutralisation and *in vivo* protection data, the full Fv region sequence, and structural data. Literature sources and notes tagged to each entry provide ready access to additional information on characteristics.

Approximately 52% of the entries in Pox-AbDab were contained in GenBank and therefore retrieved by PLAbDab (27), showing the utility of this resource in generating initial datasets of target-associated sequences whose antigen specificity can be confirmed by inspection of the source literature. However, we could find substantially more data through manual curation, highlighting the diverse documentation of antibody sequence information across studies, including through Supplementary Tables and Supplementary Files, and even figures displaying sequence alignments. The sequences of antibodies mentioned in several sources were not obtainable—older papers do not share sequence data as reliably as newer ones, while the sequences of some antibodies commonly used as baselines still have restricted access (e.g. Mab 69-126-3–7 and 1G10) or are restricted from reusage/distribution (44).

A particular challenge underpinning the need for manual curation was the heterogeneity in both virion and antigen naming, as independent studies have frequently referred to the same viral protein by its VACV ortholog and virus-specific nomenclature. We provided a reference table of orthologous protein names alongside the web application to assist new entrants to the field, although a longer-term solution would be a community effort to establish a molecular function-based antigen naming scheme. The diversity of species and strain usage for binding, neutralisation, and protection assays, even within a study (45), also poses a challenge for any attempt to extract accurate functional labels in an automated fashion.

As with all literature-based curations of antigen-specific data, biases exist in Pox-AbDab that should be taken into account when

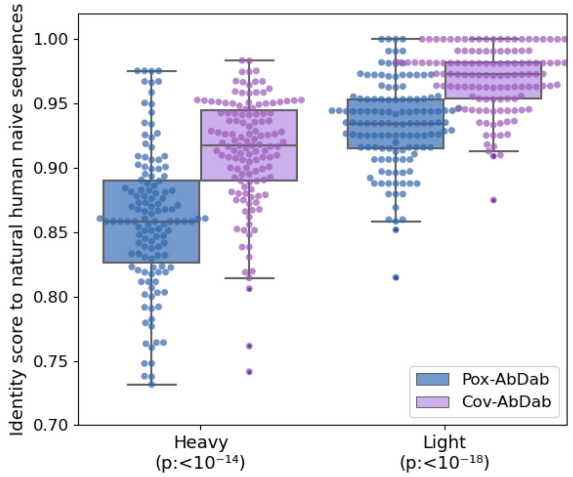

FIGURE 5
Antibody heavy and light sequence identity score to a set of human antibodies from naive B cells. The 130 full-length human antibody sequences in Pox-AbDab (blue) and 130 randomly selected human antibody sequences from CoV-AbDab (3) (purple) were compared against human naive B-cell receptor sequences from OAS (39, 40) (28.3M heavy chains from 12 studies and 24.6M light chains from five studies). The highest sequence identity observed was recorded. p-Values of the Mann–Whitney U test are indicated on the x-axis. OAS, Observed Antibody Space.

interpreting analyses. For example, VACV is the most studied orthopox species and is therefore the most represented virus species among the data in Pox-AbDab. This predominance may have focused research towards antigens that are less cross-reactive in other species. In MPXV-focused studies, neutralisation and protective capacity of the antibody are often tested only in VACV due to data availability and safety regulations around BSL-3 pathogens (38, 46, 47). Biases towards the MV compared to the EEV are caused by the fragile outer membrane of the envelope virion, which is hard to study (18). Other knowledge gaps identified in Pox-AbDab (see Figure 2) do not have obvious origins in regulatory or technical challenges and may be readily remedied by focused research efforts.

The aggregate data in Pox-AbDab already reveal immunologically relevant patterns amongst human antibodies to orthopoxviruses, such as their tenancy to accrue higher levels of somatic hypermutation than their coronavirus-binding counterparts. We also highlighted evidence of sequence variability in human antibody epitopes for certain surface antigens and that only a moderate number of antibodies in the database have been shown to cross-neutralise both VACV and MPXV. These immune evasion patterns should be considered in new vaccination designs, although current knowledge may be biased by the focus of historic vaccination strategies. As we accrued more orthopoxvirus-specific lineages from post-vaccination/post-infection B-cell receptor repertoires, immunodominant clones may emerge as they did in CoV-AbDab (3). The presence or absence of such signals would add useful context to our understanding of the potential for orthopoxvirus immune evasion.

As a pandemic preparedness measure, Pox-AbDab provides an immediate library of molecular designs that could be tested as laboratory reagents or diagnostic, prophylactic, or therapeutic antibodies in the context of an emergent orthopoxvirus outbreak. It also acts as a central location where specific antibody data could be deposited as studies into the immune response to existing or new orthopoxviruses emerge, akin to CoV-AbDab (3). This not only accelerates analyses into the potentially protective properties of these clones but also provides a ready source of machine learning-grade data that could be leveraged to design new molecules with desired orthopoxvirus reactivity and neutralisation profiles.

Methods

Data curation

Academic papers and patents containing antibodies binding orthopoxvirus pathogenic for humans were sourced by querying PubMed, Elsevier Mpox Information Center, Google Patents, and Google Scholar, and the publicly available maintained databases PLAbDab (27), PLAbDabnano (28), IEDB (29), and INDI (48) with the following search terms: orthopox, vaccinia, VACV, variola, VARV, monkeypox, mpox, MPXV, cowpox, and CPXV. Antibodies included in Pox-AbDab bind at least one of these four species pathogenic to humans, and at least the antibody V-gene(s) and CDRH3 are available. Various binding assays, such as surface plasmon resonance (SPR), bio-layer interferometry (BLI), enzyme-linked immunosorbent assay (ELISA), protein microarray, and Western blotting, were considered evidence of binding to capture the largest possible collection of relevant antibodies.

Antibody identification in Pox-AbDab

Curated antibodies were named according to the source naming convention. In some cases, the last name of the first author in which the antibody was initially described was used as a suffix to reduce the risk of duplicate names. In some cases, antibodies with the same variable region sequence were given different names depending on the source; we labelled these entries with both names. The originating species and the antibody construct were extracted from the paper.

Antibody functionality captured by Pox-AbDab

To consistently store detailed binding data, information on virus species, strain, location, and protein was combined into a single identifier separated with underscores (e.g. VACV_WR_MV_H3). For MPXV, clade information was specified when known (e.g. MPXV-IIb). Common abbreviations were used for concise strain identification. The database stores antibodies against the VACV

strains Western Reserve (WR), Lister, Elstree, Copenhagen, Connaught, New York City Board of Health (NYCBOH), Munich 1 (Munich1), International Health Division J (IHD-J), Tiantan, recombinant Tiantan strain expressing GFP (TT-FGP), and the smallpox vaccine strain ACAM2000. MPXV strains Zaire 1979 (Zaire79), Zaire96-I-16, Zaire599, and China-C-Tan-CQ01; VARV strains Solaiman, Bangladesh-1975, India-1967, and India-1967-Ind3a; and CPXV strains Grishak and Brigthon Red (BR) are included in the database. The location placeholder is used for the MV virion and the EEV virion and to indicate secreted proteins. Proteins are identified according to the antibody paper source. VACV protein orthologs are indicated by the suffix "(o)". For example, MPXV protein A35 is identified as the ortholog of VACV A33 and can be indicated by "A33(o)" or "A35" depending on the nomenclature in the source. Recombinant proteins are indicated by the suffix "(r)" and translated proteins by the suffix "(t)" when information is provided in the source.

As neutralisation assays are not performed on specific proteins, we used the virus species, strain, and location (again concatenated with underscores) as identifiers. Protection was indicated by virus species and strain. For consistent binding, neutralisation, and protection identifiers, question marks (?) are placeholders for missing data.

Antibody sequence information

V-gene and CDRH3 data are the minimum criteria for including antibodies in Pox-AbDab. Where available, VH or VHH and VL sequence information is stored, as well as V-gene, J-gene, and both CDRH3 and CDRL3 sequences. ANARCI (49) was used to identify CDR3 sequences and gene information in case sequences, but no or incomplete gene and CDR information was available. We excluded allele information for consistency. CDRs are defined based on the based on the international ImMunoGeneTics information system (IMGT) definition. Complete entries [e.g. JF11 and JE10 (50)] or part of the sequence information [e.g. full VH and VL sequence of A26C7 (19)] was excluded when ANARCI was unable to number the sequence and/or ImmuneBuilder (ABodyBuilder2 for antibodies, NanoBodyBuilder2 for VHHs) (51) was unable to structurally model the antibody. Extra sequence information beyond the VH and VL, as determined by ANARCI, was removed. Modified or inconsistent sequences of a single entry in multiple sources were stored as separate entries (e.g. VACV-138-v1 and VACV-138-v2).

Structural data

Where available, structure information was stored using the Protein Data Bank identifier (PDB ID) (52). When unavailable, ABodyBuilder2 structural models are provided. Epitope information was labelled as either conformational or linear based on whether or not epitope information was provided as a contiguous string of amino acids (i.e. a binding domain or loop) or as a set of sequentially discontinuous residues.

Web application

The data were stored in a relational database, using MariaDB[1], with a schema defined using the SQLModel library for Python[2]. The web application communicates with the database by means of a REST API conforming to version 3.1.0 of the OpenAPI Specification[3]. Both the API and the web application itself were created using the FastAPI web framework[4].

Database analysis

The database on current information storage was summarised, and immunoinformatic analysis of the data was performed. The origin and format of the antibody were summarised, as well as the source information. The type of sequence data available, the targeted virus species and antigens, the epitope identified, the ability of cross-neutralisation, and the importance of the complement system were also summarised.

The sequence diversity of the database was analysed based on V-gene usage and CDR length of the antibody per originating species, as well as the targeted proteins. Diversity of the human sequences was compared against a randomly sampled set of 5,000 antibodies collected from healthy individuals by Jaffe et al. (2022) (53) as stored in OAS (39, 40).

For structural analysis, the diversity of the targeted epitope within the four orthopoxvirus species was determined. The native epitope was identified in the available PDB structures based on a 1.4 probe radius and a 1.5 buried surface area (BSA) cutoff. The epitope footprint, as indicated in the solved crystal structure, was compared to the ortholog antigens in the other species. Here, accession numbers OP868847.1 (VACV), DQ441428.1 (VARV), HM172544.1 (MPXV), and AF482758.2 (CPXV) were used.

As a case study, the sequence-structural conservation of the recently identified Borealpox virus B6 ortholog protein was studied. The crystal structure of MPXV B6 [PDB ID: 8XS3 (38)] was compared against an AlphaFold3 (37) model of the Borealpox B6 ortholog (GenBank entry: MN240300.1). Sequence alignments [by Clustal Omega (54)] and visualisation of sequence conservation were performed using ChimeraX (v 1.10) (55). Interacting residues were defined as residues with a BSA ≥15 Å^2.

Immunoinformatics

We further analysed antibody sequence diversity and clustered antibodies using clonotyping, paratyping, and SPACE2 (56) to check for antigen-binding convergence of antibodies in Pox-AbDab.

1 https://mariadb.com/.
2 https://sqlmodel.tiangolo.com/.
3 https://spec.openapis.org/oas/v3.1.0.html.
4 https://fastapi.tiangolo.com/.

The 130 available human VH and VL sequences were compared against a naive set of human antibodies using KASearch (41). The naive dataset contained 5,000 randomly sampled unpaired heavy and light sequences from the OAS database (39, 40), collected on 21 January 2024. Distances to the full OAS naive and memory dataset were determined based on the provided "OAS-aligned" dataset of KA-Search. To compare distance scores against coronavirus-binding antibodies, 130 human full-length antibody sequences from CoV-AbDab were randomly selected. A non-parametric Mann–Whitney U test was used to statistically compare identity scores observed for Pox-AbDab against CoV-AbDab (3).

Clonotyping was performed on all entries in Pox-AbDab and carried out based on matching Immunoglobulin heavy chain variable (IGHV) and joining (IGHJ) region genes identities, identical CDRH3 lengths, and ≥80% CDRH3 sequence identity.

Functional convergence beyond sequence similarity was studied by clustering antibodies on their CDR conformations using SPACE2 (56). The 147 antibodies in Pox-AbDab with a complete Fv sequence were modelled using ABodyBuilder2 (51) and clustered according to the author's recommendation of 1.25 Å, in either length-restricted mode (all antibodies in a cluster have identical CDR lengths) or length-unrestricted mode root-mean squared deviations (RMSDs calculated as dynamic time warping distances).

Data availability statement

The database is accessible without restriction or registration at https://opig.stats.ox.ac.uk/webapps/poxabdab, and all data within Pox-AbDab can be freely downloaded.

Author contributions

HC: Writing – original draft, Data curation, Methodology, Software, Investigation, Visualization, Formal analysis. EW: Formal analysis, Software, Visualization, Writing – original draft, Investigation, Methodology. BW: Visualization, Software, Writing – original draft. CD: Resources, Conceptualization, Supervision, Funding acquisition, Writing – review & editing, Formal analysis. MR: Formal analysis, Project administration, Data curation, Supervision, Methodology, Conceptualization, Writing – review & editing, Funding acquisition.

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Conflict of interest

CD discloses membership of the Scientific Advisory Board of Fusion Antibodies plc and AI Proteins, and is a founder of Dalton Tx.

The remaining author(s) declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Generative AI statement

The author(s) declare that Generative AI was not used in the creation of this manuscript.

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References

1. Wambani J, Were T, Okoth P. Monkeypox: genetic, clinical, molecular, diagnostic, and therapeutic perspectives. *J Rare Dis*. (2024) 3:18. doi: 10.1007/s44162-024-00042-1

2. Kangbai JB, Sesay U, Vickos U, Kagbanda F, Fallah MP, Osborne A. Mpox in Africa: What we know and what is still lacking. *PLoS Negl Trop Dis*. (2025) 19: e0013148. doi: 10.1371/journal.pntd.0013148

3. Raybould MIJ, Kovaltsuk A, Marks C, Deane CM. CoVAbDab: the coronavirus antibody database. *Bioinformatics*. (2020) 37:734–5. doi: 10.1093/bioinformatics/btaa739

4. Kotagiri P, Mescia F, Rae WM, Bergamaschi L, Tuong ZK, Turner L, et al. B cell receptor repertoire kinetics after SARS-CoV-2 infection and vaccination. *Cell Rep*. (2022) 38:110393. doi: 10.1016/j.celrep.2022.110393

5. Cao Y, Wang J, Jian F, Xiao T, Song W, Yisimayi A, et al. Omicron escapes the majority of existing SARS-CoV-2 neutralizing antibodies. *Nature*. (2022) 602:657–63. doi: 10.1038/s41586-021-04385-3

6. Wu C-r, Yin W-c, Jiang Yi, Xu HE. Structure genomics of SARS-CoV-2 and its Omicron variant: drug design templates for COVID-19. *Acta Pharmacologica Sin*. (2022) 43:3021–33. doi: 10.1038/s41401-021-00851-w

7. Howley PM, Knipe DM, Whelan S, Freed EO. *Fields virology: RNA viruses*. Philadelphia, Pennsylvania, U.S.: Lippincott Williams & Wilkins (2022).

8. Cambaza EM. A review of the molecular understanding of the Mpox virus (MPXV): genomics, immune evasion, and therapeutic targets. *Zoonotic Dis*. (2025) 5:3. doi: 10.3390/zoonoticdis5010003

9. Likos AM, Sammons SA, Olson VA, Frace AM, Li Yu, OlsenRasmussen M, et al. A tale of two clades: monkeypox viruses. *J Gen Virol*. (2005) 86:2661–72. doi: 10.1099/vir.0.81215-0

10. Happi C, Adetifa I, Mbala P, Njouom R, Nakoune E, Happi A, et al. Urgent need for a non-discriminatory and non-stigmatizing nomenclature for monkeypox virus. *PLoS Biol*. (2022) 20:e3001769. doi: 10.1371/journal.pbio.3001769

11. Forni D, Cagliani R, Molteni C, Clerici M, Sironi M. Monkeypox virus: the changing facets of a zoonotic pathogen. *Infection Genet Evol*. (2022) 105:105372. doi: 10.1016/j.meegid.2022.105372

12. Alakunle E, Kolawole D, Diaz-Canova D, Alele F, Adegboye O, Moens U, et al. A comprehensive review of monkeypox virus and mpox characteristics. *Front Cell Infection Microbiol*. (2024) 14:1360586. doi: 10.3389/fcimb.2024.1360586

13. Nikitin VN, Merkuleva IA, Shcherbakov DN. Monoclonal antibodies in light of Mpox outbreak: current research, therapeutic targets, and animal models. *Antibodies*. (2025) 14:20. doi: 10.3390/antib14010020

14. Moss B. Poxvirus entry and membrane fusion. *Virology*. (2006) 344:48–54. doi: 10.1016/j.virol.2005.09.037. ISSN 0042-6822.

15. McFadden G. Poxvirus tropism. *Nat Rev Microbiol*. (2005) 3:201–13. doi: 10.1038/nrmicro1099

16. Appleyard G, Hapel AJ, Boulter EA. An antigenic difference between intracellular and extracellular rabbitpox virus. *J Gen Virol*. (1971) 13:9–17. doi: 10.1099/0022-1317-13-1-9

17. Payne LG. Significance of extracellular enveloped virus in the *in vitro* and *in vivo* dissemination of vaccinia. *J Gen Virol*. (1980) 50:89–100. doi: 10.1099/0022-1317-50-1-89

18. Moss B. Smallpox vaccines: targets of protective immunity. *Immunol Rev*. (2011) 239:8–26. doi: 10.1111/j.1600-065X.2010.00975.x

19. Matho MH, Schlossman A, Meng X, Rafii-El-Idrissi Benhnia M, Kaever T, Buller M, et al. Structural and functional characterization of anti-A33 antibodies reveal a potent cross-species orthopoxviruses neutralizer. *PLoS Pathog*. (2015) 11:e1005148. doi: 10.1371/journal.ppat.1005148

20. Lantto J, Hansen MH, Rasmussen SørenK, Steinaa L, Poulsen TR, Duggan J, et al. Capturing the natural diversity of the human antibody response against vaccinia virus. *J Virol*. (2011) 85:1820–33. doi: 10.1128/JVI.02127-10

21. Gilchuk I, Gilchuk P, Sapparapu G, Lampley R, Singh V, Kose N, et al. Cross-neutralizing and protective human antibody specificities to poxvirus infections. *Cell*. (2016) 167:684–94. doi: 10.1016/j.cell.2016.09.049

22. Mellors J, Carroll M. Direct enhancement of viral neutralising antibody potency by the complement system: a largely forgotten phenomenon. *Cell Mol Life Sci*. (2024) 81:22. doi: 10.1007/s00018-023-05074-2

23. Lustig S, Fogg C, Whitbeck JC, Moss B. Synergistic neutralizing activities of antibodies to outer membrane proteins of the two infectious forms of vaccinia virus in the presence of complement. *Virology*. (2004) 328:30–5. doi: 10.1016/j.virol.2004.07.024

24. Rafii-El-Idrissi Benhnia M, McCausland MM, Moyron J, Laudenslager J, Granger S, Rickert S, et al. Vaccinia virus extracellular enveloped virion neutralization *in vitro* and protection *in vivo* depend on complement. *J Virol*. (2009) 83:1201–15. doi: 10.1128/JVI.01797-08

25. Cohen ME, Xiao Y, Eisenberg RJ, Cohen GH, Isaacs SN. Antibody against extracellular vaccinia virus (EV) protects mice through complement and Fc receptors. *PLoS One*. (2011) 6:e20597. doi: 10.1371/journal.pone.0020597

26. Hubert M, Guivel-Benhassine F, Bruel Timothée, Porrot Françoise, Planas D, Vanhomwegen J, et al. Complement-dependent mpox-virus-neutralizing antibodies in infected and vaccinated individuals. *Cell Host Microbe*. (2023) 31:937–48. doi: 10.1016/j.chom.2023.05.001

27. Abanades B, Olsen TH, Raybould MIJ, Aguilar-Sanjuan B, Wong WKi, Georges G, et al. The Patent and Literature Antibody Database (PLAbDab): an evolving reference set of functionally diverse, literature-annotated antibody sequences and structures. *Nucleic Acids Res*. (2024) 52:D545–51. doi: 10.1093/nar/gkad1056

28. Gordon GL, Greenshields-Watson A, Agarwal P, Wong A, Boyles F, Hummer A, et al. PLAbDabnano: a database of camelid and shark nanobodies from patents and literature. *Nucleic Acids Res*. (2025) 53:D535–42. doi: 10.1093/nar/gkae881

29. Vita R, Blazeska N, Marrama D, IEDB Curation Team Members, Duesing S, Bennett J, et al. The immune epitope database (IEDB): 2024 update. *Nucleic Acids Res*. (2025) 53:D436–43. doi: 10.1093/nar/gkae1092

30. Moss B. Vaccinia virus: a tool for research and vaccine development. *Science*. (1991) 252:1662–7. doi: 10.1126/science.2047875

31. Zajonc DM. Antibody recognition of immunodominant vaccinia virus envelope proteins. In: *Macromolecular Protein Complexes: Structure and Function*. Cham: Springer (2017). p. 103–26.

32. Unger B, Traktman P. Vaccinia virus morphogenesis: A13 phosphoprotein is required for assembly of mature virions. *J Virol*. (2004) 78:8885–901. doi: 10.1128/JVI.78.16.8885-8901.2004

33. Hendrickson RC, Wang C, Hatcher EL, Lefkowitz EJ. Orthopoxvirus genome evolution: the role of gene loss. *Viruses*. (2010) 2:1933–67. doi: 10.3390/v2091933

34. V'kovski P, Kratzel A, Steiner S, Stalder H, Thiel V. Coronavirus biology and replication: implications for SARS-CoV-2. *Nat Rev Microbiol*. (2021) 19:155–70. doi: 10.1038/s41579-020-00468-6

35. Carabelli A, Peacock TP, Thorne LG, Harvey WT, Hughes J, The COVID-19 Genomics UK Consortium, et al. SARS-CoV-2 variant biology: immune escape, transmission and fitness. *Nat Rev Microbiol*. (2023) 21:162–77. doi: 10.1038/s41579-022-00841-7

36. Douglass N. Borealpox (Alaskapox) virus: will there be more emerging zoonotic orthopoxviruses? *Lancet Microbe*. (2024) 5:100883. doi: 10.1016/S2666-5247(24)00106-X

37. Abramson J, Adler J, Dunger J, Evans R, Green T, Pritzel A, et al. Accurate structure prediction of biomolecular interactions with AlphaFold 3. *Nature*. (2024) 630:493–500. doi: 10.1038/s41586-024-07487-w

38. Zhao R, Wu L, Sun J, Liu D, Han Pu, Gao Y, et al. Two noncompeting human neutralizing antibodies targeting MPXV B6 show protective effects against orthopoxvirus infections. *Nat Commun*. (2024) 15:4660. doi: 10.1038/s41467-024-48312-2

39. Kovaltsuk A, Leem J, Kelm S, Snowden J, Deane CM, Krawczyk K. Observed antibody space: A resource for data mining nextGeneration sequencing of antibody repertoires. *J Immunol*. (2018) 201:2502–9. doi: 10.4049/jimmunol.1800708

40. Olsen TH, Boyles F, Deane CM. Observed Antibody Space: A diverse database of cleaned, annotated, and translated unpaired and paired antibody sequences. *Protein Sci*. (2022) 31:141–6. doi: 10.1002/pro.4205

41. Olsen TH, Abanades B, Moal IH, Deane CM. KA-Search, a method for rapid and exhaustive sequence identity search of known antibodies. *Sci Rep*. (2023) 13:11612. doi: 10.1038/s41598-023-38108-7

42. Robinson SA, Raybould MIJ, Constantin S, Wong WKi, Marks C, Deane CM. Epitope profiling using computational structural modelling demonstrated on coronavirus-binding antibodies. *PLoS Comput Biol*. (2021) 17:e1009675. doi: 10.1371/journal.pcbi.1009675

43. Yefet R, Battini L, Hubert M, Rakayev K, Guivel-Benhassine F, Rattner N, et al. Potent neutralization by antibodies targeting the Mpox A28 protein. *bioRxiv*. (2025), 2025–05. doi: 10.1101/2025.05.22.655505

44. Li M, Chen J, Wang F, Kuang J, Peng Y, Asghar S, et al. Bispecific antibodies targeting MPXV A29 and B6 demonstrate efficacy against MPXV infection. *J Virol*. (2025) 99:e02320–24. doi: 10.1128/jvi.02320-24

45. Chen N, Li G, Liszewski MK, Atkinson JP, Jahrling PB, Feng Z, et al. Virulence differences between monkeypox virus isolates from West Africa and the Congo basin. *Virology*. (2005) 340:46–63. doi: 10.1016/j.virol.2005.05.030

46. Wang H, Yin P, Zheng T, Qin L, Li S, Han Pu, et al. Rational design of a 'two-in-one'immunogen DAM drives potent immune response against mpox virus. *Nat Immunol*. (2024) 25:307–15. doi: 10.1038/s41590-023-01715-7

47. Yang X, Guo Li, Duan H, Fan M, Xu F, Chi X, et al. Identification of neutralizing nanobodies protecting against poxvirus infection. *Cell Discov*. (2025) 11:31. doi: 10.1038/s41421-025-00771-7

48. Deszyński P, Młokosiewicz J, Volanakis A, Jaszczyszyn I, Castellana N, Bonissone S, et al. INDI—integrated nanobody database for immunoinformatics. *Nucleic Acids Res*. (2022) 50:D1273–D1281. doi: 10.1093/nar/gkab1021

49. Dunbar J, Deane CM. ANARCI: antigen receptor numbering and receptor classification. *Bioinformatics*. (2016) 32:298–300. doi: 10.1093/bioinformatics/btv552

50. Sela-Culang I, Rafii-El-Idrissi Benhnia M, Matho MH, Kaever T, Maybeno M, Schlossman A, et al. Using a combined computational-experimental approach to predict antibody-specific B cell epitopes. *Structure*. (2014) 22:646–57. doi: 10.1016/j.str.2014.02.003

51. Abanades B, Wong WKi, Boyles F, Georges G, Bujotzek A, Deane CM. ImmuneBuilder: Deep-Learning models for predicting the structures of immune proteins. *Commun Biol*. (2023) 6:575. doi: 10.1038/s42003-023-04927-7

52. Berman HM, Westbrook J, Feng Z, Gilliland G, Bhat TN, Weissig H, et al. The protein data bank. *Nucleic Acids Res*. (2000) 28:235–42. doi: 10.1093/nar/28.1.235

53. Jaffe DB, Shahi P, Adams BA, Chrisman AM, Finnegan PM, Raman N, et al. Functional antibodies exhibit light chain coherence. *Nature*. (2022) 611:352–7. doi: 10.1038/s41586-022-05371-z

54. Madeira Fábio, Madhusoodanan N, Lee J, Eusebi A, Niewielska A, Tivey ARN, et al. The EMBL-EBI Job Dispatcher sequence analysis tools framework in 2024. *Nucleic Acids Res*. (2024) 52:W521–5. doi: 10.1093/nar/gkae241

55. Meng EC, Goddard TD, Pettersen EF, Couch GS, Pearson ZJ, Morris JH, et al. UCSF ChimeraX: Tools for structure building and analysis. *Protein Sci*. (2023) 32:e4792. doi: 10.1002/pro.4792

56. Spoendlin FC, Abanades B, Raybould MIJ, Wong WKi, Georges G, Deane CM. Improved computational epitope profiling using structural models identifies a broader diversity of antibodies that bind to the same epitope. *Front Mol Biosci*. (2023) 10:1237621. doi: 10.3389/fmolb.2023.1237621