# MAST

Motif Alignment & Search Tool

For further information on how to interpret these results https://meme-suite.org/meme/doc/mast.html.

To get a copy of the MEME software please access https://meme-suite.org.

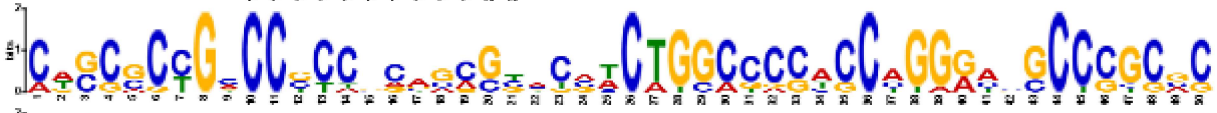
If you use MAST in your research, please cite the following paper:

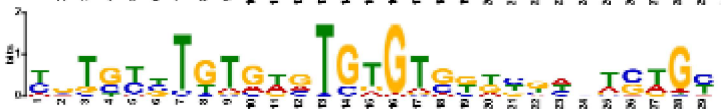
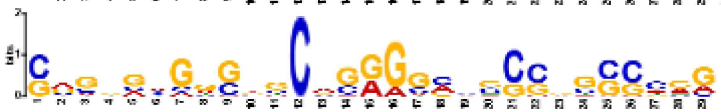
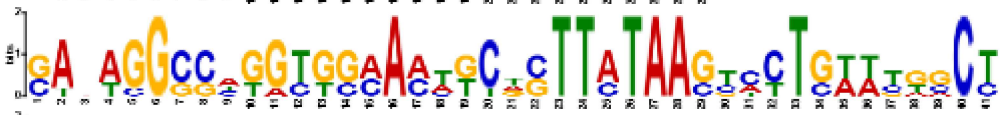
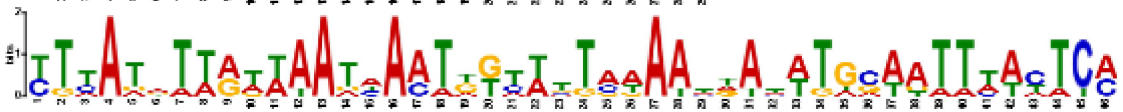
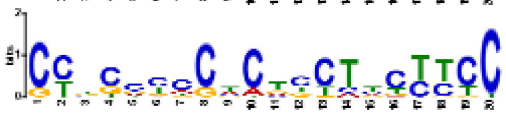
Timothy L. Bailey and Michael Gribskov, "Combining evidence using p-values: application to sequence homology searches", *Bioinformatics*, **14**(1):48-54, 1998. [full text]

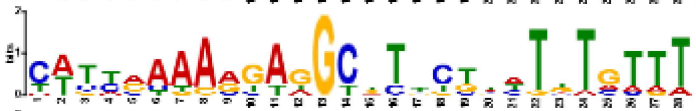
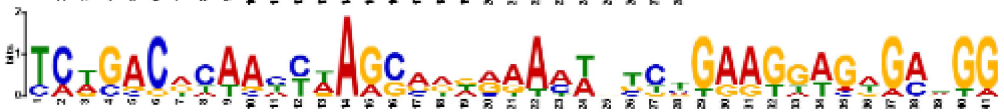
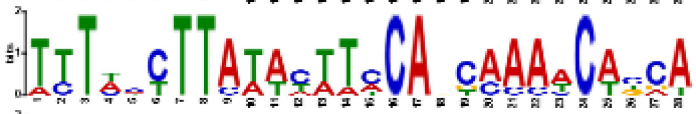
MOTIFS | SEARCH RESULTS | INPUTS & SETTINGS | PROGRAM INFORMATION | RESULTS IN TEXT FORMAT | RESULTS IN XML FORMAT

## MOTIFS

Next Top

| | Logo | Name |
|---|---|---|
| 1. | | AAAAMAAAAAARAAAAWRAVAWNAARAAA |
| 2. | | GGGBGSKGGGGVSGGGGMGGG |
| 3. |  | CWSCSCYGMCCSCCNCASCGBMCVWCTGGCCCCWCCMG |
| 4. | | AMAYTTTYTATRTAAAAGGAACTTACGAACKGCAATTTAATTY |
| 5. | | TWCWKAGMAGWWCATTSYWGGKKSWTTKTTTWCWYWST |
| 6. | | ACYMWGCMKTGGSYGCSKCCGKGRAWYMRGTGCWAMKC |
| 7. | | TACTTWTGDTHWGATWGVVDTGCTGGTTDGWTTTGGGGA |

| | Logo | Name |
|---|---|---|
| 8. | | AAAGVYGRGCCCDBTTCCWGTCTTVCCAGCYAHGTDCAAAR |
| 9. | | CTGACCCTGGACCCTGGGACCGCACACCGCCGCCTGCTCAT |
| 10. |  | YSTSYBTGTGWGTGTGTSKKBGHNTSTGY |
| 11. | | AAMTTWGKCCVGGCRYGGTGGCTCACGCCTGTAATCCCAG |
| 12. |  | SRGVGMGGSRGCAGRGGMNSCSBGSSCRG |
| 13. |  | SANAGGCCHGGTGGMAMWKCDSTTATAAGYMCTGWWYKS |
| 14. | | YTCCRGMYTGKGHAMCAGAGVGWGACBSK |
| 15. |  | YTYATRTTRWWAATHAATKKYWTTMWAAWDAWWTGSAATT |
| 16. | | SSTGGTMTCTGKGGGCWYCCCTGCCTGGG |
| 17. | | CTKABCYCAGDCCTCHCTGCC |
| 18. | | TGGTMHGTGGSAGAMACTYGTAACWCHGKGRYBSCCSRGT |
| 19. |  | CYKCCYCCTCTYCTTCYYCC |

| | Logo | Name |
|---|---|---|
| 20. | | AKNYAAGRCMRRAASNCRGTCATGKGYYKWKVWRAMSCMV |
| 21. |  | CWTYVAAARGAGGCKTTCTHHTKTGTTT |
| 22. |  | TCWGACDCAAHYWAGSADDRAAMWNTCTGAAGGWGDGM |
| 23. | | RGYTGVVAGCKGATCVDAGCGCHBSGGBS |
| 24. | | TGGAVSCRCATCCASGYCCAC |
| 25. | | WCMKBAWGARAGARAHKTCTRACTCASAG |
| 26. |  | TTTWMCTTATAYTTMCANCAAAWCABCA |
| 27. | | TBCYTTAATGTCTBCWYDKTG |
| 28. | | AAACCCADCVCGAACBAGRGAHGAVVTTWCCTTGTTCAWC |
| 29. | | ATADTAWTGMNKRAMRGAGTRAAYANAWGARRKVRTADAD |
| 30. | | GAGAGHGSATTCAGMGHAAVCADAGGWVAYCTTCTTVGTK |

## Search Results

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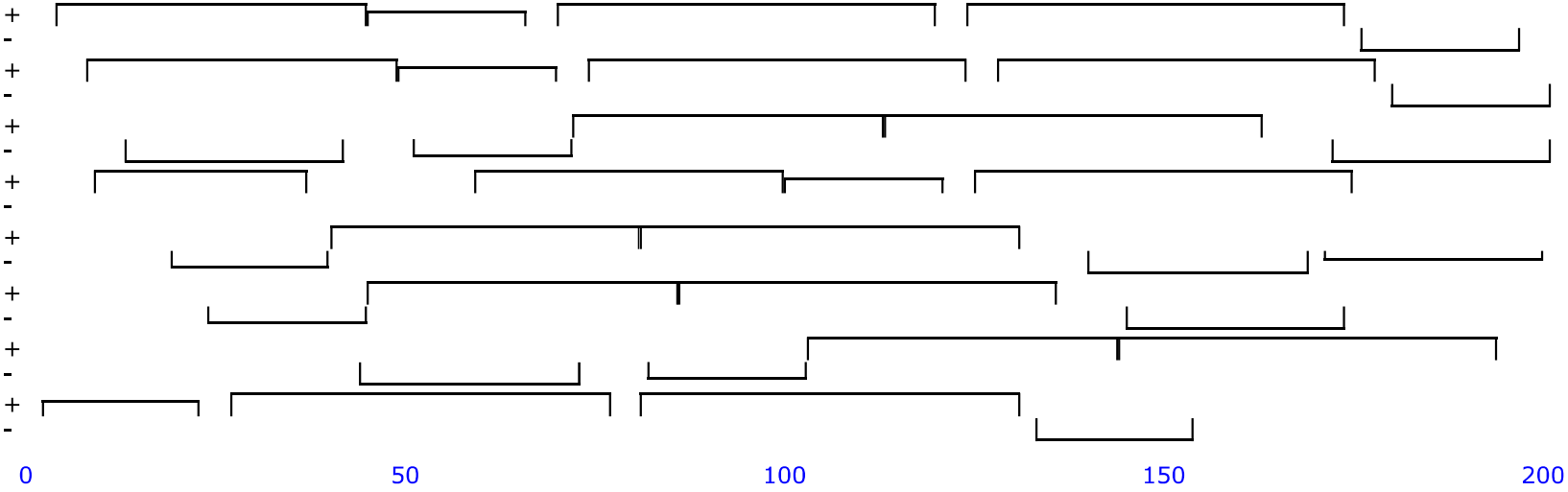
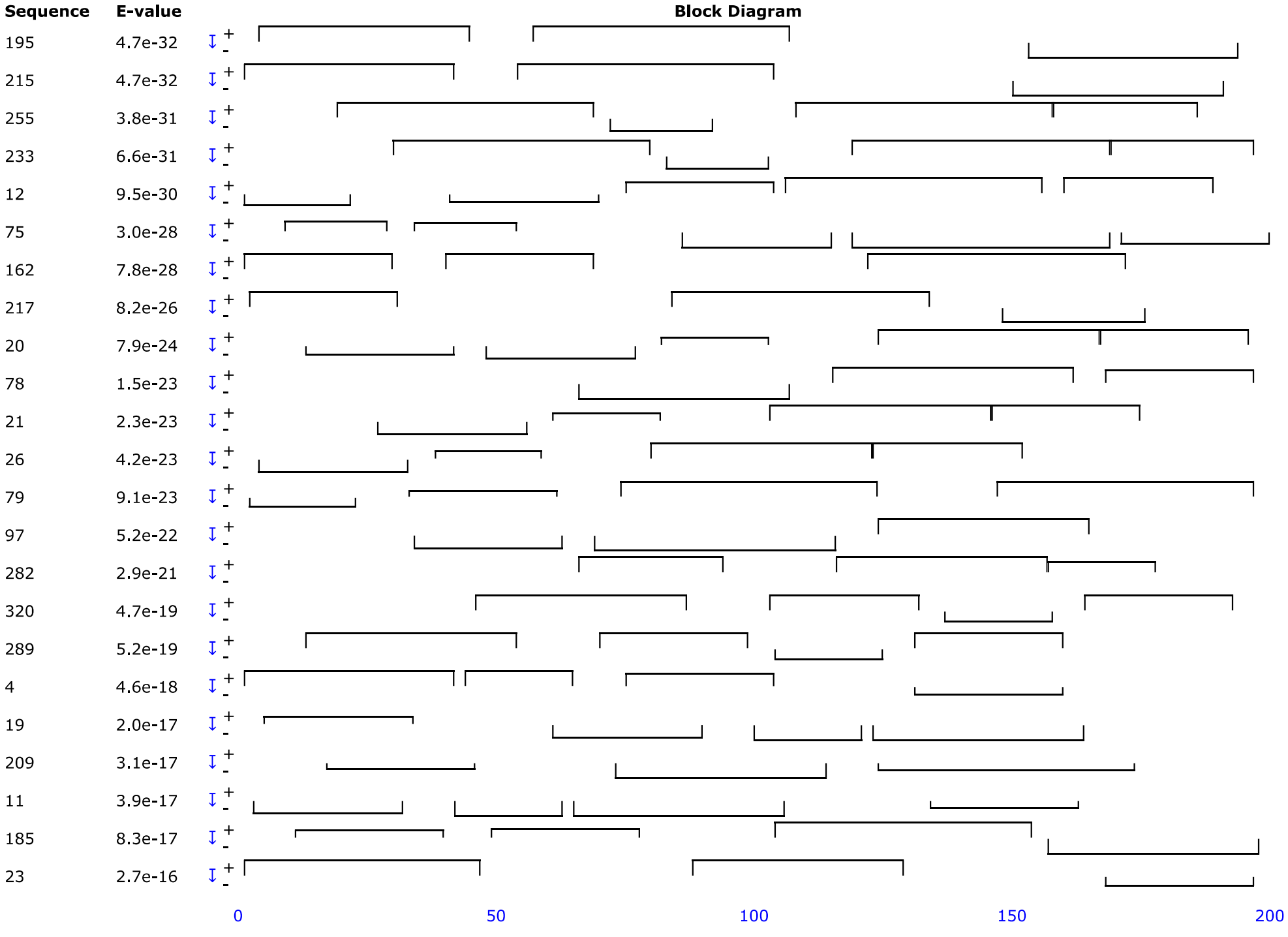
### Top Scoring Sequences

Each of the following 250 sequences has an *E*-value less than 10.
The motif matches shown have a position *p*-value less than 0.0001.
**Hover the cursor** over the sequence name to view more information about a sequence.
**Hover the cursor** over a motif for more information about the match.
**Click on the arrow** (↧) next to the *E*-value to see the sequence surrounding each match.

AAAAMAAAAAARAAAAWRAVAWNAARAAA GGGBGSKGGGGVSGGGGMGGG CWSCSCYGMCCSCCNCASCGBMCVWCTGGCCCCWCCMGGRMNGCCCGCVC
AMAYTTTYTATRTAAAAGGAACTTACGAACKGCAATTTAATTYAAAGACA TWCWKAGMAGWWCATTSYWGGKKSWTTKTTTWCWYWSTGMC
ACYMWGCMKTGGSYGCSKCCGKGRAWYMRGTGCWAMKCARRGG TACTTWTGDTHWGATWGVVDTGCTGGTTDGWTTTGGGGAASCAGCATTVA
AAAGVYGRGCCCDBTTCCWGTCTTVCCAGCYAHGTDCAAAR CTGACCCTGGACCCTGGGACCGCACACCGCCGCCTGCTCAT
YSTSYBTGTGWGTGTGTSKKBGHNTSTGY AAMTTWGKCCVGGCRYGGTGGCTCACGCCTGTAATCCCAGC SRGVGMGGSRGCAGRGGMNSCSBGSSCRG
SANAGGCCHGGTGGMAMWKCDSTTATAAGYMCTGWWYKSCT YTCCRGMYTGKGHAMCAGAGVGWGACBSK
YTYATRTTRWWAATHAATKKYWTTMWAAWDAWWTGSAATTWAYTCM SSTGGTMTCTGKGGGCWYCCCTGCCTGGG CTKABCYCAGDCCTCHCTGCC
TGGTMHGTGGSAGAMACTYGTAACWCHGKGRYBSCCSRGTGYACGKYKTC CYKCCYCCTCTYCTTCYYCC
AKNYAAGRCMRRAASNCRGTCATGKGYYKWKVWRAMSCMWGRHWGAKGRA CWTYVAAARGAGGCKTTCTHHTKTGTTT
TCWGACDCAAHYWAGSADDRAAMWNTCTGAAGGWGDGMHGG RGYTGVVAGCKGATCVDAGCGCHBSGGBS TGGAVSCRCATCCASGYCCAC
WCMKBAWGARAGARAHKTCTRACTCASAG TTTWMCTTATAYTTMCANCAAAWCABCA TBCYTTAATGTCTBCWYDKTG
AAACCCADCVCGAACBAGRGAHGAVVTTWCCTTGTTCAWCCCAKTCCHBA ATADTAWTGMNKRAMRGAGTRAAYANAWGARRKVRTADADW
GAGAGHGSATTCAGMGHAAVCADAGGWVAYCTTCTTVGTKACGAAGA

| Sequence | E-value | Block Diagram |
|---|---|---|
| 248 | 1.7e-59 | ↧ + - |
| 274 | 1.7e-59 | ↧ + - |
| 287 | 4.7e-52 | ↧ + - |
| 266 | 4.1e-43 | ↧ + - |
| 216 | 1.3e-42 | ↧ + - |
| 227 | 1.5e-42 | ↧ + - |
| 265 | 1.4e-41 | ↧ + - |
| 281 | 8.7e-39 | ↧ + - |

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E-value
Block Diagram
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255 3.8e-31
233 6.6e-31
12 9.5e-30
75 3.0e-28
162 7.8e-28
217 8.2e-26
20 7.9e-24
78 1.5e-23
21 2.3e-23
26 4.2e-23
79 9.1e-23
97 5.2e-22
282 2.9e-21
320 4.7e-19
289 5.2e-19
4 4.6e-18
19 2.0e-17
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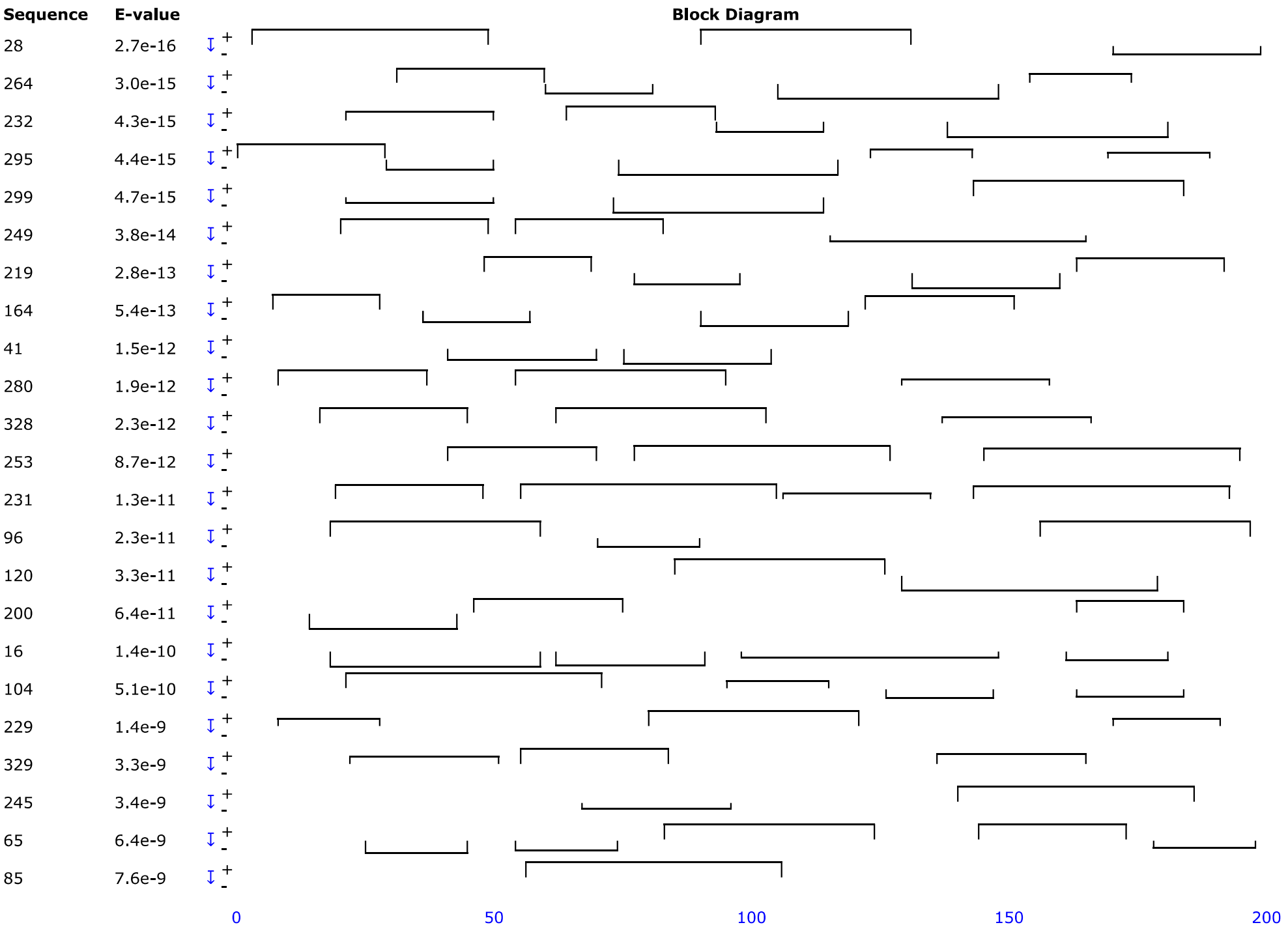
11 3.9e-17
185 8.3e-17
23 2.7e-16
0
50
100
150
200


Sequence
E-value
Block Diagram
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264 3.0e-15
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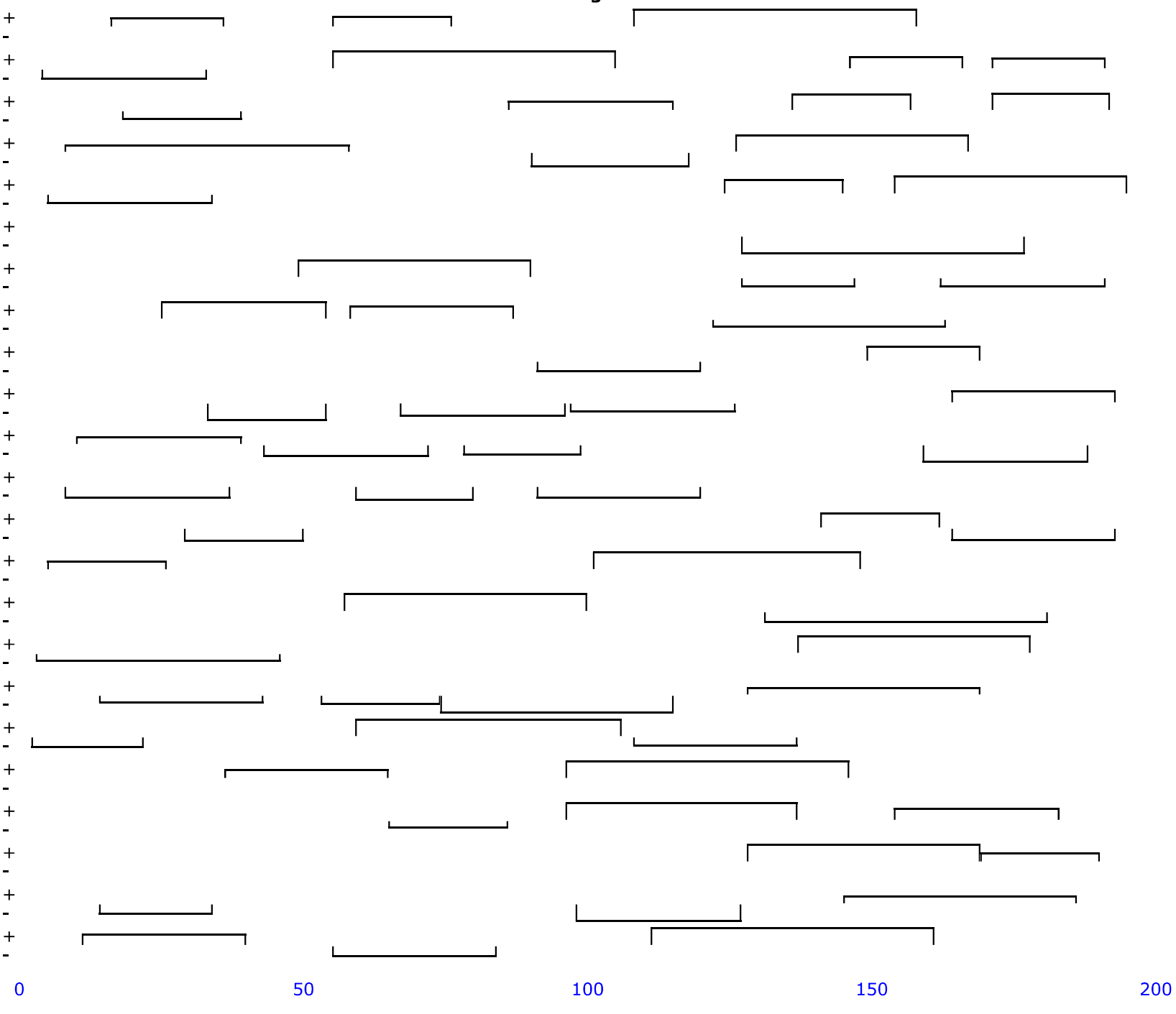
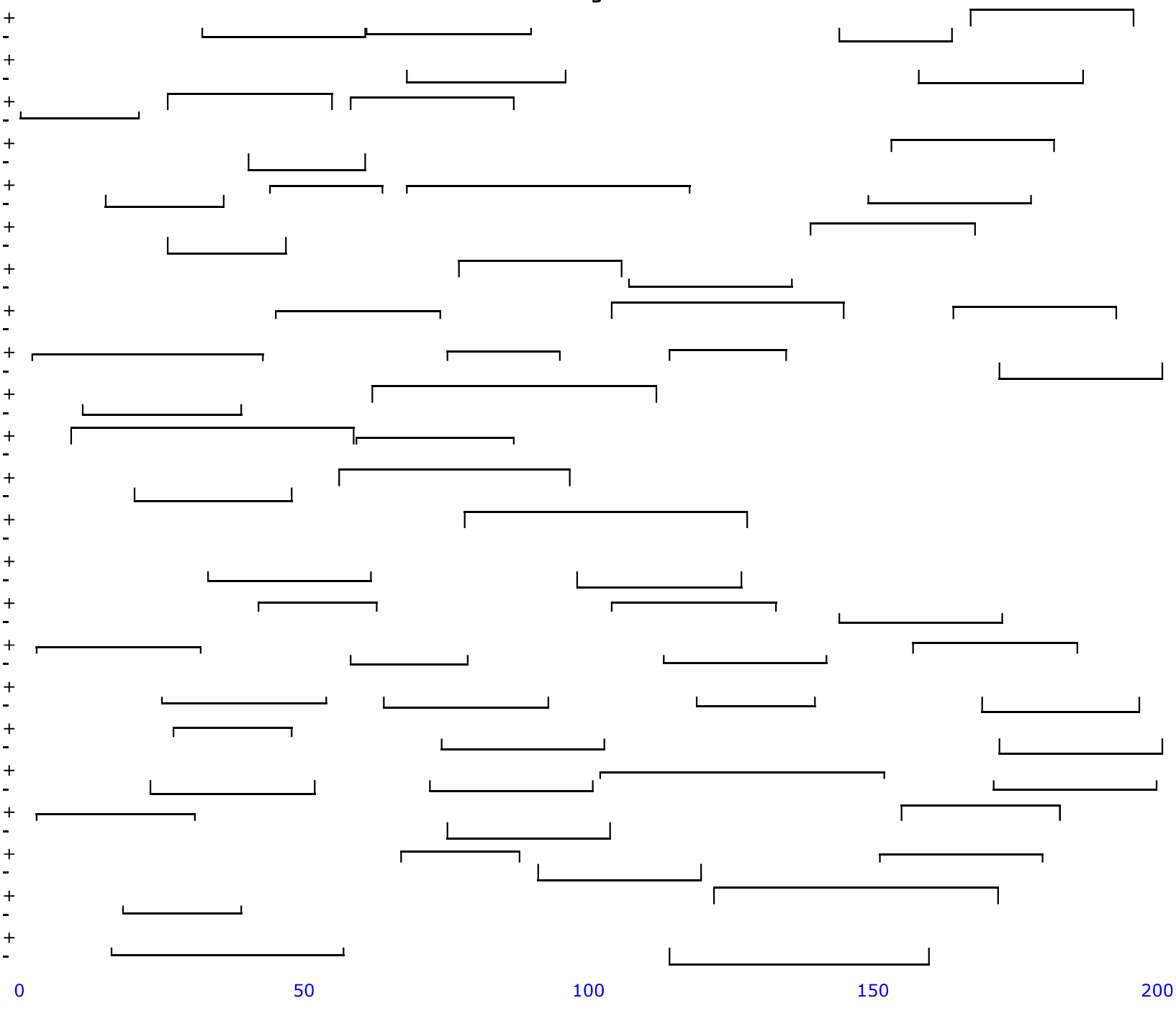
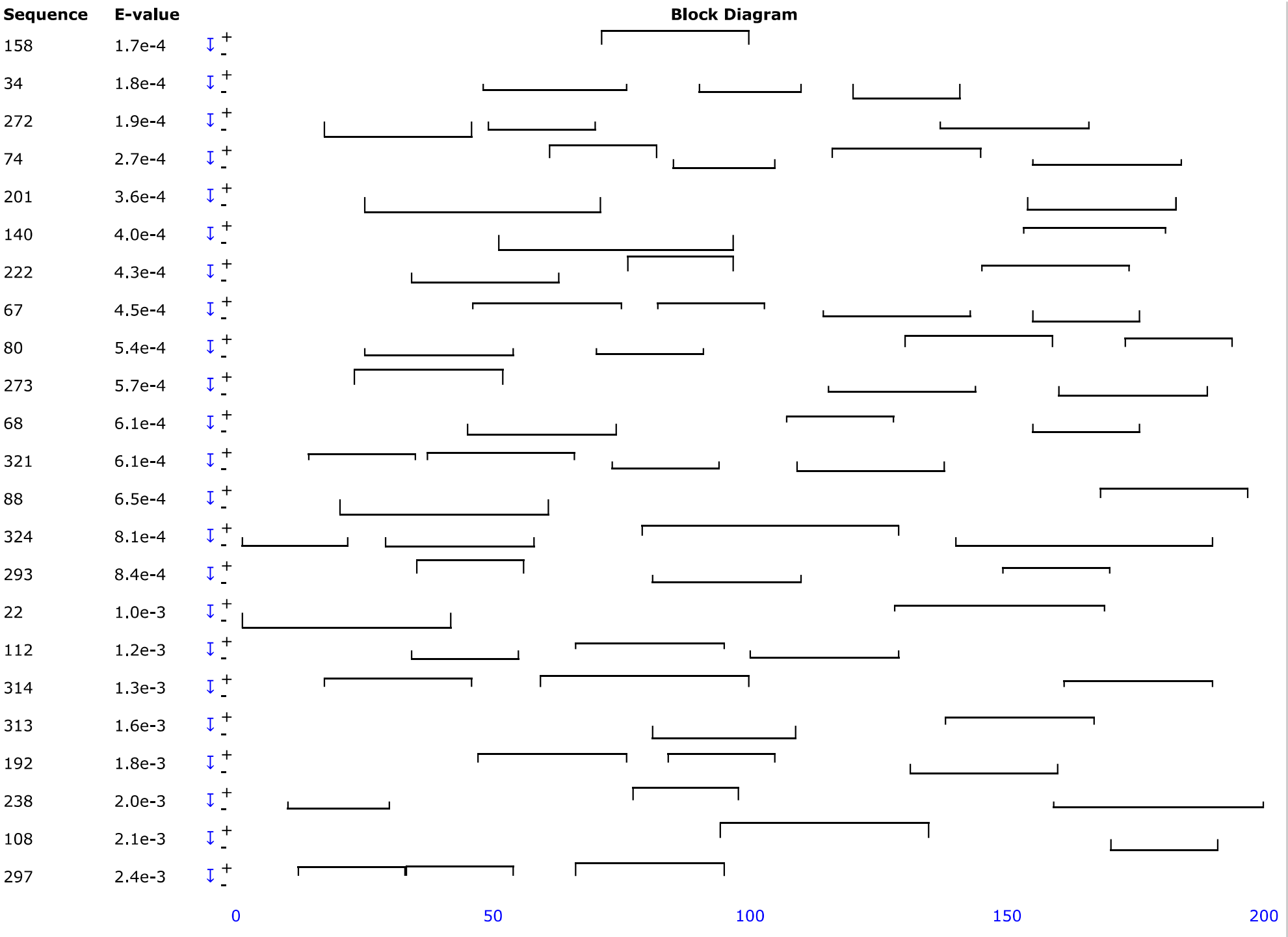
299 4.7e-15
249 3.8e-14
219 2.8e-13
164 5.4e-13
41 1.5e-12
280 1.9e-12
328 2.3e-12
253 8.7e-12
231 1.3e-11
96 2.3e-11
120 3.3e-11
200 6.4e-11
16 1.4e-10
104 5.1e-10
229 1.4e-9
329 3.3e-9
245 3.4e-9
65 6.4e-9
85 7.6e-9
0
50
100
150
200

| Sequence | E-value | Block Diagram |
|---|---|---|
| 165 | 1.2e-8 | |
| 24 | 1.6e-8 | |
| 43 | 4.2e-8 | |
| 35 | 4.6e-8 | |
| 129 | 4.6e-8 | |
| 105 | 4.7e-8 | |
| 223 | 5.5e-8 | |
| 131 | 5.9e-8 | |
| 239 | 1.1e-7 | |
| 9 | 1.3e-7 | |
| 46 | 2.7e-7 | |
| 132 | 3.2e-7 | |
| 2 | 3.9e-7 | |
| 7 | 4.4e-7 | |
| 89 | 4.7e-7 | |
| 303 | 5.9e-7 | |
| 98 | 9.8e-7 | |
| 130 | 1.1e-6 | |
| 173 | 1.1e-6 | |
| 163 | 1.3e-6 | |
| 57 | 1.6e-6 | |
| 210 | 2.2e-6 | |
| 8 | 2.7e-6 | |



| Sequence | E-value | Block Diagram |
|---|---|---|
| 225 | 3.0e-6 | |
| 160 | 3.0e-6 | |
| 6 | 3.2e-6 | |
| 277 | 4.1e-6 | |
| 56 | 5.9e-6 | |
| 279 | 6.2e-6 | |
| 323 | 7.3e-6 | |
| 25 | 7.3e-6 | |
| 161 | 8.7e-6 | |
| 77 | 9.0e-6 | |
| 47 | 1.1e-5 | |
| 17 | 1.6e-5 | |
| 154 | 1.7e-5 | |
| 33 | 1.7e-5 | |
| 308 | 2.2e-5 | |
| 326 | 2.8e-5 | |
| 147 | 3.3e-5 | |
| 213 | 6.4e-5 | |
| 116 | 7.2e-5 | |
| 110 | 1.0e-4 | |
| 247 | 1.2e-4 | |
| 278 | 1.4e-4 | |
| 168 | 1.4e-4 | |

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E-value
Block Diagram
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34 1.8e-4
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140 4.0e-4
222 4.3e-4
67 4.5e-4
80 5.4e-4
273 5.7e-4
68 6.1e-4
321 6.1e-4
88 6.5e-4
324 8.1e-4
293 8.4e-4
22 1.0e-3
112 1.2e-3
314 1.3e-3
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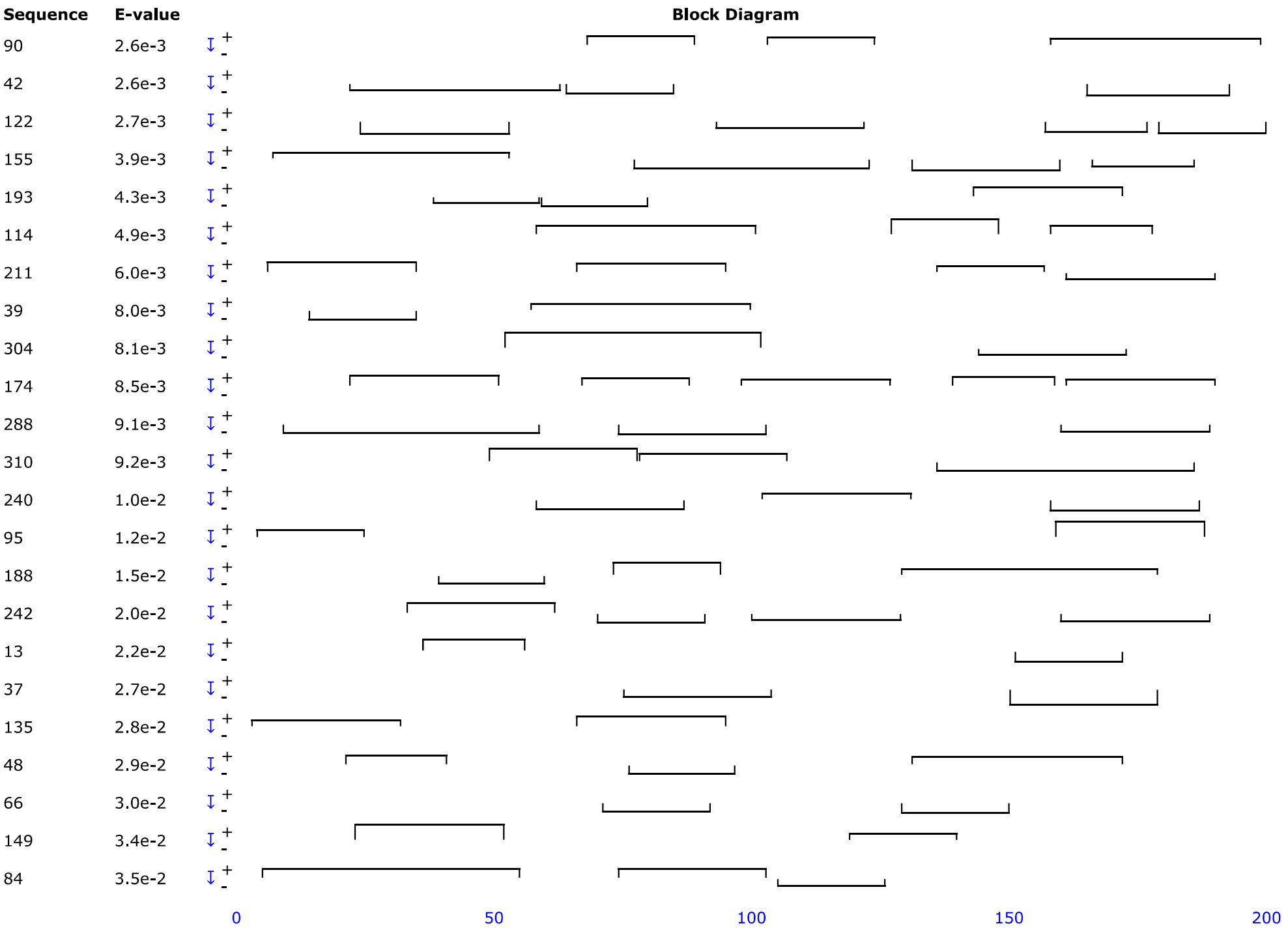
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E-value
Block Diagram
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193 4.3e-3
114 4.9e-3
211 6.0e-3
39 8.0e-3
304 8.1e-3
174 8.5e-3
288 9.1e-3
310 9.2e-3
240 1.0e-2
95 1.2e-2
188 1.5e-2
242 2.0e-2
13 2.2e-2
37 2.7e-2
135 2.8e-2
48 2.9e-2
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100
150
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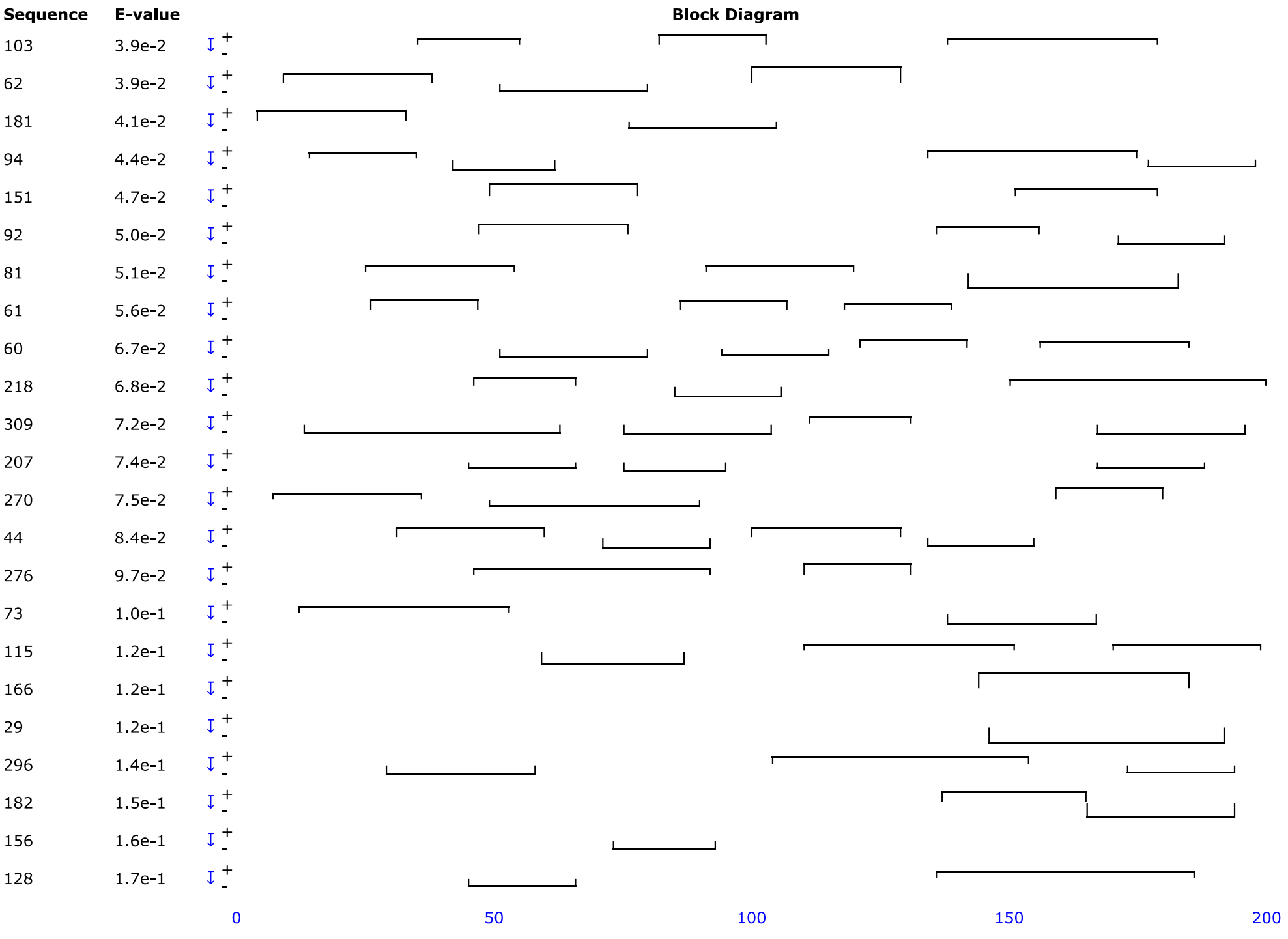
Sequence
E-value
Block Diagram
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62 3.9e-2
181 4.1e-2
94 4.4e-2
151 4.7e-2
92 5.0e-2
81 5.1e-2
61 5.6e-2
60 6.7e-2
218 6.8e-2
309 7.2e-2
207 7.4e-2
270 7.5e-2
44 8.4e-2
276 9.7e-2
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166 1.2e-1
29 1.2e-1
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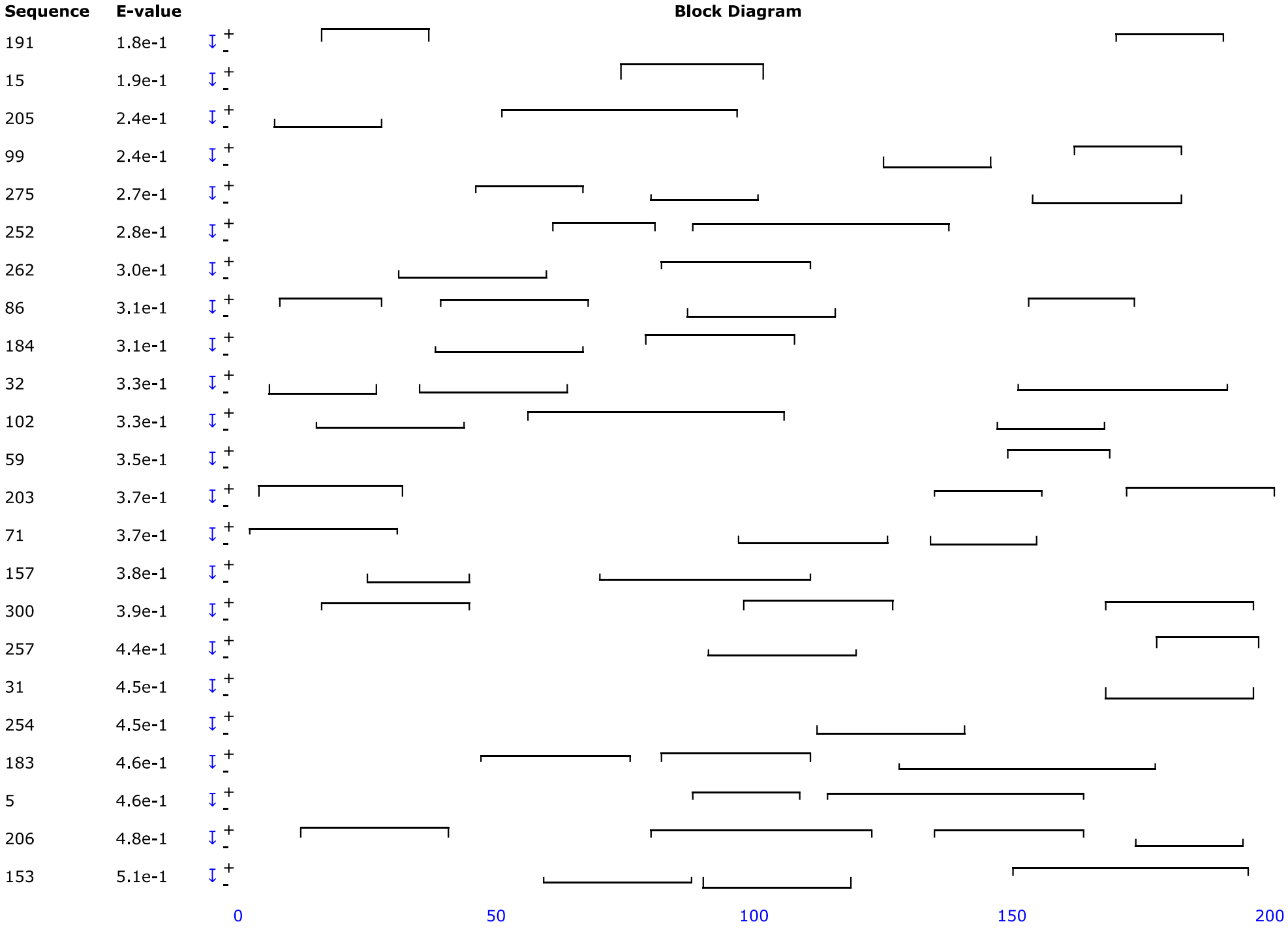
182 1.5e-1
156 1.6e-1
128 1.7e-1
0
50
100
150
200


Sequence
E-value
Block Diagram
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205 2.4e-1
99 2.4e-1
275 2.7e-1
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184 3.1e-1
32 3.3e-1
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59 3.5e-1
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71 3.7e-1
157 3.8e-1
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183 4.6e-1
5 4.6e-1
206 4.8e-1
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0
50
100
150
200

| Sequence | E-value | Block Diagram |
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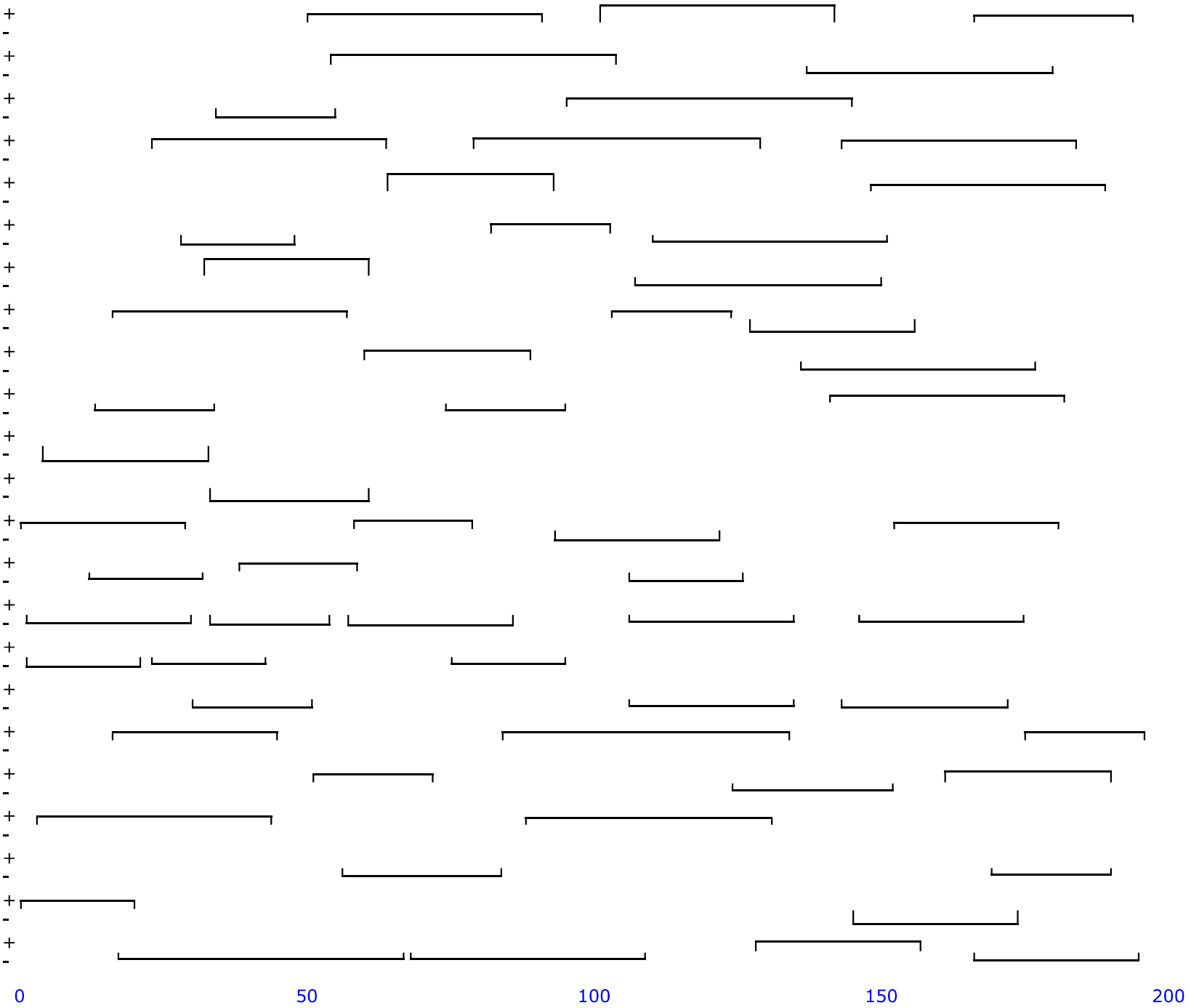
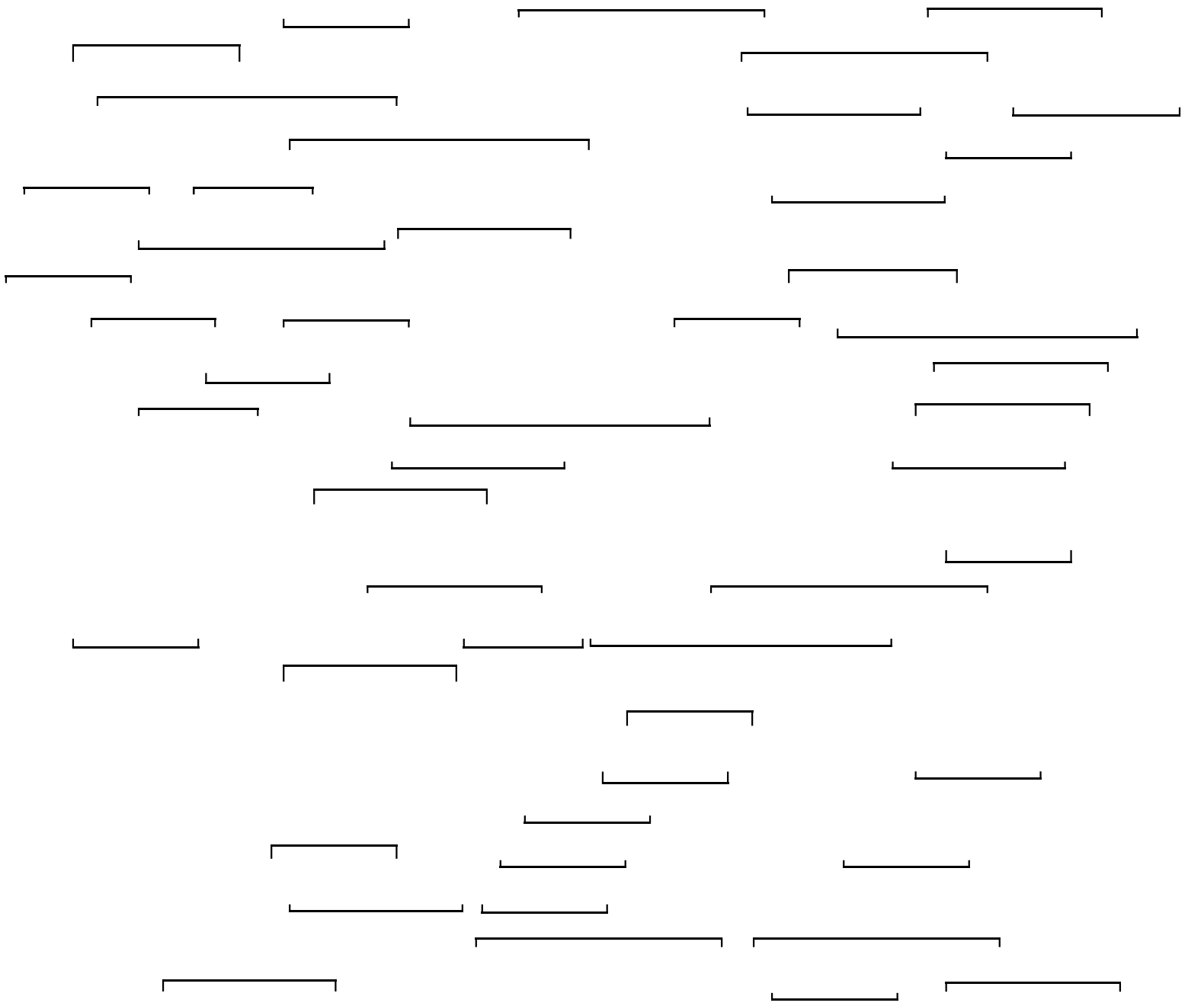
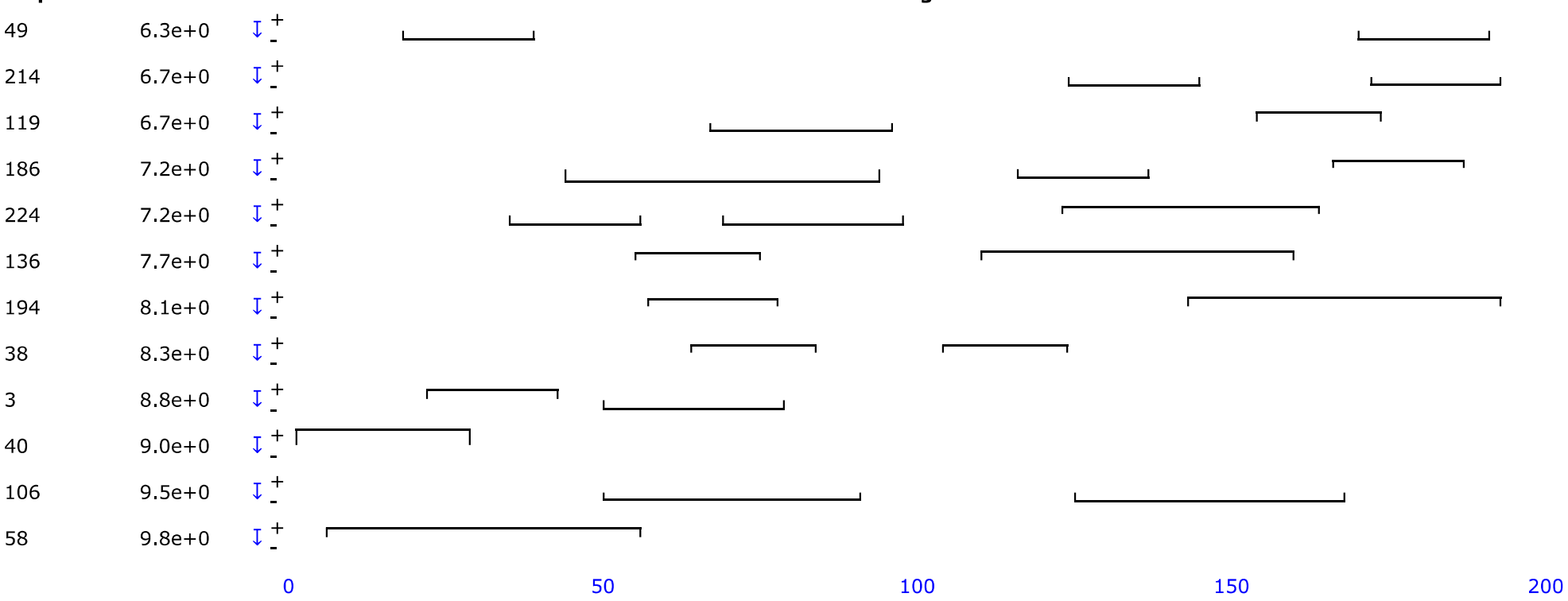
| 171 | 6.0e-1 |  |
| 170 | 6.2e-1 | |
| 51 | 6.4e-1 | |
| 319 | 6.6e-1 | |
| 107 | 7.1e-1 | |
| 137 | 7.4e-1 | |
| 69 | 8.5e-1 | |
| 91 | 8.6e-1 | |
| 169 | 8.9e-1 | |
| 180 | 9.3e-1 | |
| 113 | 9.5e-1 | |
| 251 | 9.7e-1 | |
| 190 | 1.1e+0 | |
| 317 | 1.1e+0 | |
| 285 | 1.4e+0 | |
| 30 | 1.4e+0 | |
| 72 | 1.4e+0 | |
| 167 | 1.6e+0 | |
| 305 | 1.6e+0 | |
| 172 | 1.8e+0 | |
| 260 | 1.9e+0 | |
| 316 | 1.9e+0 | |
| 237 | 2.0e+0 | |

| Sequence | E-value | Block Diagram |
|---|---|---|
| 269 | 2.0e+0 |  |
| 189 | 2.1e+0 | |
| 175 | 2.1e+0 | |
| 244 | 2.2e+0 | |
| 179 | 2.5e+0 | |
| 36 | 2.5e+0 | |
| 268 | 2.8e+0 | |
| 292 | 2.9e+0 | |
| 176 | 3.3e+0 | |
| 121 | 3.5e+0 | |
| 50 | 3.8e+0 | |
| 159 | 3.8e+0 | |
| 177 | 3.8e+0 | |
| 14 | 4.3e+0 | |
| 52 | 4.6e+0 | |
| 111 | 5.6e+0 | |
| 144 | 5.6e+0 | |
| 294 | 5.6e+0 | |
| 83 | 5.7e+0 | |
| 64 | 5.8e+0 | |
| 54 | 5.8e+0 | |
| 202 | 5.8e+0 | |
| 146 | 6.2e+0 | |

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AAAGVYGRGCCCDBTTCCWGTCTTVCCAGCYAHGTDCAAAR CTGACCCTGGACCCTGGGACCGCACACCGCCGCCTGCTCAT

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TGGTMHGTGGSAGAMACTYGTAACWCHGKGRYBSCCSRGTGYACGKYKTC CYKCCYCCTCTYCTTCYYCC

AKNYAAGRCMRRAASNCRGTCATGKGYYKWKVWRAMSCMWGRHWGAKGRA CWTYVAAARGAGGCKTTCTHHTKTGTTT

TCWGACDCAAHYWAGSADDRAAMWNTCTGAAGGWGDGMHGG RGYTGVVAGCKGATCVDAGCGCHBSGGBS TGGAVSCRCATCCASGYCCAC

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☐ AAACCCADCVCGAACBAGRGAHGAVVTTWCCTTGTTCAWCCCAKTCCHBA ☐ ATADTAWTGMNKRAMRGAGTRAAYANAWGARRKVRTADADW

☐ GAGAGHGSATTCAGMGHAAVCADAGGWVAYCTTCTTVGTKACGAAGA

# Inputs & Settings

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## Alphabet

**Background Source:** an old version of the NCBI non-redundant database

| Name | Bg. | | | | Bg. | Name |
|---|---|---|---|---|---|---|
| Adenine | 0.274262 | A | ~ | T | 0.274262 | Thymine |
| Cytosine | 0.22521 | C | ~ | G | 0.22521 | Guanine |

## Sequences

The following sequence database was supplied to MAST.

| Database | Sequence Count | Residue Count | Last Modified |
|---|---|---|---|
| SS_dmp_cpg_sequences.fasta | 329 | 66129 | Sat Jun 21 04:18:58 2025 |
| **Total** | 329 | 66129 | |

## Motifs

The following motif database was supplied to MAST.

| Database | Last Modified |
|---|---|
| meme.xml | Sat Jun 21 06:37:19 2025 |

## Other Settings

| | |
|---|---|
| **Strand Handling** | The result of scanning both strands is **combined**. When matches overlap the non-overlapping combination with the best p-value is shown. |
| **Max Correlation** | Motifs with a correlation greater than **0.6** are marked for potential removal dependant on the `--remcorr` option. |
| **Remove Correlated** | Correlated motifs exceeding the threshold are **highlighted** and their removal is recommended. |
| **Max Sequence *E*-value** | Sequences with an *E*-value less than **10** are included in the output. |
| **Adjust Hit *p*-value** | The hit *p*-value is **not adjusted** for the length of the sequence. |

| | |
|---|---|
| **Displayed Hits** | The *p*-value of a hit must be less than **0.0001** to be shown in the output. |
| **Displayed Weak Hits** | Weak hits are **not displayed**. |



**MAST version 5.5.8**
(Release date: Thu May 15 15:01:46 2025 -0700)

**Reference**
Timothy L. Bailey and Michael Gribskov, "Combining evidence using p-values: application to sequence homology searches", *Bioinformatics*, **14**(1):48-54, 1998. [full text]

**Command line summary**

```
mast -oc . -nostatus meme.xml SS_dmp_cpg_sequences.fasta
```

Ran in 0.553 seconds on Sat Jun 21 06:37:20 2025 on noble-meme.grid.gs.washington.edu