HuBMAP Reference Atlas: Toward a human [reference] map

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An **atlas** is an oversized, bound book of maps. It has descriptive text, an index, possibly other data visualizations.
An human cell atlas might show a landscape of all cells, or Maps of cells per tissue type/anatomical structure.
A human reference atlas might use human anatomy as a ‘basemap,’ or an abstract space.

https://bodyworlds.com

Weber, 1978

**Single cell and ‘omics assays**
- Genomics
- Epigenomics
- Transcriptomics
- Proteomics
- Metabolomics

**Multiplexed spatial assays**
- Protein
- RNA
- Lipids / metabolites

**Map assembly and data query**
- Landmark A
- Landmark B
- Image registration
- Feature ID
- Anatomy
- Histology
- Reference coordinates
- Cell population
- Common coordinate framework (CCF)

Fig. 3 | Map generation and assembly across cellular and spatial scales. HuBMAP aims to produce an atlas in which users can refer to a histological slide from a specific part of an organ and, in any given cell, understand its contents on multiple ‘omic levels—genomic, epigenomic, transcriptomic, proteomic, and/or metabolomic. To achieve these ends, centres will apply a combination of imaging, ‘omics and mass spectrometry techniques to specimens collected in a reproducible manner from specific sites in the body. These data will be then be integrated to arrive at a high-resolution, high-content three-dimensional map for any given tissue. To ensure inter-individual differences will not be confounded with collection heterogeneity, a robust CCF will be developed.
CCF Requirements

The CCF must capture major anatomical structures, cell types, and biomarkers and their interrelations across multiple levels of resolution.

It should be semantically explicit (using existing ontologies, e.g., Uberon, CL) and spatially explicit (e.g., using 3D reference organs for registration and exploration).
ASCT+B Tables

Anatomical Structures, Cell Types, and Biomarkers (ASCT+B) tables aim to capture the partonomy of anatomical structures, cell types, and major biomarkers (e.g., gene, protein, lipid or metabolic markers).

<table>
<thead>
<tr>
<th>Structure/Region</th>
<th>Substructure/Subregion</th>
<th>Cell Type</th>
<th>Subset of Marker Genes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Renal Corpuscle</td>
<td>Bowman’s Capsule</td>
<td>Parietal epithelial cell</td>
<td>CRB2*, CLDN1*</td>
</tr>
<tr>
<td></td>
<td>Glomerulus</td>
<td>Podocyte</td>
<td>NPHS2*, PODXL*, NPHS1*</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Capillary Endothelial Cell</td>
<td>EHD3*, EMCN*, HECW2*, FLT1*, AQP1*</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Mesangial Cell</td>
<td>POSTN*, PIEZO2*, ROBO1*, ITGAB*</td>
</tr>
</tbody>
</table>

Partial ASCT+B Table from
XMAS 2020 release supports
• AS, CT, B Search
• Table comparison
# ASCT+B Tables vs. 3D Reference Organs

ASCT+B for 10 organs on 11/30/2020, 5:37pm ET:

<table>
<thead>
<tr>
<th>Organ</th>
<th>#AS</th>
<th>#CT</th>
<th>#B</th>
<th>#AS-CT</th>
<th>#CT-B</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brain</td>
<td>184</td>
<td>127</td>
<td>254</td>
<td>127</td>
<td>346</td>
</tr>
<tr>
<td>Heart</td>
<td>23</td>
<td>16</td>
<td>35</td>
<td>73</td>
<td>42</td>
</tr>
<tr>
<td>Kidney</td>
<td>39</td>
<td>53</td>
<td>83</td>
<td>63</td>
<td>131</td>
</tr>
<tr>
<td>Large Intestine</td>
<td>22</td>
<td>33</td>
<td>45</td>
<td>306</td>
<td>72</td>
</tr>
<tr>
<td>Liver</td>
<td>16</td>
<td>27</td>
<td>34</td>
<td>29</td>
<td>35</td>
</tr>
<tr>
<td>Lung</td>
<td>18</td>
<td>62</td>
<td>103</td>
<td>110</td>
<td>128</td>
</tr>
<tr>
<td>Lymph nodes</td>
<td>34</td>
<td>30</td>
<td>50</td>
<td>63</td>
<td>110</td>
</tr>
<tr>
<td>Skin</td>
<td>14</td>
<td>32</td>
<td>57</td>
<td>37</td>
<td>99</td>
</tr>
<tr>
<td>Small Intestine</td>
<td>20</td>
<td>32</td>
<td>48</td>
<td>195</td>
<td>55</td>
</tr>
<tr>
<td>Spleen</td>
<td>33</td>
<td>26</td>
<td>46</td>
<td>48</td>
<td>72</td>
</tr>
</tbody>
</table>

**Vasculature**

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- [https://www3.cs.stonybrook.edu/~ari/](https://www3.cs.stonybrook.edu/~ari/) (male colon)
CCF Exploration User Interface (EUI)

https://portal.hubmapconsortium.org/ccf-eui
Register your data via [https://hubmap-ccf-ui.netlify.app/rui/](https://hubmap-ccf-ui.netlify.app/rui/) so it can be spatially/semantically explored in EUI.
http://gehlenborglab.org/research/projects/vitessce/
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References


