ASHI Proficiency Testing Program

2020 HT-1 Survey Instructions

Ship date: February 18, 2020
Result Submission due date: March 27, 2020

(Significant changes from 2019 HT-2 instructions highlighted)

Survey Description: The ASHI HLA Typing (HT) Survey is designed to assess laboratory performance in HLA typing by any method. The survey consists of two shipments yearly, each comprised of five whole blood specimens in ACD anticoagulant. Included in this Survey, the HT samples can also be used to demonstrate proficiency for the detection of HLA-B27 antigen or alleles in whole blood samples. Participants should HLA type the specimens using the method(s) they normally use with patient specimens. The HT survey allows the reporting of serological, low-resolution molecular and high resolution molecular results. Laboratories that clinically use two or more methods independently are expected to have interpreted the reported results independently. Analytes in the HT survey are defined as HLA Class I typing by serology, HLA Class II typing by serology, low resolution HLA Class I typing by molecular methods, low resolution HLA Class II typing by molecular methods, high resolution HLA Class I typing by molecular methods, and high resolution HLA Class II typing by molecular methods. Laboratories will specify the method utilized to type each locus of each sample (methods include: Serology, SSO, SSP, SBT, RT-PCR, NGS, “Other”). Laboratories can specify multiple methods for each locus of each sample.

Addressing CMS Regulations: Laboratories that are subject to Centers for Medicare and Medicaid Services (CMS) regulation must refer to the most recent guidance document released by the ARB in regards to testing for proficiency samples and analytes for multiple methods. Laboratories are encouraged to contact their ARB commissioners or CMS with questions regarding adherence to CMS proficiency testing regulations.

Deadline: For the HT-1 2020 survey, the deadline for submitting results is due on March 27, 2020 at 11:59 PM, Pacific Time, 38 days after the shipment date. The specific due date can be found in the PT Shipping Schedule posted on the ASHI PT website, inside the ASHI PT Lab Center and is included as a separate notice with this shipment. Late submission of results will not be accepted.

Online Entry of Results: Results are to be entered online at https://www.ashi-pt.com/. A pre-registered user ID and password are required. If you have forgotten your password, follow the on-screen instructions to have it sent to your e-mail address. To enter the HT results select the current year ‘2020’ in the first dropdown in the dashboard page. Click “Enter Results” under the “Actions” column for “Shipment 1” and “HT” (which indicates HT-1 2020) for the current HT event. Enter sample quality responses by selecting the “Specimen Verification and Quality Assessment” tab. Enter individual sample results by selecting the “Enter Results” tab and proceeding through each individual sample tab. For HT/B27 subscribers, in the ASHI PT Lab Center, HLA-B27 results will be entered in the separate “B27” section of Lab Center, which can be found under the current year ‘2020’ and “Enter Results” under the “Actions” column for “Shipment 1” and “B27” (which indicates B27-1 2020) for the current HT event.

Specimens: To accommodate the volumes of blood required, laboratories have been divided into two groups that receive two different sets of specimens. Laboratories must verify that the samples they received are correctly noted in ASHI PT Lab Center. Specimen numbers will be noted in the “Specimen Verification and Quality Assessment” tab under the heading “Verify Specimens”. Verify that the specimen ID numbers noted correspond with the specimens received. If specimen IDs do not correspond to those received, choose the correct specimen IDs from the drop down menus in the “Specimen Verification and Quality Assessment” tab under the heading “Verify Specimens”.

Specimen Quality: For each specimen tested, and for each specimen not tested because of specimen problems, indicate the quality of the specimen. Enter sample quality responses within the “Enter Results” tab by selecting the appropriate sample quality for each sample included in the HT-1 Survey under each sample ID heading and under the section labeled “Quality of Specimen”.

- “Good” is appropriate for specimens that produced reliable results with no sample processing or testing problems.
**Testing Methods:** Select the method(s) used to HLA type each locus of each specimen tested. Under each individual sample tab in the “Enter Results” section, at least one method must be selected for each locus. If, for any locus of any sample, typing was not performed, select “Not Tested” for that locus/loci under the appropriate sample tab. If a typing method other than those listed was used, select “Other” and specify the method in the Comment Field space provided at the bottom of each sample’s page. Click “Save” at the bottom of each results entry page to save your selections at any time. Please review the method selected for each sample carefully and ensure that it corresponds to the results entered for that method. Inaccurate method selection can result in lack of grading for that particular assay.

**B27 Test Results:** For HT/B27 subscribers, in the ASHI PT Lab Center, HLA-B27 results will be entered in the separate “B27” section of Lab Center, which can be found under the current year ‘2020’ and “Enter Results” under the “Actions” column for “Shipment 1” and “B27” (which indicates B27-1 2020) for the current HT event. For each sample ID tab, select if HLA-B27 was “positive/present” or “negative/absent”. Save your results by clicking the “Save” button at the bottom of the result entry screen.

**HT Test Results:** Once the current HT event has been selected in ASHI PT Lab Center, select the “Enter Results” tab. Select the tab with the sample number corresponding to the first sample received and tested by your laboratory. In the “Resolution to be graded” drop down menu, select the molecular typing resolution desired for grading that pertains to your laboratory “High Resolution Only” or “Grade Low Resolution and High Resolution based on data entered.”

Here are examples of how the choices above will affect the way your data is graded:

**If you select “High Resolution Only”, and enter the following data in Lab Center, this is how you would be graded:**

<table>
<thead>
<tr>
<th>1st Field</th>
<th>2nd Field</th>
</tr>
</thead>
<tbody>
<tr>
<td>A* 02</td>
<td>√</td>
</tr>
<tr>
<td>A* 24</td>
<td>√</td>
</tr>
</tbody>
</table>

- **Allele #1** – This allele will receive a high-resolution grade for A*02:01. No low resolution grade for the A*02 portion of the response will be assigned.
- **Allele #2** – This allele will receive no grade as no high-resolution response was given. This allele would not receive a discrepant grade, but would simply not be graded.

**If you select “Grade Low Resolution and High Resolution based on data entered”, and enter the following data in Lab Center, this is how you would be graded:**

<table>
<thead>
<tr>
<th>1st Field</th>
<th>2nd Field</th>
</tr>
</thead>
<tbody>
<tr>
<td>A* 02</td>
<td>√</td>
</tr>
<tr>
<td>A* 24</td>
<td>√</td>
</tr>
</tbody>
</table>

- **Allele #1** – This allele will receive a low-resolution grade for the A*02 portion of the response AND will receive a high-resolution grade for A*02:01.
- **Allele #2** – This allele will receive a low-resolution grade for A*24. No high-resolution grade will be assigned for this allele, as no high-resolution response was given. This allele would not receive a discrepant high-resolution grade, but would simply not be graded for high resolution.

If only serologic typing methods were utilized, no change to the “Resolution to be graded” drop down field is necessary. Select the method utilized to type each locus. Multiple methods may be selected for each locus, and different methods may be selected for different loci. Low resolution, high resolution, and serologic results for a specimen are entered on the same page. The default entry for all loci is NT1 (not tested, method not used in laboratory).

**Important Typing Data Entry Changes:**

Several differences in the way HT participants reported typing data in prior HT surveys have led to significant delays during the review and grading process. These differences include the use of dashes “-” when reporting homozygous typing and reporting antigens/alleles in reverse numerical order. These practices have made it very
challenging to calculate the consensus and grade the results. In order to avoid these issues and improve the review and grading process, several data entry changes and data correction prompts have been implemented within the ASHI PT Lab Center. These changes will affect data entry starting with the 2020 HT-1 survey and are described in detail in the following sections. Subscribers are required to follow the new data entry instructions. Failing to do so will result in error messages during the data entry process. These error messages should prompt participants to enter results according to the new HT result entry instructions.

1) All typing results must be entered in the numerical order in which they appear in the drop-down menus. For example, as shown below for a low resolution molecular type of B*14, B*27 being reported including the serologic equivalents B65, B27, enter 14 in the first allele field, and 27 in the second allele field, because that is the order they are found in the molecular drop-down menu. Enter the serologic equivalent, 65, in the “serological equivalent” column corresponding with the first allele (identified as B*14).

In cases when typing results are not entered in the numerical order in which they appear in the drop down menu, the subscriber will be prompted to correct the entry during the saving process. Example below shows a low resolution molecular type of B*14, B*27 entered in reverse order.

Upon saving the incorrectly entered results shown in the example above, the following error (see left panel below) will appear, “Error: Specimen not saved. Please resolve the issue above to save”, prompting the subscriber to enter HLA-B* locus alleles in numerical order (“B*: Values must be entered in numerical order”). In addition, the incorrectly entered allele pair will be highlighted in pink (see right panel below) guiding subscriber to the result that requires correction. When correcting the allele order in the “1st Field” column, the subscriber must ensure that any values entered in the corresponding “Serological Equivalent” fields, and/or the 2nd, 3rd and 4th molecular fields (in cases of high resolution typing entry) for the two alleles are also corrected. Please note that the specimen data will not be saved until all order entry errors are corrected for the sample.

B* locus alleles entered in reverse order are highlighted for correction.
2) Dashes "-" are no longer available for selection from drop down menus in the "1st Field", "Serological Equivalent", and in "Serological Typing" fields. In addition, dashes "-" cannot be entered in the 2nd, 3rd and 4th high resolution molecular typing fields. Subscribers attempting to enter "-" values in any of the high resolution molecular typing fields will be prompted to enter "alpha numeric" values instead. Thus, in cases of a homozygous typing at a locus, the same numerical values must be entered for both alleles in all applicable fields. An example of a homozygous high resolution HLA-A (3 field resolution) and HLA-B (2 field resolution) typing entry, as well as a homozygous low resolution HLA-C typing entry is shown below:

3) For specimens that do not have any DRB3, DRB4 or DRB5 type (such as occurs in association with any combination of DRB1*01, DRB1*08, and DRB1*10 alleles), subscribers must select the "not present" value from the "1st Field" molecular drop-down menu for both DRB3/4/5 alleles. For specimens that have only one DRB3, DRB4 or DRB5 type (ex. in association with DRB1*04/DRB1*10 typing), subscribers must select the "not present" value from the "1st Field" drop-down menu for the first DRB3/4/5 allele and then select the appropriate DRB3, DRB4 or DRB5 type from the "1st Field" drop-down menu for the second DRB3/4/5 allele. This is because the "not present" value precedes all numerical DRB3, DRB4 and DRB5 values in the "1st Field" molecular drop-down menu for DRB3/4/5 alleles. Subscribers will be prompted to correct any reverse numerical order entries for DRB3/4/5 alleles during the data saving process. Examples of correct low resolution typing entries when a) no DRB3/4/5 alleles are present, b) one DRB3/4/5 allele is present, c) two different DRB3/4/5 alleles are present, and d) two homozygous DRB3/4/5 alleles are present, are shown below:

Please note that the “not present” value has also been added to the “Serologic Typing” drop-down menu for DR51/52/53 antigens and that data entry for “Serologic Typing” should follow the numerical order result entry rules described above for molecular typing.
4) High resolution molecular typing results at the “2nd Field”, as well as the 3rd and 4th fields if applicable, must be entered in numerical order in cases where the two alleles are otherwise identical at all preceding fields. Examples of correct numerical order high resolution typing entries at a) “2nd Field”, b) 3rd field and c) 4th field resolution are shown below:

a) 2nd field resolution

| A* | 03 | ✓ | 01 | ✓ | NA | ✓ |
| A* | 03 | ✓ | 02 | ✓ | NA | ✓ |

b) 3rd field resolution

| A* | 03 | ✓ | 01 | : | 01 | ✓ | NA | ✓ |
| A* | 03 | ✓ | 01 | : | 02 | ✓ | NA | ✓ |

c) 4th field resolution

| A* | 03 | ✓ | 01 | : | 01 | ✓ | NA | ✓ |
| A* | 03 | ✓ | 01 | : | 02 | ✓ | NA | ✓ |

An example of incorrect, reverse order high resolution typing result entry at the “2nd Field” is shown below. Note the A locus alleles are homozygous at the “1st Field”.

A* locus alleles in reverse order at 2nd Field

Upon saving of the incorrectly entered results shown in the example above, the following error (see left panel below) will appear, “Error: Specimen not saved. Please resolve the issue above to save”, prompting the subscriber to enter HLA-A* locus alleles in numerical order (“A*: Values must be entered in numerical order”). In addition, the incorrectly entered allele pair will be highlighted in pink (see right panel below) guiding the subscriber to the result that requires correction. Please note that the specimen data will not be saved until all order entry errors are corrected for the sample.

A* locus alleles entered in reverse order are highlighted for correction at 2nd field
"NT" options: All drop-down lists of possible results include six different "NT" results:
NT1: Not Tested, method not used in laboratory (DEFAULT)
NT2: Not Tested due to sample quality problem
NT3: Not Tested due to reagent problem/technical failure (e.g. unavailable from vendor, QC failure, dropped tray)
NT4: Not reported due to ambiguity of high resolution typing
NT5: Not reported due to limitations of serology typing (see instructions below to add NT5 for that scenario)
NT6: Other, specify why in comments
This feature will allow labs to better document the different reasons that a gradable result was not submitted. All "NT" codes will be ungraded.

Serologic Typing: The "Serologic typing" fields are reserved for results derived from serologic typing methods. Some laboratories use serology as a "stand-alone" method for certain types of samples, but perform both serological and molecular typing on proficiency samples. If those laboratories have a serologic result for an antigen that they would not report clinically without reflex molecular typing (e.g. a possible A36 in the presence of A1), they should report the overall serologic typing but enter “NT5” for that specific antigen in the serology section. The reported serological typing results will be graded and any individual "NT5" antigen(s) will not be figured into the composite grade. Conversely, laboratories that only perform molecular typing should NOT enter serologic equivalents (antigen level typing) for molecular typing results in the "Serologic typing" fields. Serologic equivalents of molecular typing results should be entered in the "Serological Equivalent" typing fields, as applicable.
For serology results, if only one antigen was detected for any A, B, C, DR or DQ locus, the same value must be entered in both fields for the locus as the dash "-" values are no longer available in the drop-down menus for "Serologic Typing" fields, in order to avoid inversion problems as discussed above. For samples that have no serologically detectable HLA-C types, select "NT5" for both HLA-C fields. HLA-C "molecular" antigens cannot be entered in the serological typing results. For samples that don't have any DR51, DR52 or DR53 type, select "not present" value for both DR51/52/53 fields. For samples that have only one DR51/DR52/DR53 type, enter the "not present" value in the first DR51/52/53 antigen field and the correct DR51/52/53 type in the second DR51/52/53 antigen field.

Low Resolution Molecular Typing: To enter low resolution molecular typing results select the two digit types from the drop-down menus in the first column of fields labeled "1st Field". Please note that typing results must be entered in the numerical order in which they appear in the drop-down menus. If only one antigen was detected for any A, B, C, DRB1, DQA1, DQB1, DPA1, DPB1 locus, the same value must be entered in both allele fields for the locus. Dash "-" value is no longer available in the drop-down menus for the "1st Field" columns.

For specimens that do not have any DRB3, DRB4 or DRB5 type (such as occurs in association with any combination of DRB1*01, DRB1*08 and DRB1*10 alleles), subscribers must select the "not present" value from the "1st Field" molecular drop-down menus for both DRB3/4/5 alleles. For specimens that have only one DRB3, DRB4 or DRB5 type (e.g. in association with DRB1*04/DRB1*10 typing), subscribers must select the "not present" value from the "1st Field" drop-down menu for the first DRB3/4/5 allele and then select the appropriate DRB3, DRB4 or DRB5 type from the "1st Field" drop-down menu for the second DRB3/4/5 allele. This is because the "not present" value precedes all numerical DRB3, DRB4 and DRB5 values in the "1st Field" molecular drop-down menu for DRB3/4/5 alleles.

For laboratories reporting the serological equivalent: If your laboratory reports molecular results for patients as serologic equivalents or antigen level typing, the results must be reported in the low-resolution molecular typing fields "1st Field". For serologic equivalents that are either a single digit (A1, 2, 3, etc.) or have the same value as the molecular low-resolution type (A11, 23, 24, etc.), select the "1st Field" low-resolution type that is numerically equivalent (01, 02, 03, 11, 23, 24, etc.). For serologic equivalents that are more specific than their low resolution types (i.e., B60, B61, B62, B63, B64, B65, B70, B71, B72, B75, B76, B77, C9, C10, DR17, DR18, DQ7, DQ8, DQ9), you should report those results by selecting the appropriate low resolution molecular type from the "1st Field" column drop-down menu (ex. B15) and then by selecting the appropriate corresponding serologic equivalent from the "Serological Equivalent" column drop-down menu (ex. B62). Serologic equivalents for DRB3/4/5 (DR51, 52 and 53) are also provided in the "Serological Equivalent" columns. Do not enter low resolution typing only for HLA-DPB1 alleles as only high-resolution typing for DPB1 is supported by nomenclature standards. The nomenclature suffix N ("null" allele) is now provided for selection in the "Suffix" column fields and is to be utilized with corresponding alleles as appropriate.

Do not leave molecular low resolution "1st Field" or high resolution fields "2nd Field" blank, nor should you use "not present" value for DRB3/4/5 alleles, to indicate the detection of null alleles. While this is a common reporting practice for laboratories, especially utilizing low resolution typing, this does not sufficiently allow for grading and assessment of a laboratory’s ability to detect/distinguish null alleles in a proficiency testing context when molecular methods are utilized. Laboratories should utilize the nomenclature suffix "N" provided in the "Suffix" column fields to convey that a null allele has been detected when reporting either low resolution and/or high resolution molecular typing results as shown in the
example below. If a laboratory leaves a field “blank”, or notes “-”, and simply comments on the null, this response cannot be graded and proficiency cannot be adequately assessed.

This is the correct way to report null alleles for high resolution (top allele/allele #1) and low-resolution (bottom allele/allele #2) proficiency testing grading:

```
<table>
<thead>
<tr>
<th>1st Field</th>
<th>2nd Field</th>
<th>Suffix</th>
<th>Serological Equivalent</th>
</tr>
</thead>
<tbody>
<tr>
<td>DRB3/4/5</td>
<td>DRB4*01</td>
<td>:03</td>
<td>N</td>
</tr>
<tr>
<td>DRB3/4/5</td>
<td>DRB4*01</td>
<td>:03</td>
<td>N</td>
</tr>
</tbody>
</table>
```

Suffixes are no longer available in the “1st Field” column drop-down menus, the “N” suffix can only be selected by utilizing the “Suffix” drop-down menu. Laboratories supporting NMDP and UNOS should be aware of specific requirements for resolving common null alleles from expressed antigens. For the most current list of NMDP defined “common” null alleles refer to the “NMDP Policy for Adult Donor and Patient HLA Confirmatory Typing” at [https://bioinformatics.bethematchclinical.org/Policies](https://bioinformatics.bethematchclinical.org/Policies). For the most current list of the “common” null alleles that must be distinguished by OPTN/UNOS labs refer to the guidance for ASHI standard D.5.3.2.2.7. Further detail regarding common null alleles in the context of proficiency testing and ASHI PT grading can be found in the ASHI PT Operations Manual available on the ASHI PT Website at the following link: [ASHI 2019 PT Operations Manual](https://bioinformatics.bethematchclinical.org/). (The 2020 PT Operations Manual will be available by the end of the first quarter.)

**High Resolution Molecular Typing:** The high resolution, “2nd Field” columns use WHO nomenclature (see link below for further information) and are continuations of the types selected in the low-resolution “1st Field”. For example, if a specimen typed as B*08:01 and B*27:05, 08 and 27 should be selected in the low-resolution “1st Field” columns of the B locus, and :01 and :05 should be selected in the high resolution “2nd Field” columns adjacent to the low resolution types they refer to. Note that the high resolution extensions are not specific for the low resolution types entered; it is possible to select a low/high combination type that is not valid (for example, B*07:01 or DRB3:02). If a specimen is heterozygous at the high-resolution level, but homozygous at the low-resolution level, select the same low-resolution “1st Field” result twice. For example, if a sample types as B*27:01 and B*27:05, select 27 in both low-resolution B-locus “1st Field” columns, and :01 and :05 in the high-resolution “2nd Field” columns. The “2nd Field” results in such cases must be entered in numerical order, i.e. :01 must be entered for the first allele and :05 for the second allele. Whenever a single high resolution A, B, C, DRB1, DQB1, DQA1, DPB1 or DPA1 type is identified for a locus, enter the same numeric values for the first and second allele in the “1st Field”, “2nd Field” columns, as well as any additional fields (3rd and 4th) that are applicable depending on typing resolution. (You will not be able to save a high-resolution type for any locus if you selected an “NT” code for the “1st Field”). The nomenclature suffixes N, G, P, L and Q are now provided for selection in the “Suffix” column fields and are to be utilized with corresponding alleles as appropriate. These suffixes will no longer be available in the “1st Field” column drop-down menus and should NOT be typed into high resolution “2nd Field” columns.

If you believe a previously non-described HLA allele is present in a specimen, select “New” in the “Suffix” column field and describe your findings in the “Comments” box. In relation to reporting “NEW” alleles, careful discretion should be taken when utilizing sequencing or other methodologies which include data outside of traditional exons in assigning “NEW” alleles. If data which cannot be supported by IMGT sequences are utilized in assigning a “NEW” allele, the grade assigned may be “NG3” for the reported “NEW” allele.

The single letter suffixes G or P, as provided for by WHO Nomenclature Rules, should be selected if the laboratory cannot exclude one or more alternative P or G group alleles that only differ from the designated allele in nucleic acid or amino acid sequence, respectively, outside exons 2 and 3 for Class I alleles or outside exon 2 for Class II alleles. Complete definitions and current lists of the G and P allele groups can be found at: [http://hla.alleles.org/alleles/index.html](http://hla.alleles.org/alleles/index.html). The ASHI PT committee strongly recommends review of currently defined G and P groups prior to submission of results. G or P groups not officially recognized by WHO nomenclature (non-existing P and G groups) will be graded as ‘Discrepant’. For example, if a typing ambiguity includes DPB1*105:01 and DPB1*463:01 alleles, both of which belong to the DPB1*04:02P group, the typing using a P group nomenclature should be reported as DPB1*04:02P. Laboratories reporting either DPB1*105:01P (non-existent in P group nomenclature) or DPB1*463:01P (non-existent in P group nomenclature) will be graded as “Discrepant”. Utilize only the “Suffix” column drop down fields to indicate G or P groups. Do not type “G” or “P” in “2nd Field” columns.
Note - If you are unable to distinguish ambiguous alleles that are not in the same G or P group, and would report them as not excluded for clinical samples, you should list those in the Comments section as documentation that you are treating PT specimens in the same manner as clinical samples. However, if you choose to enter one allele as the "correct" type and another allele in the comments, you are at risk for a "Discrepant" grade should the allele in the comments be the one that reaches consensus. Comments will not be considered as part of the results and will not be used for determining gradable proficiency testing results. If your typing method cannot distinguish two alleles that are not in the same G or P group, and that are both on the list of Common and Well Documented Alleles, then you do not have a high resolution typing result. It is recommended that in such cases you leave the result for that allele as NT4 (not reported due to ambiguity of high resolution typing) and enter the ambiguous alleles in the comments. For the most recent list of the alleles that are currently considered to be "Common and Well Documented" please refer to: http://cwd.immunogenomics.org

Note – When entering Low and High Resolution results, the first box is designed for entering the low-resolution “1st Field” values. The second box is for laboratories that would need to enter the high-resolution “2nd Field” values only. The boxes after that are for the 3rd and 4th fields, to accommodate NGS labs. If laboratories duplicate low-resolution "1st Field" data in the "2nd Field" column, inappropriately, they will be graded as discrepant.

Example:

<table>
<thead>
<tr>
<th>1st Field</th>
<th>2nd Field</th>
</tr>
</thead>
<tbody>
<tr>
<td>DRB1*12:01</td>
<td>12</td>
</tr>
<tr>
<td></td>
<td>01</td>
</tr>
</tbody>
</table>

Correct high-resolution entry for DRB1*12:01:

Incorrect high-resolution entry for DRB1*12:01 with duplication of "1st Field“: DRB1*12:12:01 will receive a 'Discrepant' grade.

Please refer to the ASHI PT Operations manual for further detail regarding reporting of common null alleles, G-groups and P-groups, reporting of "NEW" alleles as well as other details of ASHI PT grading, at the following link:

ASHI 2019 PT Operations Manual. (The 2020 PT Operations Manual will be available by the end of the first quarter.)

Comments: Enter any relevant comments about your test results at the bottom of each specimen result entry page. If you believe a new allele is present, describe it in the Comments box, indicating, if possible, how the new allele differs from the closest previously described allele. Comments will not be considered as part of the results and will not be used for determining gradable proficiency testing results.

Save: Clicking the “Save” button at the bottom of any specimen page saves all entries for the specimen, but does not cause the results to be submitted. If Save is attempted but there is a problem with the results, a message describing the nature of the problem will appear. If changes are made to any result entry, a prompt to save the changes will appear if a user attempts to navigate away from the page without saving the changes.

Cancel: Clicking the "Cancel" button closes the specimen’s result entry page and any unsaved entries will be lost. Using your browser’s back arrow or closing your browser will also cause unsaved entries to be lost. The system will prompt users to save data if navigation away from a page is detected prior to saving changes.

Print: Select and hit "Control P” for printing the result summary screen after you have saved your data. Each specimen’s results can be printed separately by clicking "Control P” while in the results entry of a specimen tab, or a summary of all data entry can be printed by clicking “Control P” while in the “Review/Submit” tab. You are strongly encouraged to print a copy of all your entered results immediately before submitting them.

Laboratories are strongly encouraged to print out all results IMMEDIATELY PRIOR TO SUBMISSION and review for accuracy and completeness of entered and saved data. Revisions of data entry can be additionally reviewed prior to submission of results by clicking on the 'Revisions' icon at the top right-hand corner of the results submission pages of ASHI PT Lab Center.

Submit Results: Click the “Submit Results” button on the bottom of the ”Review/Submit” tab page only after you have double-checked the accuracy of your entries for every specimen and are ready to submit your final results. Clicking the “Submit Results” button will submit your results and finalize your submission. Saved entries that have not been submitted will not automatically be submitted once the submission deadline has passed. Results can be edited and re-submitted up until the deadline for result submission. A clock counting down remaining time for submission is visible within ASHI PT Lab Center. After the submission due date, it will be possible to print the submitted results.
Problems: If you experience problems entering or submitting your ASHI proficiency testing results, please contact the ASHI Central Office. Problems may be reported by clicking the ‘Report Issues’ Icon 📝 at the top right-hand corner of any page within the result entry area of ASHI PT Lab Center. Problems submitted using the ‘Report Issues’ icon will be sent to the ASHI Central Office.

Data Entry Mistakes: After submitting results, if you discover that you have made an error entering results, you may re-enter ASHI PT Lab Center and edit your entries and re-submit your results up until the deadline for submission. Mistakes reported to the ASHI Proficiency Testing Program after the deadline has passed cannot be corrected.

ASHI PT Program cannot correct data entry errors that are detected by laboratories after a Discrepant result has been received.

Replacement Materials: To identify the specimens you require, please contact the ASHI Central Office immediately by phone, email or by using the ‘Report Issues’ Icon in ASHI PT Lab Center.

HT and B27 GRADING CRITERIA

Grading of HLA-B27 and HLA typing serological and molecular results requires a minimum of 5 participants, as well as 80% or higher consensus among participants. If fewer than 5 results are submitted for any challenge, those results will be ungraded. Performance grades are assigned separately for serological, low resolution and high-resolution typing results. Each assigned antigen or allele is analyzed and graded separately but composite laboratory performance evaluation considers each complete Class I or Class II typing for each sample as a separate analyte. For more detailed information regarding grading criteria, please refer to the ASHI PT Operations Manual under the section “Survey” and the appropriate survey name. A downloadable PDF version of the Manual is also available via the following link: ASHI 2019 PT Operations Manual. (The 2020 PT Operations Manual will be available by the end of the first quarter.)