# Automatic Identification of Cuneiform Fragments Using String Alignment Algorithms 

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#### Abstract

The literature from ancient Mesopotamia is still riddled with textual lacunas. Scores of fragments which could potentially fill those lacunas lie unidentified in museums's cabinets, but their identification has traditionally been slow and laborious due to the ambiguities of cuneiform script. The present article presents a novel method for dealing with these ambiguities by using a string alignment algorithm adapted for cuneiform, which makes identification much easier and speeds up the process dramatically. The availability of this algorithm and of corpora on which to use it will advance significantly the reconstruction of Mesopotamian literature.


## 1 Introduction

The literary works from ancient Mesopotamia are in a state of reconstruction. The vehicle in which they were written, clay tablets inscribed with cuneiform script, is enormously durable but also brittle, so the masterpieces of Babylonian literature have come down to us in a fragmentary form. Since their rediscovery in the mid-nineteenth century, cuneiformists have striven to put together the classics of Mesopotamian literature from scores of fragments scattered throughout the world's museums, but the process is far from finished. Most texts are still riddled with textual lacunae and tens of thousands of fragments lie unidentified in museums' cabinets.

Most literary texts were copied on more than one clay tablet (so-called "manuscripts" of a text), often kept together in one and the same library. Frequently sections of texts are preserved in fragments from different manuscripts (referred to as "(partial) duplicates"), which partially overlap. Each fragment typically preserves a few signs not preserved on its duplicate; with the help of this signs other duplicates can be identified. The identification of these duplicates has traditionally been the
key for the reconstruction of Babylonian literature. Their potential in this respect is far from exhausted, since many hitherto unidentified fragments will, once identified, turn out to be duplicates of other fragments.

The identification of new fragments is rendered particularly challenging by the ambiguities of cuneiform script. Each sign has several possible phonetic renderings (so-called "readings"), and most syllables can be represented by means of different signs. There was never a strict orthography of any language written in cuneiform script, so the same word, e.g. Akkadian aparras, "I will divide", can be written phonetically with various combinations of signs (such as a-par-ra-as, a-pa-ar-ra-as, and $a-p a-r a-a s)$, and also by means of a word-sign (so-called "logogram", such as KUD). The variation is particularly pronounced in manuscripts from the first millennium BCE: the original triptotic declension of the Akkadian language had been lost in the spoken variety, but was still preserved in the written language. The vowels represented in the written language, however, no longer correspond with the use in previous periods, and a large degree of variation occurs at word end: for instance, the word lemutta in the 'Epic of Creation' I 44 is written in four manuscripts in four different ways, as le-mut-ta, le-mut-tu, le-mut-tu 4 , and le-mut-ti.

The identification of fragments has traditionally been done manually, making use of existing dictionaries (in particular the Chicago Assyrian Dictionary $=$ Oppenheim et al. 1956-2011), or else of concordances compiled ad-hoc (see Borger 1991, p. 51). Due to the peculiarities of cuneiform script, however, it is often difficult to make out individual words from sequences of signs bereft of context: if no unequivocal word can be made of the signs preserved, or if the word is a common one, such dictionaries and concordances are of limited use. For this reason, the identification has always depended on chance, and the success has, consequently, been
limited: thus, the catalogue of small fragments in the Nineveh collection, whose compilation took almost twenty years of painstaking work of the foremost cuneiformist at the time (Lambert, 1992), succeeded in identifying some 335 of the 5,400 pieces catalogued, i.e. $6.2 \%$. Due to the low success rate, the reconstruction is an extremely slow process: it took, for instance, over 100 years to identify the beginning of the 'Epic of Gilgameš' in a small fragment kept in a museum's drawer (Kwasman, 1998).

The potential in the use of computers for automatic identification of cuneiform fragments has long been noticed, but never realised, perhaps because of the skepticism with which some of the foremost specialists regarded the process. ${ }^{1}$

We obtained the corpus of literary texts that have been made available to the community by the "Electronic Babylonian Literature" project ${ }^{2}$. The availability of this data enables the development of algorithms to account for the ambiguities of cuneiform script, described above. Such ambiguities are best addressed by means of alignment algorithms that account for gaps and variations in the aligned sequences. The present paper presents the first use of string alignment algorithms for the identification of cuneiform fragments. We have created a search system that allows searches of cuneiform fragments using the sign mapping described below (3). Moreover, we have integrated the string alignment algorithms into the search system, thus enabling specialists to perform alignments on cuneiform fragments entered using the lightweight transliteration system referred to as $\mathrm{ATF},{ }^{3}$ the standard in the field.

## 2 Previous Work

We review previous work on solving similar alignment problems. Multiple sequence alignment has been applied successfully in linguistics (Prokić et al., 2009; List, 2011), but it does not produce optimal alignment, and our use case only requires pairwise alignment. Sanchez-Perez et al. (2014) propose a graph-based approach to text alignment for plagiarism detection, but the algorithm does

[^0]not account for gaps or lacunae and does not output the actual alignment. Williams et al. (2014), Williams (2015), and Brusuelas (2016) describe the adaptation of the BLAST algorithm for the Greek alphabet ("Greek-BLAST") in the framework of the Ancient Lives project ${ }^{4}$, which involved the implementation of a Greek Letter Oriented Substitution Matrix (GLOSUM) in lieu of the BLOSUM (BLOcks Substitution Matrix) substitution matrix. Greek manuscripts, however, do not contain the same sort of orthographic variation that can be found in cuneiform texts: this variation, described above, means that the background frequency that is at the core of GLOSUM cannot be used for cuneiform. Momtaz et al. (2016) use a sentence similarity measure for text alignment for text reuse detection. The approach works on the sentence level, but many fragments do not contain complete sentences or lines. Shmidman et al. (2016) present a method that uses only the two most infrequent letters for comparison purposes: this system accounts well for orthographic variation in Hebrew script, since the most frequent signs are those that appear most frequently in orthographic variations (e.g. י in דלמא vs. דילמא). It is, however, inappropriate for the sorts of variations that are common in cuneiform, which do not involve the insertion or removal of any sign in particular.

## 3 Methodology

As we have described above, the alignment of cuneiform fragments is challenging. After carrying out the survey of previous work in the previous section, we determined that the best solution would be to use sequence alignment. In order to account for the sort of variations that are common in cuneiform script, and for the sort of gaps that occur in cuneiform fragments, we needed a string alignment library in which the scoring could be defined programmatically instead of specifying the whole scoring matrix (due to a large number of cuneiform signs, such a matrix would be unpractically large). For that reason, we choose the library python-alignment ${ }^{5}$. We chose the library because it is pure Python, works with arbitrary vocabulary and can perform local (Smith and Waterman, 1981) and global alignments (Needleman and Wunsch, 1970).

[^1]The sign mapping problem Cuneiform signs are polyvalent, i.e., the same sign (e.g. UD) can have multiple phonetic readings (e.g. tam, tú, par, $u t$, hiš), and the same phonetic readings can be expressed with several discrete signs: for instance, the syllable $/ t u /$ can be written with the sign TU (the reading is then $\left.t u_{(1)}\right)$, UD $\left(=t u_{2}\right)$, $\mathrm{DU}\left(=t u_{3}\right)$, TUM $\left(=t u_{4}\right)$. The complexity of the system is further compounded by the fact that the repertoire of signs changed over time: signs that originally had distinct shapes coalesced into the same signs (e.g. the sign forms $\mathrm{KU}, \mathrm{TUG}_{2}$, and EŠ2, originally independent, coalesced into the same sign, which had $k u, t u g_{2}$, and $e \check{s}_{2}$ as possible readings). This fact means that the sign mapping adopted for the alignment should be geared towards the specific period of the texts involved. For this reason, the cuneiform Unicode block ( $\mathrm{U}+12000-\mathrm{U}+123 \mathrm{FF}$, $\mathrm{U}+12400-\mathrm{U}+1247 \mathrm{~F}, \mathrm{U}+12480-\mathrm{U}+1254 \mathrm{~F}$ ) cannot be used for the alignment, because its sign repertoire amalgamates several different periods (Studt, 2007). The repertoire that fits best manuscripts from the first millennium BCE is the list from Assyrisch-Babylonische Zeichenliste (henceforth $\mathrm{ABZ},=$ Borger 1988). In total, our sign database contains:

- 2490 signs ( 1936 composite and 554 simple) with 9194 readings.
- 826 signs with ABZ, which can be mapped to 694 ABZ numbers.
Readings, logograms, numbers, and compound graphemes in ATF format are converted to a sequence of ABZ numbers by getting a sign with matching reading or name from the sign list and using the ABZ value of that sign. If the sign does not have an ABZ number, the sign name is used instead. Compound graphemes and numbers can be arbitrary, so if they do not match a sign or reading from the sign list, they are used as is. For example 2 is a reading of MIN (ABZ570), but 9 is not a reading. " 2 " would become "ABZ570" but " 9 " would stay as " 9 ".

Some signs are formed by combining several signs (e.g. the sign ŠAB consists of PA +IB ): to account for this phenomenon, we treat juxtaposed signs outside of groupings as individual signs (e.g. |PA.IB| from ŠAB will be become PA IB, but $\mid G_{2} \times($ ME.EN $) \mid$ would remain unchanged.).

Scoring Since no reference alignments exist for cuneiform texts, we determined parameters in preliminary experimentation on aligning fragments
to the manuscripts. We ran local and global alignments of fragments presented in table 2 in appendix A against all the manuscripts, starting with default values: 2 for a match, -1 for substitution, and -2 for a gap.

Line breaks are essential in literary texts which have an established line structure. Therefore we assigned a high score for line break match and a significant penalty for substitution.

Some signs are transliterated as variants when the correct sign is unclear. Substituting a variant to one of those signs should not be penalized, and we use the maximum score of all possible combinations for the score of the alignment substitution.

Some substitutions are common, and some signs have a similar meaning. Therefore, these substitutions should not be penalized, and to determine common pairs, we performed local alignments, filtered out alignments with similarity less than $80 \%$, and calculated the frequency of each pair. From the most frequent pairs, we selected those which made sense (Table 3 in appendix C). These common substitutions have a positive but smaller score than the exact match.

The textual lacunae are problematic for the alignment, and we extended the python-alignment library with an affine gap penalty (Gotoh, 1982) has a significant penalty, but the extension is very cheap to allow the gap to cover the missing signs. Such a low penalty usually is not recommended (Smith and Waterman, 1981), but it is needed to get good results in our case. In the case of a lacuna, we are not dealing with actual addition or removal but missing data in the other sequence. When a gap is cheaper than a substitution, there are two ways to arrange the gaps:

$$
\begin{array}{lllllll}
\mathrm{a} & \mathrm{a} & - & - & - & \mathrm{a} & \mathrm{a} \\
- & - & \mathrm{b} & \mathrm{~b} & \mathrm{~b} & \mathrm{~b} & - \\
\hline
\end{array}
$$

If there are many such gaps, the number of possible alignments with an equal score grows exponentially. To overcome the issue, we modified the global backtracking algorithm to return only a single alignment. The final scoring is presented in Table 1. To filter out uninteresting results, we ignore alignments scoring less than or equal to 100.

We used global alignment for the final results because local alignment resulted in too many irrelevant matches. Furthermore, we discovered that global alignment was better even in the case of fragments that contain excerpts from different texts and that therefore match different texts in the corpus: in

| Type | Score |
| :--- | ---: |
| match | 16 |
| substitution | -5 |
| common substitution | 7 |
| break match | 6 |
| break substitution | -10 |
| gap start | -5 |
| gap extension | -1 |
| break gap extension | -10 |
| variant | max of all combinations |

Table 1: Scoring
these cases, the score of the global alignment, even with the penalty for the non-matching sections, was higher than that of the local alignments. An example alignment of the fragment K. 17700 is shown in appendix D.

## 4 Evaluation

To evaluate the results, we picked 100 manuscripts with at most 20 lines from 'Poem of Creation' (Enūma eliš) (Appendix B). The size of less than 20 lines corresponds to the average size of a fragment in the collection of fragments put at our disposal by the eBL project. ${ }^{6}$ We ran a global alignment against all the manuscripts. A chapter matches if any of the manuscripts in the chapter has a score larger than 100 . The method was able to assign the correct chapter to most of the inputs (recall 0.92 ), but produced many false positives (precision 0.39 ). The $\mathrm{F}_{1}$-measure is 0.55 and $\mathrm{F}_{2}$-measure is 0.73 . The $\mathrm{F}_{2}$-measure is more suited to our use case because the goal is to identify as many fragments as possible, and we can tolerate false positives but must avoid false negatives. The identifications have to be validated by an expert, and they can filter out the false negatives.

The traditional approach to sign identification was slow and laborious: it often took weeks to identify a single fragment, and decades to catalogue collections thereof (see Section 1). Even so, the success was rather limited, and ca. $90 \%$ of the pieces could not be identified. The method proposed here speeds up the process dramatically, improves the success rate, and renders it possible to compare masses of transliterated fragments with large text corpora. As a first step we implemented the sign

[^2]mapping with ABZ numbers described above (3) and a simple transliteration search allowing us to query signs in consecutive lines. We made that system available to the eBL Team, who was able to identify hundreds of pieces that had escaped undetected with the traditional method (see Jiménez et al. 2018 and Jiménez et al. 2019). While that system was successful, it still required the user to construct queries and would find only exact matches, so it was not fully automatic. A simple possibility to achieve full automatization is querying systematically with the whole fragment, but that procedure does not yield interesting results. To find matching texts, domain knowledge is required to construct a clever query that would match divergent texts. A simple improvement could be to replace one sign at a time with a wildcard matching any sign in the target sequence, but the approach is unfeasible for large fragments as a query needs to be performed for each sign in the fragment, and what can match is also limited. Our string alignment approach allows for more drastic changes in the sequences, which do occur in practice, and, importantly, the whole process of searching for matches is fully automated.

## 5 Conclusion

We identify fragments of clay tablets written with cuneiform script. Mesopotamian literature can be reconstructed on the basis of fragments that match partially other known fragments. The detection of these partial matches is paramount for progress in knowledge. The traditional method for detecting these matches was slow and inefficient. In order to account for the ambiguities of cuneiform script, in particular for the polyvalence of the sign and for signs composed of other signs, we implemented a sign mapping that transforms a transliteration into a sequence of signs that correspond to the specific period in which the fragment was written. Then we implemented a string alignment algorithm in order to align those signs, and fine-tuned the scoring to adapt it to our needs, which included adding a series of common substitutions that should not be penalized. We used an affine gap penalty to account for gaps, an exceedingly common feature of fragments. The method described was able to assign $92 \%$ of the fragments to a correct context. The method will speed up considerably the task of assigning fragments to texts, and therefore accelerate the reconstruction of Mesopotamian literature.

## References

Rykle Borger. 1988. Assyrisch-babylonische Zeichenliste. Neukirchen-Vluyn.

Rykle Borger. 1991. Ein brief sin-idinnams von larsa an den sonnengott sowie bemerkungen über joins und das joinen. Nachrichten der Akademie der Wissenschaften in Göttingen. I. Philologisch-historische Klasse, (1991/2):39-84.

James Brusuelas. 2016. Engaging Greek: Ancient Lives, pages 187-204. Ubiquity Press.

Osamu Gotoh. 1982. An improved algorithm for matching biological sequences. Journal of Molecular Biology, 162.

Enrique Jiménez, A. Heinrich, A. Hätinen, Zs. Földi, T. Mitto, J. Peterson, and U. Gabbay. 2019. From the electronic babylonian literature lab 8-15. KASKAL. Rivista di storia, ambienti e culture del Vicino Oriente Antico, (17):231-279.

Enrique Jiménez, A. Hätinen, Zs. Földi, A. Heinrich, and T. Mitto. 2018. From the electronic babylonian literature lab 1-7. KASKAL. Rivista di storia, ambienti e culture del Vicino Oriente Antico, (16):75-94.

Theodore Kwasman. 1998. A new join to the epic of gilgameš tablet i. Nouvelles Assyriologiques Brèves et Utilitaires, (1998/99).

Wilfred G. Lambert. 1992. Catalogue of the Cuneiform Tablets in the Kouyunjik Collection of the British Museum: Third Supplement. British Museum Press, London.

Johann-Mattis List. 2011. Multiple sequence alignment in historical linguistics. a sound class based apporach. pages 241-260.

Mozhgan Momtaz, Kayvan Bijari, Mostafa Salehi, and Hadi Veisi. 2016. Graph-based approach to text alignment for plagiarism detection in persian documents. volume 1737, pages 176-179. CEUR-WS.

Saul B. Needleman and Christian D. Wunsch. 1970. A general method applicable to the search for similarities in the amino acid sequence of two proteins. Journal of Molecular Biology, 48.
A. L. Oppenheim, E. Reiner, and M. Roth. 1956-2011. The Assyrian Dictionary of the Oriental Institute of the University of Chicago. Oriental Institute, Chicago.

Jelena Prokić, Martijn Wieling, and John Nerbonne. 2009. Multiple sequence alignments in linguistics.

Miguel A. Sanchez-Perez, Grigori Sidorov, and Alexander Gelbukh. 2014. The winning approach to text alignment for text reuse detection at pan 2014: Notebook for pan at clef 2014. volume 1180, pages 1004-1011. CEUR-WS.

Avi Shmidman, Moshe Koppel, and Ely Porat. 2016. Identification of parallel passages across a large hebrew/aramaic corpus. CoRR, abs/1602.08715.
T. F. Smith and M. S. Waterman. 1981. Identification of common molecular subsequences. Journal of Molecular Biology, 147.

Margret Studt. 2007. A practical and critical guide to the unicode blocks »cuneiform« and »cuneiform numbers« of unicode standard version 5.0.

Alex C. Williams. 2015. Computationally Accelerated Papyrology. Ph.D. thesis, Middle Tennessee State University, Murfreesboro, Tennessee.

Alex C. Williams, Hyrum D. Carroll, John F. Wallin, James Brusuelas, Lucy Fortson, Anne-Francoise Lamblin, and Haoyu Yu. 2014. Identification of ancient greek papyrus fragments using genetic sequence alignment algorithms. In 2014 IEEE 10th International Conference on e-Science, volume 2, pages 5-10.

## A Development Fragments

Our development fragments in Table 2 were chosen because they are known to match one chapter ("fragment") or more than one ("school"). The "fragments" contain significant gaps of the type that is common in cuneiform fragments. The nonmatching fragments were chosen at random.

| Museum number | Type |
| :--- | :--- |
| K. 19352 | Fragment |
| K. 17700 | Fragment |
| BM.36681 | School |
| BM.36688 | School |
| BM. 99811 | School |
| BM. 101558 | School |
| K. 20949 | School |
| K. 17591 | Fragment |
| K. 18617 | Fragment |
| K. 19604 | Fragment |
| K. 20637 | Fragment |
| K. 21209 | Fragment |
| Rm. 468 | Fragment |
| K. 20074 | not in Corpus, random |
| BM. 110295 | not in Corpus, random |
| BM. 82855 | not in Corpus, random |
| K. 20703 | not in Corpus, random, colophon |
| K. 15836 | not in Corpus, random, colophon |

Table 2: Development fragments

## B Test Fragments

To evaluate the results, we picked 100 manuscripts with at most 20 lines from 'Poem of Creation' (Enūma eliš) and compared it against all existing texts in a corpus of cuneiform literary texts. The size of less than 20 lines corresponds to the average size of a cuneiform fragment. The manuscripts chosen are:

- SB VII NinNAQuo2b
- SB I BabaNBQuo1
- SB V NinNACom1
- SB I BabaNBSch14
- SB I AššNA8
- SB I BabaNB9
- SB V NinNACom2
- SB VI NinNACom5
- SB V BabaNBSch2
- SB III BabaNBQuo1
- SB I SipNBSch1
- SB IV NinNA1b
- SB VI NinNA5
- SB VII SipNBQuo2
- SB II KalNA1
- SB VII BabaLBSch1
- SB I BabaNBSch12
- SB II NinNA1
- SB I AššNA4
- SB VI BabaNBCom2
- SB II BabaLBSch7
- SB I BabaNBSch4
- SB VII BabaNB1
- SB I BabaNBSch22
- SB VI BabaNBSch1
- SB II NinNA4
- SB IV BabaLBQuo3
- SB VII AššNACom1a
- SB VII NinNAQuo2a
- SB I BabaNBQuo3
- SB VI AššNA3
- SB I BabaNBSch7
- SB VI NinNACom3
- SB I BabaNBSch13
- SB I BabaNBSch5
- SB III HuzNAQuo1
- SB V BabaLBQuo1
- SB I NinNA1c
- SB VII NinNACom3
- SB VI BabaNBCom3
- SB V BabaLBQuo3
- SB IV BabaNBSch2
- SB IV BabaNBSch4
- SB VI BabaNBSch3
- SB V BabaNBCom3
- SB IV BabaNBSch1
- SB V NinNAQuo2
- SB III NinNACom1
- SB VI NinNAQuo2
- SB II BabaLBSch6
- SB IV HuzNA4a
- SB I BabaNBSch24
- SB I BabaNBSch15
- SB VII BabaNBQuo2
- SB IV HuzNA2
- SB I NinNA6b
- SB VII BabaNBSch4
- SB II BabaNBQuo2
- SB V BabaLBQuo2
- SB VI BabaNBSch2
- SB VII NinNA4c
- SB V BorNBQuol
- SB III AššNAQuo1
- SB VII BabaNBCom3
- SB I BabaNBSch8
- SB V BabaNBSch6
- SB I BabaNBSch11
- SB I BabaNBSch1
- SB V NinNA6a
- SB VII BabaLBQuo3
- SB VII NinNAQuo4
- SB VI SipLBSch1
- SB I BabaNB7
- SB II BabaNBSch1
- SB IV AššMA1c
- SB V NinNA3
- SB I BabaNBSch6
- SB III BabaNBSch1
- SB I NinNA1d
- SB I NinNACom1
- SB VII NinNACom4
- SB I AššNASch1
- SB I AššNA7
- SB VI KalNA1
- SB VII AššNAQuo1
- SB III BabaNBSch5
- SB III BabaLBQuo1
- SB IV BabaNBCom2
- SB VI BabaLBQuo2
- SB II BabaLBSch3
- SB III BabaLBSch1
- SB VII BabaNBQuo1
- SB VII BabaLBQuo4
- SB V AššNA1
- SB VII NinNAQuo3
- SB IV NinNACom1
- SB III BabaNBSch3
- SB III BabaNBSch2
- SB VII Ǎ̌šNAQuo2
- SB VII HuzNA1c


## C Substitutions

Although there are usually more than two ways of writing a word in cuneiform, some sign substitutions are particularly common (e.g. $\mathrm{TU}=\mathrm{ABZ58}$ vs $\mathrm{TI}=\mathrm{ABZ73}$ in le-mut-tu vs le-mut-ti). In order to determine the most common substitutions, we performed local alignments, filtered out alignments with similarity less than $80 \%$, and calculated the frequency of each pair. These common substitutions have a positive but smaller score than the exact match. The list is shown in table 3.

| ABZ58 | ABZ139 |
| :--- | :--- |
| ABZ75 | ABZ231 |
| ABZ142 | ABZ579 |
| ABZ70 | ABZ75 |
| ABZ55 | ABZ59 |
| ABZ308 | ABZ142 |
| ABZ537 | ABZ55 |
| ABZ73 | ABZ207 |
| ABZ75 | ABZ312 |
| ABZ367 | ABZ449 |
| ABZ214 | ABZ371 |
| ABZ84 | ABZ586 |
| ABZ73 | ABZ139 |
| ABZ86 | ABZ328 |
| ABZ352 | ABZ138 |
| ABZ597 | ABZ353 |
| ABZ104 | ABZ7 |
| ABZ376 | ABZ73 |
| ABZ61 | ABZ427 |
| ABZ207 | ABZ139 |
| ABZ532 | ABZ427 |
| ABZ5 | ABZ371 |
| ABZ318 | ABZ411 |
| ABZ545 | ABZ354 |
| ABZ58 | ABZ73 |
| ABZ381 | ABZ207 |
| ABZ461 | ABZ536 |
| ABZ68 | ABZ86 |
| ABZ342 | ABZ61 |
| ABZ318 | ABZ142 |
| ABZ597 | ABZ545 |
| ABZ68 | ABZ328 |

Table 3: Common substitutions

## D Example Alignment

The global alignment of the fragment K. 17700 against the manuscript SB I NinNA3 from 'Poem of Creation' (Enūma eliš) has significant gaps due to parts broken away from the fragment. An affine gap penalty with a low cost for gap extension allows for significant gaps. $88 \%$ of the signs in the preserved regions are identical. Line-break (\#) matches have a high score so that the lines will stay aligned.


K. 17700 - $\quad$ - $\quad$ -

NinNA3 ABZ449 ABZ537 ABZ461 ABZ142 ABZ342 ABZ231 ABZ73 ABZ367
K. 17700 ABZ86 ABZ308 ABZ73 - $\quad$ - $\quad$ -

NinNA3 ABZ86 ABZ308 ABZ73 ABZ332 ABZ545 \# ABZ367 ABZ78 ABZ6
K. 17700 - $\quad$ - ABZ401 ABZ579


[^0]:    1"It is impracticable to use computers to identify such pieces, since the ambiguities of cuneiform script and the lack of reconstructed texts to be used as a basis for machine identifications rule out any such method. It is accordingly necessary to rely on the human memory and on aids such as dictionaries and glossaries" (Lambert, 1992, p. ix).
    ${ }^{2}$ eBL, https://www.ebl.lmu.de/
    ${ }^{3}$ http://oracc.org/doc/help/ editinginatf/index.html

[^1]:    4https://www.ancientlives.org/
    5https://github.com/eseraygun/ python-alignment

[^2]:    ${ }^{6}$ https://www.ebl.lmu.de/fragmentarium
    The average size is 259,641 lines $/ 19,053$ fragments $=13.62$ lines.

