An Integrated Approach to the Characterization of Immune Repertoires Using AIMS: An Automated Immune Molecule Separator

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Abstract

The adaptive immune system employs an array of receptors designed to respond with high specificity to pathogens or molecular aberrations faced by the host organism. Binding of these receptors to molecular fragments - collectively referred to as antigens - initiates immune responses. These antigenic targets are recognized in their native state on the surfaces of pathogens by antibodies, whereas T cell receptors (TCR) recognize processed antigens as short peptides, presented on major histocompatibility complex (MHC) molecules. Recent research has led to a wealth of immune repertoire data that are key to interrogating the nature of these molecular interactions. However, existing tools for the analysis of these large datasets typically focus on molecular sets of a single type, forcing researchers to separately analyze strongly coupled sequences of interacting molecules. Here, we introduce a software package for the integrated analysis of immune repertoire data, capable of identifying distinct biophysical differences in isolated TCR, MHC, peptide, antibody, and antigen sequence data. This integrated analytical approach allows for direct comparisons across immune repertoire subsets and provides a starting point for the identification of key interaction hotspots in complementary receptor-antigen pairs. The software (AIMS - Automated Immune Molecule Separator) is freely available as an open access package in GUI or command-line form.

INTRODUCTION

To control infection and disease, the adaptive immune system of higher organisms utilizes a complex collection of receptors and signaling pathways specifically tailored to each individual immunological challenge [1–4]. Over the past decade, researchers have increasingly leveraged these receptors, specifically antibodies and T cell receptors (TCRs), to generate novel therapeutics [5–11]. Generally, the success of natural immune responses or therapeutics are strongly dependent on the ability of these receptors to recognize and appropriately respond to pathogenic threats. However, recognition of pathogens is a dynamic challenge for the immune system as the generation of its receptors is dependent on the identity of the pathogens, and the pathogens themselves are frequently capable of generating compensatory mutations that, in turn, require adaptations in the immune responses.

Both sides of this competition are subject to a balancing act; successful pathogens must mutate and generate variants that reduce detection by the host immune system yet maintain a sufficient level of biological fitness, whereas successful immune responses must recruit or generate receptors that bind with high affinity and specificity to a given pathogen yet ideally maintain sufficient breadth to adapt quickly to these pathogenic variants [12–14]. This biological back and forth is encapsulated by the amino acid sequences that determine the interaction strength between the molecular players involved in adaptive immune recognition. The costs for determining these amino acid sequences of immune receptors has been decreasing rapidly [15], thereby providing access to datasets exponentially increasing in size [16–20]. Likewise, current sequencing technologies allow us to follow the evolution of viruses and identify variants of concern in real-time across the globe [21]. Characterization of the peptides presented by MHC, also referred to as the immunopeptidome, relies on mass spectrometry-based identification. While this method severely limits the coverage of each experiment, single immunopeptidomic assays can yield thousands of identified pathogenic or self-peptides [22]. As these sequence databases continue to expand, methods for analyzing their large datasets must keep pace, helping researchers to identify key distinguishing features of the sequences identified in any given immunological niche.

Excellent software exist for the analysis of TCR sequences [23–28], antibodies [25, 29–32], and peptides [33–35]. Conversely, the analyses of viral sequences are largely dependent on multi-sequence alignments, phylogenetic analysis, or custom pipelines from researchers in a specific viral sub-field. While each of these approaches are powerful tools in their respective fields, they make comparisons across immune repertoires difficult. Software that compares, for instance, peptide and TCR repertoires typically give a simple binary "yes" or "no" to questions of binding, making the identification of trends within or across these repertoires difficult. Further, a majority of the analyses are developed for a very specific task, such as prediction of peptide binding to a specific MHC allele or identification of the evolutionary trajectory of a given antibody sequence. General characterizations of a given immune repertoire are often done via an in-house analysis, focusing on simplified quantities such as net biophysical properties of sequences, as well as their lengths or conservation.

To address some of these shortcomings, we developed the AIMS (Automated Immune Molecule Separator) software to take into account the fundamental biophysical properties of amino acid sequences to characterize, differentiate, and identify clusters within immune repertoires. While the initial input of sequences into AIMS is different for each of the distinct molecular classes of immune repertoires, the downstream analysis is identical and allows for cross-receptor analysis and the identification of patterns in the corresponding trends of interacting molecules. The application of AIMS for targeted investigations of specific biological systems has been previously described [36–38]. Here, we outline applications of the software to each immune repertoire class with a specific focus on the software's integrated analytical capabilities for cross-repertoire analyses.

RESULTS

Encoding of Amino Acid Sequences and Their Biophysical Properties

An ideal repertoire analysis approach would build on experimentally determined molecular complex structures and perform a direct biophysical analysis of each interaction. While such an approach to the study of receptor recognition events has been historically productive, the scale of modern receptor repertoires makes crystallization of each complex structure impossible. Structural modeling is an intriguing alternative, whereby these immune receptor complexes can be computationally predicted [28]. While this technology has made exceptional progress over the past decade, predictions of the conformations adopted by the flexible TCR or antibody CDR loops and the placement of the antigen-contacting amino acid side chains on these loops are unreliable, even for the most advanced structural prediction software to date [39]. Given the high degree of conservation of the key structural features in antibodies, TCR, MHC, and presented peptides, the relative placement of side chains takes on an outsized importance in immune recognition events compared to most protein-protein interactions.

Angstrom-scale discrepancies between computationally predicted and experimentally determined structures can have significant consequences in immune contexts. For instance, an incorrectly modeled structure may suggest a salt bridge is a key feature of an antibody-antigen interaction, when in reality these residues primarily participate in a more intricate hydrogen-bonding network. These potentially incorrect assumptions can lead to misguided experimental efforts, with point mutation studies or efforts to improve binding affinity focused on the wrong amino acid interactions. The encoding scheme employed by AIMS overcomes this problem via a hybrid approach to repertoire analysis. AIMS takes advantage of the structural conservation inherent to immune molecules, selecting out only the regions involved in the interaction interface. These conserved interacting regions, which are highly variable at the sequence level, are then aligned in matrix form using a pseudo-structural approach. By incorporating general structural features, rather than explicit contact predictions, AIMS reduces the bias of the analysis.

The exact encoding scheme adopted varies across the available analysis modes for each molecular species. Among TCR-peptide-MHC complexes, the interaction interface is strikingly similar, with crystal structures consistently finding nearly identical docking angles between the two [37, 40–44]. TCRs contact the peptide and the MHC α-helices via their six complementarity determining region (CDR) loops, which are in turn connected via stem regions to their well conserved framework regions. These stem regions adjacent to the CDR loops are never found within 5 Å of the antigen [26]. Further, in most organisms studied in immunology, specifically humans, mice, and non-human primates, these stem regions are easily identified by highly conserved amino acids, allowing for the exclusion of framework regions from the analysis. In a majority of structures, assuming the conserved stem regions are defined as endpoints, the central 4-5 residues of the CDR3 loops contact the central residues of the peptide [26] (Fig. 1A, B). From these general structural rules, we can inform the encoding of TCR sequences into AIMS, imposing a "central" alignment scheme as the standard.

In the central alignment scheme, we align each sequence to the central residue of each user-defined CDR loop. Whereas most analysis tools segregate TCR sequences by length, thereby artificially segmenting the data, the central alignment scheme of AIMS allows for receptors of all lengths to be analyzed simultaneously while focusing on the key regions of the receptor. Due to the length differences of the TCR sequences in a given dataset, signals from the CDR stem regions will be averaged out, thus prioritizing signals from the center of the CDR loops. We can visualize an example of this encoding for a test dataset of paired TCRα and TCRβ sequences from the VDJ database [16] (Fig. 1C). In this matrix, we can see that each amino acid is encoded as a unique number in the matrix 1 to 21, or a unique color in the figure, with padded zeros between CDR loops represented by white space in the figure. To control for potential artifacts introduced by this approach, analysis can be repeated with "left" or "right" alignment of the sequences, aligning to the N- or C-termini, respectively, of the given sequences (Fig. S1).

The standard AIMS encoding for peptides is slightly different from this central TCR alignment scheme. For class I MHC, the flanking regions of bound peptides are 'buried' as highly conserved anchor residues that bind to the MHC platform and are unable to contact TCR (Fig. 1A,B). The majority of TCR contacts are made with the central regions of the peptides that bulge out of the MHC binding groove in the case of longer peptides [45]. Further, the length distribution of peptides presented by class I MHC is narrow [33], subverting some of the sequence length concerns present in the TCR analysis. As such, peptide encoding in AIMS adopts a "bulge" scheme. The bulge scheme aligns the N- and C-terminal residues to either edge of the matrix, along with a user-defined number of additional flanking residues. Zeros are padded between these flanking regions and the remaining residues are centrally aligned as in the case of the TCR sequences, again adopting the same numeric amino acid encoding scheme (Fig. 1D). We can see clearly for this subset of HLA-A2 presented *Influenza* peptides taken from the Immune Epitope Database (IEDB) [46] the relative conservation at anchor position 2, compared to the variability at the center of the peptide sequences. Importantly, this bulge alignment can also be applied to TCR and antibody sequences, putting more focus on their conserved stem regions.

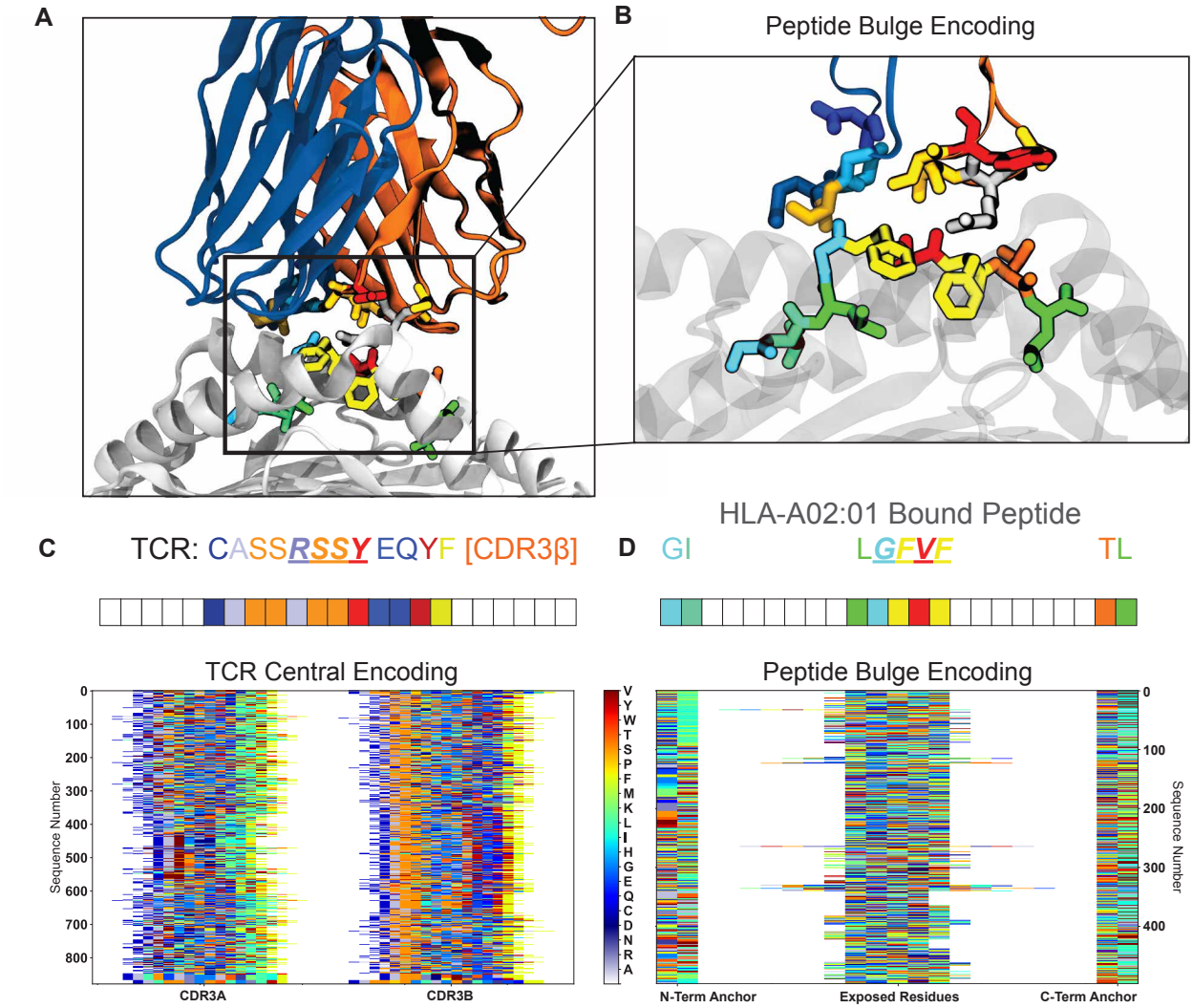

Figure 1: Example of AIMS encoding for the analysis of TCR-peptide interactions. (A) Rendering of a specific TCR-pMHC interaction (PDB ID: 1OGA) with TCRα shown in blue, TCRβ in orange, MHC in white. (B) Inset shows a zoom in on this TCR-peptide interface, with the MHC now translucent. Representative AIMS encoding of the single TCR CDR3β sequence (C, central-encoding) or the peptide sequence (D, bulge-encoding) in panel A. Below these single encodings are examples of full TCR repertoire (C) or immunopeptidome (D) AIMS-encoded matrices. Each amino acid in the structures, the single encoded sequences, and the matrices is represented by a unique color.

AIMS is capable of analyzing other molecules with conserved structural features and localized interfacial heterogeneity, including antibodies [36], MHC and MHC-like molecules [37], and, more generally, any molecular subset that can be successfully aligned using existing multi-sequence alignment software [38]. Antibody sequences can be treated in the same manner as TCRs due to their structural similarity, adopting as a default a central alignment scheme (Fig. S2A). It is important to note however, that somatic hypermutation can alter the framework regions of antibodies, which can subsequently change the flexibility of CDR loops [47], so careful analysis should utilize multiple alignment schemes to check for patterns in the data. In the case of non-immunoglobulin molecules the conserved structural features

such as interaction interfaces of Dpr-DIP proteins (Fig. S2B), α-helices and β-strands of MHC-like molecules (Fig. S2C), and antigenic sites of the *Influenza* hemagglutinin protein (Fig S2D) are the central focus of the multi-sequence alignment. The generalized AIMS encoding scheme allows for any molecular biologist or bioinformatician to take advantage of the downstream biophysical characterization tools of AIMS for their application of interest.

Methods for Repertoire Characterization

All downstream repertoire characterization follows from this initial encoding, and takes identical paths regardless of the immune repertoire under consideration. This initial encoding, where each amino acid is encoded as a number (i.e., Ala = 1, Arg = 2, Asn = 3, and so on), is projected into 61 corresponding biophysical property spaces (see Table S1). New matrices are added to the dataset encoding the biophysical properties corresponding to each amino acid, generating a three-dimensional array of shape i x j x k, where i = the number of sequences in a given dataset, j = the number of amino acid encoded positions in the datasets, and k = the number of biophysical properties (Fig. 2A). Users can optionally exclude or include additional property-encoding dimensions as desired.

The default AIMS analysis parses through this high-dimensional matrix, removing highly correlated vectors and normalizing each property to a mean of 0 and a standard deviation of 1 (Fig. 2B). This normalization is critical for identifying biophysical similarities (and differences) between the receptors in a given dataset, but users can choose to forgo this normalization and correlated vector removal if desired. From this parsed high-dimensional matrix, three primary paths can be followed through the analytical pipeline. When analyzing an unsorted population or a mixture of molecules with a non-obvious data structure such as TCR sequences acquired from peripheral blood, antibody or B-cell receptor (BCR) sequences isolated from germinal centers, or peptides identified from whole tissues, the best first step is immediate clustering of these sequences based on biophysical similarity (Fig. 2C). From this clustering, specific clusters of interest can be selected for further characterization.

If, instead, the data are antigenically well-defined, through tetramer sorting, isolation of B cells from immunized organisms, or elution of peptides from cancerous cells, AIMS can be used to either identify discriminating features between distinct repertoires (Fig. 2D) or directly characterize each well-defined repertoire biophysically (Fig. 2E, F). To identify these discriminating features, we utilize a supervised learning algorithm, specifically linear discriminant analysis (LDA) an interpretable algorithm that overcomes the typical "black box" problem in machine learning (Fig. 2D). Users may be less interested in specific, nuanced differences between repertoires, and instead require a full characterization of their repertoire of interest. If so, they can either directly opt for biophysical (Fig. 2E) and information-theoretic (Fig. 2F) characterization of direct user inputs or of the clusters of interest identified in the cluster isolation module (Fig. 2C). Generally, the linear discriminant analysis, biophysical characterization, and information theoretic quantification works best when considering binary repertoire comparisons, and loses efficacy with the number of distinct repertoires under consideration.

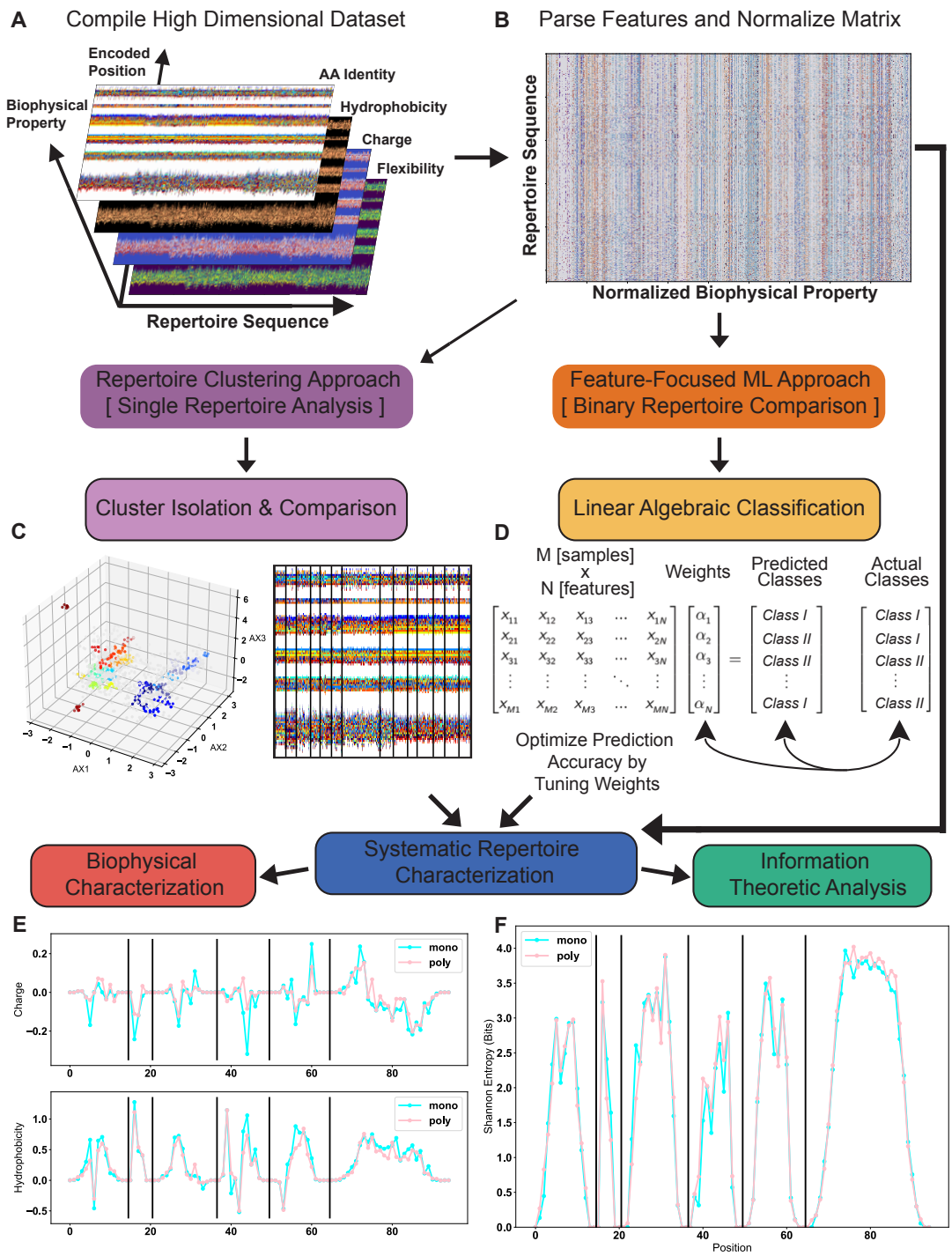

Figure 2: A graphical overview of the standard AIMS analytical pipeline. (A) Visual representation of the high-dimensional biophysical property matrix. (B) Representative parsed biophysical property matrix reshaped into two dimensions. (C) Exemplary dimensionality reduction, clustering, and re-visualization of the data in B. (D) Simplified matrix representation of the linear discriminant analysis workflow. Final repertoire characterization steps using (E) biophysical property analysis or (F) information theoretic analysis of this specific example dataset. Lines and colored boxes help guide the reader through the workflow.

In the following sections we will thoroughly describe these distinct AIMS modules, selecting the applications which best highlight the capabilities of these modules, rather than opting for a contiguous application to a single dataset. Given the flexibility and strong dependence on user input for AIMS analysis, we will highlight several typical examples for each module. More extensive descriptions of all AIMS options are provided in the supplementary material accompanying this manuscript.

Unsupervised Clustering of a TCR Repertoire from an Unsorted Dataset

For the exploratory analysis of datasets, the AIMS dimensionality reduction and clustering modules are frequently a good starting point. As an example, we generate a new AIMS analysis from the paired-chain data derived from VDJdb [16] and as shown in Fig. 1C. These sequences are complete with metadata regarding their epitope specificity, MHC allele presentation, and the haplotype of the individual each receptor was isolated from, if it was naturally derived. As intuition and recent, quantitative work have suggested [48], paired-chain TCR sequence data greatly increases the information content from a given repertoire sequencing experiment when compared to single chain sequencing. Using the AIMS dimensionality reduction and clustering module, we can determine precisely how strongly the analysis changes upon inclusion of the CDR3α sequences.

We first generate the AIMS-encoding and biophysical property matrices discussed above for both the paired-chain dataset and the CDR3β-only dataset. From this biophysical property matrix, the sequences are projected onto a three-dimensional space using the uniform manifold approximation and projection (UMAP) dimensionality reduction algorithm [49], and subsequently clustered using the density-based OPTICS (Ordering Points To Identify the Clustering Structure) clustering algorithm [50] with a minimum cluster size of 10. For best visual representation, the two-dimensional projection of the three-dimensional space is shown (Fig. 3A, B). It is important to note that, for improved clarity, the projections shown here remove four outlier sequences with a proline in CDR3α and CDR3β, a very rare amino acid in TCR CDR loops. Visualizations of the projection without outliers removed can be found in Fig. S3. In addition to the dimensionality reduction and clustering methods outlined here, AIMS is alternatively capable of utilizing principal component analysis (PCA) and t-distributed stochastic neighbor embedding (t-SNE) to reduce dimensionality and K-means and DBSCAN algorithms for downstream clustering.

From the UMAP projection and OPTICS clustering of Fig. 3A, B alone we can see that the number of distinct outlier populations is increased in the paired chain dataset, suggesting the identification of a higher number of biophysically distinct sequences. Visualizing just a subset of the clusters back as AIMS-encoded matrices (Fig. 3C, D) we see that this is likely due to the clustering of the paired chain data picking up unique motifs in both CDR3α and CDR3β, suggesting that these strong outliers can come from either chain. These clusters can then be analyzed for cluster membership compared to their original dataset identifiers, here based on the antigen recognized by each TCR (Fig. 3E, F). Importantly, cluster purity can be measured relative to metadata of the user's choice, such as antigenic species source, allele of presenting MHC, organism haplotype, or virtually any other identifiable characteristic a

user can encode as metadata for the sample (Fig. S4).

This visualization of antigen recognition for each cluster (Fig. 3E, F) highlights subtle differences between the paired-chain and single-chain datasets. We see that despite a nearly equal number of clusters identified, the average cluster purity is higher for the paired chain data at 0.50 ± 0.28 when compared to the single chain data at 0.37 ± 0.24, although not significantly so. We notice however that the few pure or close to pure clusters are coming from the same two antigens, NLVPMVATV and LLWNGPMAV, largely because these antigens make up 43 and 23 percent of the total dataset, respectively.

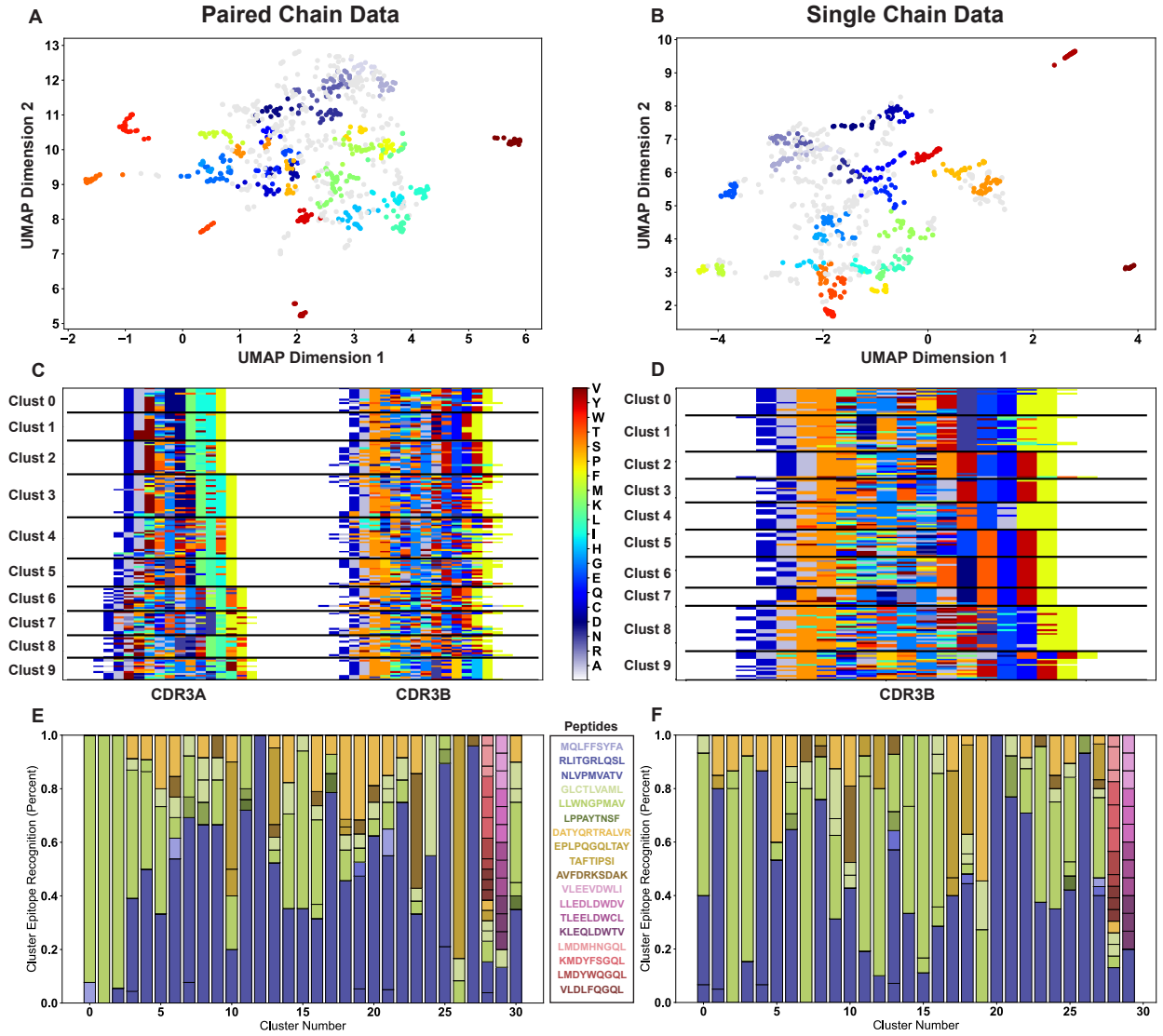

Figure 3: Comparison of the purity of receptor clustering using paired chain (left) or single chain CDR3B (right) data. Dimensionality reduction using UMAP, followed by density based OPTICS clustering subsects the data into biophysically similar paired chain (A) and single chain (B) receptors. The first ten of these clusters are then re-visualized in their AIMS-encoded matrix, with black lines marking different clusters (C, D). The antigen specificity of each of these clusters is then quantified by percentages (E, F), with the colors corresponding to specific peptides as shown in the key.

Regardless of the number of included CDR loops, two striking clusters are identified for each dataset. These two clusters, which are primarily comprised of three TCRs isolated from tumors and tested against an array of yeast-displayed peptides [11], are otherwise biophysically unassuming. Interestingly however, the fourth TCR from this study, referred to as "1A", is left unclustered by the OPTICS algorithm in both the paired-chain and CDR3β-only datasets. Coincidentally, TCR 1A is the only one of these four tumor-isolated TCRs for which the authors can find no stimulatory endogenous antigens [11], potentially suggesting that autoreactive TCRs are more frequently biophysical outliers. Overall, these results show that while unique CDR3α motifs are critically important for antigen recognition and for understanding the full breadth of receptor diversity, a fairly accurate picture of sequence diversity and similarity can still be generated from CDR3β sequences alone.

In the last step of clustering, users may choose to further analyze isolated clusters, running these sequence subsets through the AIMS biophysical characterization and information theoretic pipeline. This step, outlined in the next section, gives AIMS users the ability to identify nuanced differences in specific clustered sequence subsets within a given repertoire.

Going Beyond Receptor Clustering and Motif Analysis

The next key module in the analysis pipeline is unique to AIMS, and takes advantage of the architecture of the AIMS biophysical property matrix. As mentioned previously, the analysis of this and the next section can be carried out with individual clusters of sequences derived from unstructured data, as outlined in the previous section, or from antigenically well defined populations (see Fig. S5 or Boughter et al. [36] for examples). In highlighting the features of the biophysical property analysis, we select the two antigenically purest clusters of Fig. 3 from both the paired-chain and single chain datasets with specificity to the NLVPMVATV and LLWNGPMAV antigens (Fig. 4A, B). From these cluster subsets, we can appreciate that despite having nearly the same antigenic purity in each of these clusters, the paired chain clusters surprisingly display increased CDR3β diversity. While we are able to generate sequence logos for the distinct motifs in these clusters (Fig. S6A, B), the AIMS analysis pipeline permits a richer biophysical characterization of these clusters.

Specifically, from the high-dimensional biophysical property matrix for each of these clusters, we can isolate single property masks (Fig. S6C, D) which can be averaged across repertoires (Fig. 4C, D) or across repertoires and positions (Fig. S6E, F), generating position sensitive or net average biophysical properties for the molecular subsets of interest. These biophysical property visualizations can be used to more carefully compare and contrast the clusters generated from the paired-chain and single chain datasets. We see from the position-sensitive biophysical property averages that the general trends of CDR3β are matched in the paired-chain and the single-chain clusters, despite the significant difference in diversity of CDR3β. The positively charged region of CDR3β in TCRs recognizing the LLWNGPMAV peptide is seen in both datasets, while a corresponding negative region is found in the CDR3α of TCRs recognizing the NLVPMVATV peptide.

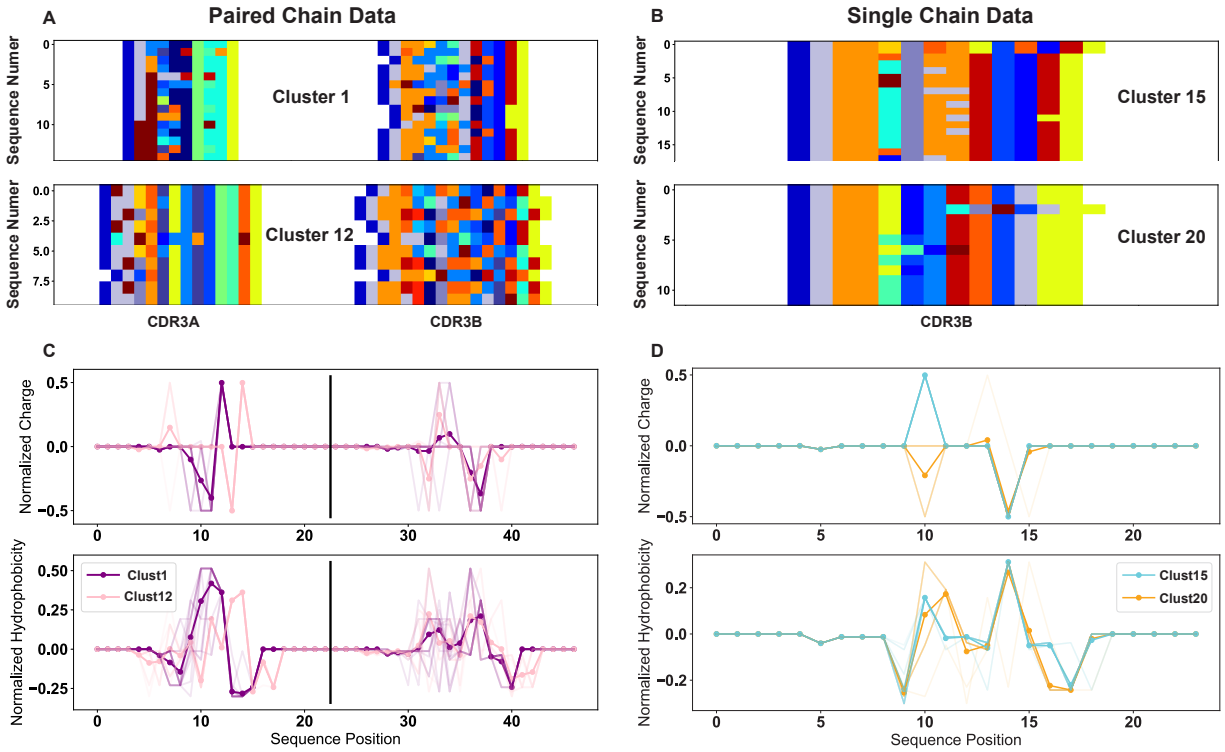

Figure 4: Isolation of individual sequence clusters and subsequent position-sensitive biophysical characterization of these sequences. A subset of clusters identified in Fig. 3 are isolated and shown as their AIMS matrix encoding for the paired chain (A) and single-chain (B) datasets. From these encodings, we can calculate the position sensitive biophysical properties for each cluster (C, D). Opaque lines with dots represent the averages over each cluster, while translucent lines trace the biophysical property value for each sequence in the cluster, adding in the visualization of variance.

Given the lack of charged residues in the peptides, the conservation of charge in these pure clusters is somewhat surprising. Conversely, the hydropathy score of the CDR3β chains is far more variable within the paired-chain clusters, although the same general trend is again followed when compared to the single-chain data, with two distinct peaks in hydropathy and a region neither lacking nor enriched in hydrophobic residues. This is a common feature in the clustering of sequences in AIMS, and may reflect the nature of the hydrophobicity metrics used, or alternatively could be suggestive of the important features in the formation of TCR-pMHC complexes. While charges in the interface must be delicately arranged to form interfacial interactions and offset the significant energetic penalties of desolvation, more hydrophobic residues are free to effectively "fill in the blanks" and pack as best they can.

While only the position sensitive charge and hydropathy are highlighted in this section, any of the 61 standard AIMS properties can be visualized in a user-specified manner, either as position-sensitive averages across receptors, or as net averages over position- and sequence-space. Parameters that are structurally related, but again do not make explicit structural predictions, are often nearly as useful as these more common biophysical properties. Amino acid size, β-sheet or α-helical propensity, and amino acid flexibility can often help to generate new hypotheses in the absence of a reference crystal structure. The analysis highlighted here

is specifically for the qualitative comparison across clusters or repertoires. For an outline of how to generate more quantitative and statistically rigorous comparison of distinct groups of sequences, we refer readers to the supplement.

Generating Quantitative Metrics of Repertoire Diversity and Amino Acid Patterning

While the biophysical characterization of immune repertoires can help answer questions regarding the mechanisms of immune recognition, complementary analysis is required to identify patterns emerging from the dynamic nature of an immune response. Understanding the broader patterns and probabilities of amino acid usage in these diverse molecules can elucidate the details of receptor or antigen generation, selection, presentation, or persistence. In AIMS, we can further quantify entire repertoires, cluster molecular subsets, or define antigenic groups using an array of statistical and information theoretic approaches.

Information theory is a powerful tool, originally formulated to develop "A Mathematical Theory of Communication" [51] that has seen a recent resurgence in immunological research [52–55]. Fundamentally, information theory is built for the analysis of sequences of inputs and outputs. Here, these inputs and outputs are the amino acids making up our immune repertoires, through the quantification of the observed probability distributions of these sequences. To illustrate the capabilities of the AIMS probabilistic and information theoretic tools, we switch from the paired chain VDJdb example to two subsets of isolated peptides from the IEDB: *Influenza A*- and *Ebolavirus*-derived peptides presented by HLA-A*02:01 and HLA-B*15:01, respectively [46].

In AIMS, we leverage the inherent position-sensitivity of the encoded matrices to build up a site-specific probability distribution (Fig. 5A) for these peptide inputs. We see from these position-sensitive probability distributions that the expected anchors at P2 and the C-terminal positions (or P1 and P14 in the AIMS encoding of Fig. S7) have the strongest amino acid preference, as expected for these positions [56, 57]. We see in comparing these two datasets that only P2 glutamine and isoleucine show up as distinct anchors for HLA-B*15 and HLA-A*02, respectively, because other strong anchors are shared between these two alleles. Due to the limited overlap in the C- terminal anchors, we see strong preferences towards HLA-B*15 peptides containing tyrosine and phenylalanine, and a similar preference towards leucine and valine anchors for HLA-A*02. However, whereas conventional sequence logo plots can generate similar inferences, albeit via a more indirect comparison, the AIMS analysis takes these probability distributions a step further. First, from the position-sensitive probability distribution, we can calculate relevant information theoretic metrics such as the Shannon entropy and the mutual information to quantify diversity and relationships among the peptide preferences for these repertoires.

In calculating the Shannon entropy we can identify trends in conserved residues, as may be present in obvious anchor positions of peptides or key contact residues of antibodies and TCRs. We show the position-sensitive entropy for these two defined peptide populations (Fig. 5B), and see that in addition to the two anchor positions, there are additional insights

into the diversity of the central amino acids. Specifically, we see that even with peptides derived from single viral clades, the diversity at the center of the peptides is nearly maximal, i.e. all 20 amino acids occurring at nearly equal probability. Given the arguments for the necessity of cross-reactivity in T cells [58], this massive diversity from singular datasets is perhaps unsurprising. Importantly, from this diversity, AIMS can pull out signals that are unique to each dataset by calculating the mutual information.

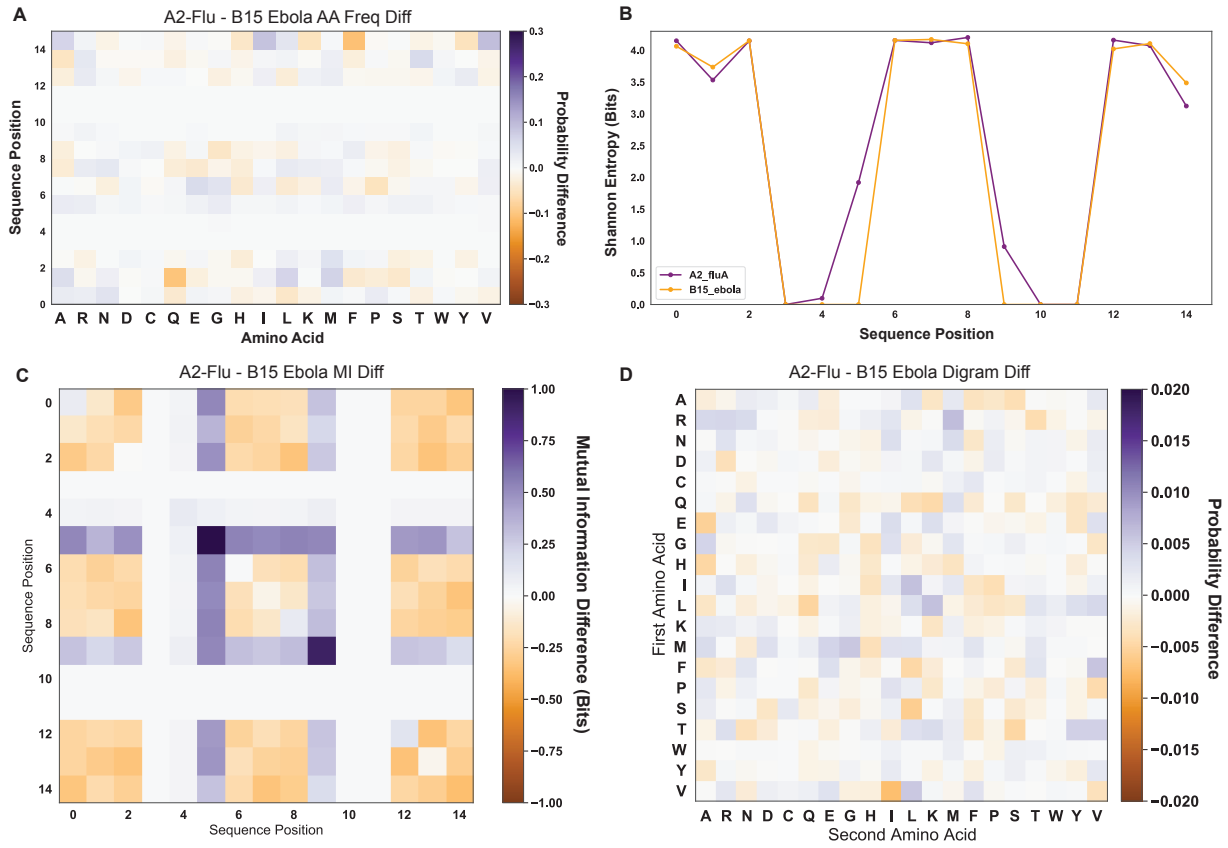

Figure 5: Statistical and information theoretic AIMS analysis of *Influenza A*- and *Ebolavirus*-derived peptides. (A) Position sensitive amino acid frequency difference between the two peptide datasets. (B) Position sensitive Shannon entropy quantification of the two peptide datasets. (C) Position sensitive mutual information difference between the two peptide datasets. (D) Di-gram amino acid frequency difference calculated between the two peptide datasets. In all difference plots, a deeper shade of purple represents a higher quantity for the HLA-A*02 presented *Influenza A* peptide dataset, while a deeper shade of orange represents a higher quantity for the HLA-B*15 presented *Ebolavirus* peptide dataset.

The mutual information, as its name suggests, is a measure of the amount of information gained from some given condition. Looking at the difference in the mutual information between the *Influenza A*- and *Ebolavirus*-derived peptides, we see strong trends of increased information between the N- and C-terminal ends of the *Ebolavirus*-derived peptides (Fig. 5C). We further see that although only the *Influenza A*-derived peptides have a varied length distribution, leading to the wider central entropy peak, there is a clear signal in these long peptides, suggesting a specific subset of amino acid usage in the peptides that tend to be longer. Generally in immune repertoire analysis, mutual information may represent

instances of co-evolution or receptor cross-talk, as has been discussed in analysis of polyreactive antibody sequences [36]. The goal of this information-theoretic analysis is to identify key regions of increased diversity, conservation, or crosstalk. For more details on the calculation of the entropy and mutual information, as well as the equations utilized for these calculations in AIMS, we refer the reader to the methods.

As a final step, we can attempt to identify the source of the patterns in the short-range mutual information through the analysis of di-gram amino acid probabilities. Removing the position sensitivity of the peptides in each dataset, we can count the raw occurrence probabilities of each peptide di-gram using a sliding window, building up a probability distribution for each amino acid pair, where the order of occurrence matters. From these di-gram probabilities, we can add significant context to our information theoretic results (Fig. 5D). Interestingly, although there are strong differences in the raw amino acid occurrence probabilities for each dataset (Fig. S7), the di-gram differences are often concentrated in precise regions. For instance, both arginine and methionine are more frequently found in the *Influenza A* dataset, and this difference can largely be attributed to an enrichment in the arginine-methionine di-gram. In addition to the standard analysis pipeline outlined here, the analysis can be extended arbitrarily to include N-gram motifs, providing the potential to identify regions with a propensity for certain triads or higher-order motifs. Due to the additive nature of Shannon entropy, the entropy summed over any of these N-gram formulations will always be equivalent to the entropy of the sequences included in the entire dataset, providing a maximum value for the diversity within the data. Likewise, the N-gram probability distributions can always be related back to the raw probability distributions of each single amino acid.

Machine-Learning Based Classification for Binary Repertoire Comparisons

While the unsupervised clustering and information theoretic analysis in AIMS is ideal for exploratory analysis of repertoires, a more targeted, supervised learning approach is also available for the identification of specific differences in distinct repertoire datasets. This supervised learning in AIMS utilizes a linear discriminant analysis (LDA)-based classifier to simultaneously sort individual sequences into their respective classes and identify key features that delineate distinct repertoires. While other algorithms may perform better in classifying repertoire data, the strength of LDA lies in its interpretability. Unlike other machine learning methods, the vectors most important for discriminating between distinct repertoires are included as output, along with their associated linear weights. Further details on linear discriminant analysis can be found in the methods. In this targeted supervised approach, users immediately identify key, position-sensitive differences between their datasets while also generating a classifier for future use in their analysis. While a key feature of the AIMS analysis, we will not discuss the application of LDA to immune repertoires further in this manuscript due to space considerations. Instead, we refer the reader to two applications of the AIMS LDA module as seen in Boughter et al. [36] and Nandigrami et al. [38]

Comparisons to Existing Software

While the AIMS analysis pipeline has been developed to address more than just TCR repertoire analysis, it shares some features with existing software such as GLIPH [26] and TCRdist [24, 59]. These software packages aim to identify TCR sequences enriched above background populations or to cluster sequences with similar amino acid motifs, taking different approaches but generating similar results to the AIMS clustering outlined above. Although a detailed comparison between different types of software with potentially non-overlapping algorithms and output options can be difficult, we should expect similar results when applied to the same problems. For GLIPH, we compare our ability to identify distinct motifs using the standard AIMS analysis, whereas in comparing to TCRdist we more quantitatively compare the TCRdist "distance" metric to the corresponding AIMS distance in the high-dimensional biophysical property space.

As a representative motif comparison, we examine the output of GLIPH from Glanville et al. [26] as applied to the *Influenza* antigen M1 presented by HLA-A*02:01 (Fig. 6).

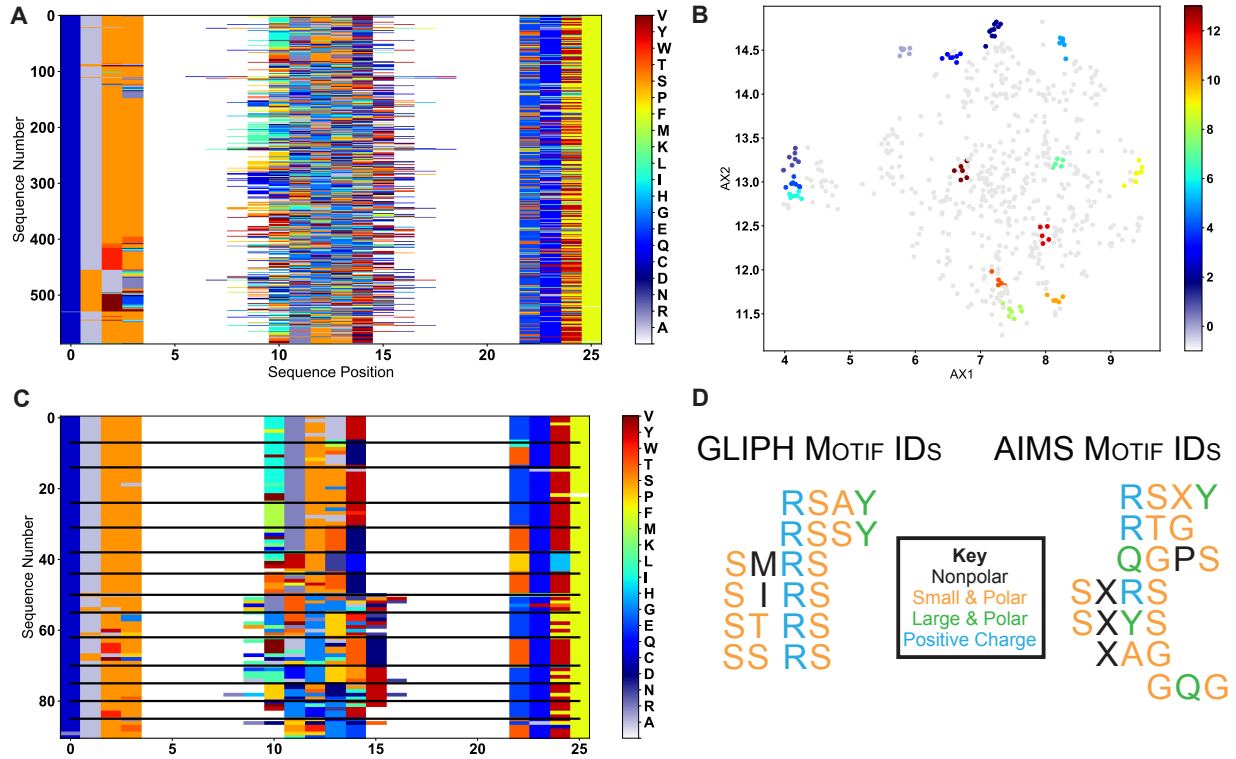

Figure 6: Comparison of AIMS TCR clustering analysis to GLIPH results. (A) The *Influenza*-reactive TCRs identified by Glanville et al. are encoded into an AIMS matrix using the bulge-encoding. (B) Each sequence is then processed using the standard AIMS pipeline, and then projected onto two dimensions using PCA and clustered using the OPTICS algorithm. (C) These clusters are then re-visualized as an AIMS matrix. (D) Finally, the motifs identified by GLIPH can be directly compared to the motifs identified by AIMS via the clustering in panel C. Biophysical properties of each amino acid in the motif are colored according to the key, and an "X" in the AIMS motif represents "any amino acid with this biophysical property", i.e. the orange "X" can represent S, T, G, or A.

In addition to the benchmarking of the results of each software, we can compare and contrast the distinct paths to these results. One such difference between AIMS and GLIPH is that there is no "reference population" needed as input for AIMS. AIMS takes the identified M1-reactive sequences (Fig. 6A), generates the previously discussed biophysical property matrix, and identifies biophysically distinct clusters in a projected space of these biophysical properties (Fig. 6B). Unlike the more diverse clusters of Fig. 3 resulting from the analysis of a broad input repertoire, this more targeted analysis of tetramer-sorted sequences results in more homogeneous clustered sequences (Fig. 6C). From these clusters, we can then identify the key sequence motifs of each cluster and compare these to the GLIPH results (Fig. 6D).

First, it is important to note that subsets of the same sequence identified by GLIPH are not included here; for instance, the motifs SIRS, IRS, and SIR are all identified as distinct by Glanville et al., but are included only as SIRS here. Further, coloring the sequences by a description of the most basic amino acid properties shows that many of the distinct GLIPH motifs are biophysically degenerate. In contrast, AIMS identifies thirteen biophysically distinct clusters, three of which fully encapsulate the results of GLIPH. While the GLIPH results seem to suggest that an arginine is a requisite for recognition of the highly hydrophobic peptide GILGFVFTL, we see this dependence on the presence of an arginine is relaxed in the AIMS results, instead suggesting the need for an enrichment of smaller amino acids (S, T, G, A) or nonpolar residues. Importantly, it is clear that a hydrophilic amino acid is well tolerated or in fact required for recognition, as six of the seven highlighted AIMS clusters have such a conserved residue in CDR3β.

We can furthermore quantitatively compare the AIMS analysis to TCRdist, an analysis software that clusters and annotates inputs of large TCR repertoires based on similarity. The "distance" metric critical to the TCRdist pipeline provides a useful quantitative comparison point for our AIMS analysis. Importantly, this distance metric is fundamentally based upon the BLOSUM62 substitution matrix [60]. The BLOSUM62 substitution matrix implicitly encodes biophysical similarities and differences between amino acids, whereas the AIMS encoding explicitly encodes all of these biophysical properties in a single high-dimensional matrix. As such, we should expect similar, but not necessarily identical results when calculating the TCR distances using both TCRdist and AIMS.

Using the mouse TCR repertoire data of Dash et al. [24], we first generated the AIMS encodings for either the CDR3 loops of the sequenced TCRs (Fig. 7A) or for all six CDR loops of these same TCRs (Fig. 7B) with the intention of matching the two main distance output options in TCRdist. We next generated the high-dimensional biophysical property matrices for each of these AIMS-encoded matrices, normalized each feature as discussed previously, and removed highly correlated vectors from each matrix. While the next step in the standard AIMS analysis pipeline is the reduction of these high dimensional matrices, the UMAP and PCA projections do not conserve the distances between points. As such, we instead calculate the raw Euclidean distances in the high-dimensional space, and directly compare these to the TCRdist values.

From these panels, we see reasonably strong correlation for the CDR3-only distances (Fig. 7C, α and β chain correlation coefficients of 0.73 and 0.72, respectively) and a stronger

correlation for the full CDR loop calculations (Fig. 7D, α and β chain correlation coefficients of 0.83 and 0.75, respectively). In both datasets, we see that as the TCRs get more dissimilar, the AIMS distances seem to level off even as the TCRdist metric continues to get larger. This may be due in part to well known issues with the calculation of distance metrics in high-dimensional spaces [61], but is likely not a point of concern in the standard AIMS analysis as clusters are generated in the projected spaces. In recent applications of TCRdist [59], a distance cutoff of 20 has been used to define similar CDR3 loops of TCRs. Using this same definition and then a distance cutoff of 60 for all six CDR loop distances, we see that the correlation coefficients improve for more similar TCRs, with CDR3 (all CDR) correlation coefficients of 0.85 (0.86) for the α-chain and 0.85 (0.82) for the β chain. Comparisons with a wider range of antigens from Mayer-Blackwell et al. [59] show similar agreement (Fig. S8).

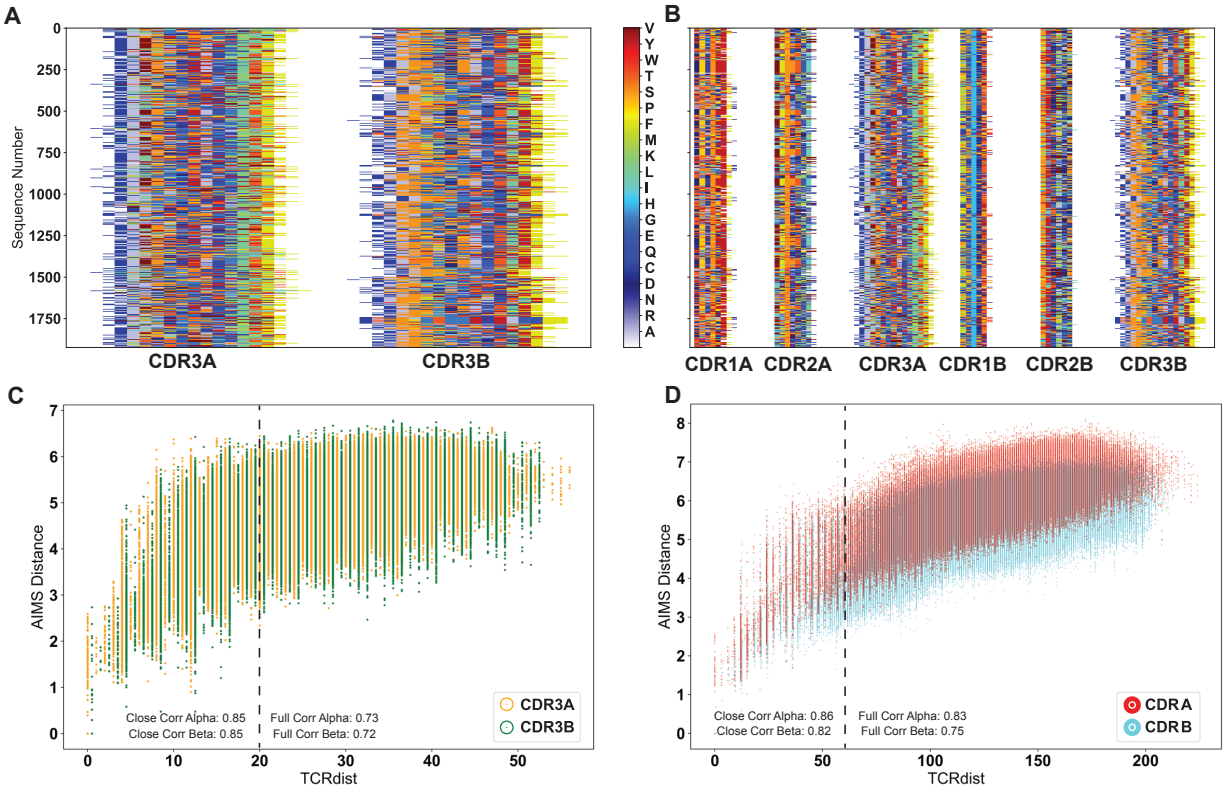

Figure 7: Quantitative comparison of distance metrics used in AIMS and TCRdist. Both the CDR3-only sequences (A) and the full-CDR sequences (B) of Dash et al. are encoded into AIMS matrices. Sequence distances calculated via TCRdist and AIMS are then directly compared for these CDR3-only sequences (C) or full-CDR sequences (D) for the TCRα- and β-chains. Correlation coefficients between these distance metrics are reported for the full set of sequences and for closely related sequences, which are delineated by the dashed vertical lines.

Thus, in searching through the high-dimensional biophysical space for the same distinct repertoire clusters as GLIPH and TCRdist, AIMS provides not just the identification of these clusters but also the biophysical similarities within these clusters; effectively providing the explanations for why sequences are grouped into the same clusters. Further, comparisons between clusters or even separate datasets can be made at a level deeper than the motif

scale. In highlighting the functionality and unique strengths of AIMS, we set out to show that previous results from TCRdist and GLIPH can be reproduced, and that these results can subsequently be expanded upon with new analyses.

DISCUSSION

Immune molecules and the pathogens which they protect against represent a unique case study for bioinformatic analysis approaches. The variable or polymorphic regions of TCRs, antibodies, and MHC molecules in humans are concentrated in select regions of these proteins, specifically in their key intermolecular interaction sites, while the rest of their three-dimensional structures are exceptionally well conserved. This structural conservation and localized variability appears to point towards molecular modeling as a key tool, but modern computational approaches are either too costly i.e., slow and inefficient, or too inaccurate to allow for detailed conclusions regarding the proximity of specific amino acids [28, 39, 62]. Many of the best performing machine learning approaches are "black box" algorithms that do not allow the user to determine how or why certain classifications are made. While more interpretable structural modeling approaches are capable of approximate placement of TCR protein backbones on the pMHC surface, even the best structure prediction software struggles to place receptor side chains in the proper position on the antigenic surface [28, 39]. Proper placement of these side chains, to Angstrom-level precision, is key for proper inference of the interaction strength between receptors and their cognate antigens.

AIMS was developed specifically as an interpretable tool for immune repertoire analysis, capable of utilizing the information provided by conserved structural features of immune molecules for unique analytical approaches while reducing the potential for errors arising from insufficient resolution offered by structural predictions. The generality of the AIMS analysis pipeline allows for the simultaneous characterization of all adaptive immune molecules, including peptides, conserved viral structures, antibodies [36], MHC molecules [37], T cell receptors, and broadly any protein subset with structurally conserved features and localized diversity [38]. Currently the standard AIMS pipeline analyzes each of these molecular subsets individually, and subsequently allows users to compare and contrast biophysical features of paired TCR-pMHC or antibody-antigen interactions. Recently developed features and further ongoing work is aimed at incorporating mixed repertoire analysis from the pipeline initialization. These features will provide insights into the intricacies and inter-relationships of all of the molecular players involved in an adaptive immune response.

Of the existing software packages available for the analysis of molecular subsets of adaptive immunity, T cell receptor repertoire analysis is likely the most mature of the fields, and therefore serves as the primary point of comparison for AIMS. Despite not being developed explicitly for T cell receptor analysis, we find that AIMS can reproduce the results of two of the most popular programs developed for TCR analysis, namely GLIPH and TCRdist [24, 26, 59]. GLIPH and TCRdist both utilize distance based metrics to identify unique motifs from TCR repertoire datasets. Extending sequence analysis beyond clustering, AIMS quantifies the biophysical differences between identified clusters of sequences to determine the

various approaches TCRs take to recognize single antigenic targets. In the analysis of large experimental datasets, users have the option of clustering using GLIPH or TCRdist, and subsequently importing these sequences into AIMS for the downstream analysis, providing an opportunity for comparisons of multiple approaches to repertoire analysis.

AIMS fundamentally is built around the identification of biophysically distinct molecular subsets. Independent of any biases in the experimental approaches used, AIMS aims to find the receptor subsets that most strongly span the biophysical space of the input dataset. While still susceptible to some of the issues that plague all analysis in the regime of strong undersampling, by focusing on those receptors that are the most biophysically distinct, rather than those that are the most similar according to a variety of distance metrics, we can identify the limits of molecular recognition. This may under-emphasize the importance of convergence towards certain motifs in immune responses, but it enhances our understanding of the diverse paths adaptive immune systems take towards solving the same problems of pathogenic recognition.

METHODS

This section should serve as a reference for the conceptual considerations and assumptions that are key features in AIMS. For a more practical discussion of the implementation of AIMS using either the graphical user interface (GUI) for non-computational researchers or the Jupyter notebooks for more advanced users, we direct the reader to download the code through GitHub [https://github.com/ctboughter/AIMS] and follow the walkthroughs available at [https://aims-doc.readthedocs.io/en/latest/].

Dimensionality Reduction and Unsupervised Clustering

In the analysis of immune repertoires, and broadly of amino acid sequences, thorough characterization of these sequences requires the generation of a high-dimensional space comprised of assorted descriptive properties. To systematically analyze this high-dimensional space of data, AIMS employs both linear and non-linear dimensionality reduction techniques with extensive flexibility in the application of these techniques given to users.

Often, we recommend starting with the linear dimensionality reduction, principal component analysis (PCA). PCA is a highly interpretable dimensionality reduction technique that projects the data onto linear combinations of the input vectors corresponding to the orthogonal vectors spanning the dimensions of highest variance in the data. PCA is a powerful and interpretable tool for analysis of high-dimensional datasets, as the identified principal components are fundamental linear algebraic properties of the matrix. Due to the linear nature of PCA, the precise biophysical properties used to create the principal components are easily inferred from the data. Unfortunately, in the analysis of immune repertoires, the axes of highest variance are not always those that best separate the key biophysical features in a given dataset. In antibody and TCR data particularly, the vectors of highest variance in

the data will generally be in the center of the CDR3 loops. While this frequently also means that CDR3 will be the most distinguishing feature of a given antibody or TCR sequence, this need not always be the case.

If needed, users can instead turn to the nonlinear dimensionality reduction techniques, specifically t-stochastic neighborhood embedding (t-SNE) and uniform manifold approximation projection (UMAP). Fundamentally these nonlinear algorithms attempt to reduce dimensionality while preserving distance between and within clusters of data points in the original input space. Users should become familiar with each algorithm by reading the relevant literature, but certain key features will be discussed here. Perhaps most importantly, both t-SNE and UMAP as implemented in python are inherently stochastic algorithms. This means that if users want reproducible analysis, care must be taken to first specify a specific seed from which the stochastic algorithm will start from. Further, as nonlinear algorithms the resultant projections are not easily interpreted, making the identification of biophysical differences in localized clusters of data points difficult. Notably however, some of the downstream analytical tools in AIMS can help overcome this shortcoming.

Once the data have been projected onto a lower-dimensional space, users must define their clustering algorithm of choice. The default, Kmeans clustering, is the most conceptually straightforward, breaking the data into N clusters, where N is defined by the user. Kmeans clustering is especially useful if users should expect *a priori* some specific number of clusters arise within their data. In using AIMS for more exploratory studies, density-based clustering is recommended instead, using either OPTICS or DBSCAN algorithms. These algorithms are not biased by a user-defined number of clusters, and instead identify clusters based on localized concentrations of data points. Each algorithm comes with its own advantages and disadvantages, so again users are encouraged to read further on these to inform their analysis. In the body of this manuscript, UMAP is used to reduce the dimensionality, while the OPTICS algorithm is used to cluster the data.

Linear Discriminant Analysis

As discussed briefly in the main text, linear discriminant analysis (LDA) is described in greater detail in Boughter et al. [36] and Nandigrami et al. [38]. Briefly, LDA is useful for two distinct purposes, the generation of classifiers to be used in future applications, and the identification of key features that discriminate between two well-defined datasets. Importantly, both of these applications require large amounts of well-defined data to be confident in the results and a discrete number of labels that can be applied to these data. Unlike much of the data used as examples here, which are more heterogeneous or comprised of mixed populations of data. Despite this, here we briefly define how linear discriminant analysis works in AIMS.

LDA is conceptually similar to PCA, in that the data are projected onto axes generated via a linear combination of the input vectors. However, in LDA the classes which each sequence belongs to are added as input, and the identified axes are those which both minimize within-class distance while maximizing distance between classes. Further, unlike PCA, users

must be aware of a potential for overfitting. To avoid this, AIMS includes multiple preprocessing steps before the LDA calculation, including the removal of highly correlated vectors in the biophysical property matrices and a range of algorithms for the selection of a subset of key vectors. When the LDA calculation is completed, the key outputs used in AIMS are the linear weights for each input vector. These weights can then be sorted by magnitude to identify the key properties that best discriminate between the input datasets. These properties can then be visualized in AIMS using the standard biophysical property analysis. For the generation of interpretable classifiers using LDA, more advanced knowledge of machine learning is recommended.

Information Theoretic Calculations

Information theory, a theory classically applied to communication across noisy channels, is incredibly versatile in its applications, with high potential for further applications in immunology [51,52,63–66]. In AIMS, we utilize two powerful concepts from information theory, namely Shannon entropy and mutual information.

Shannon entropy, in its simplest form, can be used as a proxy for the diversity in a given input population. This entropy, denoted as H, has the general form:

$$H(X) = -\sum_{X} p(x) \log_2 p(x) \tag{1}$$

Where $p(x)$ is the occurrence probability of a given event, and X is the set of all events. We can then calculate this entropy at every position across AIMS-encoded matrices, where X is the set of all amino acids, and $p(x)$ is the probability of seeing a specific amino acid at the given position. In other words, we want to determine, for a given site in the AIMS matrix, how much diversity (or entropy) is present. Given there are only 20 amino acids used in naturally derived sequences, we can calculate a theoretical maximum entropy of 4.32 bits, which assumes that every amino acid occurs at a given position with equal probability.

Importantly, from this entropy we can calculate an equally interesting property of the dataset, namely the mutual information. Mutual information is similar, but not identical to, correlation. Whereas correlations are required to be linear, if two amino acids vary in any linked way, this will be reflected as an increase in mutual information.

In AIMS, mutual information $I(X;Y)$ is calculated by subtracting the Shannon entropy described above from the conditional Shannon entropy $H(X|Y)$ at each given position as seen in equations 2 and 3:

$$H(X|Y) = -\sum_{y \in Y} p(y) \sum_{x \in X} p(x|y) \log_2 p(x|y) \tag{2}$$

$$I(X;Y) = H(X) - H(X|Y) \tag{3}$$

Putting these equations into words, we are effectively asking how the knowledge of the identity of an amino acid at one site changes the entropy at another site. If the entropy at the "test site" is zero, i.e. $H(X) = 0$, then no matter what we know of the amino acid identity at another site the change in entropy at the test site will still be zero, and therefore the mutual information will be zero. Likewise, if the entropy remains unchanged at this test site despite the knowledge of the amino acid identity at another site, the mutual information will again be zero. There is only a meaningful mutual information between a test site and a given amino acid site if the knowledge of that given amino acid reduces the entropy at the test site. The mutual information cannot be negative, so the reverse situation, i.e. an increase in diversity with the knowledge of amino acid identity at a given site, cannot occur.

Statistical Considerations in AIMS

The position sensitive averages in AIMS in particular are critical for comparing repertoires from distinct sources or subsets of repertoires, and are capable of identifying different modes of recognition for these molecules. Importantly, these averages are difficult to compare statistically, as they are not normally distributed due to the discrete nature of the 20 amino acids composing protein sequences. As such, the AIMS standard for statistical analysis of these repertoires is to bootstrap a normal distribution of receptor averages, with the bootstrapped average and the bootstrapped standard deviation reported as the final statistically-relevant values. More information on this bootstrapping can be found on the GitHub page. By default, general trends are identified using AIMS first, without bootstrapped values (due to computational cost), and should the user choose to calculate these bootstrapped values, they can do so using code provided solely for this application.

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Competing Interests

The authors declare no competing interests.

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Chomont, Nelson L. Michael, Merlin L. Robb, Nittaya Phanuphak, Jintanat Ananworanich, Julie A. Ake, Siriwat Akapirat, Meera Bose, Evan Cale, Phillip Chan, Sararut Chanthaburanun, Nampueng Churikanont, Peter Dawson, Netsiri Dumrongpisutikul, Saowanit Getchalarat, Surat Jongrakthaitae, Krisada Jongsakul, Sukalaya Lerdlum, Sopark Manasnayakorn, Corinne McCullough, Mark Milazzo, Bessara Nuntapinit, Kier On, Madelaine Ouellette, Praphan Phanuphak, Eric Sanders-Buell, Nongluck Sangnoi, Shida Shangguan, Sunee Sirivichayakul, Nipattra Tragonlugsana, Rapee Trichavaroj, Sasiwimol Ubolyam, Sandhya Vasan, Phandee Wattanaboonyongcharoen, and Thipvadee Yamchuenpong. Safety and efficacy of VRC01 broadly neutralising antibodies in adults with acutely treated HIV (RV397): a phase 2, randomised, double-blind, placebo-controlled trial. *The Lancet HIV*, 2019.

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Supplemental Figures

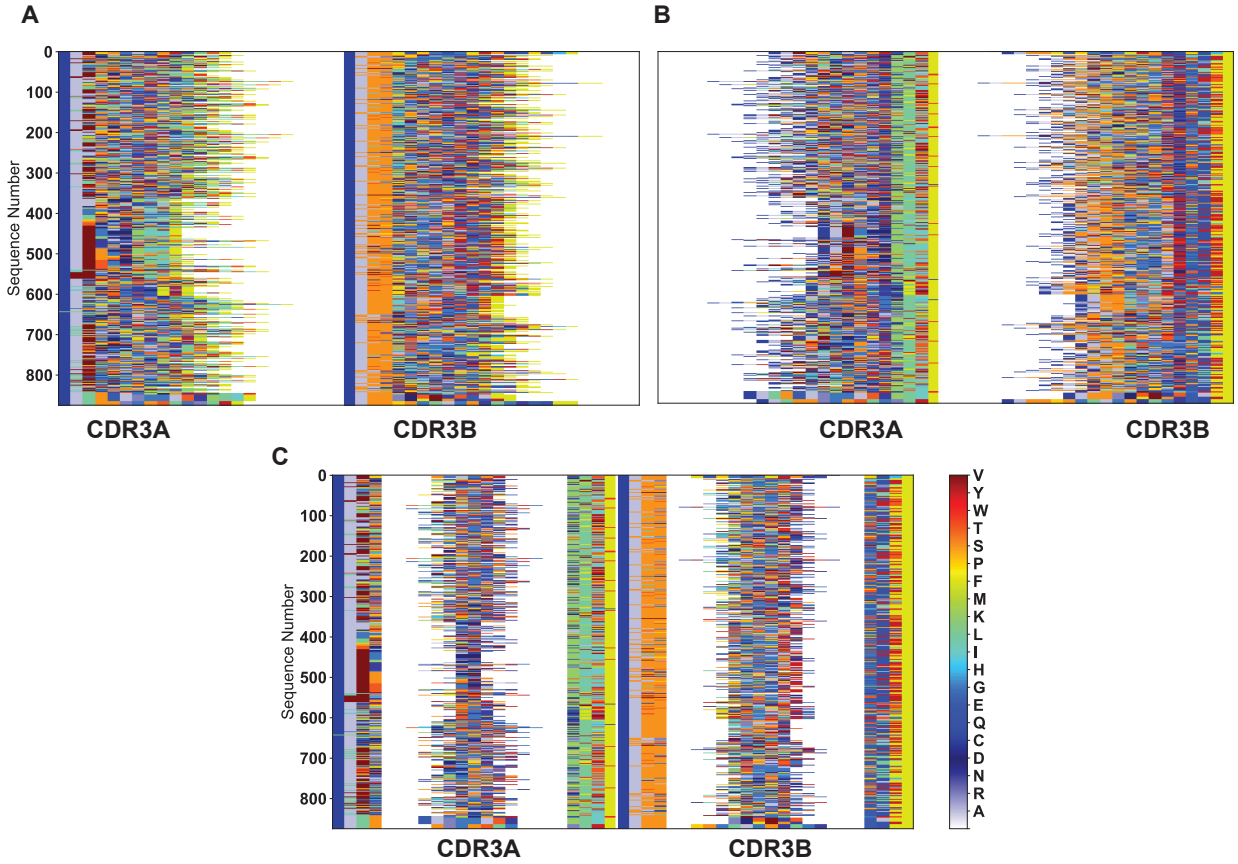

Figure S1: Alternate numerical encoding alignment schemes in AIMS using the same repertoire data as Fig. 1C. Each of these schemes are independently applied to individual key structural features by aligning to the (A) N-terminal amino acids, (B) C-terminal amino acids, or (C) "bulge" encoding as discussed in the peptide analysis described in the main text. Here the bulge padding is set to 6, i.e. 3 amino acids padding the N- and C- termini are separated for alignment, and the remaining amino acids are centrally aligned.

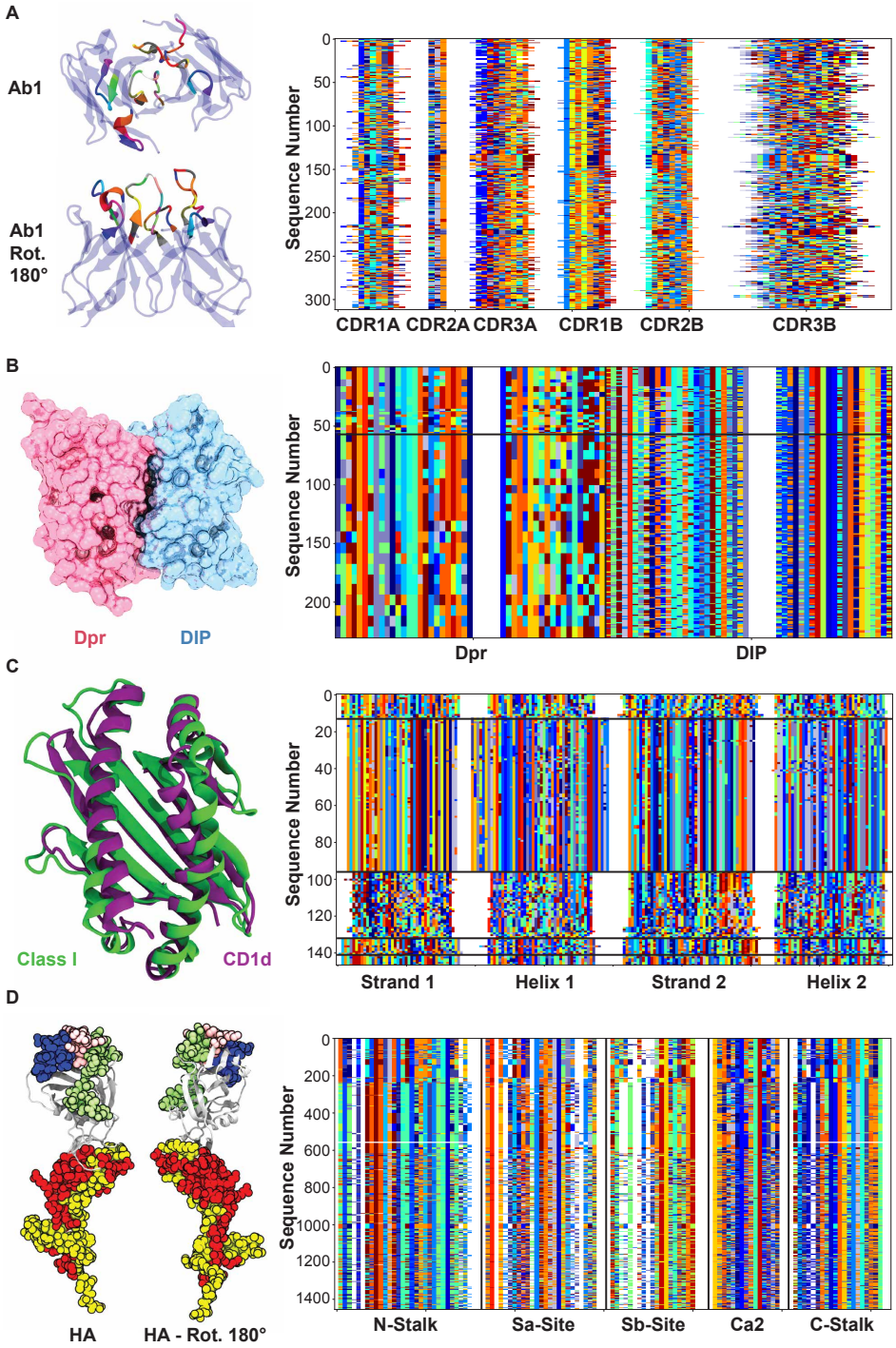

Figure S2: Examples of the input flexibility available in AIMS, with molecular structures on the left and AIMS encodings of subsets of these structures on the right. (A) Antibody encoding of all six CDR loops, structure via Marta Borowska et al. [Unpublished]. (B) Multiple sequence alignment encoding as discussed in Nandigrami et al. [38]. (C) MHC and MHC-like encoding of the α-helices and β-strands of these related molecules, structures via PDBs: 2XPG, 1ZT4. (D) Multiple sequence alignment encoding of *Influenza* hemagglutinin (HA) protein, structure via PDB: 1RUZ. *Influenza* MSA via 3DFlu [67].

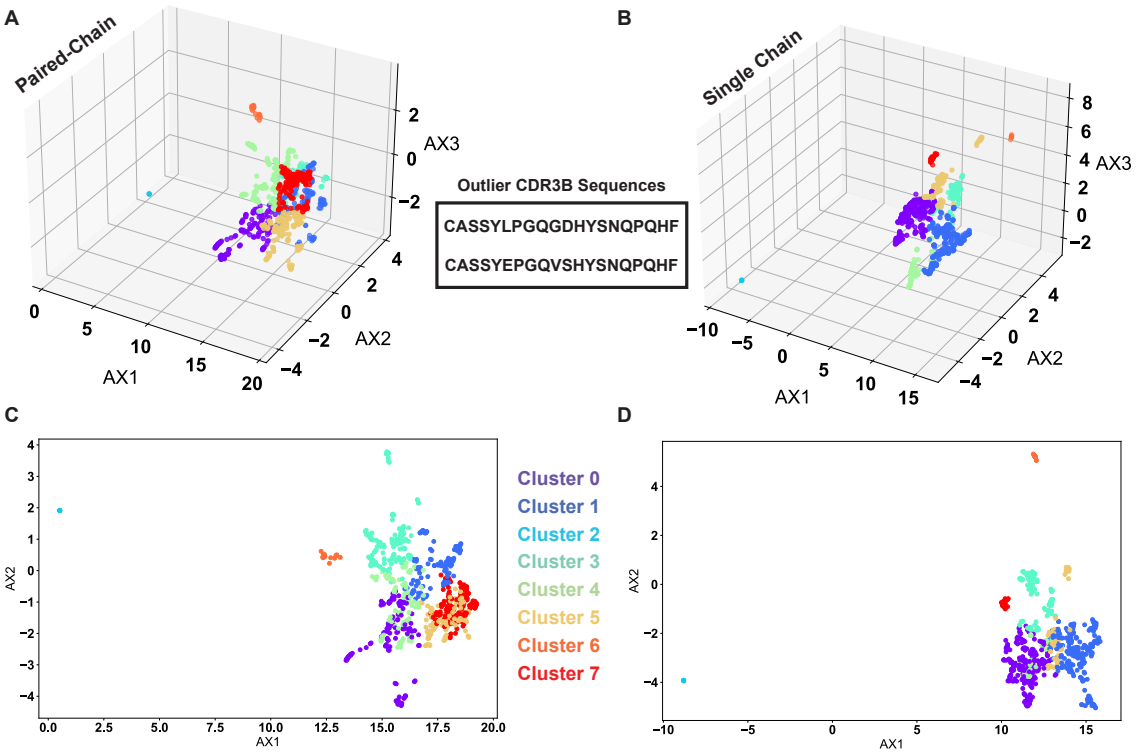

Figure S3: VDJdb repertoire dimensionality reduction and clustering analysis including proline-containing outlier sequences. Shown are the three-dimensional clustering results for the paired chain (A) and single chain (B) data and the two-dimensional projections of these same figures for the paired chain (C) and single chain (D) data. CDR3β amino acid sequences of these outliers are highlighted in the center of the figure. Both sequences were confirmed to be the outliers in the paired chain and single-chain data.

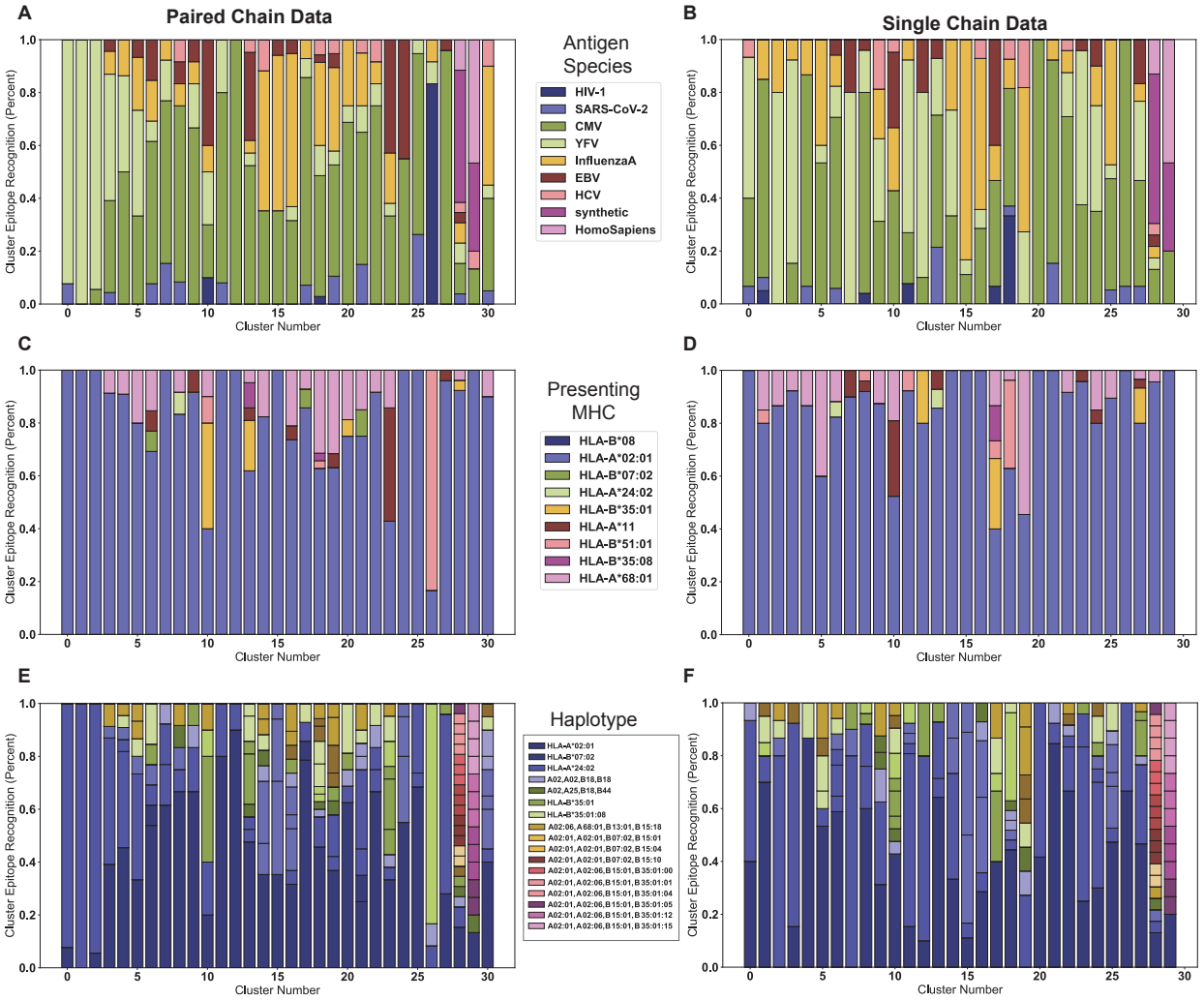

Figure S4: Cluster purity quantification for an array of metadata from the VDJ database when comparing paired chain (left column) and single chain (right column) clustering results. Antigen species source for each cluster member, with a cluster purity of 0.52 ± 0.26 (paired, A) and 0.39 ± 0.24 (single, B). Presenting MHC of each tested epitope for each cluster member, with a cluster purity of 0.68 ± 0.35 (paired, C) and 0.646 ± 0.37 (single, D). Organism haplotype for each cluster member, with a cluster purity of 0.46 ± 0.26 (paired, E) and 0.38 ± 0.22 (single, F). Legends are comprehensive for panels A, B, C, and D but only show a subset of the groups for panels E, F.

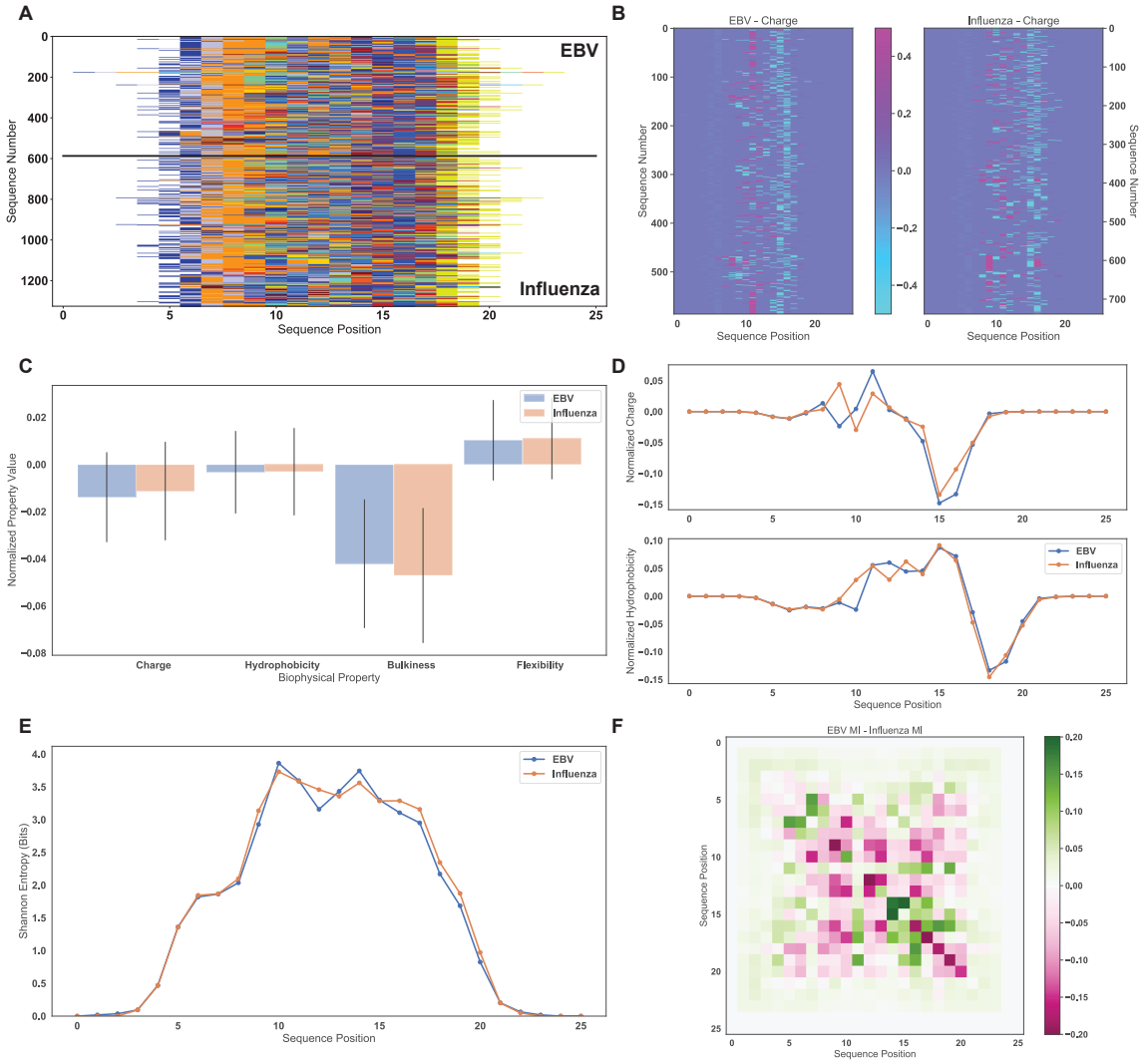

Figure S5: Biophysical and information theoretic analysis, as in Fig. 4 and 5, for the defined antigenic sequences reactive to either *Influenza* or EBV peptides as used in Glanville et al. (A) Initial AIMS encoding separated by antigenic reactivity, using the central alignment scheme. (B) Example of a biophysical property mask applied to the data in (A), here specifically showing the position- and sequence-sensitive normalized charge of each sequence. (C) Net biophysical properties, i.e. averaged over all positions and all sequences, for each antigen specificity. (D) Position sensitive charge and hydropathy, i.e. averaged over the y-axis of panel B, for each antigen specificity. Information theoretic analysis concludes the characterization of an antigen-specific repertoire, with the position sensitive entropy (E) and mutual information difference (F).

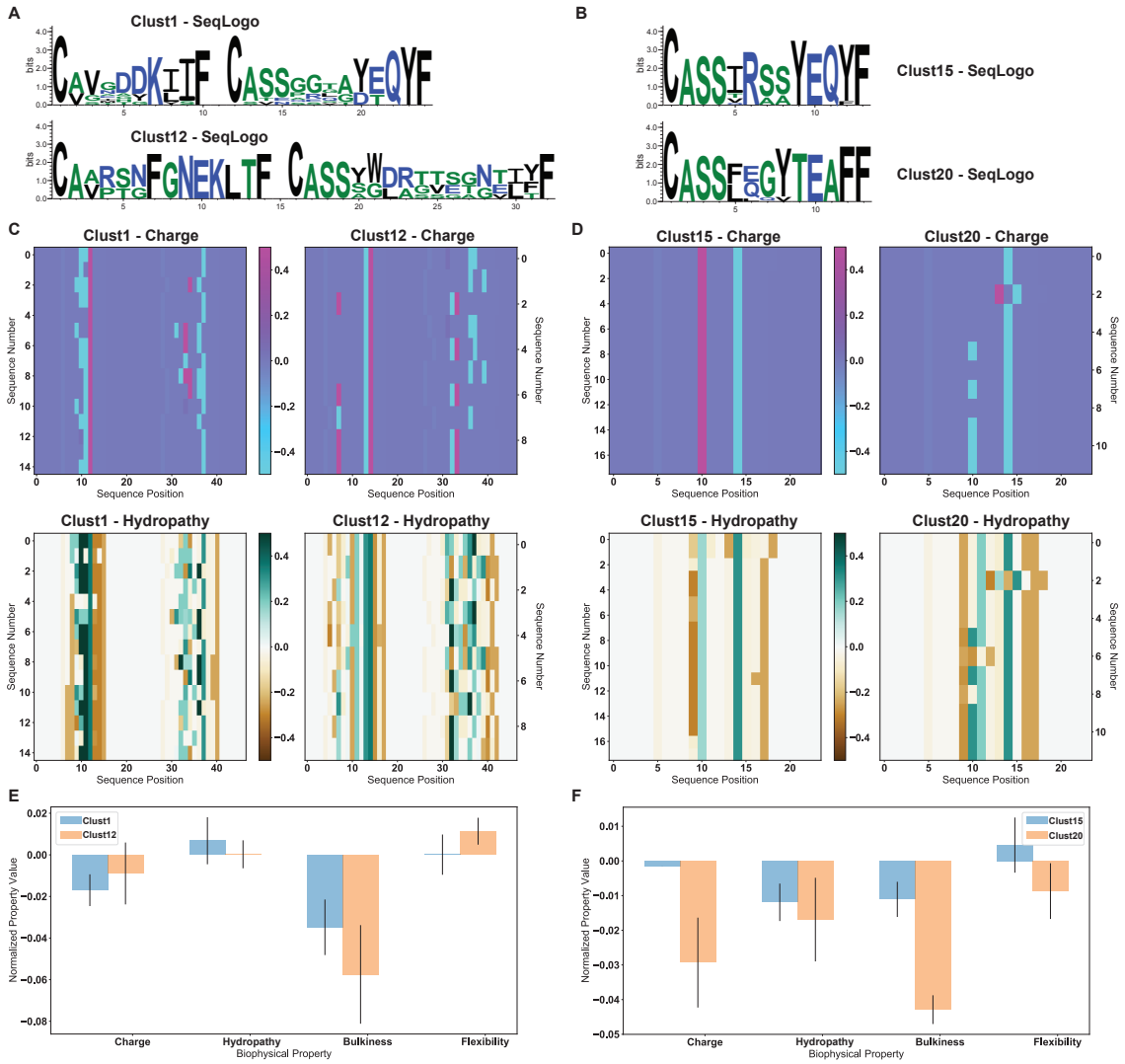

Figure S6: Detailed biophysical analysis done in parallel with Fig. 4 for the paired chain (left column) and single chain (right column) selected clusters. (A, B) Sequence logos of the selected clusters of Fig. 4A, B, as generated by WebLogo [68]. (C, D) Biophysical property masks of charge (top) and hydropathy (bottom) for each cluster of sequences. The position-sensitive biophysical property masks of Fig. 4C, D are generated by averaging over the y-axis of these plots. (E, F) Net averaged biophysical properties, i.e. averages over the x- and y-axes of panels C and D, of four out of the sixty-one available AIMS properties for each cluster of sequences.

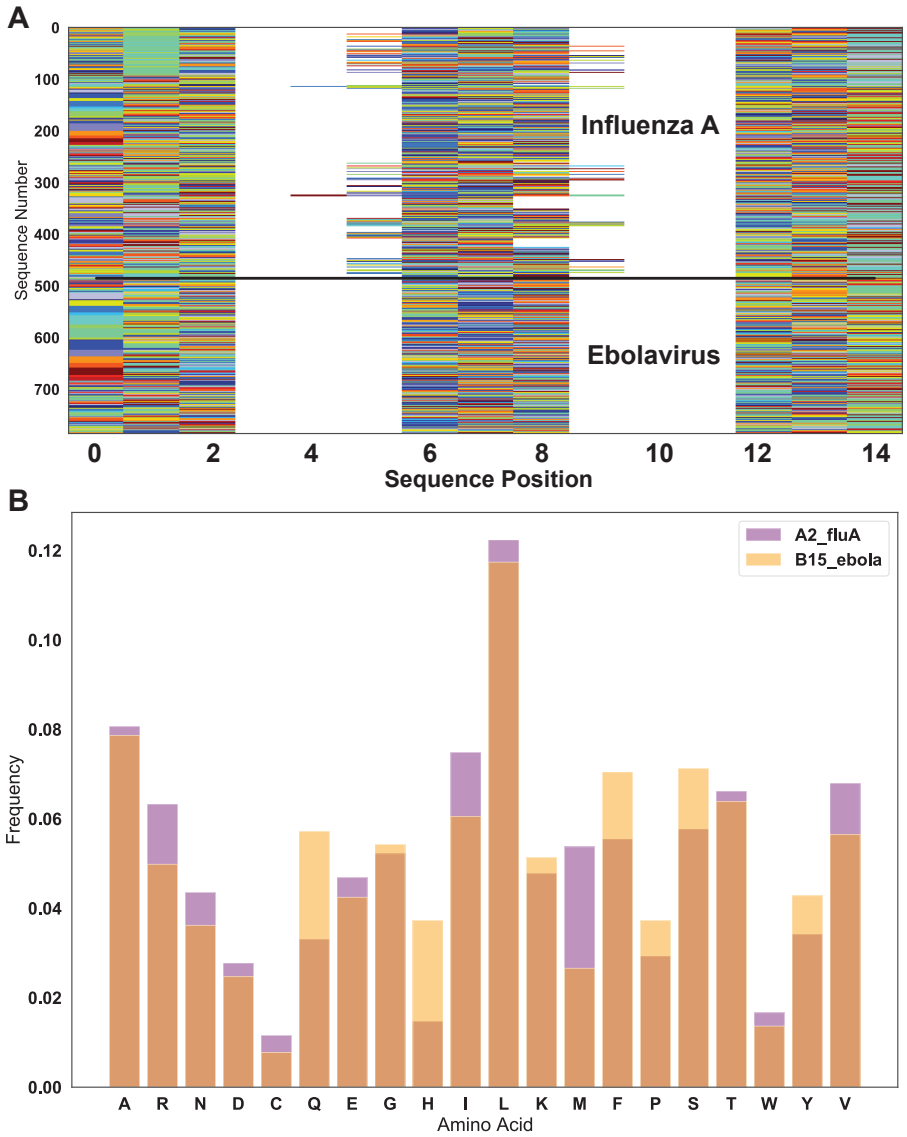

Figure S7: Associated figures for the peptide analysis of Fig. 5. (A) AIMS-encoding using the bulge alignment scheme of the dataset of *Influenza A* and *Ebolavirus* derived peptides. (B) Position-independent amino acid frequencies for the HLA-A2 presented *Influenza A* peptides and the HLA-B15 *Ebolavirus* peptides.

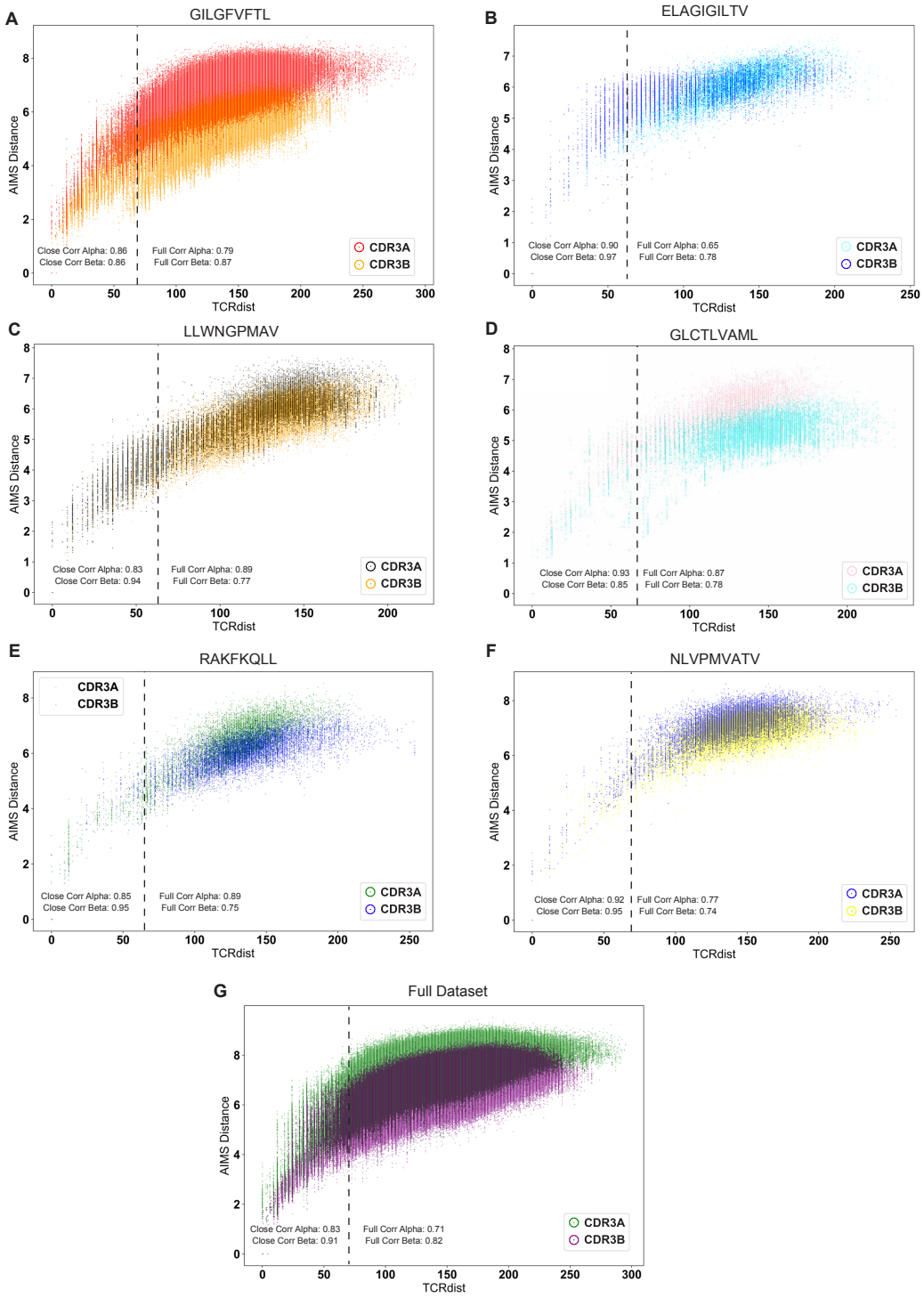

Figure S8: Quantitative comparison of distance metrics used in AIMS and TCRdist. Here only the sequence distances calculated via TCRdist and AIMS between full-CDR sequences of Mayer-Blackwell et al. are compared directly for the TCRα- and β-chains. Correlation coefficients between these distance metrics are reported for the full set of sequences and for closely related sequences, which are delineated by the dashed vertical lines at a TCRdist of 60 units. TCRs are isolated from human T cells in response to each antigen listed above the plots (A-F) or for the full dataset of TCRs (G).

Table S1: List of all of biophysical properties used for this study. For hotspot detecting variables (HS) a simplified form of the description is used. For more in-depth descriptions, the original reference should be used.

Property Shorthand	Description
Phob1	Hydrophobicity Scale [-1,1]
Charge	Charge [ec]
Phob2	Octanol-Interface Hydrophobicity Scale
Bulk	Side-Chain Bulkiness
Flex	Side-Chain Flexibility
KD1	Helix/Bend Preference
KD2	Side-Chain Size
KD3	Extended Structure Preference
KD4	Hydrophobicity
KD5	Double-bend Preference
KD6	Flat Extended Preference
KD7	Partial Specific Volume
KD8	Occurrence in alpha-region
KD9	pK-C
KD10	Surrounding Hydrophobicity
HS1	Normalized Positional Residue Freq at Helix C-term
HS2	Normalized Positional Residue Freq at Helix C4-term
HS3	Spin-spin coupling constants
HS4	Random Parameter
HS5	pK-N
HS6	Alpha-Helix Indices for Beta-Proteins
HS7	Linker Propensity from 2-Linker Dataset
HS8	Linker Propensity from Long Dataset
HS9	Normalized Relative Freq of Helix End
HS10	Normalized Relative Freq of Double Bend
HS11	pK-COOH
HS12	Relative Mutability
HS13	Kerr-Constant Increments
HS14	Net Charge
HS15	Norm Freq Zeta-R
HS16	Hydropathy Scale
HS17	Ratio of Average Computed Composition
HS18	Intercept in Regression Analysis
HS19	Correlation coefficient in Reg Anal
HS20	Weights for Alpha-Helix at window pos
HS21	Weights for Beta-sheet at window pos -3
HS22	Weights for Beta-sheet at window pos 3
HS23	Weights for coil at win pos -5
HS24	Weights coil win pos -4
HS25	Weights coil win pos 6

HS26	Avg Rel Frac occur in AL
HS27	Avg Rel Frac occur in EL
HS28	Avg Rel Frac occur in A0
HS29	Rel Pref at N
HS30	Rel Pref at N1
HS31	Rel Pref at N2
HS32	Rel Pref at C1
HS33	Rel Pref at C
HS34	Information measure for extended without H-bond
HS35	Information measure for C-term turn
HS36	Loss of SC hydropathy by helix formation
HS37	Principal Component 4 (Sneath 1966)
HS38	Zimm-Bragg Parameter
HS39	Normalized Freq of ZetaR
HS40	Rel Pop Conformational State A
HS41	Rel Pop Conformational State C
HS42	Electron-Ion Interaction Potential
HS43	Free energy change of epsI to epsEx
HS44	Free energy change of alphaRI to alphaRH
HS45	Hydrophobicity coeff
HS46	Principal Property Value z3 Wold et. al. 1987

Table S2: Table used for the second version of the AIMS scoring of pairwise amino acid interactions. The table attempts to recapitulate the interactions between amino acids at the level of an introductory biochemistry course.

Res/Res	A	G	L	M	F	W	K	Q	E	S	P	V	I	C	Y	H	R	N	D	T
A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
G	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
L	0	0	1	1	1	1	-2	-1	-2	-0.5	1	1	1	-0.5	-0.5	-0.5	-2	-1	-2	-0.5
M	0	0	1	1	1	1	-2	-1	-2	-0.5	1	1	1	-0.5	-0.5	-0.5	-2	-1	-2	-0.5
F	0	0	1	1	1	1	-2	-1	-2	-0.5	1	1	1	-0.5	-0.5	-0.5	-2	-1	-2	-0.5
W	0	0	1	1	1	1	-2	-1	-2	-0.5	1	1	1	-0.5	-0.5	-0.5	-2	-1	-2	-0.5
K	0	0	-2	-2	-2	-2	-2	1	2	0.5	-1	-2	-2	0.5	1	1	-2	1	2	0.5
Q	0	0	-1	-1	-1	-1	1	1	1	0.5	-1	-1	-1	0.5	1	1	1	1	1	0.5
E	0	0	-2	-2	-2	-2	2	1	-2	0.5	-1	-2	-2	0.5	1	1	2	1	-2	0.5
S	0	0	-0.5	-0.5	-0.5	-0.5	0.5	0.5	0.5	0.5	-0.5	-0.5	-0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
P	0	0	1	1	1	1	-1	-1	-1	-0.5	0	1	1	-0.5	-0.5	-0.5	-2	-1	-2	-0.5
V	0	0	1	1	1	1	-2	-1	-2	-0.5	1	1	1	-0.5	-0.5	-0.5	-2	-1	-2	-0.5
I	0	0	1	1	1	1	-2	-1	-2	-.0.5	1	1	1	-0.5	-0.5	-0.5	-2	-1	-2	-0.5
C	0	0	-0.5	-0.5	-0.5	-0.5	0.5	0.5	0.5	0.5	-0.5	-0.5	-0.5	2	0.5	0.5	0.5	0.5	0.5	0.5
Y	0	0	-0.5	-0.5	-0.5	-0.5	1	1	1	0.5	-0.5	-0.5	-0.5	0.5	1	1	1	1	1	0.5
H	0	0	-0.5	-0.5	-0.5	-0.5	1	1	1	0.5	-0.5	-0.5	-0.5	0.5	1	1	1	1	1	0.5
R	0	0	-2	-2	-2	-2	-2	1	2	0.5	-2	-2	-2	0.5	1	1	-2	1	2	0.5
N	0	0	-1	-1	-1	-1	1	1	1	0.5	-1	-1	-1	0.5	1	1	1	1	1	0.5
D	0	0	-2	-2	-2	-2	2	1	-2	0.5	-2	-2	-2	0.5	1	1	2	1	-2	0.5
T	0	0	-0.5	-0.5	-0.5	-0.5	0.5	0.5	0.5	0.5	-0.5	-0.5	-0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5