

Command line	Training Set	First Motif	Summary of Motifs	Termination	Explanation
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Search sequence databases with these motifs using [MAST](#).

Submit these motifs to [BLOCKS multiple alignment processor](#).

Build and use a motif-based hidden Markov model (HMM) using [Meta-MEME](#).

[MEME - Motif discovery tool](#)

MEME version 3.5.3 (Release date: 2006-04-30 01:41:24 -0700 (Sun, 30 Apr 2006))

For further information on how to interpret these results or to get a copy of the MEME software please access <http://meme.nbcr.net>.

This file may be used as input to the MAST algorithm for searching sequence databases for matches to groups of motifs. MAST is available for interactive use and downloading at <http://meme.nbcr.net>.

[REFERENCE](#)

If you use this program in your research, please cite:

Timothy L. Bailey and Charles Elkan, "Fitting a mixture model by expectation maximization to discover motifs in biopolymers", Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology, pp. 28-36, AAAI Press, Menlo Park, California, 1994.

[TRAINING SET](#)

DATAFILE= pasted_sequences					
ALPHABET= ACDEFGHIKLMNPQRSTVWY					
Sequence name	Weight	Length	Sequence name	Weight	Length
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PY04084	1.0000	283	PY05820	1.0000	330
PY07022	1.0000	323	PY01595	1.0000	307
PY04430	1.0000	288	PY07516	1.0000	269
PY01873	1.0000	321	PY07501	1.0000	271
PY06567	1.0000	622	PY00308	1.0000	338
PY06374	1.0000	279	PY07849	1.0000	287
PY03760	1.0000	279	PY07653	1.0000	266
PY03042	1.0000	287	PY06126	1.0000	290
PY02671	1.0000	279	PY06514	1.0000	299
PY00284	1.0000	362	PY06763	1.0000	307
PY00494	1.0000	299	PY02564	1.0000	299
PY02312	1.0000	338	PY06851	1.0000	312
PY03948	1.0000	277	PY07838	1.0000	292
PY06829	1.0000	295	PY02565	1.0000	296
PY05708	1.0000	295	PY03636	1.0000	297
PY04516	1.0000	302	PY00988	1.0000	345
PY07327	1.0000	295	PY05781	1.0000	297
PY03177	1.0000	297	PY07331	1.0000	297
PY07421	1.0000	327	PY02278	1.0000	297
PY05923	1.0000	313	PY05871	1.0000	339
PY07021	1.0000	307	PY01184	1.0000	323
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PY02652	1.0000	304	PY03729	1.0000	304
PY07027	1.0000	304	PY02298	1.0000	304
PY05769	1.0000	304	PY01774	1.0000	304
PY06666	1.0000	262	PY04083	1.0000	296
PY07413	1.0000	304	PY06227	1.0000	300

MEME					
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PY01111	1.0000	316	PY07533	1.0000	288
PY02543	1.0000	309	PY04979	1.0000	293
PY06796	1.0000	293	PY06220	1.0000	322
PY03987	1.0000	285	PY07594	1.0000	292
PY07342	1.0000	292	PY03973	1.0000	292
PY05912	1.0000	317	PY07422	1.0000	294
PY05146	1.0000	351	PY00055	1.0000	315
PY07264	1.0000	311	PY04795	1.0000	308
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PY06742	1.0000	317	PY02660	1.0000	346
PY06877	1.0000	271	PY06151	1.0000	290
PY03983	1.0000	324	PY05244	1.0000	317
PY03991	1.0000	329	PY04554	1.0000	299
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PY02973	1.0000	288	PY00580	1.0000	288
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PY02572	1.0000	283	PY02131	1.0000	288
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PY04755	1.0000	274	PY07160	1.0000	274
PY05560	1.0000	269	PY05624	1.0000	298
PY03438	1.0000	323	PY04327	1.0000	298
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PY07411	1.0000	295	PY00997	1.0000	300
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PY00177	1.0000	281	PY02971	1.0000	281
PY06732	1.0000	322	PY07111	1.0000	319
PY07080	1.0000	301	PY05816	1.0000	306
PY02970	1.0000	329	PY07454	1.0000	285
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PY04466	1.0000	293	PY02687	1.0000	323
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PY07187	1.0000	653	PY03359	1.0000	359
PY05688	1.0000	330	PY07035	1.0000	359
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PY00754	1.0000	586	PY01963	1.0000	545
PY00552	1.0000	325	PY04773	1.0000	325
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PY04733	1.0000	343	PY06499	1.0000	291
PY01981	1.0000	653	PY03091	1.0000	291
PY03332	1.0000	332	PY06020	1.0000	316
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PY01834	1.0000	347	PY01872	1.0000	282
PY07226	1.0000	338	PY03016	1.0000	275
PY04786	1.0000	275	PY03331	1.0000	275
PY04787	1.0000	283	PY07405	1.0000	344
PY02782	1.0000	331	PY03010	1.0000	318
PY06339	1.0000	350	PY01871	1.0000	323
PY00297	1.0000	273	PY05648	1.0000	318
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[COMMAND LINE SUMMARY](#)

This information can also be useful in the event you wish to report a problem with the MEME software.

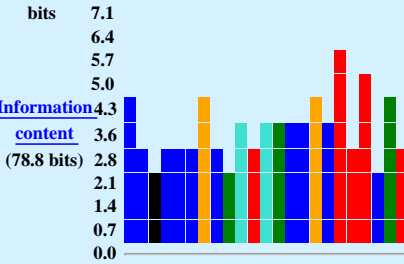
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model:  mod=      zoops      nmotifs=      20      evt=      1e+100
object function=  E-value of product of p-values
width:  minw=      6      maxw=      50      minic=      0.00
width:  wg=      11      ws=      1      endgaps=      yes
nsites:  minsites=    2      maxsites=    184      wnsites=      0.8
theta:  prob=      1      spmap=      pam      spfuzz=      120
em:      prior=      megap      b=      292390      maxiter=      20
       distance=      1e-05
data:    n=      58478      N=      184

sample: seed=      0      seqfrac=      1
Dirichlet mixture priors file: prior30.plib
Letter frequencies in dataset:
A 0.029 C 0.026 D 0.067 E 0.054 F 0.060 G 0.038 H 0.011 I 0.084 K 0.115
L 0.087 M 0.020 N 0.100 P 0.020 Q 0.024 R 0.020 S 0.092 T 0.047 V 0.032
W 0.007 Y 0.065
Background letter frequencies (from dataset with add-one prior applied):
A 0.029 C 0.026 D 0.067 E 0.054 F 0.060 G 0.038 H 0.011 I 0.084 K 0.115
L 0.087 M 0.020 N 0.100 P 0.020 Q 0.024 R 0.020 S 0.092 T 0.047 V 0.032
W 0.007 Y 0.065
```

PN MOTIF 1 width = 23 sites = 161 llr = 8790 E-value = 6.1e-3023

[Simplified](#) A 914:::2:::1:::
[pos.-specific](#) C :::::
[probability matrix](#) D :::::
E :::::
F ::36::1:::a:9::4::
G ::::9:::a:::
H :::::
I :7:6::8:::
K :::::a:::a1:2a
L ::1:39:::a:::
M :::::
N :::::
P ::2:::
Q :::::8:
R :::::a:9::
S ::2:::7::a:::3::
T :::::
V :1:::2:::1:::
W :::::
Y :::::a:a:::



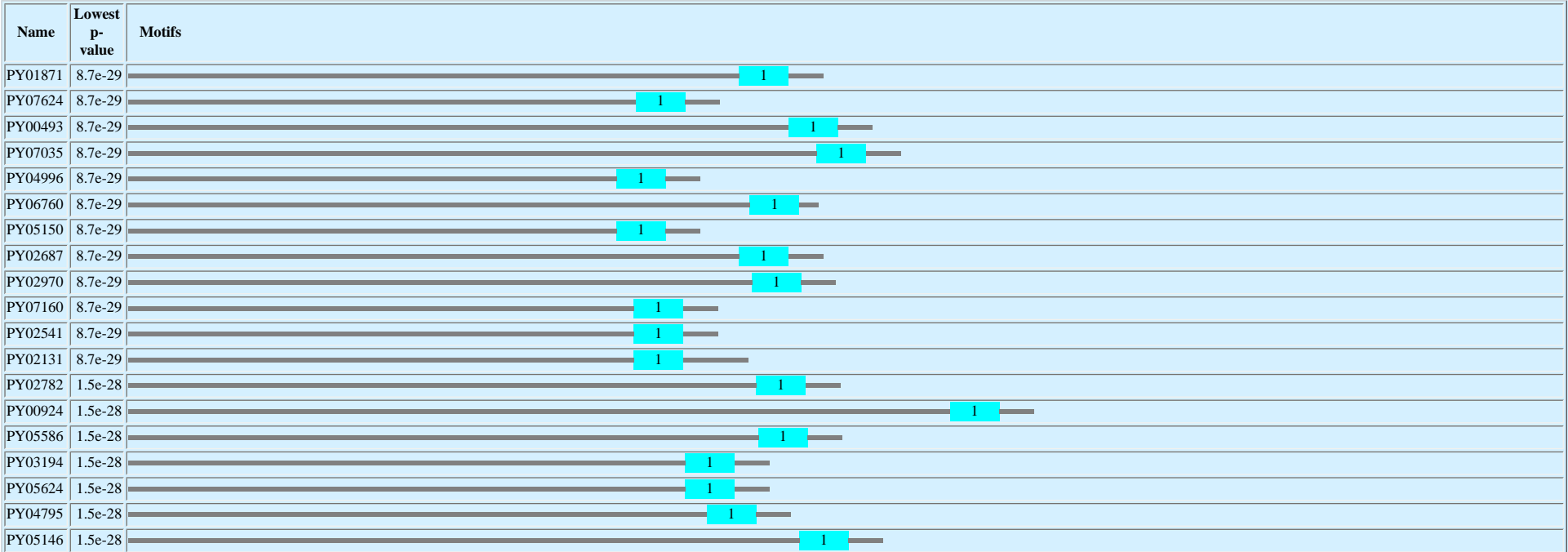
[Multilevel consensus sequence](#) AIAIFLGISYKYSLFGFRKRFQK
SFL A SK
P

NAME	START	P-VALUE	SITES
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PY07624	237	8.74e-29	SLISIAFIFV AIP IFLGIS YKY SLFG FRKRFQK QKLREKIKNI
PY00493	308	8.74e-29	KLIPVLLIFP AIP IFLGIAY KY SLFG FRKRFQK QKLREKLKNV
PY07035	321	8.74e-29	KLFIVLSIFG AIP IFLGIAY KY SLFG FRKRFQK QKLREKLKNV
PY04996	228	8.74e-29	SLISIAFIFV AIP IFLGIS YKY SLFG FRKRFQK QKLREKIKNI
PY06760	290	8.74e-29	KLIPVLLIFG AIP IFLGIS YKY SLFG FRKRFQK QKLREKLKK
PY05150	228	8.74e-29	SLISIALIFV AIP IFLGIS YKY SLFG FRKRFQK QKLREKIKNI
PY02687	285	8.74e-29	KLFIVLSIFG AIP IFLGIAY KY SLFG FRKRFQK QKLREKLKNV
PY02970	291	8.74e-29	KLIPVLLIFA AIP IFLGIAY KY SLFG FRKRFQK QKLREKLKNV
PY07160	236	8.74e-29	SLISIAFIFV AIP IFLGIS YKY SLFG FRKRFQK QKLREKIKNI
PY02541	236	8.74e-29	SLISIALIFV AIP IFLGIS YKY SLFG FRKRFQK QKLREKIKNI
PY02131	236	8.74e-29	SLISIALIFV AIP IFLGIS YKY SLFG FRKRFQK QKLRFYVVEP
PY02782	293	1.50e-28	KLIPVLSIFV AIAFFL GIS YKY SLFG FRKRFQK QKLREKLKNV
PY00924	383	1.50e-28	RLFTVLSIFG AIAFFL GIS YKY SLFG FRKRFQK QKLREKLKNI
PY05586	294	1.50e-28	NLFIVLSIFG AIAFFL GIS YKY SLFG FRKRFQK QKLREKLKNI
PY03194	260	1.50e-28	RLFTVLSIFG AIAFFL GIS YKY SLFG FRKRFQK QKLREKIKNI
PY05624	260	1.50e-28	KLFTVLSIFG AIAFFL GIS YKY SLFG FRKRFQK QKLREKLKNI
PY04795	270	1.50e-28	TIISVLSIFG AIAFFL GIS YKY SLFG FRKRFQK QKLREKLKNI
PY05146	313	1.50e-28	NLFIVLSIFG AIAFFL GIS YKY SLFG FRKRFQK QKLREKLKNI
PY05769	266	1.50e-28	KLFTVLSIFG AIAFFL GIS YKY SLFG FRKRFQK QKLREKIKNI
PY02298	266	1.50e-28	RLFTVLSIFG AIAFFL GIS YKY SLFG FRKRFQK QKLREKIKNI
PY02652	266	1.50e-28	KLFTVLSIFG AIAFFL GIS YKY SLFG FRKRFQK QKLREKIKNX
PY06204	266	1.50e-28	KLFTVLSIFG AIAFFL GIS YKY SLFG FRKRFQK QKLREKIKKI
PY06829	257	1.50e-28	RLFTVLSIFG AIAFFL GIS YKY SLFG FRKRFQK QKLREKIKNI
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PY05688	300	3.47e-28	KLIIIVLSIFG AIAIFL GIS YKY SLFG FRKRSQK HLREKLKK
PY04554	268	3.47e-28	KLIPVLSIFP AIP IFLGIAY KY SLFG FRKRSQK QHIREKLKK
PY06742	286	3.47e-28	KLIPVLSIFG AIAIFL GIS YKY SLFG FRKRSQK QHLKEKLKK
PY06666	231	3.47e-28	KLIPILSILV AIP IFLGIAY KY SLFG FRKRSQK QHLREIVKK
PY01872	244	6.85e-28	KLFTVLSIFG AIAFFL GIS YKY SLFG FRKRAQK QYLREKIKNI
PY00177	243	6.85e-28	KLFTVLSIFG AIAFFL GIS YKY SLFG FRKRAQK QHLREKIKKI
PY05410	260	6.85e-28	KLFTVLSIFG AIAFFL GIS YKY SLFG FRKRAQK QYLREKIKKI
PY00580	250	6.85e-28	RLFAVLSIFG AIAFFL GIS YKY SLFG FRKRAQK QYLREKIKKI
PY03991	291	6.85e-28	KLFTVLSIFG AIAFFL GIS YKY SLFG FRKRAQK QYLREKIKKI
PY07342	254	6.85e-28	KLFTVLSIFG AIAFFL GIS YKY SLFG FRKRAQK QYLREKIKNI
PY06796	255	6.85e-28	KLFTVLSIFG AIAFFL GIS YKY SLFG FRKRAQK QYLREKIKKI
PY05708	257	6.85e-28	KIFTVLSIFG AIAFFL GIS YKY SLFG FRKRAQK QYIREKIKNI
PY04733	313	7.99e-28	KLIPVLLILG AIP IFLGIAY KY SLFG FRKRVQK HLREKLKK
PY07594	254	7.99e-28	KLIPILSILV AIAIFL GIS YKY SLFG FRKRVQK QYLREKIKNI
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PY03729	266	9.62e-28	KLFTVLLIFG AIAFLL GIS YKY SLFG FRKRFQK QQIREKIKNI
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PY01873	290	1.67e-27	KLIPVLLIFG AIP ILLGVSY KY SLFG FRKRFQK QKLREKLKK
PY07411	255	2.19e-27	KLIRVLSILV AIP IFWGIS YKY SLFG FRKRSQK QNLREKLKKI
PY03636	259	2.59e-27	KLFTVLSIFG AIAFLL GIS YKY SLFG FRKRAQK QYLREKIKKI
PY06020	285	3.60e-27	KLVTVLSIFG AIAILL GVSY KY SLFG FRKRSQK QHLREKLKK
PY02971	243	3.60e-27	RLFTILSIFG AIAFFL GIF YKY SLFG FRKRFQK QKLREKIKNI
PY07021	269	3.60e-27	KLFIVLSIFG AIGIFL GIS YKY SLFG FRKRFQK QKLREKLKNI
PY03010	286	4.17e-27	KLIPVVSIFV AISFFL GIS YKY SLFG FRKRSQK HLREKVDVMF
PY03983	293	5.44e-27	KLIPVLSIIV AIP IFL GIF Y KY SLFG FRKRSQK QHLREKIKK
PY05781	259	6.69e-27	KLLLLLSIFG AIAIFL GIS YKY SLFG FRKRFKK QQIREKIKNI
PY01834	316	7.50e-27	KLFIVLSIFA AIPFFL GIAY KY SLFG FRKRTQK HHLRENLKK
PY00085	260	7.50e-27	TLISIGFIFV AVSIFL GIAY KY SLFG FRKRFQK QKLREKIKNI
PY04755	236	7.50e-27	TLVPIAFIFV AVSIFL GIAY KY SLFG FRKRFQK QKLREKIKNI
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PY04988	270	8.95e-27	KLFTVLSIFG AIAFFL GIS YKY SLFG FRKRFKK QQIREKIKKI
PY07017	225	8.95e-27	KLISVLSIFG AIAFFL GIS YKY SLFG FRKRFKK QQIREKIKNI
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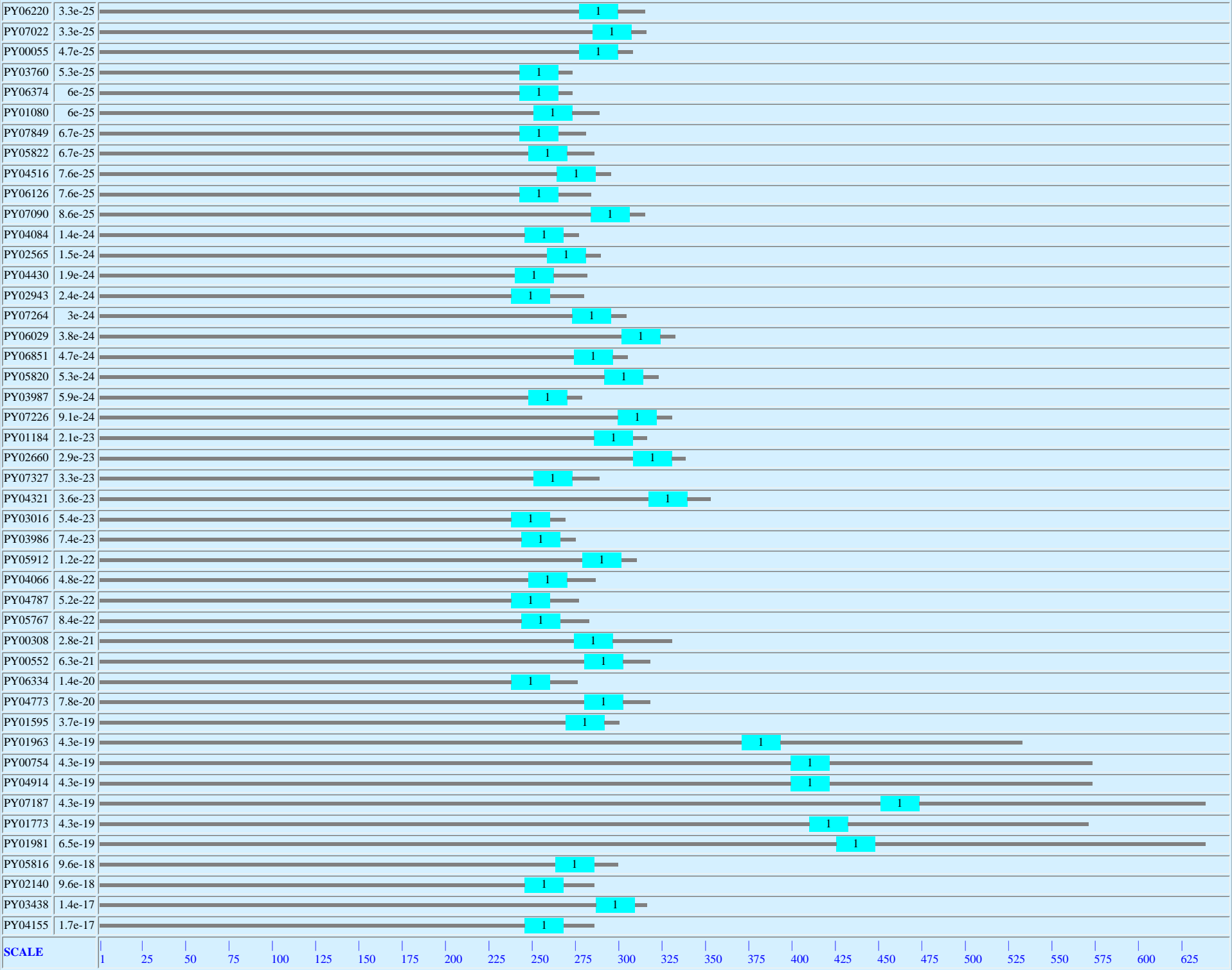
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PY06514	261	8.95e-27	NLFIIVLSIFG	AIAFFFGISYKYSLFGFRKRQK	QKLREKIKNI
PY01110	288	1.38e-26	KLIVIVLPILA	AIIFLGIAYKYSLFGFRKRSKK	QHLREKLKK
PY04786	244	1.57e-26	TLISIGFIFV	AVSIFLGIAYKYSLFGFRKRSQK	QHLREMLKK
PY02688	243	1.57e-26	KLISVLSIFG	AIGFLLGISYKYSLFGFRKRQK	QKLREKIKNI
PY02312	307	1.57e-26	KLVPILSIFV	AIAIFFGISYKYSLFGFRKRAQK	QHLREKLKK
PY07653	228	1.57e-26	SLISIAFIFV	AIIFFGISYKYSLFGFRKRAQK	QYLRETIKNI
PY02940	254	1.57e-26	KLISVLSIFG	AIGFLLGISYKYSLFGFRKRQK	QKLREKIKNI
PY00297	235	1.84e-26	SLISIAFIFV	AASILLGVSYKYSLFGFRKRQK	QKLREXLKNI
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PY06227	269	1.84e-26	TLISIAIIFV	AASILLGVSYKYSLFGFRKRQK	QKLRENLLK
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PY06877	240	3.67e-26	TLITIAIIFV	AASILLGVSYKYSLFGFRKRSQK	QHLREMLKK
PY07533	239	3.67e-26	ILITIAIIFI	AASILLGVSYKYSLFGFRKRSQK	QHLREMFLCC
PY06886	255	3.67e-26	ILITIAIIFV	AASILLGVSYKYSLFGFRKRSQK	HHLREKLKK
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PY05923	282	3.67e-26	MLITIAIIFV	AASILLGVSYKYSLFGFRKRSQK	QHLREMLKK
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PY07516	228	3.67e-26	MLITIAIIFV	AASILLGVSYKYSLFGFRKRSQK	QHLREKLKNS
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PY02827	313	5.54e-26	KLIPVLSIIV	AIIFLGIIFYKYSLFGFRKRTQK	QHIREKLKK
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PY05244	286	5.54e-26	KLIPVLSIIV	AIIFLGIIFYKYSLFGFRKRTQK	QHLRKKLLK
PY06151	252	5.54e-26	TLISITFIFV	ATISICLGIAYKYSLFGFRKRQK	QKLREKLKNV
PY05719	284	8.28e-26	KLFIIVLSIFG	AIGIFLGISYKYSLFGFRKRFKK	QQIREKIKNI
PY03042	249	8.28e-26	NLLVLSIFG	AIGIFLGISYKYSLFGFRKRFKK	QQIREKLKNI
PY07111	288	1.08e-25	KLIPVLSIFV	AIAILGGISYKYSLFGFRKRVQK	QHLREKLKK
PY06619	285	1.23e-25	KLLVLSIFA	TIAIFLGIAYKYSLFGFRKRVQK	QYLREKIKNI
PY06732	291	1.23e-25	KLIPVLSIVV	AIAFFFGISYKYSLFGFRKRSQR	QHLREKLKK
PY07406	286	1.23e-25	KLIPVLLIFA	AIIFLGISYKYSLFGFRKRSQX	QYLREKIKNI
PY02614	269	1.23e-25	KLFTVLSIFG	AIAFLLGVSYKYSLFGLRKRFQK	QKLREKLKNI
PY05673	290	1.57e-25	KLIPVLLIFT	AIIFLGIIVKYSLFGFRKRFKK	QQIREKIKNI
PY02973	250	2.27e-25	RLFAVLSIFG	AIAFFLGISYKYSLFGFRKRQK	QYLREKIKNI
PY00500	270	2.91e-25	KLFIIVLSIFG	AIGIFWGISYKYSLFGFRKRFKK	QQIREKIKNI
PY02671	249	2.91e-25	TLMSIGPIFF	AVSIFLGISYKYSLFGFRKRSKK	HLREKLKK
PY03359	328	3.30e-25	KLILIPIFIIV	ATLILLGIAYKYSLFGFRKRSQK	QHLRKKIKT
PY06782	272	3.30e-25	KLILIPIFIIV	ATLILLGIAYKYSLFGFRKRSQK	QYXREXIKX
PY06220	284	3.30e-25	KLISIPFIFV	ATLILLGIAYKYSLFGFRKRSQK	QYLREKIKNI
PY07022	292	3.30e-25	KLISIPFILV	ATLILLGIAYKYSLFGFRKRSQK	QHLREKLKK
PY00055	284	4.71e-25	KIIPVLSIFA	AILFFGGISYKYSLFGFRKRSQK	QHLREKIKK
PY03760	249	5.32e-25	TLISIASIFV	AVSTFLGISYKYSLFGFRKRQK	HLRKKLLK
PY06374	249	5.98e-25	TLMSIGVFV	AASILLGVSYKYSLFGFRKRSKK	HLREKLKK
PY01080	257	5.98e-25	RLFTVLSIFG	VIAFLLGISYKYSLFGFRKRFKK	QQIREKIKNI
PY07849	249	6.74e-25	TLIPIAFIFV	TVSIFLGIAYKYSLFGFRKRQK	QKLREKIKNI
PY05822	254	6.74e-25	KLISVLSILV	AIAFLGGISYKYSLFGFRKRFKK	QQIKEKIKNI
PY04516	271	7.57e-25	IIITIAIIFV	AVSILLGVSYKYSLFGFRKRFKK	QHLREKLKK
PY06126	249	7.57e-25	TLISIGFIFV	AVSIFLGIAYKYSLFGFRKRSQK	QCLREKIKNI
PY07090	291	8.56e-25	KLIPVLSIIV	AIIFLGIIFYKYSLFGFRKRTKK	QHLKEKIKK
PY04084	252	1.36e-24	TLITIAIIFV	AASILLVVSYKYSLFGFRKRSQK	QHLREMLKK
PY02565	265	1.53e-24	TLIPIAIIFV	VASFFFGISYKYSLFGFRKRQK	QKLREKIKK

PY04430	246	1.93e-24	TLISIGFIFV	AVSILLGIAYKYSLLGFRKRSQK	QCLRERIKNI
PY02943	244	2.42e-24	ALIPIAFIFV	AVLIFLGIAYKYSLLGFRKRSQK	QCLRERIKNI
PY07264	280	3.03e-24	TLIPIAIIFV	AASILLGVSYKYSLFGFRKQSQK	QHLREKLKK
PY06029	309	3.80e-24	KLIPVLSIFG	AIVFFLGISYKYSLFGSRKRSQK	QHLREKLKK
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PY05820	299	5.29e-24	KLISIPFIFV	VTLLILGIAYKYSLFGFRKRSQK	QQIREKLKK
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PY03016	244	5.44e-23	TLITIGIIFV	AASILLGVSYKYSLFGFRKRFCK	QHLREMLKK
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PY05912	286	1.22e-22	KLILVLSILA	AIAISLVISYKYSLFGFRKRARK	QYLRENLKK
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PY00308	281	2.81e-21	NTVIPGLSIF	AIPVFLGVAYKYSLFGFKLFPQR	QYIRKKLKKF
PY00552	287	6.33e-21	KLILALSIFS	AITIFLGIFYKGSFLVLRKRAQK	QHLREKLKNI
PY06334	244	1.40e-20	TLPIAFMLV	ALSIFLGIYKYSSLGFRKRSQK	QCLREKIKNI
PY04773	287	7.77e-20	KLILALSIFS	AMTIFLGIFYKCSLFLRKRQSQK	QHLREKLKNI
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PY05816	270	9.64e-18	KLIIALSIFT	AIIFWRIFYKYSLFGLRKNSKT	IFKRKAKTVK
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PY03438	294	1.40e-17	KFISIPFIFV	VTLLILGIAYKYSLFKSRKPFPR	PIQKKKK
PY04155	252	1.75e-17	NFYILLLIFG	IIIVFIGIYKYSLSGFRNRPKK	LYLRKKLKKM

Motif 1 block diagrams



PY02564	9e-27	1
PY06514	9e-27	1
PY01110	1.4e-26	1
PY04786	1.6e-26	1
PY02688	1.6e-26	1
PY02312	1.6e-26	1
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PY07422	2.8e-26	1
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PY07546	3.2e-26	1
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PY06499	3.7e-26	1
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Motif 1 position-specific scoring matrix

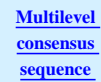
Motif 1 position-specific probability matrix

PN MOTIF 2 width = 21 sites = 183 llr = 6601 E-value = 9.8e-2010

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A : ..... 6 : .....
C : ..... a : .....
D 3: 5: 15: ..... 5 : ..... 1:
E : ..... 1: ..... 2: ..... 2:
F : ..... 7: ..... 8: .....
G : .....
H : ..... 1: ..... 1
I : 6: 6: 25: ..... 11: 11
K : 141: 6: 1: 8: ..... 1:
L : ..... 1: 2: 22: 49: 1:
M : 4: ..... 3: ..... 8:
N 5: 3121: 3: ..... 1: 4: 1
P : ..... 1: ..... 1: .....
Q : .....
R : .....
S 1: 111: 8: ..... 1: 3: 1:
T : .....
V : ..... 1: .....
W : .....
Y : ..... a : ..... 7

```



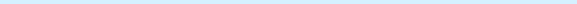
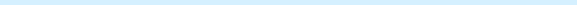
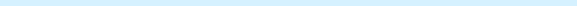
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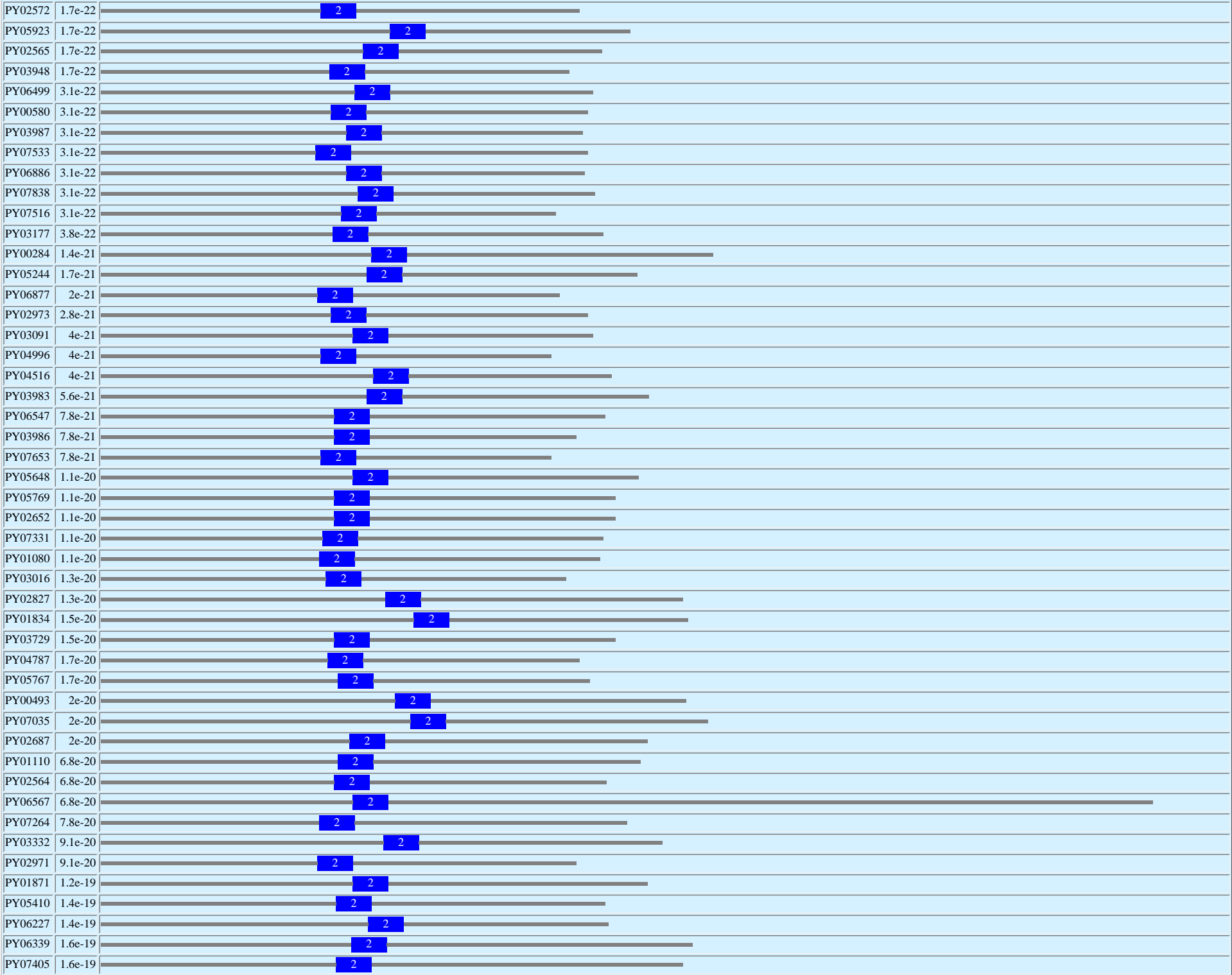
MEME

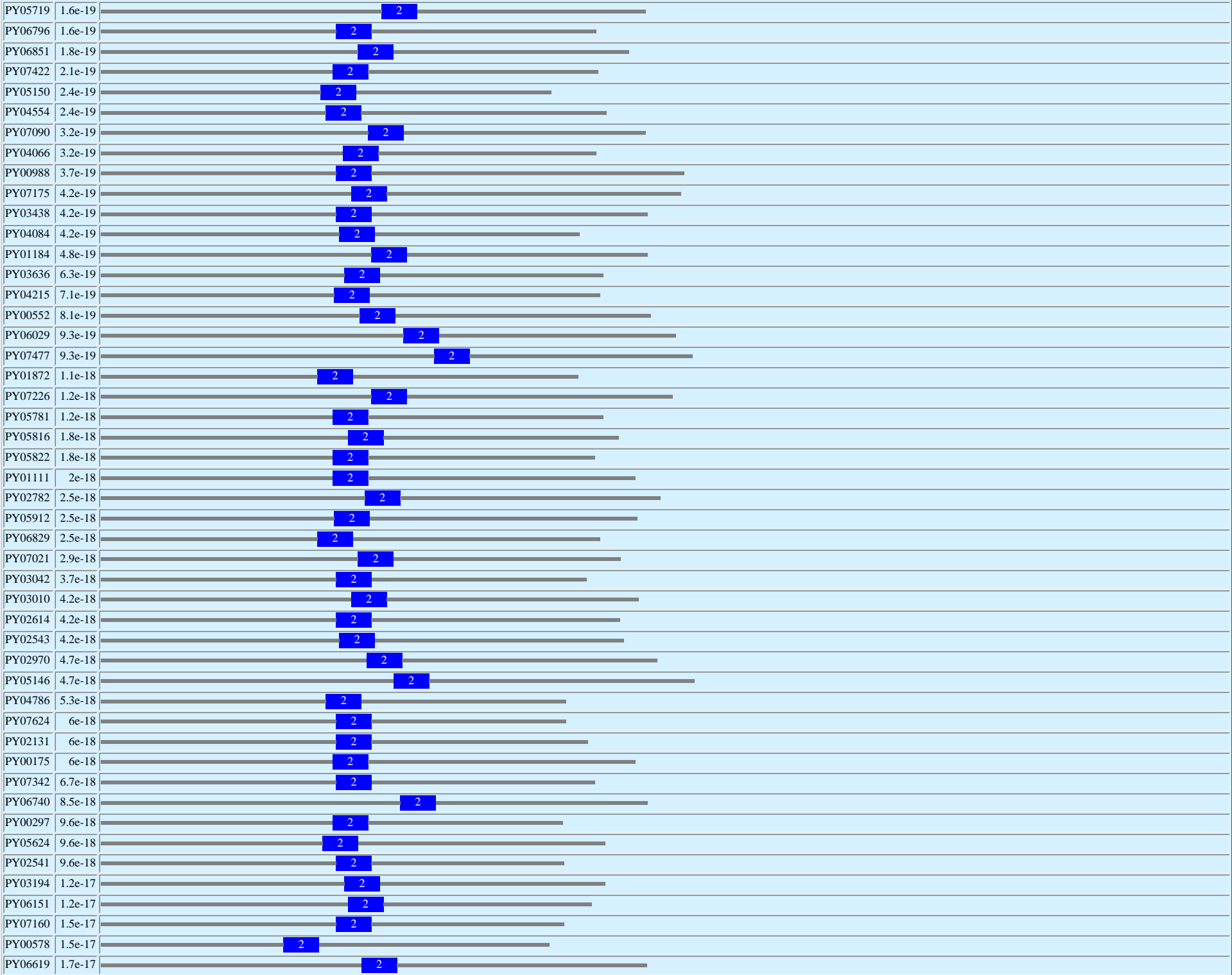
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PY02036	131	1.84e-23	SVIENKIKSM NMDIKDISNFYDAFKSLCNMY SEIELYNYQC
PY05560	129	1.84e-23	DLIGEKIRLM NMDIKDISNFYDAFKSLCNMY SEIDSISDCK
PY02572	131	1.69e-22	EVISAKIKSM NIDIKDISNFYDAFKSLCNMY SEIGAEDNPC
PY05923	172	1.69e-22	DVIDTKIESM NIDIKDISNFYDAFKSLCNMY SEFDPEKSTE
PY02565	156	1.69e-22	DVIETKIRSI NIDIKDISNFYDAFKSLCNMY SEIGAEDYQC
PY03948	136	1.69e-22	DDICKIKISM NIDIKDISNFYDAFKSLCNMY SEIIAEDYQC
PY06499	151	3.07e-22	DDIGNKIKSI DIDIKDISNFYDAFKSLCNMY SERDAITQCK
PY00580	137	3.07e-22	EYMKKRNDLM NINIEDMSKLYDAFKLLCNMY SEVATNKDDN
PY03987	146	3.07e-22	DVIKKKIESM DIDIKDISNFYDAFKSLCNMY NEIVADDDQC
PY07533	128	3.07e-22	EVIDTKIKSM DIDIKDISNFYDAFKSLCNMY SEFDPEENTE
PY06886	146	3.07e-22	NVICKKIKSM DIDIKDISNFYDAFKSLCNMY SEISVEDYEF
PY07838	153	3.07e-22	DDIGNKIKLM DIDIKDISNFYDAFKSLCNMY IEVDAENYQC
PY07516	143	3.07e-22	GVIDEKIESM DIDIKDISNFYDAFKSLCNMY IEIGTEKNTK
PY03177	138	3.78e-22	EFMKERTDLL NMNIKDMSKFYDAFKLLCIMY DNYSTNKDNK
PY00284	161	1.40e-21	EIIFKNMDFS NIDIKDISKFYDAFKLLCKMY DELNDGKLEC
PY05244	158	1.67e-21	EFIEKNEYLM NIGINDMSKFYDAFKPLCNMY TELNANDASD
PY06877	129	1.99e-21	DVIEKKMKSM NMNIKDISNFYDAFKSLCNMY SELDPEKNT
PY02973	137	2.83e-21	EFMDKKNDLL NINIEDMSKFYDAFKLLCIMY NADATNKDDN
PY03091	150	3.99e-21	DVIKKQISSM NIDIKDISNFYDALKSLCNMY SELDENNNQC
PY04996	131	3.99e-21	DLINKKNYLM EMNIKDISKFYDAFKSLCEMY TEFDEDNQKC
PY04516	162	3.99e-21	DVIYKKIKST NIDIKDISNFYDALKSLCNMY SEIDPEDYEC
PY03983	158	5.59e-21	EFIEKNKYLM NIGINDMSNFYDAFKPLCNMY TELDANDTDN
PY06547	139	7.78e-21	EIIDQKSDLL DINIKDMSDFYDAFKSLCNMY NSVATSKHDT
PY03986	139	7.78e-21	DVIENKIKSM NMNIKDVSNFYDAFKSLCNMC SEISAEANTE
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PY02652	139	1.07e-20	YLIDKKKYFL DMDKKIISNFYDAFKLLCEMY AEFDDNSQYC
PY07331	132	1.07e-20	DLIDQKKYLV DMDKKIISNFYDAFKLLCEMY AEFDDNSQYC
PY01080	130	1.07e-20	DLIDQKKYLI DMDKKIISNFYDAFKLLCEMY AEFDDNSQYC
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PY02827	169	1.26e-20	EFIEGNEYFT NMDMNIMSNFYDAFKLLCTMY TEFNENEPDC
PY01834	186	1.48e-20	ELIEKNECLM NISINDISKFYDAFKILCNMY IDYNGNSSNC
PY03729	139	1.48e-20	DLIDKKTYYFL NMNRNIISKFYDAFKLLCEMY AEFDDNTPYC
PY04787	135	1.73e-20	AVIDKKIKSM NMNIKDISNFYDAFKSLCKMY IEVDASNQCM
PY05767	141	1.73e-20	DVIKNKIKSM NMNIKDISNFYDAFKSLCKMY IEVDANNQCM
PY00493	175	2.03e-20	GLIDTKIDVL NMDSKIIVSKFYKAFKLLCEMY TEFDEKKNDC
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PY02687	148	2.03e-20	KDLIDKKNVF GMDSNDVSKFYDAFKLLCEMY TEFDENASNC
PY01110	141	6.78e-20	TEETKEYMDI NININDMSKFYELLKLLCNMY TSYDNNSSQ
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PY01871	150	1.21e-19	KLLDKKNYVL NMNSNIVSKFYDAFKSLCEMY TEFDENTSNC
PY05410	140	1.39e-19	EFMNERNDFM NINIEDLSKFYDASKLLCNMY GNVKNNANDT
PY06227	159	1.39e-19	TVIEKKIRSM DIDIKDIYNFYDAFKSLCNMY SETDVDNYKC
PY06339	149	1.60e-19	ELLDKKNDVL NMDSKIIVSKFYKAFKSLCEMY TEFDENKENC
PY07405	140	1.60e-19	KLLDKKNNDVL NMDSKIIVSKFYKAFKSLCEMY TEYDENKENC
PY05719	167	1.60e-19	IDKNHNLKNT DMDSNIISSELYDAFKLLCEMY SEFDGSTSNC
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PY06851	153	1.84e-19	EFIEKNEYLM NIGINDISNFYDAFKPLCKMY TELNANESKC
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PY05150	131	2.43e-19	DLMNKKKYLM EMNIKVISKFYDAFKSLCEMY TEFDEDNPKC
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PY04066	144	3.20e-19	AVIEKKIKSM NMNIKDISNFYDAFKSLCNLY RELDANNKQC
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PY07175	149	4.19e-19	GLIDTKMEVL NMDSNNVSKFYKAFKSLCEMY NELDDDKTKC
PY03438	140	4.19e-19	DLINKKKEYI DIDIKDMSKLYDAFKILCKMI INADKKDDGK
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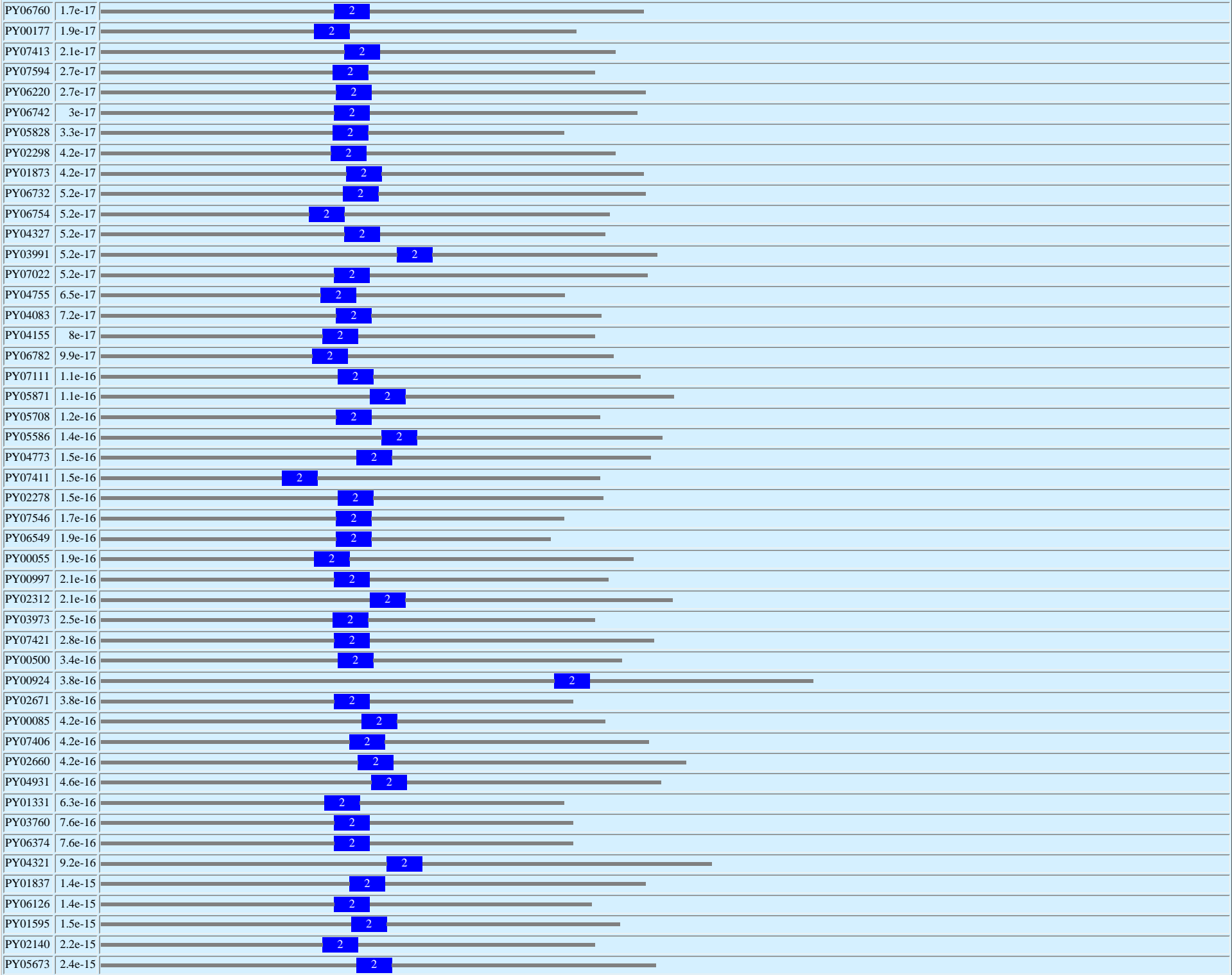
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PY04773	152	1.51e-16	EIIIVKNMDLL NIMFEDISKFFE AFKLLCKMH DEFNEKTLEC
PY07411	108	1.51e-16	KIIDEIKEYM DINISIMSRFYK LLKLLCNMN TAYTRNSSSK
PY02278	141	1.51e-16	IEKRHNLMNK DMDKNSISTLYD AFKLLCKMY TDFNKDTSNK
PY07546	140	1.68e-16	KLIDKNNYFL SMDKSIIIFKFYD AFKSLCNLY NELDDNQCK
PY06549	140	1.86e-16	EFINKQKDLF NINIENLSKFYD ASKLLICSMY GNFATNINKD
PY00055	127	1.86e-16	EIIDVIKEYM DINITIMSKFYEL LLKLLCKMN TSYTNGKSND
PY00997	139	2.06e-16	KIIDKVEEYM NINIDNMPKFYES LKLLCNMY TAYTKNNNSD

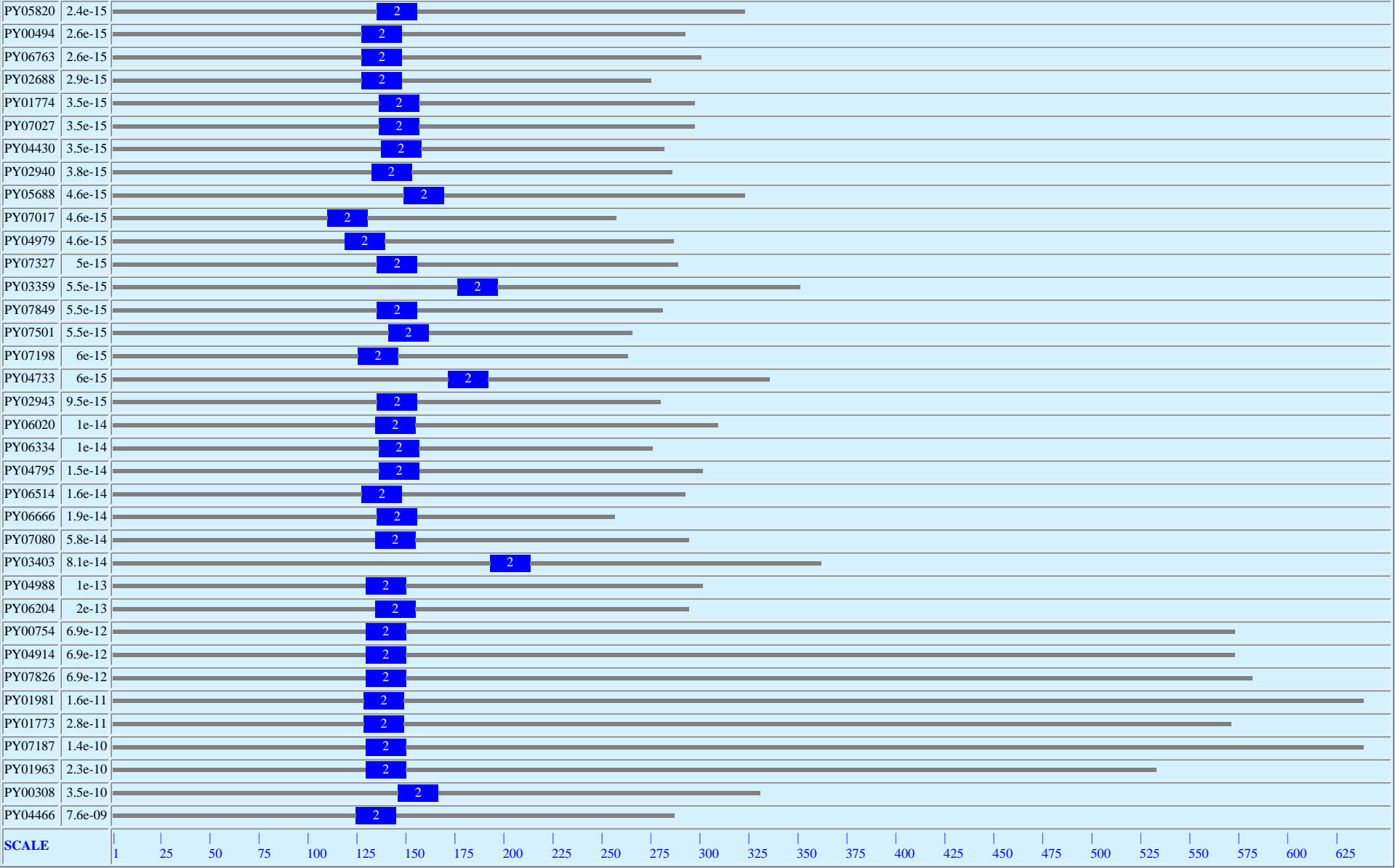
Motif 2 block diagrams

Name	Lowest p-value	Motifs
PY03331	1.8e-23	 2
PY02036	1.8e-23	 2
PY05560	1.8e-23	 2









[Motif 2 in BLOCKS format](#)

to [BLOCKS multiple alignment processor](#).

[Motif 2 position-specific scoring matrix](#)

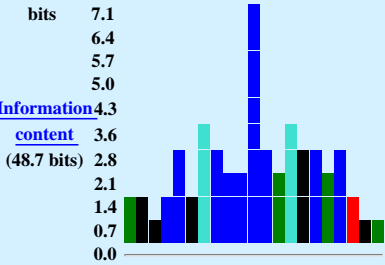
[Motif 2 position-specific probability matrix](#)

Time 575.85 secs.

PN [MOTIF 3](#) width = 21 sites = 183 llr = 6173 E-value = 1.2e-1827

[Simplified
pos.-
specific
probability
matrix](#)

A	:	1	:	1	:	2	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
C	:	:	:	:	:	1	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
D	:	1	:	1	:	2	:	:	:	:	:	:	:	:	:	:	:	:	:	:	1
E	:	1	:	3	:	:	:	:	:	:	:	:	:	:	:	:	:	:	1	1	:
F	:	:	:	2	1	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
G	:	:	:	:	:	:	:	:	:	1	:	:	:	:	:	:	:	:	:	:	:
H	:	:	:	:	:	:	:	:	:	1	:	:	:	:	:	:	:	:	:	:	1
I	:	4	:	5	1	1	:	7	4	5	:	:	1	:	:	1	:	:	:	:	:
K	:	2	1	:	:	:	:	:	:	:	:	:	:	4	:	1	:	7	3	:	:
L	:	:	1	:	1	:	2	3	:	9	:	:	9	:	6	:	:	:	:	:	:
M	:	:	:	:	:	:	4	:	:	:	:	4	:	:	:	:	:	:	:	:	:
N	5	1	4	:	:	:	:	:	:	:	:	:	7	:	1	:	2	:	:	:	:
P	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	1	:	:	:	:
Q	:	:	:	:	:	:	:	:	:	:	:	:	3	:	2	:	:	:	:	:	:
R	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
S	1	:	:	:	:	:	1	:	8	:	:	1	:	1	1	:	:	:	:	:	:
T	1	:	:	1	:	:	:	:	:	:	:	:	:	2	1	:	:	:	:	:	:
V	:	:	1	6	1	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
W	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
Y	1	:	:	:	9	:	:	:	:	:	:	9	:	:	:	:	:	:	:	:	:



[Multilevel
consensus
sequence](#)

NINIVYIIIWLSYMLNLKKx

DMLKQ

NAME	START	P-VALUE	SITES
PY04083	75	1.80e-25	SQLFKSVANS NINIVYIIIWLSYMLNLKKEQ TGNDTNLQYF
PY01774	75	1.80e-25	SELFKSVANS NINIVYIIIWLSYMLNLKKEQ TGSDSNLQFF
PY07027	75	1.80e-25	SELFKSVANS NINIVYIIIWLSYMLNLKKEQ TGSDSNLQFF
PY07327	74	1.80e-25	SQLFKSVANS NINIVYIIIWLSYMLNLKKEQ TGNDTNLQYF
PY05624	67	5.90e-23	KDSSVFKHHK NINIVYILIWLSYMLNLKKQ VGITNLRIFY
PY05586	102	1.65e-22	SSVFKSYAKS NIDVVEYIIIWLSYMLNLKEH VGKTNLQYFY
PY06514	65	2.14e-22	SSVFKSDAKS NINIVYIIIWLSYMLSLKKQ VGDKNLQYF
PY04466	74	2.73e-22	SELFTSVANN NINIVDYILIWLSYMLNLKKEQ TGNDNNLQFF
PY03729	74	2.73e-22	SEFFKSVANS NINIVDYILIWLSYMLNLKKEQ PGNDSNLKFF
PY06567	385	2.73e-22	SSVFRSYAKS NTNIVYIIIWLSYMLNLKKEQ FGKTNLQYFY
PY01080	66	2.73e-22	SELFKSVANS NINIVDYILIWLSYMLNLKKEQ VGISNLQYFY
PY05769	75	8.94e-22	SELFKSVANS NINIVDYILIWLSYMLNLKPE GTMSNIHFFY
PY02652	75	8.94e-22	SELFKSVANS NINIVDYILIWLSYMLNLKPE GTMSNIHFFY

PY05822	74	1.40e-21	SSVFQSVAKN	NINIV EY IMIWL S YML KL KK N	EGSDSLKYFY
PY07021	85	2.71e-21	ASVFRSVAKS	NIDIV DY IIIWL S YML NL KE N	TGSTISHIKH
PY07198	72	6.27e-21	SSESYNVQN	NINV DY IIIWL S YML NL K ST	QDDTITNLNN
PY05146	109	6.27e-21	SSVFMSDAKG	NTNIV EY IIIWL S YML NL KK S	EENMSNLQYF
PY00494	74	6.27e-21	SSGSLYNVEN	NINV EY IILWL S YML NL K ST	QDDTITNLNN
PY06763	74	6.27e-21	SSGSLYNVEN	NINV EY IILWL S YML NL K ST	QDDTITNLNN
PY00493	111	7.70e-21	CGMVPPPARN	NINIV DY ILIWL S YML NL KE S	EKDNTTCFYS
PY01871	85	9.41e-21	CGVSHSPLKN	NINIV DY IMIWL S YML NL G KS	EEDNITGFY
PY02940	79	2.07e-20	SGLFNSRETS	NINV EY IMIWL C YML NL K ST	QDGSFTNLNN
PY06619	89	6.36e-20	SDLFSQYAKN	YMNIV EY IMIWL S YML NL K ND	APGLTNLEHF
PY02688	74	7.62e-20	SSGLSYNVQN	NTNIV EY IILWL S YML NL K ST	QDDSTITNLNN
PY07331	66	7.62e-20	SELFKTIVANS	NINIV DY IILTWL S YML NL K QQ	VGDETNPQYF
PY06126	74	9.12e-20	SDTFSINSKN	NINIV EY IIIWL S YIL SL K PH	EGITNLNDFY
PY06829	65	1.09e-19	SSESSYYAQN	NINIV DY IMLW V SYML NL K ET	EPNNGLKIFY
PY03042	73	1.30e-19	SSLFEKVAKN	NINIV DY IIIWL S YML SL ME S	ELKESLVFFY
PY06374	74	1.55e-19	VDSFTVNAKS	NINIV DY IIIWL S YML SL N KN	MNYKNIYDFY
PY06886	77	1.84e-19	LNMFGCEEDID	GDKIV EY AILWL S Y KL N Q K T H	NGTTKLYDFY
PY04979	65	2.18e-19	SSGSSYDEQN	IINV EY IILWL S YML NL K ST	EDDTITNLNN
PY06204	74	2.18e-19	SGLFNNNVKN	NINV EY IIIWL S YML NL K DK	NGNILTTTFYN
PY00500	75	2.59e-19	SDLFKSVAKS	NINIA G YIMIWL S YML NL KK S	VEGITNVKHF
PY02298	73	2.59e-19	SSGSSRYAQN	DINV DY IILWL S YML NL K PE	GNISNLQIFY
PY02687	85	3.62e-19	CNVVSSPAKN	SINM V DYILIWL S YML NL KE S	EKDNTTCFYS
PY02943	74	4.27e-19	SDSFNSVAKG	NINIV EY IMIWL S YML N FT T I	DESGSIELFY
PY07849	74	4.27e-19	STSFSEFIAG	NTNIV EY IMIWL S YML N F K K I	DENETIKHFY
PY07546	74	5.03e-19	ADLFKSVAKS	NIDIV EY IMIWL S Y MV N L K NN	EPNLTNQQHF
PY05648	85	6.96e-19	CGVKPSPVK	IINV DY IMIWL S YML NL D KS	EKKNNINDFY
PY03331	70	6.96e-19	EDTDNEENLE	GDKIV EY AILWL S Y KL N Q K KE	NRSTKLYDFY
PY03760	74	6.96e-19	SYSFRNYAKN	NINM VY IIIWL S YML SL KS	DNINNLKEFY
PY03973	74	8.17e-19	ISAFRMTVKG	NIDIV EY ILIWL S YML SL IK S	KEDNRKHFYN
PY02671	74	8.17e-19	SGSFEINAKS	SINIV DY IIIWL S YML SL N KN	MDYKNIHDFY
PY01331	66	9.58e-19	LNMFGEGDID	SDKLV EY AILWL S Y KL N Q K T Q	NGTTKLYDFY
PY07653	66	9.58e-19	SLSPKKYANS	NINV VY ILVWL S Y KL N Q K T N	NGITQFMDFY
PY04084	77	9.58e-19	LNMFGCEEDIG	SDKLV EY AILWL S Y KL N Q K T Q	NGTTKLDDFY
PY07175	84	1.12e-18	CGVVPSPSKN	NP INIV DY ILIWL S YML NL G KS	EDEDNITGFY
PY06782	62	1.12e-18	SYNFSSNANG	NMNIV TY IMTWIS Y KL N Q K P Q	KEITKFNDFY
PY07022	74	1.12e-18	SYNFSSNANG	NMNIV IY IMTWIS Y KL N Q K P Q	NEITNLKDFY
PY06151	81	1.31e-18	SYSFKTYAKN	NINM VY IMIWL S YIL SL KK D	NSIKNLKEFY
PY07594	73	1.31e-18	VSAFEMAACS	NINTV EY ILIWL S YML N L IK T	KENNSIDSFY
PY04996	66	1.53e-18	SVSPKKYANS	NINV VY ILVWL S Y KL N Q K T D	NGITKLMDFY
PY05150	66	1.53e-18	SVSPKKYANS	NINV VY ILVWL S Y KL N Q K T D	NGITKLMDFY
PY07017	56	1.53e-18	SGLFKSCETS	NINV EY ITMIWL C YML NL K ST	QDDNITNLNN
PY07421	74	1.53e-18	SYNFSSNANG	NMNIV TY IMTWIS Y KL N Q K K Q	DGITTTFNDFY
PY05719	101	2.09e-18	SDLFNSVAKG	NINIV DY IILWL N YML SL KE N	QAKNSLNHFY
PY02572	66	2.09e-18	LNMLNPETID	GDKIV EY AILWL S Y KL N Q K T Q	NGTIKLDDFY
PY02970	94	2.43e-18	CGVDPPPARN	NINIV DY ILIWL S YML TL KE S	EKDNTTCFYS
PY04988	69	3.28e-18	SGVLKDNAKN	YINAV EY IIIWL S YML NL K DN	KGNILNNFYE
PY04795	74	3.28e-18	SSVFESVSKS	NVNIV EY IMIWL N YML NL ME P	SGSTTNLEFY
PY03986	76	3.81e-18	LNMIGEEGID	GKLV EY AILWL S Y KL N Q K T Q	NGTTTLNEFY
PY03948	73	4.41e-18	TLLTLFNGID	SDKLV EY AILWL S Y KL N Q K KE	NETTKLYDFY
PY06339	84	5.11e-18	CGVDPSTAKN	NINIV DY IMIWL S Y MIN L K YS	EESNIITCFY
PY03987	79	5.11e-18	NDNNKNENLA	GDKLV EY AILWL S Y KL N Q K KE	NGTILNDFY
PY05781	73	5.91e-18	KDNSVFKYHN	NINM VY IFIWL S YML NL KE Q	VGDVNNLQYF
PY02564	75	5.91e-18	SDLFNFDEKS	KNDIF DY IMIWL S YML NL KE N	ISNDSLQYFY
PY00988	73	6.83e-18	SDLFQSVAKS	NTNIV DY IIIWL S YML SL MD N	ELKESLGFFY
PY03010	84	7.89e-18	FNSYTDNAKK	KIDIV Y IIIWL S YML SL KK KE	NEINKLNDFY
PY01595	74	7.89e-18	EQLFVKNKKS	NINTV QY IIIWL S Y KL N Q K K Y	DGIKDLNEFY
PY04786	69	1.39e-17	FNDINDENID	SEKLV EY AILWL S Y KL N Q K KE	DETIISNEFY
PY05767	78	1.60e-17	ERIDNHEKLE	SKLAE EY AILWL S Y KL N Q K T Q	NGTTKLYDFY
PY06877	65	1.60e-17	LNMLGDDKTD	GKLV EY AILWL S Y KL N Q K KE	NEMTILNDFY
PY02782	93	1.83e-17	CGVAPSPAKD	IINIV DY ILIWL N YML NL N KS	EKDNVTCFYI
PY07160	75	1.83e-17	KTVFSHYANK	NIDIV VY IMMWL G Y KL N KL N	TEFSNINEFY
PY06742	74	1.83e-17	QFSISLDLPT	YKDAV V CIMIWL S Y KL N Q K SE	NGINTLKDFY
PY06227	92	2.10e-17	LKKLDEESLE	SDQIV EY ASLWL S Y KL N Q K K Q	NGTTRLNEFY
PY02543	75	2.41e-17	SSGLSNKAKN	NINF V DYIMTWL IY ML SL KS N	PDKNSLKHFY
PY07838	92	3.16e-17	LKMFGSENLE	SDQIV EY ASLWL S Y KL N Q K KE	IGITKLYDFY

PY02036	66	3.61e-17	LKNLDESFE	SDKIVQYASLWLS SKLNQKTQ	NGTTKLYNFY
PY05673	85	4.13e-17	CGLLPPPARN	NTNIVDYILIWLRYMLNLNKT	IKNNNINDFY
PY07035	121	4.13e-17	CNVVSSPAKN	SINMVDYILIWLRYMLNLKES	EKDNTTCFYS
PY07406	84	4.13e-17	CGVVSPEKN	IINIVDYILIWLSTLNLKKS	EKDNITCFYK
PY07516	76	4.13e-17	LMNIGEEDIN	GDKLVEYAILWLSYKLNQKKK	NGTTILNDFH
PY04787	69	4.71e-17	NGMDDVENLE	SDKLAEYAILWLSYKLNQKTE	NGTTKLYDFY
PY06499	90	4.71e-17	MLLNKLENLE	SDEIVQYASLWLS SKLNQKKQ	NGTTRLDDFY
PY06760	75	4.71e-17	SGVLPSPKDS	NPYIVDYILIWLSTMLNLTNS	KGDNIKSFYS
PY05560	64	4.71e-17	MLLKKLADLG	SDKIVQYACLWLS SKLNQKTQ	NGTTTLNDFY
PY01873	77	4.71e-17	SGVLPSPSKS	NPYIVDYILIWLSTMLNLTNS	KEKDNITFFY
PY04066	78	4.71e-17	NGMDDVENLE	SDKLAEYAILWLSYKLNQKTE	NGTIKLYDFY
PY05828	73	5.38e-17	YEKFNSVAKR	KINIVDYILIWLGYMLNLIKM	NENATIDLFY
PY07422	75	5.38e-17	SDLFNFDEKS	KNDIFYIYIMIWLSYMLNLKKK	ESNDSLKYFY
PY06220	75	5.38e-17	SYNFSNNANG	NMNVVVYIMIWLS SKLNKMLN	TQFSNLNEFY
PY07405	75	6.13e-17	GGILSPPARN	NINIVGYISIWLSTMLNLGKS	EEDKNIGEFY
PY04215	75	6.13e-17	SNSFNFDEKS	KNDIFYIYIMIWLSYMLNLKEN	EANNSELEFFY
PY03091	85	6.98e-17	ENLDSDENLY	SDKLVEYAILWLSYRLNQKAQ	NGTTTLNEFY
PY06754	59	6.98e-17	NGAGIDENLD	SDKIAEYAILWLG SKLNQKKE	NETTTTLNDFY
PY07533	63	6.98e-17	FEYINDDNLE	SDQLAEYAILWLSYKLNQKTE	NGTTTLNDFY
PY07411	43	7.94e-17	KHGSSVINNT	YKDDTVCMIWLSYMLNLKKS	DGINTLKSFY
PY03438	75	7.94e-17	YDKFSNNANG	KIDIVIYIMTWLGYKLNQKLN	TKFPNLNEFY
PY02278	74	7.94e-17	SYGSSYYAQN	NINVVDTILWLSYMLNLKEN	SYKDSIKHFFY
PY04321	105	9.03e-17	SYNFSNYADD	NIIVVFIMIWLGYKLNQKLN	KEFPNLKDFY
PY07413	78	1.03e-16	FNDIDDKNID	GDKLVEYGILWLSYKLNQKKQ	YGTTLKDDFY
PY04733	111	1.17e-16	DGIFPSPSNS	NPINIVDNIFIWLSYMLNLKET	NKNEGIKYFY
PY00924	204	1.70e-16	YPTKDGVINY	NKFFFLYIILWLSYKLNQNTB	ETFTTINDFY
PY02565	87	1.93e-16	ENLDSDENLD	SDKLVEYAILWLSYNLNQKTE	SEITTLNDFY
PY05820	75	1.93e-16	SENFSSYNAND	NLDIVTYIMTWLGYKLNQKLN	SEFSNINEFY
PY05816	78	2.18e-16	HRIDDLSEH	VKAFIYIYIMIWLNMYMLNLKKD	EKNNLNDLYT
PY06334	75	2.46e-16	NSVFNVAKS	NINIVFYIILWLSYMLNLTPTI	YENTSIEPFY
PY04430	73	2.46e-16	FTQFNSVAKR	KINIVDYILIWLGYMLNRIKN	NENDIISFY
PY02614	73	2.79e-16	SSGLSNKTKN	NIIFVDYIMIWLIYMLSLKDN	PNKNSLKHFY
PY03359	116	3.15e-16	PYNFSSNANG	NMSIATYIMTWISYKLNQKQP	KEISXFTDFY
PY02541	75	3.15e-16	KSVFSSYADG	KIDIVVYIMMWLGYKLN SKLN	TQFSNINEFY
PY07264	65	3.15e-16	KEVDMQNI	SDEIAEYAILWLG HILNQKTE	NRTTTLNDFY
PY04516	95	4.01e-16	PEGISDEHLE	GDKLAEYAILWLSYRLNQKKE	NGTTILNDFY
PY00284	86	4.01e-16	KGIDDLRNEQ	VEAFIYIYIMIWLNMYMLNLKKD	GKITALKDFY
PY02140	68	5.09e-16	SDNFKSNAKS	NINIVFYIMIWLSYTLNKTIN	GEKSINEFYN
PY04155	68	5.09e-16	SDNFKSNAKS	NINIVFYIMIWLSYTLNKTIN	GEKSINEFYN
PY02131	75	5.73e-16	KTVFYHYSNN	NIDIVVYIMMWLGYKLNKMVN	PQFPNINEFY
PY00297	74	6.45e-16	SSSLKNHAKN	NIGIVQYIILWLSYMLSAIKN	QENNSLKFFY
PY03983	79	6.45e-16	NRISTLSKDH	SKVFIIYVMIWLGHMLNLKKD	DKIKNLNDFY
PY00177	62	9.16e-16	YPTKGGVIEY	NKFFFLYIILWLSYKLNQKNRE	KTFTSINDFY
PY01184	82	9.16e-16	SDFNGSNDEK	NKVFFIYIMIWLSYMLKLKNV	NDFKSLKDFY
PY06666	74	1.03e-15	KSAFEKDAKG	NIYIVQYILIWLSTVLSLIKES	NQDDNRVHFY
PY00085	90	1.15e-15	KSTFENDAKG	NIYIVQYILIWLSTVLSLIES	NEAGNRTSFY
PY00175	73	1.63e-15	KAGISLYHNT	YKDATVCVMIWLSYKLNQKTE	HATTKLSDFY
PY05410	75	1.82e-15	LTGRVYNENN	TNAFFIYIISWLSYKLNQKNKE	EKFATINDFF
PY02827	94	2.04e-15	NKINSLNKEQ	VKIIVTYIMIWLSYKLNKNPD	VGITTLNEFY
PY07624	75	2.28e-15	KTVFYHYSNN	NIDIVVYIMWLGYKLNKMLK	TQFSNINEFY
PY07342	75	3.18e-15	YPTKGGIIND	TKFFFLYIILWLSYKLNQITR	KNFTKINEFY
PY06796	75	3.18e-15	YPNKGNTINS	TKFFFLYIILWLSYKLNQNSD	SKPTKIYDFY
PY06851	78	3.55e-15	NRISTLSKDY	SKVFIIYVMIWLGHMLNLKDV	NDFKNINEFF
PY05244	79	4.42e-15	NRISTLSKDH	SKVFIVYVMIWLGHMLNLKKK	EKIKNLNDFY
PY00055	62	4.93e-15	KPGSTVDSNT	YKDDVLCIMIWLSYKLSLKLFP	DDITTLNSFY
PY04755	66	6.81e-15	SDSFNSVAKG	NTNIVDYILIWLKYMLNFKRI	NENDSIESFY
PY03403	133	7.58e-15	EGLLPSPSRS	NPINIVDNIFIWLSYMLSLDPT	IKYNGIKYFY
PY05923	105	7.58e-15	NGIDIGEDLD	SDKLVEYAILWLSYNINQKKE	NRTTTLNDFH
PY03016	70	8.44e-15	KNIDDKENLE	SDKFVEYIILWLSYIINQITQ	NGTTKLYDFY
PY07226	96	8.44e-15	SYNFSSNANG	NMNIVTYIMTLISYKLNQKSQ	DGITTFNDFY
PY06020	73	1.29e-14	VSGISHYHDV	YKEVTVFIMIWLSYKLSLKLFP	ENITTLKDFY
PY00552	79	1.29e-14	YKVNYSSKEK	VKSFIYIYIMIWLSYMLNLKKD	GKITALKDFY
PY04773	79	1.43e-14	KGIDDLSDNQ	VSFIIYIMIWLNKYKLNKKD	EGTNLNDFYT
PY03991	111	1.43e-14	SLDKSYNENN	TKFFFLYIILWLSYKLNKNTE	HNTTKINDFY
PY05708	75	1.43e-14	YPKIGDNEYI	TQFFFIYIILWLSYKLNQNLD	HKTSNINEFY

PY05688	88	1.76e-14	KTGTSSYHDV	YKDV	TMCIMIWL	SYKLS	LKTF	NNITTLKDFY	
PY05912	74	1.95e-14	KAGTSVDKHT	YKDDL	VLCIMIWL	SYKLN	LKTF	DNITTLKDFY	
PY03332	103	2.39e-14	KDGTSDVKHT	YKDDI	ICIMIWL	SYKLS	LKTF	DNITTLKDFY	
PY04931	96	2.39e-14	EGLLPSPSKS	NFNIV	DIIFIWL	SYMLN	MDKT	INYDGIKYFY	
PY06029	105	2.93e-14	TRINDLSNEQ	LKVFI	IYIMWL	NYMIN	LKKD	GKINNNDIFY	
PY02971	64	3.97e-14	STNRSYNESS	TNAFF	IYIISW	FSYKLN	QNSF	HNSTQISDFY	
PY02660	88	4.39e-14	IYTCESEKES	ITLVVV	YMLAWS	SYKLN	QKTN	NGITKLNEFY	
PY06547	74	4.85e-14	HENTCYNEKN	INAIFL	IYISWL	SYKLN	QSSF	HNFTKIKDFY	
PY07111	77	4.85e-14	TSNFTFDNNT	LKDDA	VCIMIWL	GYILS	LKPP	DNIKTLNDFY	
PY07501	80	5.35e-14	KSVFENDAKG	NIYIV	QYILIWL	SYVFS	LIKS	EEKGSLNEFY	
PY05871	95	7.20e-14	KYGSSFDPRF	YKDEA	VSIMIWL	GYILN	LKSH	EGITTLIDFY	
PY06732	79	7.94e-14	NYGSSFDSTK	YKDET	VCIMIWL	GHILS	SLKSH	EGITNLMDFY	
PY07090	82	8.75e-14	SDFGSDSDEK	HKVFI	IYIMWL	NYFKLN	QTTT	AKNTEFKDFY	
PY02312	95	1.42e-13	TGGYSFDTKY	YKNE	TVCIVIW	LGYYIL	NLKS	GGINTLNDFY	
PY06740	103	1.56e-13	NKIDNLSNEK	FKMII	IYIMIWL	SHMLE	LKNV	TEFKNINAFY	
PY06549	75	2.28e-13	YPIKGNNEYN	TEPFF	IYIILWL	SNKML	QNKG	HNTTTINDFY	
PY00308	88	3.65e-13	KTLKENNTLE	DDKLA	EYAILWL	SYKLD	QKQK	DKLTDLNKFY	
PY01837	73	4.39e-13	NNIDSLSKDQ	IEIFT	IYIIMWF	SYMLN	LKNV	KEFNININEFY	
PY07080	73	4.81e-13	TYRSTGYGDN	TNPF	FLYMI	SWLSYK	LQNSV	DGSTTINGFY	
PY01872	64	6.33e-13	VIDKSYKENN	TNVFF	LYMISW	FSYKLN	QITG	NKFTKINDLY	
PY00997	74	7.59e-13	KLSFSADPNT	LKND	SVSIII	IWLGYIL	NLKPH	EGINTINDFY	
PY01110	74	9.10e-13	KSGFSADPDT	LKS	D	TVCIIIW	LGYYIL	SLKSH	EGIKTINDFY
PY00580	72	9.95e-13	YALKNKSNID	TNAFF	IYIISW	ISYK	LQSTN	ENFTTIKDFE	
PY01981	77	1.55e-12	GKYYKESENE	NNE	YITYIM	LWLSNKM	KLIKK	GSYGSVGDIFY	
PY03177	73	1.70e-12	YEFKSKSHNN	TNAFF	IYLVSW	LSYKLN	QNKG	NNFTTINDFF	
PY02973	72	1.85e-12	YALKNKSHIN	TDAFF	IYIISW	FSYK	LQFTK	ENFTTINEFY	
PY01111	73	2.03e-12	KLGFSAQQDV	LKY	D	SVCIIIW	LGYYIL	SLKSQ	DGINKLSDYY
PY03636	80	2.03e-12	SKDISYNENN	TNAFF	LYVISW	FSYK	LQNSF	HNTTKINDFY	
PY04914	78	2.41e-12	LNKNIEYENK	NNE	YITYAM	LWLSNKM	KLIKI	GSYGSVADFH	
PY01963	78	3.13e-12	DDQYIENDDK	NNE	YIMYIM	LWLSNKM	KLLK	GTYGAVSEFY	
PY07826	78	3.41e-12	LNKNIEYENK	NNE	YITYAM	LWLSNKM	KLIKY	GSYGSIGDFY	
PY01834	111	4.42e-12	SRISNLSEDP	PKVFI	TYIIIW	LNYYIL	RLLKNV	NDFKNISEIY	
PY07187	78	6.21e-12	GDEYIESEDK	NNE	YMTYIM	LWLSNKM	KLIKY	GNYSVADFY	
PY00754	78	6.76e-12	LNKNIEYENK	NNE	YITYVM	LWLSNKM	KLIKK	GSYGSVGDFF	
PY04327	80	6.76e-12	LTTNGYDQNN	TNAFF	I	MISWFSYK	LNQHEG	KKFNTINDFF	
PY07477	133	8.71e-12	LKNKTHDENS	VNTFF	IYIISW	FSYKLN	KNKKG	HNATTINDFF	
PY01773	77	2.16e-11	LNKNLESENN	NNE	YITYVM	LWLSNKM	KLIAK	GRYGSVADFY	
PY03194	80	4.84e-11	STKKIYNENT	INAFF	LYMISW	FSNKL	KQKSI	YNTTSLNDFY	
PY04554	75	1.14e-05	INSFKDNAKN	NLDV	VVYYIL	ICLKKE	NGINKL	NDFYTKHIET	
PY00578	44	1.20e-05	YKNYCPGNNC	NS	ETKITV	GFLCYQLN	QSTK	HNTTKIYDFY	

Motif 3 block diagrams

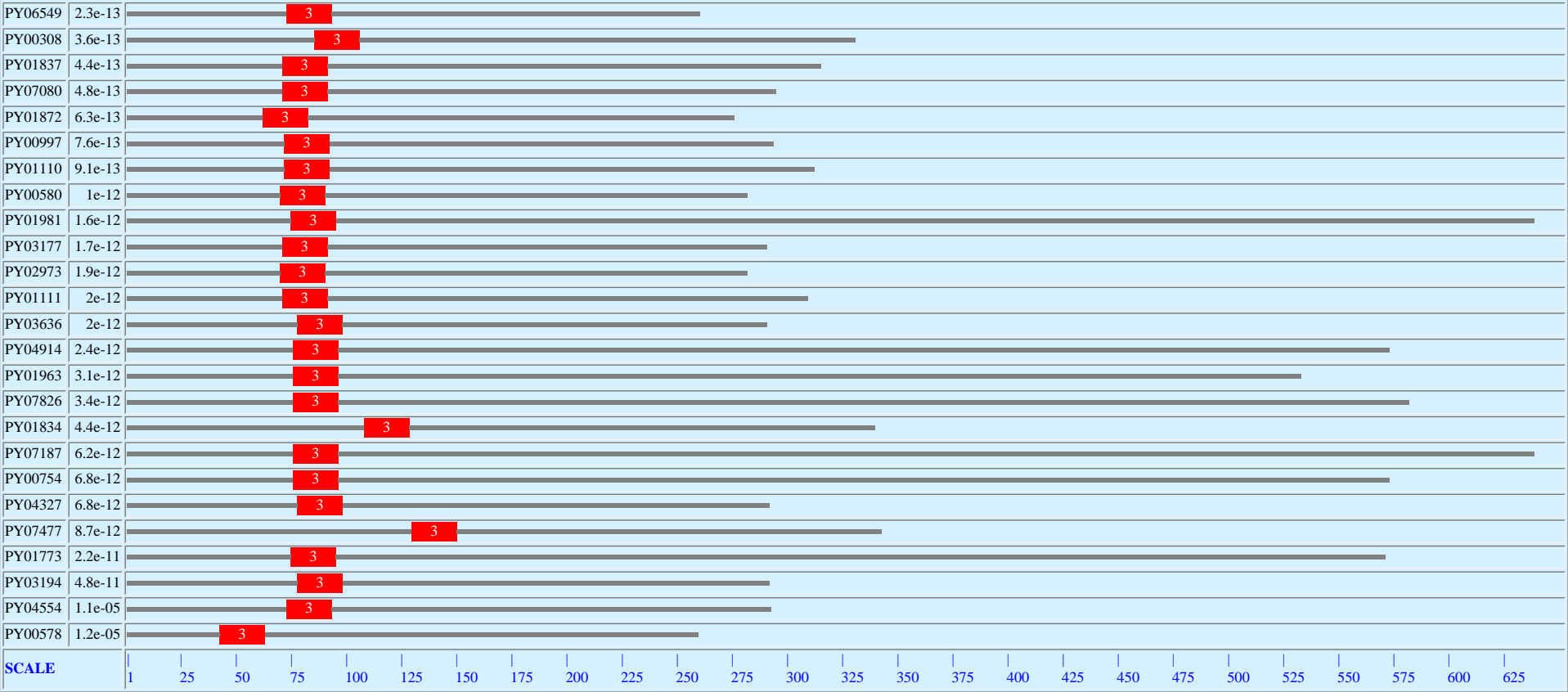


MEME

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PY01871	9.4e-21	3
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PY07849	4.3e-19	3
PY07546	5e-19	3
PY05648	7e-19	3
PY03331	7e-19	3
PY03760	7e-19	3
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PY07421	1.5e-18	3
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PY04988	3.3e-18	3
PY04795	3.3e-18	3
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Motif 3 in BLOCKS format

to BLOCKS multiple alignment processor.

Motif 3 position-specific scoring matrix

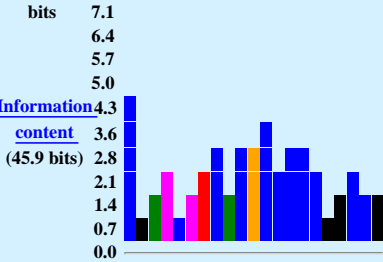
Motif 3 position-specific probability matrix

Time 811.09 secs.

FN MOTIF 4 width = 21 sites = 179 llr = 5696 E-value = 1.6e-1623

[Simplified](#) A : : : : : : : : 6 1 : : : : : 1 : : :
[pos.-specific](#) C 9 : : : : : : : : : 6 : : : : : : : :

[probability](#) D : 3 1 6 : 4 : : : : : : : : 2 : : : 1
[matrix](#) E : 1 : 1 1 3 : : : : : : : : 1 2 : : :
F : : : 1 : : : : : 4 1 1 : 4 : : 6 5 :
G : : 1 : : 1 : : : 1 7 : : : : : 1 : : 4
H : : : : : : : : : : : : : : : : : : :
I : : : : 2 : : 8 1 1 : : 2 : : 1 : : 1 1 :
K : 1 : : : 1 8 : : : : : : : : 1 1 : : 2
L : : : : 4 : : 1 : : : : 7 : 9 5 : 1 1 : :
M : : : : : : : : : : 1 : : : : : : : :
N : 2 2 1 : 1 : : 5 : : : : : : 4 : 1 1 :
P : : : : : : : : : : : : : : : : : : :
Q : 1 : : : : : : : : : : : 3 : : : : :
R : : : : : : 1 : : : : : : : : : : : : :
S : 1 3 : : : : 2 1 : : : : : : : : 1
T : : 4 : : : : : 1 : : : : : : : : 1
V : : : : : : 1 : : 1 : : : : : : : 1
W : : : : : : : : : : : 4 : : : : : : :
Y : : : : : : : : : : 4 : : : : 1 2 : :



[Multilevel](#) C D T D L D K I N A G C L W L L N Q F F G
[consensus](#) S E F Y F D E
[sequence](#)

NAME	START	P-VALUE	SITES
PY00297	42	1.57e-22	QHFKKYCNSN CDTDLLEKISAGCLYLLNEFFFG DSSSLKNHAK
PY05719	69	1.94e-22	HFKKYCTGGK CDGDLDKINAGCLYLFNAFFG SSDLFNSVAK
PY07226	64	5.47e-22	SINNYCPNRK CESDIDKINAGCLWLFFKQFFYG SSYNFSSNAN
PY03438	43	1.00e-21	TIKKYCPNKN CDS DINKI AGCLWLLNQFFYG DYDKFSNNAN
PY07411	12	1.22e-21	LKNYCPKSGN C NNDIDKINAGFLWLFFNAFFG KHGSSVINNT
PY03359	84	1.49e-21	SLNSYCPNRK CEN D D K I N A G C L W L F K Q F F Y G S P Y N F S S N A N
PY03973	42	3.88e-21	YFQEYCTGDS CDNDLDKINAGCLYLFDAFFK DISAFRMTVK
PY07331	34	6.80e-21	FLNNYCSSND CNTDLEKINGGCLYLFNF FFG SSELFKTVAN
PY04321	73	9.82e-21	TIKNYCPNRK CDS DINKI D A G C L W L F N Q F F Y G G S Y N F S N Y A D
PY04083	43	2.02e-20	FLDGYCDSYS CDTDAEKINGGCLYLFNQIFG TSQLFKSVAN
PY07327	42	2.02e-20	FLDGYCDSYS CDTDAEKINGGCLYLFNQIFG TSQLFKSVAN
PY05871	64	2.41e-20	LFKKYCLNEK C N N D L D K I N A G C L Y L F Y E F F G K Y G S S F D P R F
PY05244	48	3.42e-20	CPNRDSGETE CKTDLKINAGCLWLFEQNIV NRISTLSKDH
PY01080	34	4.07e-20	FLDSYCDGKG CDTDLAKINGGCLYLFNKFFG SSELFKSVAN
PY06829	34	5.74e-20	FLDSYCGSYS CDG D I E K I N A G F F Y L F N Q F F G S S E S S Y Y A Q N
PY06742	43	8.06e-20	VFRKYCPNDN CDTNKKINAGCLWLFNAYFG QFSISLDLPT
PY07405	43	1.57e-19	ILNNYCDNKK CQS D F D K I S A G C L Y L L D Q F Y K D G G I L S P P A R
PY07022	42	1.85e-19	GLFTKYCPNN C E N N I D K I N A G C L W L F N K F Y G S S Y N F S S N A N
PY06567	353	2.18e-19	TLNRYCSGNS CDNDLDKINAGCLYLLDSFFK DSSVFRSYAK
PY01774	43	2.56e-19	FLDGYCGSNS CDTDFEKNINGGCLYLFNKIFG TSELFKSVAN
PY07027	43	2.56e-19	FLDGYCGSNS CDTDFEKNINGGCLYLFNKIFG TSELFKSVAN
PY02614	42	3.01e-19	FLDSYCYKNE CKGDLEKINAGCLFLLNKFFG SSGLSNKTKN
PY06220	43	3.01e-19	TIKNYCPKKK CDS NVNKI AGCLWLFFKQFFYG SSYNFSNNAN
PY02543	44	3.01e-19	FLNSYCFNNE CKGDLEKINAGCLFLLNKFFG SSGLSNKAKN
PY02971	32	3.53e-19	NINKYCPDEN CNTELDKITAGFLWLLGQYFT ISTNRSYNES
PY01595	48	5.69e-19	CPNGESGDTE CKTDLDNINAGCLWLLQLFV KNKKSNIINTV
PY04554	43	6.65e-19	QNFKKYCTNS CDS NL E K I N A V C L Y L F N L F F G N I N S F K D N A K

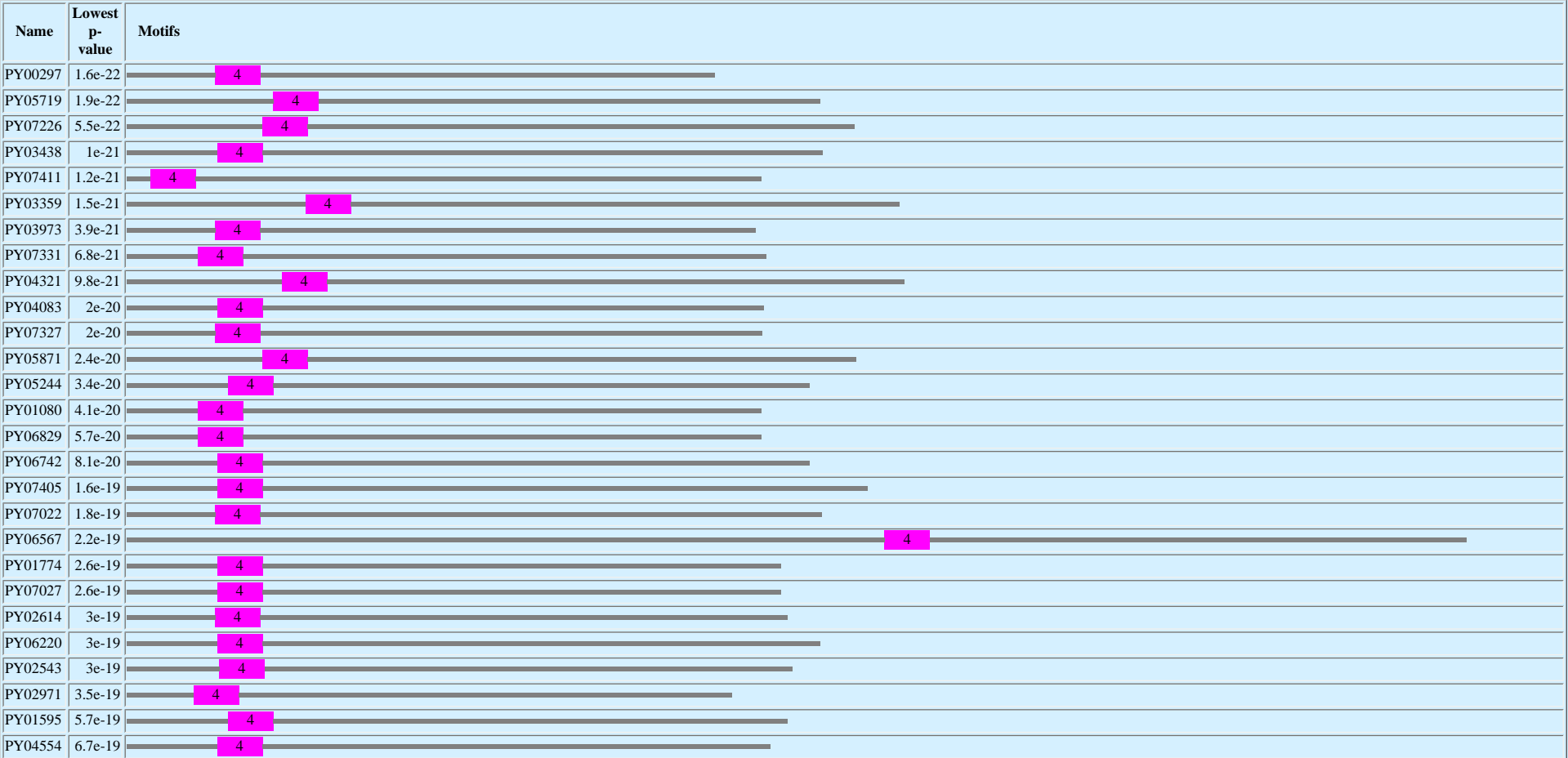
PY02298	42	7.77e-19	FLDSYCFKYK	CEGDLDKINAGFFYLLNQFIG	SSGSSRYAQN
PY05820	43	9.08e-19	FFKTYCSSNN	CDIDINKINAGCLWLFNKFFYG	DSENFSYNAN
PY06020	42	1.06e-18	IFKKYCPNKN	CGTDTDIANAGCLWLFNQFFG	VSGISHYHDV
PY03983	48	1.06e-18	CPNGSGSETK	CNTEADKINAGCLWLFEBQNIV	NRISTLSKDH
PY02140	36	1.06e-18	NFDKYCTNDS	CDSNLGKINAGCLFLFDEFFK	DSDNFKSNK
PY04155	36	1.06e-18	NFDKYCTNNS	CDSNLGKINAGCLFLFDEFFK	DSDNFKSNK
PY05781	43	1.06e-18	PIKEYCAGNS	CDDDLLEKINAGCLFLFDALFK	DNSVFKYHNN
PY02312	64	1.06e-18	AFKKYCPNNN	CDGDINKINAGCLWLFNSMFG	TGGYSFDTKY
PY00500	43	1.23e-18	HFKKYCDKEK	CDDPLEKVNAGCLYFFNEFFG	SSDLFKSVAK
PY05912	43	1.23e-18	TFKSYCSNNK	CDNDTDIVNAGCLWLINNEFFG	KAGTSVDKHT
PY01111	42	1.23e-18	FFKDYCPNKN	CNNDIEKINAGCLWLIYEFFV	KLGFSAQQDV
PY00988	41	1.23e-18	EHLKNYCISG	CDNNLEKINAGCLYLLYTFFG	SSDLFQSVAK
PY06549	43	1.95e-18	NYKNYCPSEN	CDTDLEKITIGFLWLLQYFT	EYPIKGNNEY
PY06151	49	1.95e-18	NNHSFCTNIN	CETDIDKINAGCLWLFKAIF	DSYSFKTYAK
PY05822	42	2.26e-18	FLNKYCDGSK	CDNDIEQISAGCLYLLNEFFK	NSSVFQSVAK
PY05688	57	2.62e-18	LFKKYCSSEK	CEGDVNIVNAGCLWLFNEFFG	KTGTSSYHDV
PY06782	30	2.62e-18	SLNIYCSNRK	CENDIDKINAGSLWLFKQFFYG	SSYNFSSNAN
PY07342	43	2.62e-18	NYSNYCPGKD	CNTELEKITIGFLWLLGQYFG	KYPTKGGIIN
PY06126	42	3.05e-18	LFKKEYCNKI	CGSDLDKINAVCLFLFNELF	SSDTFSINSK
PY06619	57	3.53e-18	EHLKNYCTSG	CDNALDKINAGCLYFFKEFFG	SSDLFSQYAK
PY07111	46	4.09e-18	MLKKYCPKES	CNNIDKINAGCLWLINAIFS	TSNFTFDNNT
PY07017	24	4.73e-18	FLDSYCFNDE	CNSDYGKINAGFLYLLNQFCG	VSGLFKSCET
PY03403	101	4.73e-18	EHLKKHCISK	CDNNFDKINAVCLYLLDQFFYK	HEGLLPSPSR
PY07090	48	5.47e-18	CSNGESEGTG	CKTDLDKINGGCLWLFEBQNII	NRISDFGDSS
PY01837	42	6.32e-18	CPNGSGSKNE	CKTDLDKIKAGFLWLFEBQIIV	NNIDSLSKDQ
PY05146	77	6.32e-18	ILNSYCAGNK	CSDNLAKINAGCLYLFDAFFK	NSSVFMSSDAK
PY05586	70	7.30e-18	ILSNYCSNSNE	CSDNLAKINAGCLYLLDAFFK	NSSVFKSYAK
PY07421	42	8.43e-18	SLNRYCPKNN	CETNINKIISGCLWLLKQFFYG	DSYNFSSNAN
PY06514	33	8.43e-18	ILDNYCTSSG	CTDDLAKINAGCLYLFDAFFK	NSSVFKSDAK
PY07080	42	9.72e-18	NFKNYCPDKN	CNSELEKITIGFLWLLQYFG	TYRSTGYGDN
PY00997	43	9.72e-18	TFKKYCPKES	CNNIDKINAGCLWLIYELFV	KLSFSADPNT
PY03636	48	9.72e-18	CYNQSGGVNE	CNTDLDKITVGFLLWLEQYFT	ISKDISYNN
PY06334	43	1.12e-17	DFKDYCTGNK	CNDDTGKISAGCLYLLDAFFK	DNSVFNSVAK
PY00175	42	1.12e-17	TFKKYCPSNS	CVADTDILNAGCLWLFNQFFG	KAGISLYHNT
PY01873	45	1.12e-17	FLNKYCDSNK	CQSDYDRISAGCLYLLDQFFYK	DSGVLPRPSK
PY04430	41	1.12e-17	NLKKYCDNGS	CDDYFGKVNAGCLYLFDEFFA	GFTQFNSVAK
PY02688	43	1.71e-17	FLDSYCYNGE	CSSDFGKINAGFFYLLNQFFE	SSGLSYNVQN
PY04327	48	1.71e-17	CPENGLGDNT	CNTNLDKITAGFLWLLGECYS	TLTTNGYDQN
PY02278	43	1.71e-17	FLNSYCDGNK	CDSNLEKINAGFFYLLNQFLG	SYGSSYYAQN
PY03042	41	1.71e-17	EYFKDYCTGG	CDNDFKKINAGCLYFFDAFFK	DSSLFEKVAK
PY04773	48	2.25e-17	CRDEESGETE	CKTELDKINAVCLWLLNENIA	KGIDDLNSDQ
PY06760	43	2.58e-17	FLNNYCNSNQ	CQSDYDRISAGCLYLLDQLYK	DSGVLPSPKD
PY02827	63	2.58e-17	PNGDSGSKQE	CKTELDKINAACIWLFNQIIS	NKINSLNKEQ
PY04755	34	2.58e-17	VSQKYCTDVN	CDDDINKINAVCLFLFNELF	SSDSFNNSVAK
PY00924	172	3.39e-17	NYKRYCPSGD	CNTELEKITIGFLWLLGQYFT	EYPTKDGVIN
PY07021	53	3.39e-17	HLQKYCDDGK	CNGPLDKISAGCLYFFNEFFK	DASVFRSVAK
PY05708	43	3.89e-17	NFDKYCPNNN	CDTDLEKITIGFLWLLGKYFT	KYPKIGDNEY
PY03010	52	4.45e-17	HFKQYCTNNS	CDSNLEQINSACLYLFNAFFG	DFNSYTDNAK
PY05769	43	4.45e-17	FLDSYCDDKS	CDTDFFRRIDGGCLYLFKQIFG	TSELFKSVAN
PY02652	43	4.45e-17	FLDSYCDDKS	CDTDFFRRIDGGCLYLFKQIFG	TSELFKSVAN
PY02940	47	4.45e-17	FLDSYCGDNN	CSTDYGKISAGFLYLFNGLFG	VSGLFNSRET
PY04931	64	5.09e-17	EHLKKNCISK	CDSNFDKIDAVCLYLLDQFFYK	HEGLLPSPSK
PY04733	79	5.81e-17	EYLQKYCING	CDNLDKINVGCYLLDQFFYK	HDGIFPSPSN
PY06796	43	5.81e-17	NYSNYCPGKD	CNTELEKITIGFLWLLGQYFD	KYPNKGNTIN
PY06851	47	6.64e-17	CSNGSGGETE	CNNEVDKINGGCLWLFEBQNIV	NRISTLSKDY
PY07477	101	8.65e-17	CPVTDSENE	CDNNFGKITAGFLWLLQECYS	ALKNKTHDEN
PY04215	43	8.65e-17	FLDSYCGSNS	CSDSFEKISAGFFYLLSGFFG	DSNSFNFDEK
PY03332	72	9.86e-17	TFKRYCPNNK	CSDSTNIVNAGCLWLINDFFG	KDGTSDVKHT
PY07594	41	9.86e-17	DRLKKYCTNN	CDNNLDKISAGCLYFFDTFFK	DVSAFEMAAC
PY07198	41	1.12e-16	FLDSYCNMYK	CEGDLDKINAGFFYLLNQFFW	SSESSYNVQN
PY03991	79	1.12e-16	GFKNYCPSSS	CNSELEKITIGFLWLLQYFT	ISLDKSYNN
PY04795	42	1.46e-16	HSKKYCDNGN	CNGPLDKINTVCLYLFNEFFG	NSSVFEVSK
PY00055	31	1.66e-16	ILGKYCPNEN	CNNYIDKINAGSLWLFYEFFG	KPGSTVDSNT
PY07422	43	1.66e-16	FLNSHCDGNT	CNDIEKISAGFFYLLSGFFG	GSDLFNFDEK
PY01184	48	1.66e-16	CPNGDSKEKE	CKNEVDKINAACWLWFEQNIV	NRISDFNGSN

PY00284	55	1.66e-16	CPNGNSGHN	CITELDKINAACLWLLNENIT	KGIDDLRNEQ
PY05816	47	1.88e-16	CPHGNSGNNK	CITELDKINAACLWLFEQNIS	HRIDDLSEH
PY01872	32	2.14e-16	NIKKYCPDEN	CDTDFDKNTAGFLWLLGECYS	TVIDKSYKEN
PY05624	37	2.14e-16	ILNNYCTGNN	CSSNLDKLNAGCLYLLDGLFK	DSSVFKHHKN
PY02564	43	2.14e-16	FLNGYCDGNK	CDSDFEKISAGFFYFLGGFFG	GSDLFNFDEK
PY02671	42	2.14e-16	LFKENCTNQK	CESDLAKINAVCLFFFKFFG	DSGSFEINAK
PY07546	42	2.43e-16	HFKTYCTNNN	CEMPLKINAACLYLFDGFFK	DADLFKSVAK
PY06339	52	2.76e-16	DFSNGYCNID	FKSDFDKINAGCLYLLDEFIK	DCGVDPSTAK
PY03729	42	3.54e-16	FLDSYCDGNK	CDSAFERIDGGCLYLKQIFG	TSEFFKSVAN
PY07175	52	5.14e-16	FLNNSCNNNN	FQSELDRLISAGCLYLLDQFYK	DCGVVPRPSK
PY05673	53	5.14e-16	FSNNSCNNND	FQSDLDRLISAGCLYLLDEFIK	DCGLLPPPAR
PY07849	42	5.14e-16	YFKEYCTDGQ	CEEDINKINAVCLFLFNELF	NSTSF5FIK
PY02943	42	5.82e-16	DFKEYCTDVN	CEEDINKINAACFLFLNELF	SSDSFNSVAK
PY06374	42	5.82e-16	LFKDYCDNKK	CVTDLDKIHAVCLFLFDNFXG	GVDSFTVNAK
PY06732	48	8.39e-16	FFNGYCPNNN	CESDINKITAGCLRLFNDMFG	NYGSSFD5KT
PY00494	43	8.39e-16	FLEGYCDDYE	CSTNYGKLNAGFFYLLNQFIG	SSGSLYNVEN
PY06763	43	8.39e-16	FLEGYCDDYE	CSTNYGKLNAGFFYLLNQFIG	SSGSLYNVEN
PY07501	48	9.47e-16	DFIDYCTDGE	CDDDTDKINARCLNVFDAFFK	DKSVFENDAK
PY01834	80	1.07e-15	CPIEDSGNQE	CKTDLDKIKAVFLWLFEQNII	SRISNL5EDQ
PY02970	62	1.07e-15	DFSDSYCNID	FKSDFDKISAGCLYLLDEFIK	DCGVDP5PAR
PY03760	42	1.21e-15	HFKKEYCDNEL	CDKDVVKINAGCLFLFDAIFM	DSYSFRNYAK
PY00177	30	1.36e-15	DFQKYCSNKS	CNTLEQITIGFLWLLGEYFT	EYPTKGGVIE
PY06204	42	1.36e-15	FLDSYCGNKN	CEGNLDKINAVFFYLINFFG	SSGLFNNNVK
PY05828	41	1.53e-15	KLKNYCDNGS	CDSAFGKVNAGCLYLFDLFX	DYEFNSVAK
PY07035	89	1.72e-15	ELSDHLCdni	SQSDLNKISAGCLYLLDEFIK	DCNVVSSPAK
PY02687	53	1.72e-15	ELSDHLCdni	SQSDLNKISAGCLYLLDEFIK	DCNVVSSPAK
PY05648	53	2.18e-15	LNKYSCNNNN	LQSDFDKISAGCLYLLDEFIK	DCGVKPSPVK
PY04466	42	2.45e-15	FLDSYCGGNK	CDSAFERIAGGCLYLFMQIFG	TSELF5TSVAN
PY06029	74	2.75e-15	CSNGESDGTG	CKTDHDKINGGCRWLFEQNVV	TRINDLSNEQ
PY06547	30	4.90e-15	SLKKYCPNGN	CDTNLDKIKAGFLWLFEKNCS	KYEITD5DGQ
PY07653	34	5.49e-15	NQYKQNFNKA	SYTDIDKINGWCLWLFAIFG	DSLSPKKYAN
PY01871	53	9.64e-15	LNNYSCNNNN	FKNELDRISAGCLYLLDEFIK	DCGVSH5PLK
PY00552	48	9.64e-15	CPDGESGEGK	CNTKLDKINAVCLWLLNSNIA	YKVNYS5KEK
PY06740	72	1.20e-14	HNVD5GNSKE	CKTEPDKINAACLWLVEQIII	NKIDNLSNEK
PY05410	43	1.34e-14	NFLEYCPQKN	CNSELEQITIGFLWLLGECYS	TLTGRVYNEN
PY00580	42	1.34e-14	NFKDYCPKED	CDTELEKNTIGFLWLLGBCFY	ALKNKSNI5DT
PY04786	41	1.50e-14	ILKLYCPGNN	CSSDEQKIIAGFIMLLNMFND	INDENID5EK
PY01110	43	1.67e-14	SFKKYCPDGN	CNNIDDKINAGCLRLIYDFFI	KSGFSAD5PDT
PY00085	58	2.32e-14	DYKNYCTNEN	CDNDTDKMNARCLHIFDAFFK	DKSTFENDAK
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PY02131	43	6.11e-13	TLKQYCPDKE	CKNYINLVKGGCLWLLDRFYG	SKTVFYH5YSN
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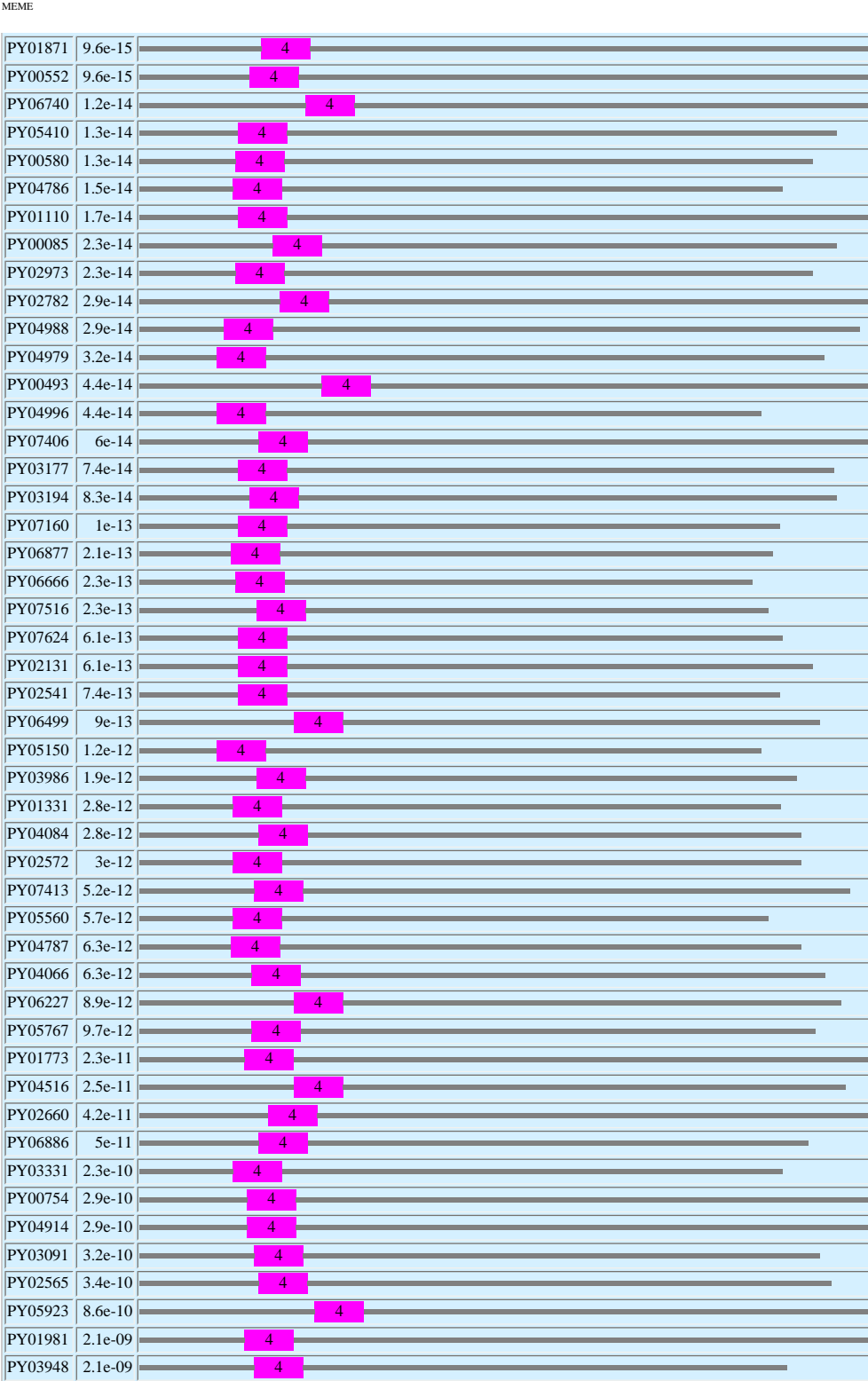
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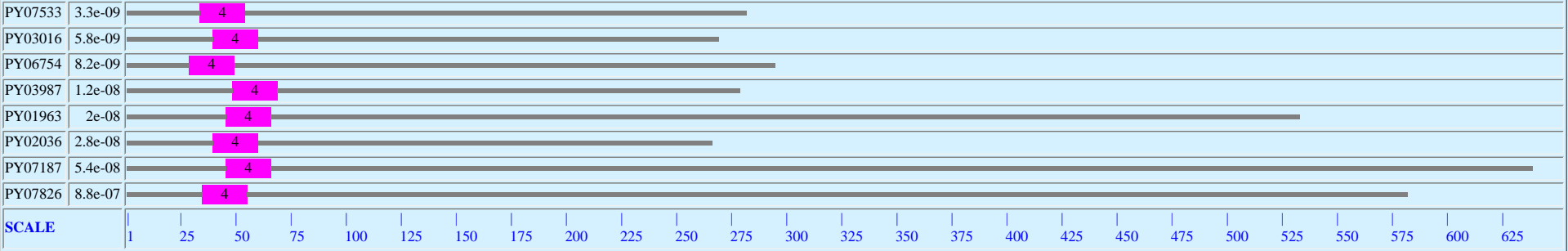
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Motif 4 block diagrams



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Motif 4 in BLOCKS format

to BLOCKS multiple alignment processor.

Motif 4 position-specific scoring matrix

Motif 4 position-specific probability matrix

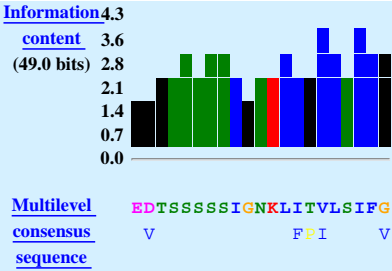
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MOTIF 5 width = 21 sites = 159 llr = 5406 E-value = 1.4e-1556

Simplified pos.-specific probability matrix

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C	:	:	2	:	:	:	:	:	:	:	:	:	:	:	:	:	:
D	:	1	2	:	:	:	:	:	:	:	:	:	:	:	:	:	:
E	:	3	:	:	:	1	:	:	:	:	:	:	:	:	:	:	:
F	:	:	:	:	:	:	:	:	:	:	:	:	3	:	:	1	:
G	:	1	:	:	:	:	:	2	:	:	:	:	:	:	:	:	5
H	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
I	:	:	1	:	:	:	:	6	:	:	:	:	:	6	1	3	:
K	:	:	:	:	:	:	:	2	1	7	:	:	:	:	:	:	:
L	:	:	:	2	:	:	1	:	1	:	:	:	9	:	1	:	7
M	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
N	:	1	:	:	:	:	:	:	:	:	:	:	7	:	:	:	:
P	:	:	:	2	:	:	:	:	:	:	:	:	:	:	2	:	:
Q	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
R	:	:	:	2	:	:	:	:	:	:	:	:	:	:	1	:	:
S	:	1	:	1	:	5	7	8	9	:	:	2	:	:	1	:	:
T	:	1	:	4	:	:	:	:	:	:	:	2	:	2	:	3	:
V	:	2	:	2	:	:	:	:	:	:	:	:	:	:	6	:	:
W	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
Y	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:

bits 7.1 6.4 5.7 5.0

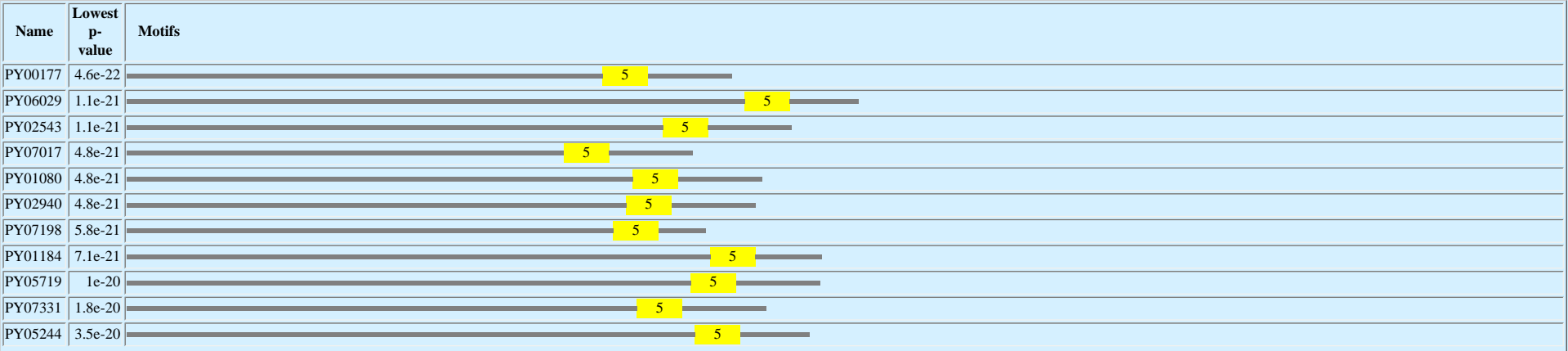


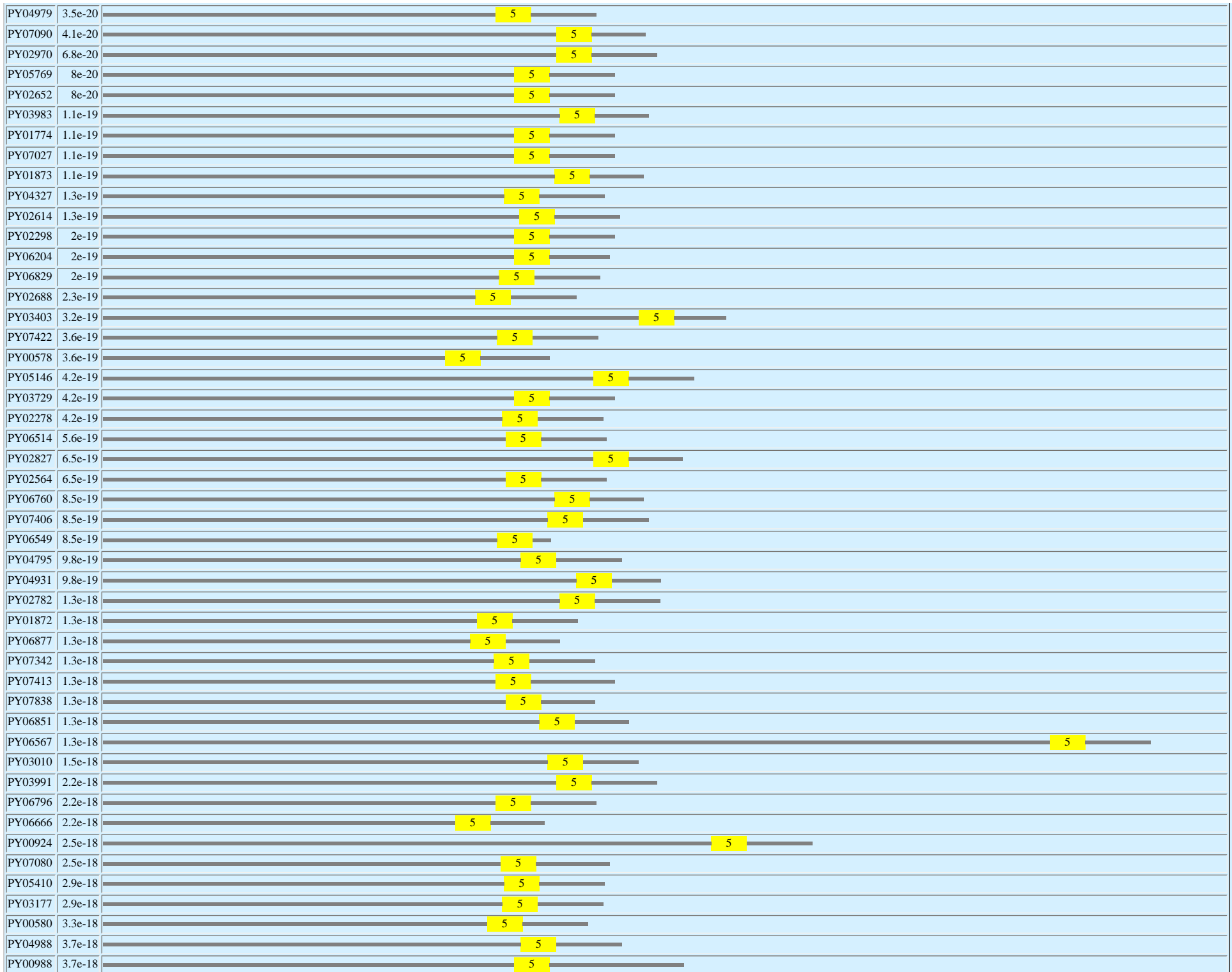
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PY07017	204	4.82e-21	GTEQILVQSS VDTSSSSSIGNKLISVLSIFG AIAFFLGISY
PY01080	236	4.82e-21	TSAQQILQIS GDTSSSSSIGNRLFTVLSIFG VIAFLLGISY
PY02940	233	4.82e-21	GTEQILVQSS VDTSSSSSIGNKLISVLSIFG AIGFLLGISY
PY07198	227	5.84e-21	EAEQILAQSS EDTSSSSSIGNKLISVLSIFG AIGFLLGISY
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PY05719	263	1.02e-20	ITKKCSAQMS GVTSSSSSIANKLFI VLSIFG AIGIFLGISY
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PY05244	265	3.50e-20	NPVQDSGQKI EATSSSSSITNKLIPVLSIIV AIPIFLGIFY
PY04979	234	3.50e-20	RAVQRLEQIS EDASSSSSITNKLFTVLSIFA AIAFFLGISY
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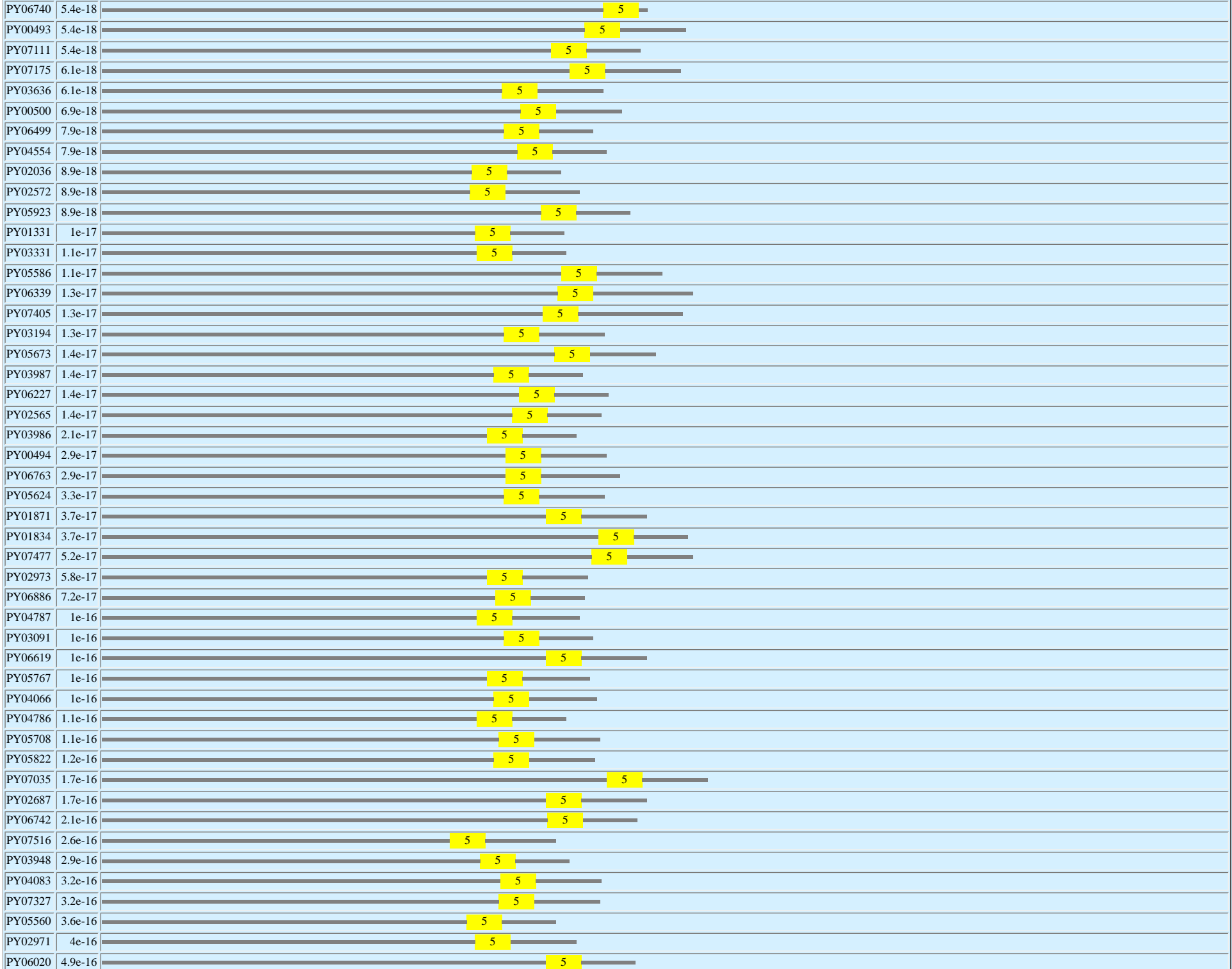
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 PY03948 225 2.91e-16 SLVCIDSSSL **VACFR**SS**VTKN**LIIP**IAIFV** AASILLGISY
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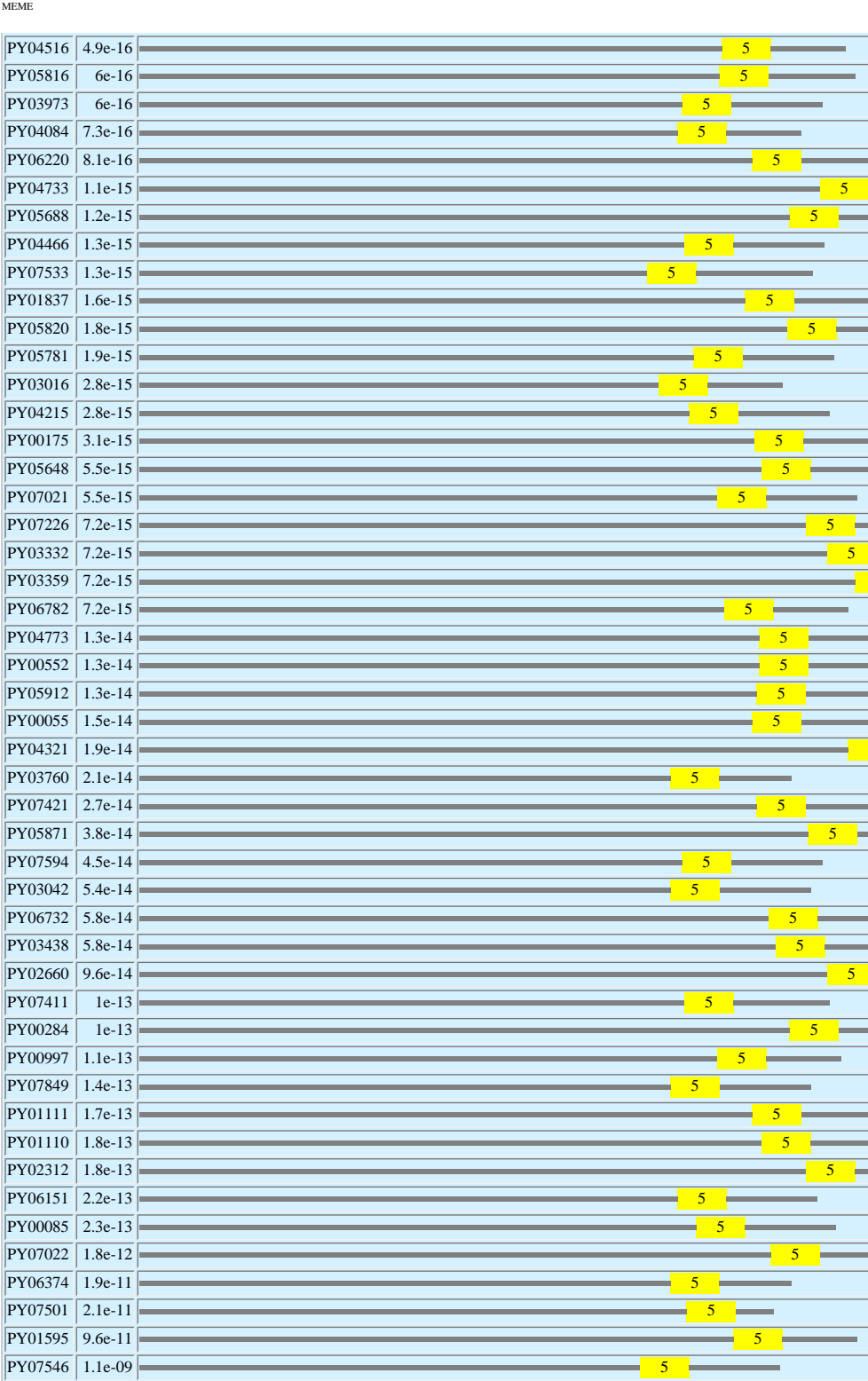
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Motif 5 block diagrams

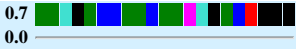








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Multilevel consensus sequence

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SKI T N L K Y

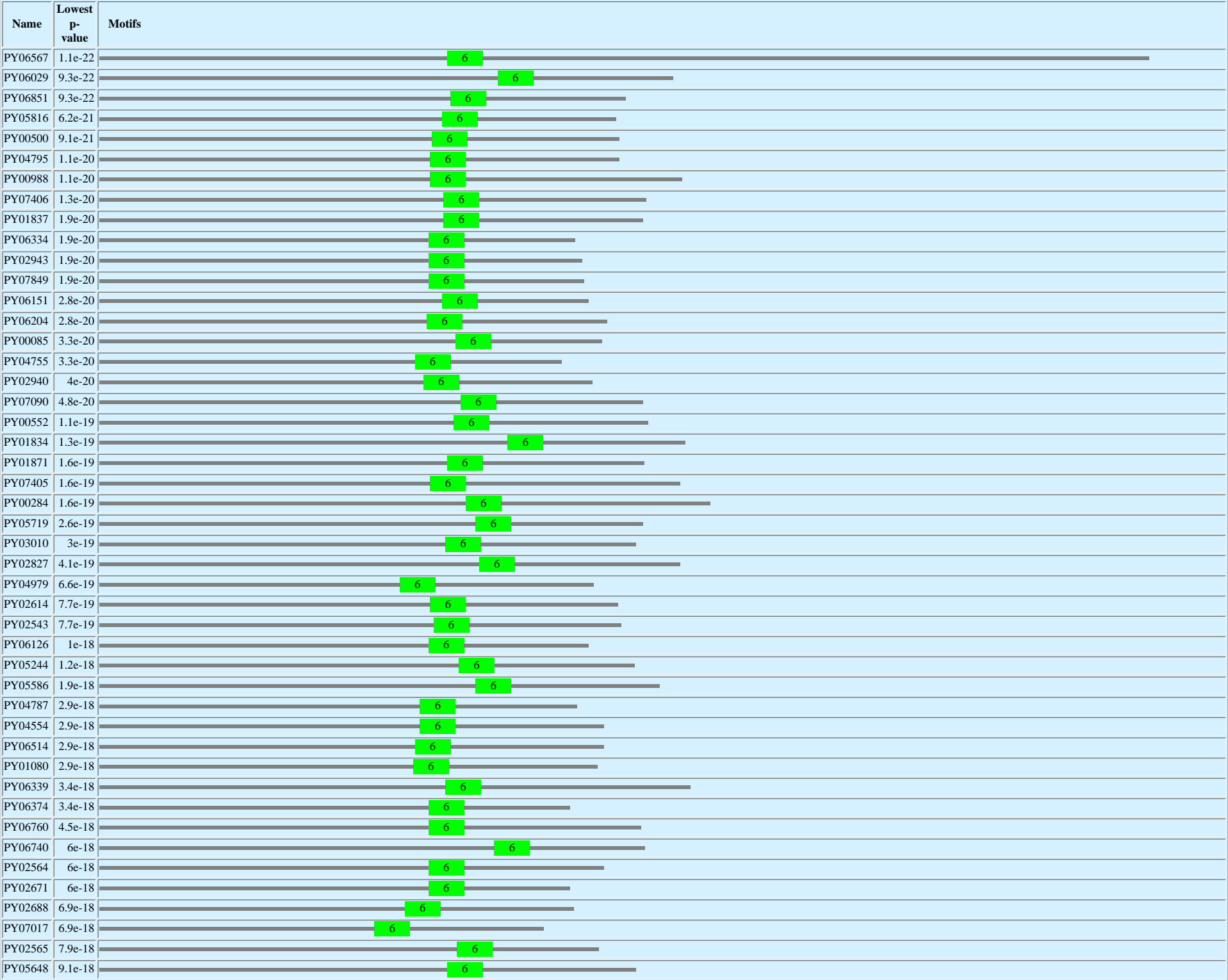
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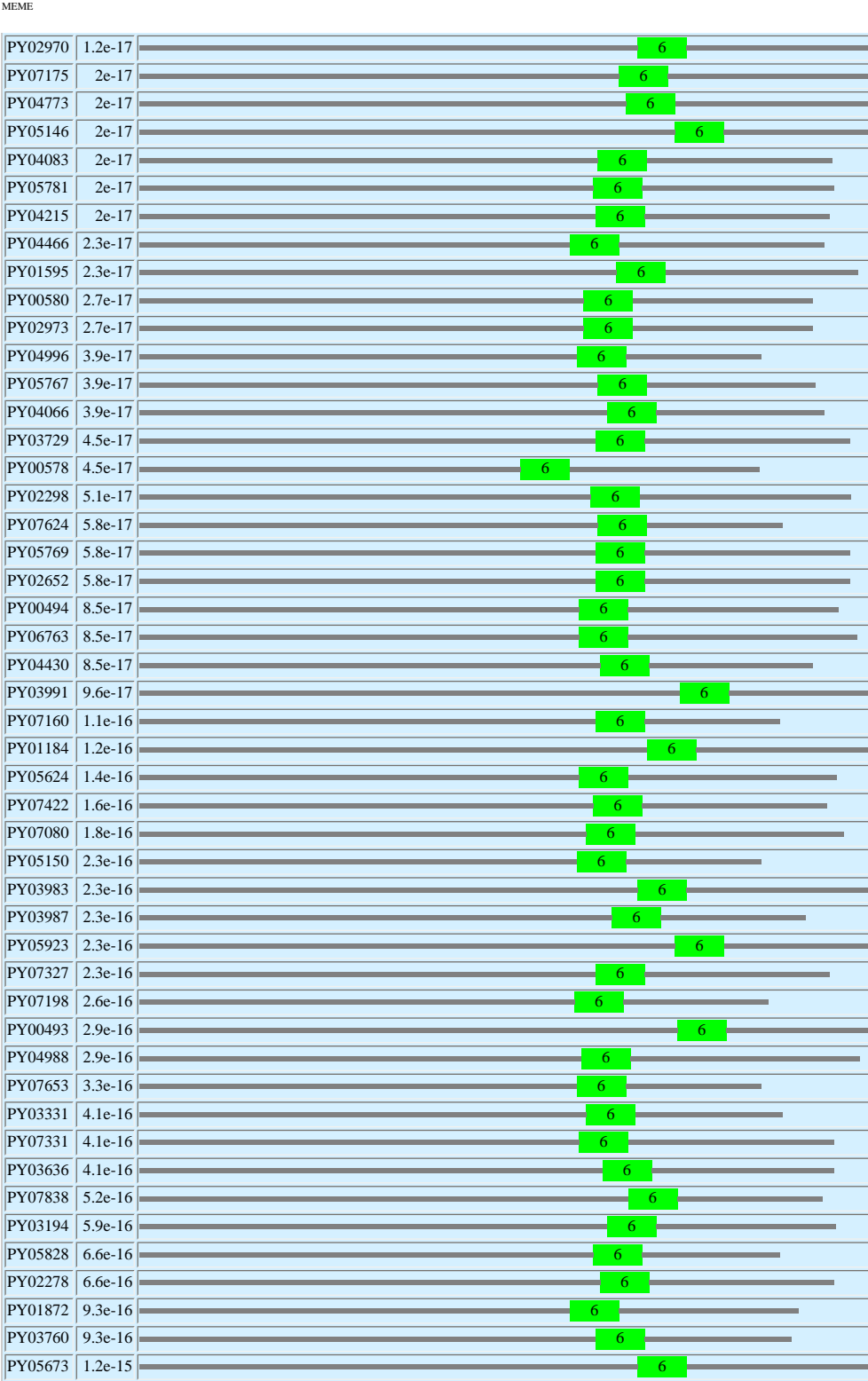
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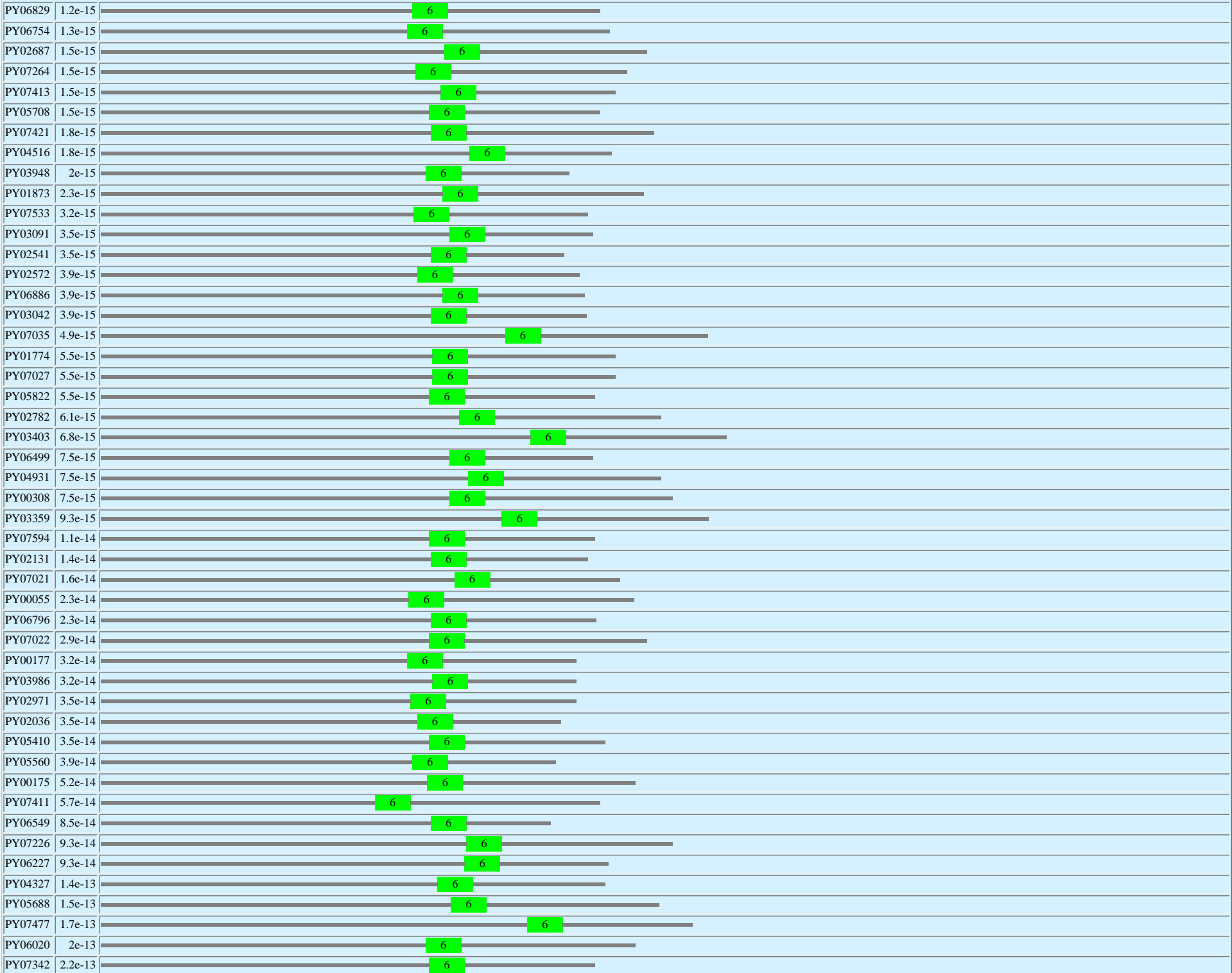
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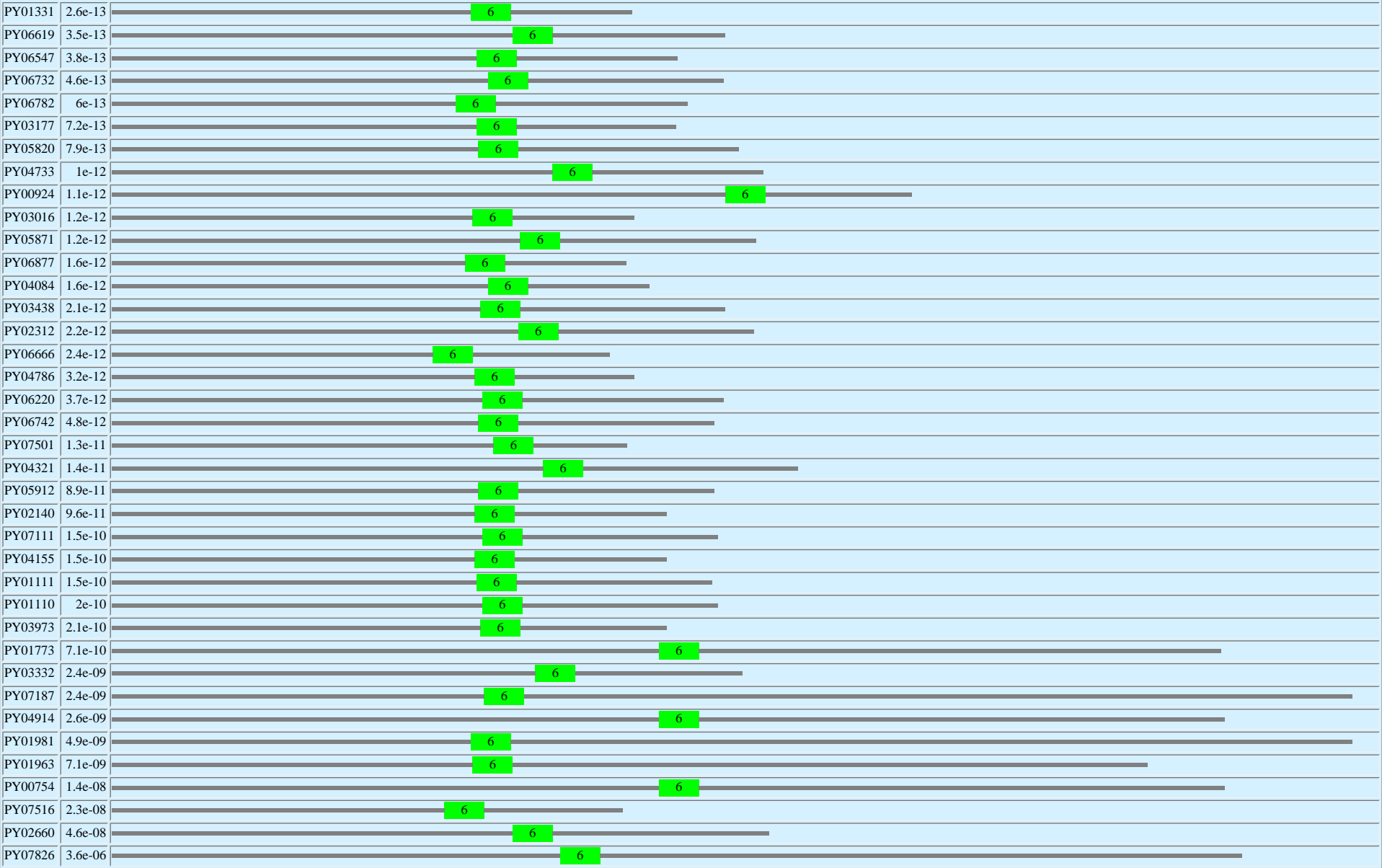
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PY00055	183	2.34e-14	LNDNDNNIDD	SSYNKVLL	LSNYYNNFEKYR	VPYNKQMKRP	
PY06796	196	2.34e-14	LNEYSNNTDD	NSYKQLLFALST	DYGNLKNKS	TNITSLPEIT	
PY07022	195	2.87e-14	LFNDNNDADG	NSYNQILSILSNDY	DYFRNSY	VNSNIQNTFP	
PY00177	182	3.17e-14	ELNNKYKDKG	TP	SKILSALSTDYNNIKGKR	KDYQTLPEIT	
PY03986	197	3.17e-14	VKNALDITKE	NSYSQLWLSLSKDY	KNFEGNY	NSIWCNNVPS	
PY02971	184	3.51e-14	ELNNDISKIEG	TARSKILSALST	DYNKLKSKY	NGFPSIPETS	
PY02036	188	3.51e-14	LKNALDINKG	SSYYELLSSLSIDY	KNFENSY	NTLWCSKGPP	
PY05410	195	3.51e-14	GLNEGYNIES	SARIKIL	FLLSTDYNNLKEKC	NNVQPRSFPP	
PY05560	185	3.87e-14	VKNVFDITKG	NSYLQLWLILSNDY	KNFESNY	NSNWCSHVPS	
PY00175	194	5.21e-14	LNDNDNNIDD	SSYSKVL	SVLSKCYDNFGDYT	LLNNTPIINRP	
PY07411	163	5.75e-14	LFNDNDNIEG	SSYNKVLRVLS	RXYNNFEKGR	SYNNISLYLP	
PY06549	196	8.49e-14	LDVDSNNTSD	SSRKQILSALST	DYGTLSKR	NDITFLPEIT	
PY07226	217	9.35e-14	LFNDNDDNEG	SSYNKILSALSSDY	YNFEKNK	VDGKSIEFPS	
PY06227	216	9.35e-14	VKNVFDITKG	SSYLQLWLSLSKDY	KDFESNY	NSFLCNTGPP	
PY04327	200	1.37e-13	DLNESYNIED	TARRKIL	FLLTIDYNNLINKC	KSFTSLPDIT	
PY05688	208	1.51e-13	LFDDDDNNNGD	NSYNKVLLVLSNWYNN	FGKGT	RYNNTSINLT	
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PY06020	193	2.00e-13	LLNDNNNIHD	SSYSKVLLVLSNYYNN	FEKSK	ALRSISIDL	
PY07342	195	2.19e-13	NLNNKYKTEG	AS	LQILSALLTIDYNNLNKEY	SDIPSFSEIE	
PY01331	190	2.64e-13	HKNALDITKG	DSYSQLWFSLLKDY	KIFENKY	NSLECSSISP	
PY06619	212	3.49e-13	LKKDLNITTN	NSYNDVLC	TLSDYD	FKNKF	KNSKCSDTSF
PY06547	193	3.82e-13	EINDYYNIEN	SPYSQILS	FLLSTDYNTFTTKN	ASKIDNSKKF	
PY06732	199	4.59e-13	LFDDDDNNIDN	NSYNKVLLVLSKYYNN	FEIGR	SYKNISIDRP	
PY06782	182	6.02e-13	LFNDNDNNEG	NSYNKILSALSSDY	YNFEKNK	VDGKPINLPS	
PY03177	193	7.20e-13	SLNNDRNIED	TVRNKIL	FVLSYND	FKNNC	NRNGVKCKDF
PY05820	194	7.87e-13	KFINDTDIEN	SSYNKILSTLSNDY	TGYGKQT	IYLHLRNKLP	
PY04733	233	1.03e-12	LKQDTSFTKN	SYDSQIF	STLLKDYDGLKREC	EVALSPQTEE	
PY00924	324	1.12e-12	ELKDGSNAEG	IPNNQIL	FALLTIDYNNKLNKKC	SNIPSFSELA	
PY03016	191	1.22e-12	VIGGSSVDKH	SSYYKLLYNLSNDY	BEYFKNKY	NSEECNNFSS	
PY05871	216	1.22e-12	FNDVDNNTDN	STYSKVL	LVMSNYYNNFEKGR	NFNSAEIKFP	
PY06877	187	1.59e-12	LKNTFDITKG	VSYSQLWSNL	IDYMIFENAY	NSFRCNNVSS	
PY04084	199	1.59e-12	HKNALDITKG	DSYSQLWFSLLKDY	KFFENEY	NRVKCGNVPS	
PY03438	195	2.06e-12	KLLNDNDTED	SSYNKILSALSNDY	TEYGYKT	IHSHVKKLHP	
PY02312	215	2.25e-12	NFDDDDNNNDG	NSYNKVLLVLSKYYD	NIGKGR	KFDNTEINLP	
PY06666	170	2.45e-12	IEFDHNIGEN	IRYL	VLINLLTIDYDNLKKNC	EHPFSTPDIK	
PY04786	192	3.16e-12	LKNSFDITKG	YLYSQLWSSLSIDY	IFESKY	NAECNNVSPL	
PY06220	196	3.74e-12	LNEDSNYEN	SSYNKIMSILSNDY	NDLKGQV	KSYDMPTLQT	
PY06742	194	4.81e-12	LLDGDNNITDN	SIYSKVLLVLSKYYNN	FESILR	VTIDTEMARP	
PY07501	202	1.28e-11	IIIDHNIGEN	IRYFYVLINLLTIDYDNLKKKC		GIFPSTPDIK	
PY04321	228	1.39e-11	FNDNDNNVEG	SSYKQILSRLSS	EYTYFRNSY	VKSIKQGTIP	
PY05912	194	8.90e-11	FLDDENNIDN	SSYDKVLCIF	SKYYNDFGKGT	RFSNISTDRP	
PY02140	192	9.59e-11	DSNITKNGLY	RKILSILY	TLSDYDNFKKKN	NNSSSLPSIK	
PY07111	196	1.49e-10	LLNDNNNDDG	STYNKVLLVL	RYYYMFGKGT	NLYSKTKVFP	
PY04155	192	1.49e-10	DSNITKNGLY	RKILSILY	TLSDYDNLKKKN	NNSSSLPSIK	
PY01111	193	1.49e-10	LFDDDDNDEG	NSYNKILNVLSIYYNN	LVKGN	KFNNTSVDRP	
PY01110	196	2.00e-10	LFDDNDNNEG	NSFNKILNVLSNYYNN	MGKGT	RFNNTSINRP	
PY03973	195	2.15e-10	FNIDHNITKD	KPYF	ALITILNGYDNLKNEC	EDFPSTPDIT	
PY01773	289	7.13e-10	FSDMFTNIGN	LYKNV	STLKDIFYGKLKNSA	DNTISYVNEL	
PY03332	224	2.39e-09	FNDIDNNIDN	SSYDKVLRV	VFFKYND	DFGKGT	RFSNISKDRP
PY07187	197	2.39e-09	VEKKKKFFED	EYYCNVLV	TLQNAQQFKNDN	NIQKKLPEIM	
PY04914	289	2.55e-09	FSSMFTNIKD	SLYENVLP	TLTDFYGKFKNFA	GNTINHVNKE	
PY01981	190	4.87e-09	VLKKKKFFED	EYYCNVLV	TLKNAYEKFKKDN	DTKKNFPEII	
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PY00754	289	1.41e-08	FSKMFTNIGN	SLYENVLP	TLTDFYGKLKNFA	GNTINHVNKE	
PY07516	176	2.28e-08	IGTEKNTKCK	CLENAGE	FLSNDYKNFKQ	EY	SAKCSSISPL
PY02660	212	4.62e-08	INENFNDTNS	KIFKR	VLSVVSNDYD	IKRTL	EVEFVRKQIP
PY07826	237	3.56e-06	KTCKQLGEEA	TTSSK	VLSVKVQDASNGKKDL	KKVEDTSKHI	

Motif 6 block diagrams









Motif 6 in BLOCKS format

to BLOCKS multiple alignment processor.

Motif 6 position-specific scoring matrix

PN MOTIF 7 width = 29 sites = 139 llr = 5235 E-value = 1.9e-1408

Category	Information Content (bits)
1	7.1
2	6.4
3	5.7
4	5.0
5	4.3
6	3.6
7	2.8
8	2.1
9	1.4
10	0.7
11	0.0
12	0.7
13	1.4
14	2.1
15	2.8
16	3.6

Multilevel

consensus

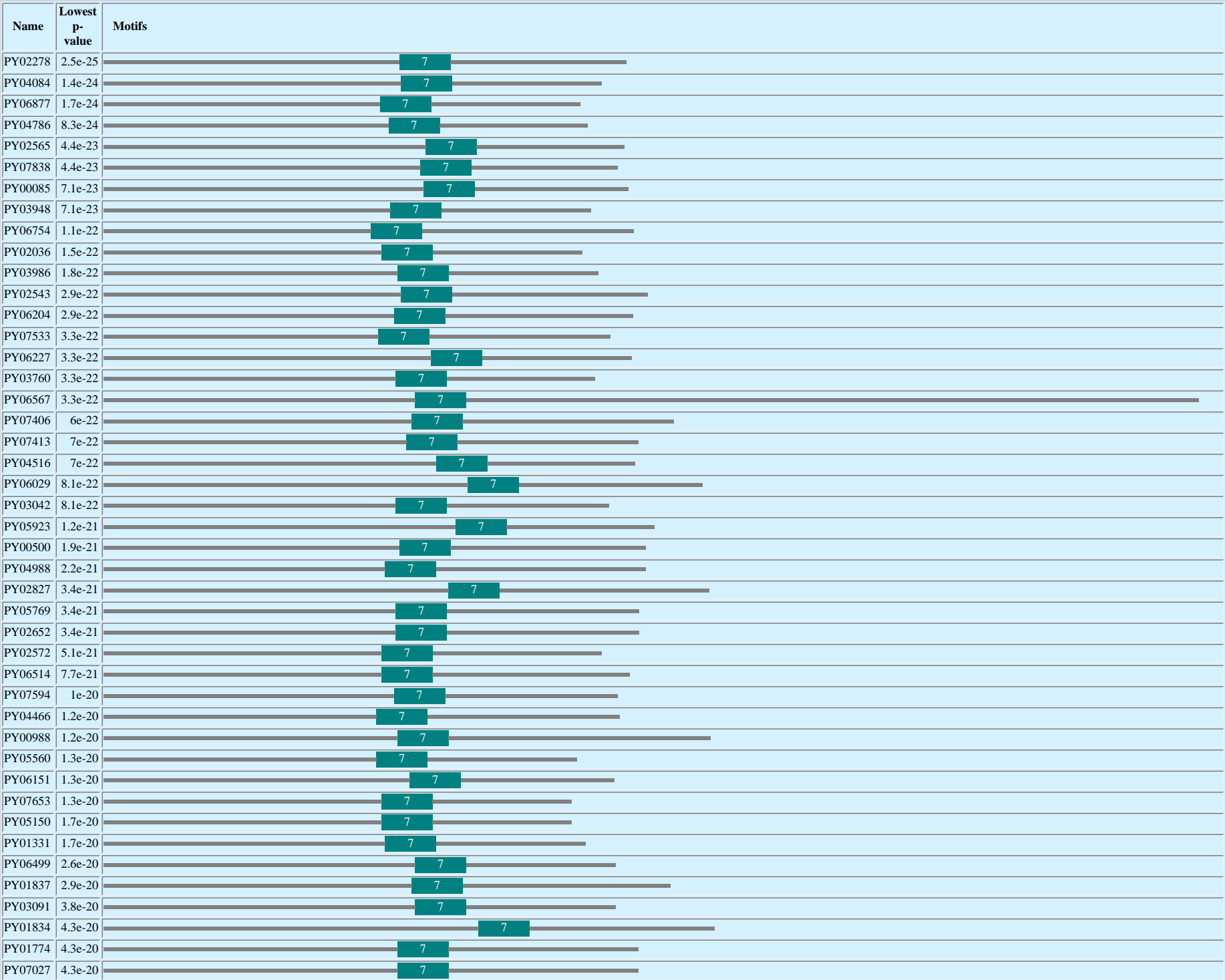
sequence

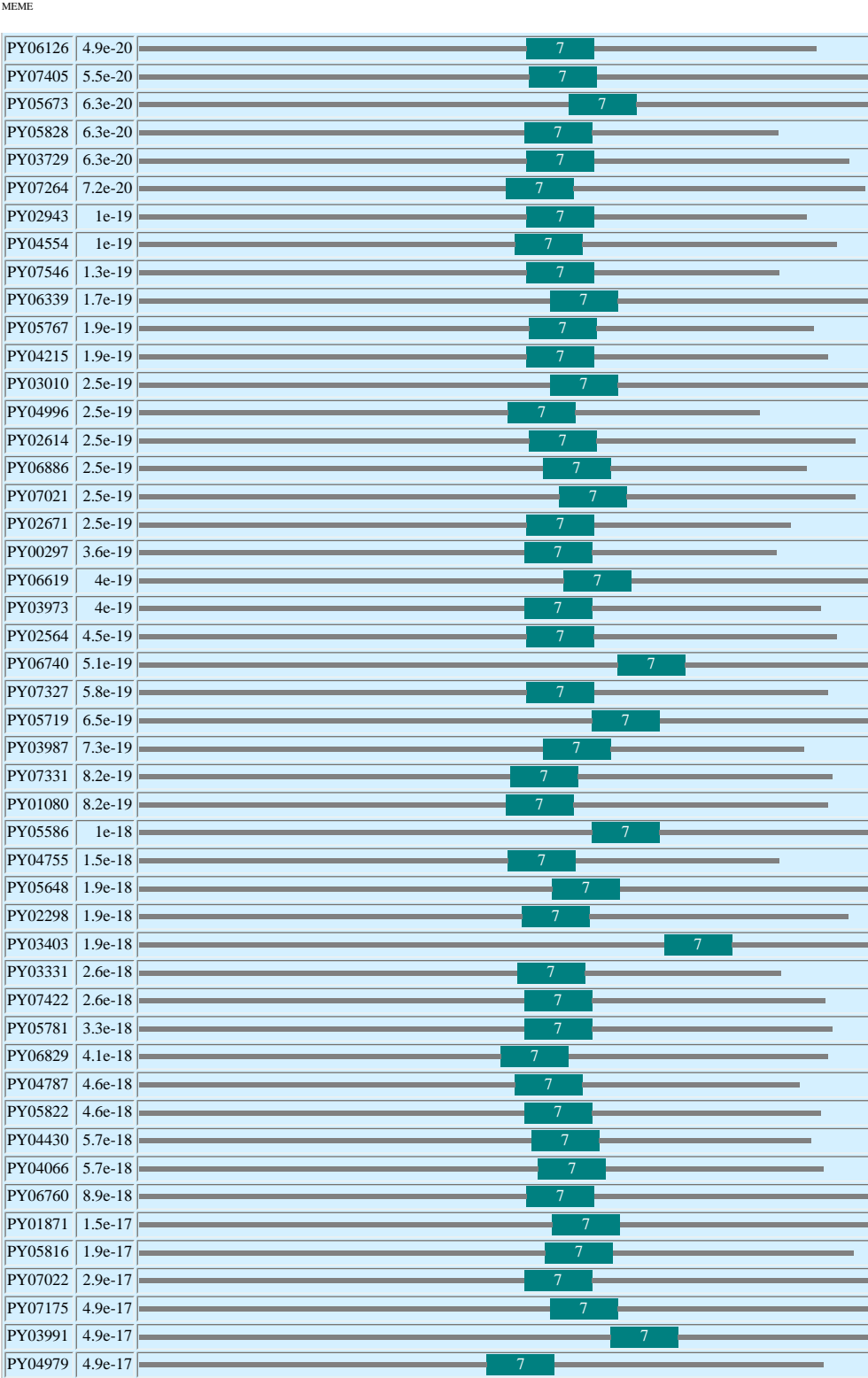
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PY04084	170	1.40e-24	NVYSELDPK TQCKTCL ENAG EFFFEYK EKNALDITKG DSYSQLWFSL
PY06877	158	1.68e-24	MYSELDPEKN TECKKCL ENAG EFFFEYK EKLKNTFDITKG VSYSQLWSNL
PY04786	163	8.26e-24	MYSEFGPEKN TQCKTCL ENAG REFFFEYK EKLKNSFDTIKG YLYSQLWSSL
PY02565	184	4.37e-23	NMYSEIGAED YQCNKCL ENAG BLFEKYK EKLKNDLDINK SSYYQLLSSL
PY07838	181	4.37e-23	NMYIEVDAEN YQCNKCL ENAG EFFFEKCEK VKNVPDITKG SSYLQLWSSL
PY00085	183	7.06e-23	DICIGVDEDR SNCDN YLEKAK EF FAKKYDEL NEDYNNKGK SPYNQLLSTL
PY03948	164	7.06e-23	NMYSEIIAED YQCNKCL ENAG EFFFEKCEK VKNVAFDINKG SSYLQLWSSL
PY06754	153	1.13e-22	MDGELDPKKK YQCNKCL ESARE FFFEKCEK VKNVAFDINKG SSYLQLLSSL
PY02036	159	1.55e-22	NMYSEIBLYN YQCNKCL ENAG BLFEKYK EKLKNALDINKG SSYYELLSSL

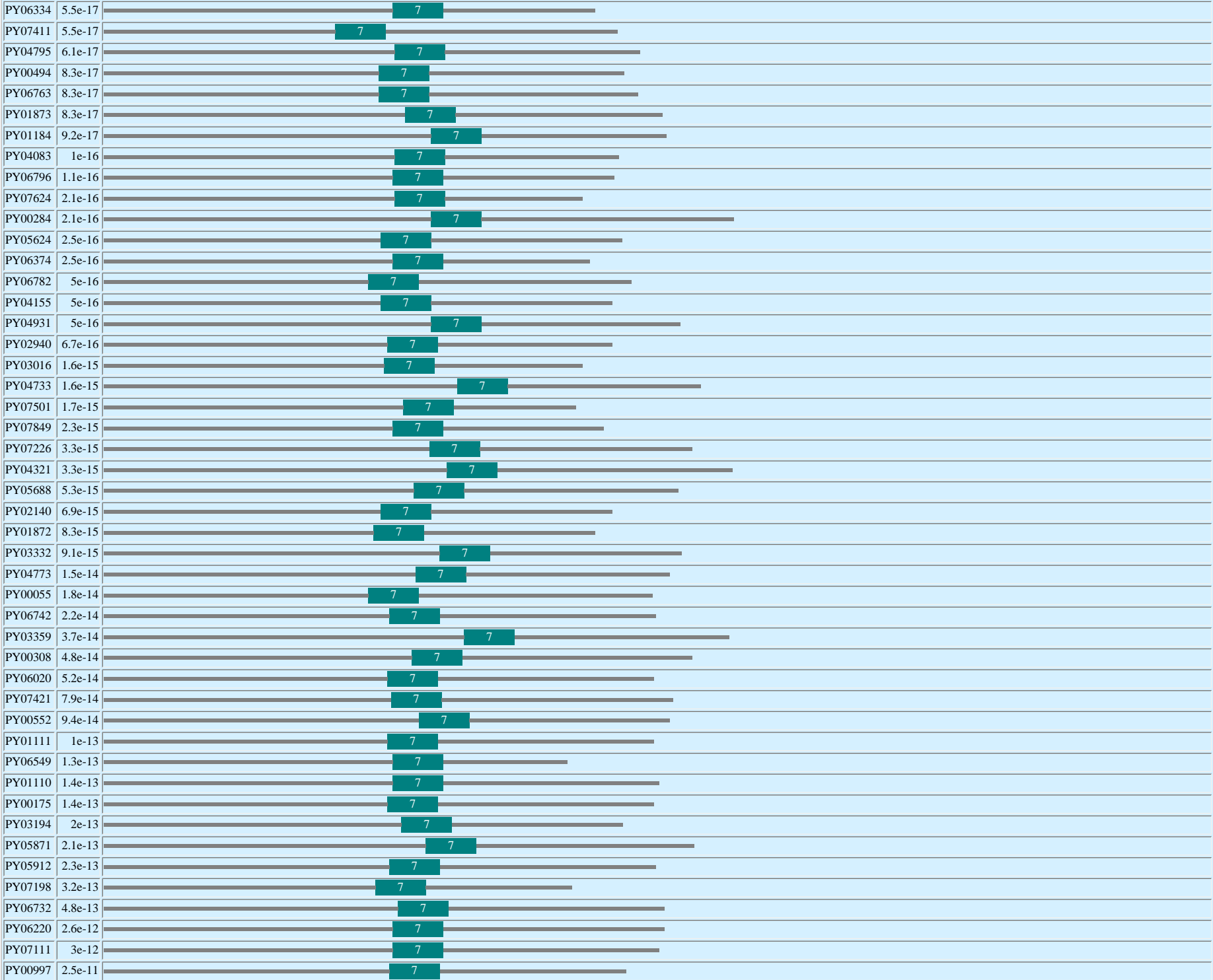
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PY06204	166	2.85e-22	NMYNKFNDST	SDCTKCLNDANEFAKKYKELNDDSSITND	SSYNKLLCTL
PY07533	157	3.32e-22	MYSEFDPEEN	TECKTCLNAGELFEKYEKLKNALDINKG	SSYYELLSSL
PY06227	187	3.32e-22	NMYSETDVVN	YKCNKCLNAGEFFKECKVKNVFDITKG	SSYLQLWLSL
PY03760	167	3.32e-22	NMHTSIDANI	SNCSKYLEKAQEFAKKYDDLNEYNNTKD	SLYNKILSTL
PY06567	178	3.32e-22	SMYTEFNANT	PDCTKYLEKANQFVVKYANLNENSNTDGG	SSYRQVLCTL
PY07406	176	6.02e-22	EIYTEFDENT	SNCTNYSETAKEFVKQYEBELYKDDNITKD	SSYSKVLCTL
PY07413	173	6.98e-22	NVYSELDPKK	TQCKTCLNAAEEFFEKLEKLNDFDITEE	DSYSQLWLSL
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PY05923	201	1.25e-21	MYSEFDPEKS	TECKTCLTAGEFFKECKVKNAFDINKG	SSYLQLWSSL
PY00500	169	1.92e-21	NMYNEFNANE	PNCDKCLEKANEFVGKYEKINEDPNNTNS	NSYRQVLCTL
PY04988	161	2.21e-21	NMYNGFNDNM	TDCKKCLNYADEFVKKYNELNGDSSITND	SSCNKLLCTL
PY02827	197	3.37e-21	TMHTEFNENE	PDCNNYLEKAREFVKKYEKLNGNYNNNEY	SSYIQLSTL
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PY06514	159	7.70e-21	TMHIEFDETN	PQCGKYLNDAKEFVKKYDELKDKDKITEG	NPYYKLLSTL
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PY04466	156	1.15e-20	EMYAEFDOKT	PYCTKSSSENANKFVKKYNELNKD SITGN	ISYNQLLSTL
PY00988	168	1.15e-20	EMYTEFNENT	SNCTKCSGKADQFVKKYEKLKNDDSSIAKN	SSYSKVLCTL
PY05560	156	1.32e-20	CNMYSEIDSI	SDCKTCLNAGEFFKECEIVKNVFDITKG	NSYLQLWLIL
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PY07653	159	1.32e-20	EMYTEFDEDN	PKCEKYLEGDNFVKKYDQLKKDS DINKD	DSYSQIFSIL
PY05150	159	1.72e-20	EMYTEFDEDN	PKCEKYLEGDNFVKKYDQLKKDS DINED	DAYSQIFSIL
PY01331	161	1.72e-20	NVYNELDPEK	KQCKTCLESGGEFFEKYEKKNALDITKG	DSYSQLWFSL
PY06499	178	2.55e-20	CNMYSERDAI	TQCKICLENAGEFFKECKVKNALDFNKG	SSYLQLWSTL
PY01837	176	2.91e-20	IVHTEFDANK	PECTKYIENAKNFVKYNELNNGSDITES	SPYYQVLSTL
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PY01774	168	4.29e-20	NMYTGLNEKN	PDCTKYITTANEFVKKYQELYGDS DNTGS	SLYRKILHNL
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PY06126	167	4.88e-20	NMYNGFDTKK	TDCKNYLKDAKNFVKKYDELNEDYNNKGK	SPYNQLLSTL
PY07405	168	5.55e-20	EMYTEYDENK	ENCTNYSKAKKEFVEQYEEKLYEDYNSNND	SSYKQVLCTL
PY05673	185	6.30e-20	EDGGDDDDEN	KDCKKYS EDNNEFFKKYKELENDSDITGN	NSYKQLLLNL
PY05828	166	6.30e-20	DICTGVNEEK	KNCDNYLEKAEFFVEKYDELNEDYYNGIN	SPYNQLLSTL
PY03729	167	6.30e-20	EMYAEFDNT	PYCSNCSKNAKQFVNKYKEMNENS DITNN	SSYNELLSTL
PY07264	158	7.15e-20	KMNNEIGTKK	IQCNTCLKNAGEFFYEQYEEKLNLD DINKG	SSYFQLWLSL
PY02943	167	1.04e-19	MMYIEFDSEN	ADCKNYLEKAKKFVEIYDELNEYYNNGKG	SPYNQLLSTL
PY04554	162	1.04e-19	EMYSAFGGNT	SNCKKCSKNFNQFVEKYKELNENYNNTDN	SPYRKILFTL
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PY03010	177	2.48e-19	EMYSEYGENT	LNCKKCSNKAIQFVEKYKELNGDSNNNDG	SPYKKILSTL
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PY02614	168	2.48e-19	EMYTDFDENT	SNCAKCS EKAFQFVENYKKLNEYFNNTNG	SSYNKILSTL
PY06886	174	2.48e-19	NMYSEISVED	YEFNKCLNARELFEKYEKLKNALDINKG	SSYKLLSSL
PY07021	181	2.48e-19	NMYTGPDENK	ANCENISEKARQFVEKYKELNVNCDITGN	SSCSKILYTL
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PY07327	167	5.76e-19	NMYIDLGENN	ADCTKYISNANEFVKKYQELYGDSNNNDN	SLYRQILYNL
PY05719	195	6.48e-19	EMYSEFDGST	SNCTKYS GKA DN FVKYKLNKNSNNTDD	SSYKQILCTL
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PY01080	158	8.21e-19	EMHAEFDNNS	QYCAKCS ENASN FVKYKEMNENS DITSN	GSYKQLLSTL
PY05586	195	1.04e-18	MMHFEFDKES	FKCNKY LKEAKEFVEKYEYLKKNYSITEN	SPYYKLLSTL
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PY02298 165 1.85e-18 EMYTNFNETR **SNCSLCSE**NANKFVSKY**KEMNKNSNITSN** SSYKQLLSTL
PY03403 226 1.85e-18 KLYNELGDEN **KNCKNYLDDNN**EFFKKY**KDLNEDTNITKN** SYYNEILSTL
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PY07422 166 2.61e-18 NMYEFGNNGN **KKCKXYLDDDD**NEFFKKY**KELKNDSDITDR** SPYKEILSAL
PY05781 166 3.27e-18 MMYIEFDDES **SNCKQCL**KYANAF**IEKYK**KLTKDSN**ITDN** SSYNQILSNL
PY06829 156 4.10e-18 CEMYTIDERN **LHSTKCS**ENANKFVSKY**KEMNKNSNITSN** SSCKQLLSTL
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PY04083 168 1.01e-16 NMYFYLDENN **P**DK**TKYIS**NA**KQF**VNNY**KELYG**DSS**NNDN** SLYRQILSNL
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PY02940 164 6.69e-16 EMYTKVDEDN **NNC**NNY**LKDDNQ**FT**KIYK**ELN**NGD**V**TND** SSYNQLLSTL
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PY04733 204 1.58e-15 KLYNGLGDGN **KNCKNYL**EDNS**EFF**KKY**NDL**KQD**TSFTKN** SYDSQIFSTL
PY07501 173 1.74e-15 DIYIDLDTNN **S**DTQD**SEKANQ**FV**EY**TK**KI**I**IDNIGEN** IRYFYVLINL
PY07849 167 2.30e-15 HIYIEVNEES **LS**CY**RFS**E**IAN**D**FAK**KY**DEL**NENY**NGKD** SPYNQLLSTL
PY07226 188 3.33e-15 CNMYINIGKK **KG**GG**YLEYAK**NFAN**EYK**KL**FND**DD**DNNEG** SSYNKILSAL
PY04321 198 3.33e-15 KMYNDISKIS **NNNKKY**IEYANK**F**AD**EYK**KL**FND**DN**DNV**E GSSYKQILSR
PY05688 179 5.27e-15 LCDMNTSYKN **NNSSKIS**ED**GNK**FV**DEYQ**KL**FDD**NN**NGD** NSYNKVLVL
PY02140 160 6.92e-15 NIHVTDAGHV **P**NC**EQCA**KAAN**GF**VTNY**EGVIS**DS**SNITKN** GLYRKILSIL
PY01872 156 8.28e-15 CIMYGRVAQN **KKDDK**LLND**AKD**FV**KKYQ**ELN**RY**SNN**TDV** SSYRQILSSL
PY03332 194 9.06e-15 LCNMHTAYTK **DKS**ND**FS**ENAN**QF**VDRY**KEL**FND**IDNNID** NSSYDKVLRV
PY04773 180 1.54e-14 KMHDEFNEKT **LE**CSKY**LG**YAN**DIVG**FK**KL**NEN**SSATR**N SSSYQIWSL
PY00055 153 1.84e-14 LCKMNTSYTN **GKS**ND**FS**EDANK**FVYEY**EKL**LND**DN**DNID** DSSYNKVLH
PY06742 165 2.19e-14 LCSMDTAYTK **NKDS**E**FMQ**DANK**FV**EKY**QEL**L**DG**DN**NTDN** SIYSKVLVL
PY03359 208 3.69e-14 CDVISNADKQ **NVR**KTY**LEYA**E**EFV**TEY**QKL**INNN**NTGT**E DSSYSQLLST
PY00308 178 4.77e-14 YLYYVFHDES **LN**CKQ**NLD**LANK**FVQ**N**VEK**L**IED**SN**NTVD** ISYNKLLSTL
PY06020 164 5.19e-14 LCNMNTAYTK **Q**NN**SDFS**KY**SNK**FVEY**EYEL**LND**NNNI** ID SSSYKVLVL
PY07421 166 7.92e-14 CNVINNAGKK **DV**SKTY**LEYA**DE**FVTEYQ**KL**IN**NN**NTDTE** NSSYSQLLST
PY00552 182 9.36e-14 KLHTEYDEDN **LK**CTEY**LG**YAN**DIVG**FN**EL**NRN**SSISGD** SSSYQVWSTL
PY01111 164 1.02e-13 LCNMYTAYNN **Q**NS**SQVS**EY**AKTF**AD**GYTEL**FDD**DN**DE**G** NSYNKILNVL
PY06549 167 1.31e-13 CSMYGNFATN **IN**KD**S**LLNNAN**EF**VIKY**QEL**D**VD**SN**NTSD** SSRKQILSAL
PY01110 167 1.42e-13 LCNMYTSYDN **NNSSQ**AS**EAK**KFANGY**TEL**F**D**ND**DNNEG** NSFNKILNVL
PY00175 164 1.42e-13 LCNMNTAYNG **K**NS**S**K**ILDY**ANK**FGE**EY**GK**LLND**DN**DN**ID** DSSYSKVLV
PY03194 172 1.97e-13 CKMHGNTVQN **QKDD**TL**S**NN**NAID**FV**KKYQ**ELN**KVYGI**GE KPYNKIFSTL
PY05871 186 2.14e-13 LCEMNTAYTT **NKSGD**FSQ**VN**KFVEY**EYK**LFND**VD**NN**TD** NSTYSKVLV
PY05912 165 2.32e-13 LCNMYNAYKN **AKS**ND**FS**E**ANK**FVSKY**KE**FLD**DENNID**N SSYDKVLCIF
PY07198 157 3.20e-13 EMYTKIDENK **KK**CNNY**LND**DN**EF**L**DEYR**KL**LTD**SD**TDNG** NSYYNQILST
PY06732 170 4.78e-13 LCDMNSYTN **E**NN**S**KY**SEV**N**KFA**VEY**QNL**FDD**DN**DN**ID**N NSYNKVLVL
PY06220 167 2.62e-12 CNMHINVGKK **DM**FNTY**SECS**N**KFI**KIY**NEL**NED**SNY**NEN SSYNKIMSIL
PY07111 167 3.05e-12 LCNMNSDIEK **KSS**DD**ILKANN**FLN**IYK**EL**LND**NNN**DDG** STYNKVLVL
PY00997 165 2.49e-11 LCNMYTAYTK **K**NN**SDFS**KY**TN**K**F**DKY**KEL**FDD**DKNIKD** SIRFNDMPID

Motif 7 block diagrams







sequence					Q
NAME	START	P-VALUE	SITES		
PY06829	280	1.81e-18	LFGFRKRFQK	QKLREKIKNIKKRMN	Q
PY06619	308	2.68e-18	LFGFRKRVQK	QYLREKIKNIKKRMN	H
PY07594	277	2.68e-18	LFGFRKRVQK	QYLREKIKNIKKRMN	K
PY05673	313	5.25e-18	LFGFRKRFFK	QQIREKIKNIKKRMN	H
PY01080	280	5.25e-18	LFGFRKRFFK	QQIREKIKNIKKRMN	H
PY04773	310	6.41e-18	LFILRKRSQK	QLREKCLKNIKKRMN	H
PY00552	310	6.41e-18	LFVLRKRAQK	QLREKCLKNIKKRMN	H
PY04795	293	7.80e-18	LFGFRKRFQK	QKLREKCLKNIKKRMN	Q
PY05146	336	7.80e-18	LFGFRKRFQK	QKLREKCLKNIKKRMN	H
PY07021	292	7.80e-18	LFGFRKRFQK	QKLREKCLKNIKKRMN	Q
PY00494	284	7.80e-18	LFGFRKRFQK	QKLREKCLKNIKKRMN	H
PY04466	278	1.96e-17	LFGFRKRFQK	QKLREKIKNIKKKMN	Q
PY02971	266	1.96e-17	LFGFRKRFQK	QKLREKIKNIKKKMN	H
PY02688	266	1.96e-17	LFGFRKRFQK	QKLREKIKNIKKKMN	Q
PY03194	283	1.96e-17	LFGFRKRFQK	QKLREKIKNIKKKMN	R
PY07546	259	1.96e-17	LFGFRKRFQK	QKLREKIKNIKKKMN	H
PY06514	284	1.96e-17	LFGFRKRFQK	QKLREKIKNIKKKMN	H
PY02940	277	1.96e-17	LFGFRKRFQK	QKLREKIKNIKKKMN	Q
PY01872	267	2.62e-17	LFGFRKRAQK	QYLREKIKNIKKKMN	H
PY07477	335	2.62e-17	LFGFRKRVQK	QYLREKIKNIKKKMN	H
PY07406	309	2.62e-17	LFGFRKRSQX	QYLREKIKNIKKKMN	H
PY02973	273	2.62e-17	LFGFRKRGGK	QYLREKIKNIKKKMN	H
PY07342	277	2.62e-17	LFGFRKRAQK	QYLREKIKNIKKKMN	R
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PY02782	316	3.33e-17	LFGFRKRFQK	QKLREKCLKNVKKRMN	H
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PY06151	275	3.33e-17	LFGFRKRFQK	QKLREKCLKNVKKRMN	H
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PY07027	289	3.77e-17	LFGFRKRFFK	QQIREKIKNIKKKMN	Q
PY07331	282	3.77e-17	LFGFRKRFFK	QQIREKIKNIKKKMN	Q
PY05781	282	3.77e-17	LFGFRKRFFK	QQIREKIKNIKKKMN	R
PY02564	284	3.77e-17	LFGFRKRFFK	QQIREKIKNIKKKMN	Q
PY00924	406	5.73e-17	LFGFRKRFQK	QKLREKCLKNIKKKMN	H
PY05624	283	5.73e-17	LFGFRKRFQK	QKLREKCLKNIKKKMN	Q
PY04083	281	8.99e-17	LFGFRKRVQK	QKLREKIKNIKKRIN	H
PY05769	289	8.99e-17	LFGFRKRFQK	QKLREKIKNIKKRIN	H
PY02298	289	8.99e-17	LFGFRKRFQK	QKLREKIKNIKKRIN	H
PY04327	283	9.61e-17	LFGFRKRVQK	QYLREKIKKIKKRMN	Q
PY03636	282	9.61e-17	LFGFRKRAQK	QYLREKIKKIKKRMN	H
PY05708	280	1.10e-16	LFGFRKRAQK	QYIREKIKNIKKKMN	R
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PY04979	278	1.65e-16	LFGFRKRFFK	QQIREKIKNIKKRIN	H
PY03729	289	2.02e-16	LFGFRKRFQK	QQIREKIKNIKKRMA	H
PY07624	260	2.27e-16	LFGFRKRFQK	QKLREKIKNIMKKMI	H
PY00085	283	2.27e-16	LFGFRKRFQK	QKLREKIKNIMKKMI	H
PY04996	251	2.27e-16	LFGFRKRFQK	QKLREKIKNIMKKMI	H
PY05150	251	2.27e-16	LFGFRKRFQK	QKLREKIKNIMKKMI	H
PY05586	317	2.27e-16	LFGFRKRFQK	QKLREKCLKNIKKRIN	H
PY07160	259	2.27e-16	LFGFRKRFQK	QKLREKIKNIMKKMI	H
PY04755	259	2.27e-16	LFGFRKRFQK	QKLREKIKNIMKKMI	H
PY02541	259	2.27e-16	LFGFRKRFQK	QKLREKIKNIMKKMI	H
PY02614	292	2.27e-16	LFGLRKRFQK	QKLREKCLKNIKKRIN	H
PY02543	294	2.27e-16	LFGFRKRFQK	QKLREKCLKNIKKRIN	H
PY07849	272	2.27e-16	LFGFRKRFQK	QKLREKIKNIMKKMI	H
PY06567	607	2.27e-16	LFGFRKRFQK	QKLREKCLKNIKKRIN	H
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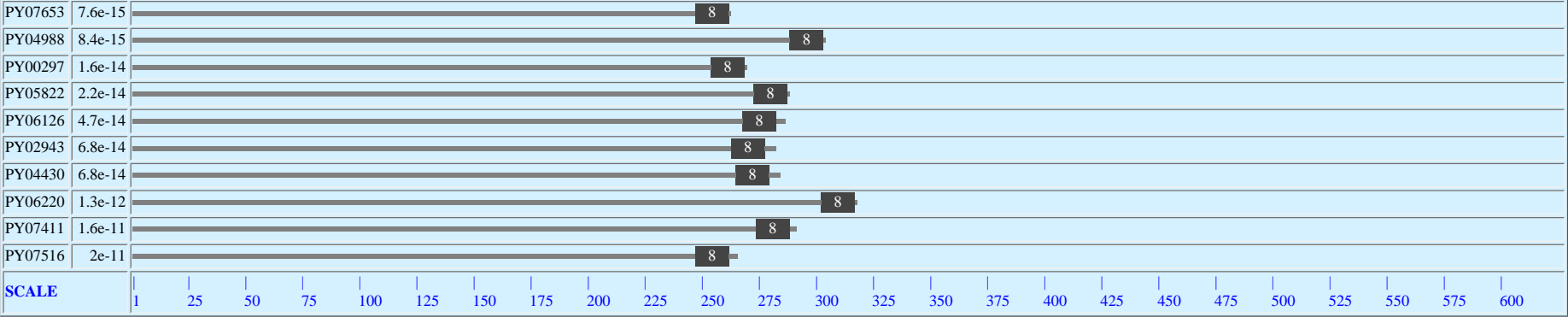
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PY03991	314	3.89e-16	LFGFRKRAQK	QYLR E KIKKKKKMN	H
PY06796	278	3.89e-16	LFGFRKRAQK	QYLR E KIKKKKKMN	H
PY04215	280	4.64e-16	LFGFRKR F QK	Q K X R EKIKNIKKRMN	H
PY05719	307	6.88e-16	LFGFRKR F KK	QQ I R E KIKNIKKKIN	Q
PY00500	293	6.88e-16	LFGFRKR F KK	QQ I R E KIKNIKKKIN	Q
PY02278	282	6.88e-16	LFGFRKR F QK	Q K L R E K I K T I KKKMN	H
PY07327	280	7.61e-16	LFG L RKRAQX	QY I R E KIKNIKKKMI	H
PY03973	277	1.81e-15	LFGFRKRGQK	QYLR E KIK I IKKKMN	H
PY03177	282	1.99e-15	LFGFRKR F KK	QQ I K E KIKNIKKRMN	H
PY02652	289	4.63e-15	LFGFRKR F QK	Q K L R E K I K N X KKRIN	H
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PY07653	251	7.63e-15	LFGFRKRAQK	QYLR E TIKNIKKKMI	H
PY04988	293	8.41e-15	LFGFRKR F KK	QQ I R E KIKKKKKIN	N
PY00297	258	1.63e-14	LFGFRKR F QK	Q K L R E X LKNIKKRIN	H
PY05822	277	2.19e-14	LFGFRKR F KK	QQ I K E KIKNIKKRIN	N
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PY02943	267	6.75e-14	LLGFRKRSQK	Q C L R E R IKNIKKKLI	INKLF
PY04430	269	6.75e-14	LLGFRKRSQK	Q C L R E R IKNIKKKLI	INKLF
PY06220	307	1.34e-12	LFGFRKRSQK	QYLR E KIKNIKN K T D	H
PY07411	278	1.57e-11	LFGFRKRSQK	Q N L R E K L K I R R K WM	INI
PY07516	251	1.96e-11	LFGFRKRSQK	Q H L R E K L K N S D Y SMN	SNND

Motif 8 block diagrams







[Motif 8 in BLOCKS format](#)

to [BLOCKS multiple alignment processor](#).

[Motif 8 position-specific scoring matrix](#)

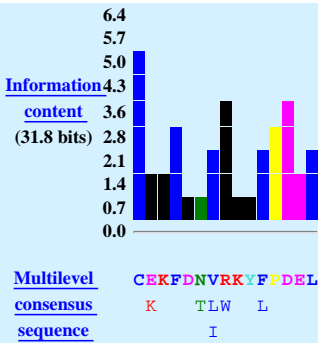
[Motif 8 position-specific probability matrix](#)

Time 1666.73 secs.

MOTIF 9 width = 15 sites = 144 llr = 3171 E-value = 3.0e-736

[Simplified pos.-specific probability matrix](#)

A : : 1 : : : : : : : :
C a : : : : : : : : : :
D : 1 : : 3 : : 2 1 1 : 1 9 2 :
E : 3 1 : 1 1 : : 2 : : : : 5 :
F : : 8 : 1 1 : : 1 6 : : : :
G : 2 : : : : : : : : : : 1 :
H : : : : : : : : : : : : : :
I : : : 2 : : 2 : : 1 1 : : : :
K : 2 3 : 2 : : 3 1 : : : 1 :
L : : : : : 1 3 : : : 3 : : : 7
M : : : : : : : : : : : : : :
N : : 1 : 2 3 : : 2 1 : : : : :
P : : : : : : : : : : 6 : : 1
Q : : 1 : 1 : : : : : : : : :
R : : 2 : : : 4 1 : : : : : :
S : 1 1 : : 1 : : : 1 : 1 : 1
T : : : : : 2 : : 1 : : : : 1 :
V : : : : : 4 : : : : : 1 : : :
W : : : : : : 3 : 1 : : : : :
Y : : : : : : : 3 : : : : : :
bits 7.1



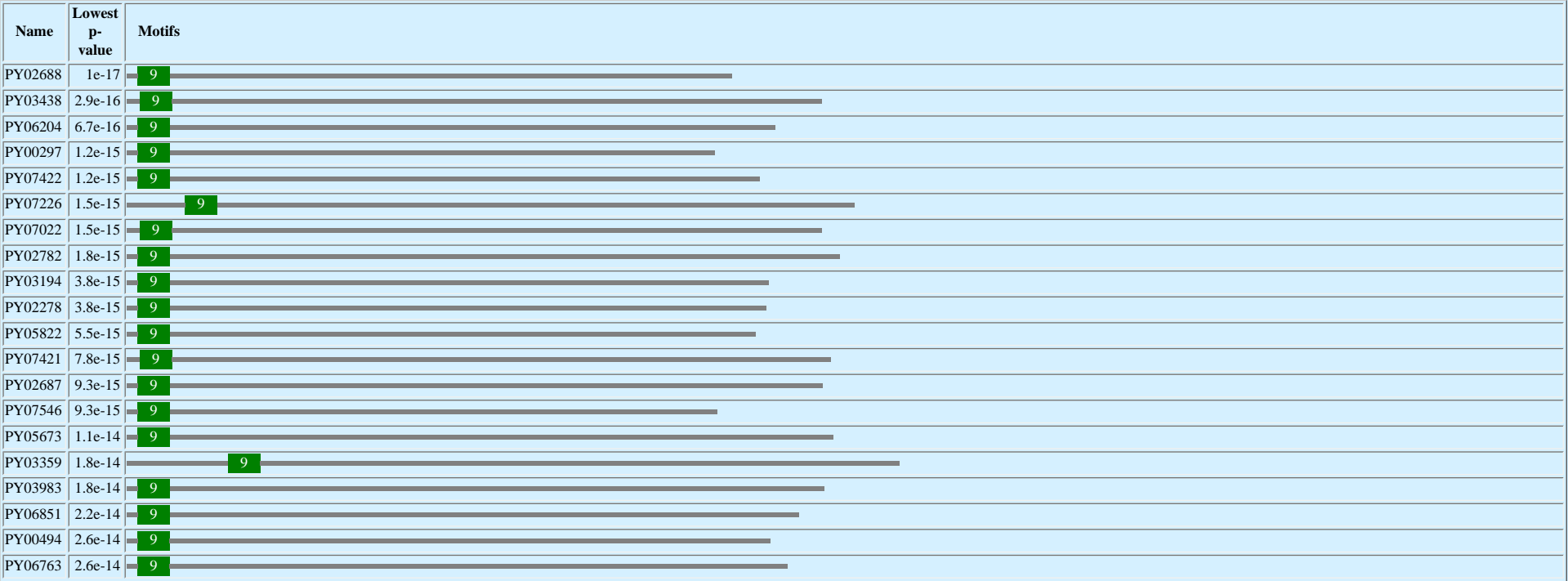
NAME	START	P-VALUE	SITES
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PY03438	7	2.92e-16	MLTSKM CGEFDTLWRFFPDEL NESGEYYISG
PY06204	6	6.69e-16	MNKKI CEKFEENVWKKFPDEL NNGEYEFKDN
PY00297	6	1.22e-15	MNKEV CKRFKNVWKKDFPDEL NNSGKYQFKN
PY07422	6	1.22e-15	MDKKV CEKFEINIWEAFDEL NSSGEYKFKD
PY07226	28	1.49e-15	DQSKYLQFKA CGEFDTFWRFFPDEL KTSGEYDFKV
PY07022	7	1.49e-15	MLTSKM CGEFDTFWRFFPDEL NESGSYNFKK
PY02782	6	1.81e-15	MNKEV CEKFKNIWKWLPDEL IEGKYQFNDN
PY03194	6	3.82e-15	MDDTL CGQFDFFVRKYLDEL SKEAEFELND
PY02278	6	3.82e-15	MDKNL CEKFEENVWEDFPDTL TDDGKYQLKD
PY05822	6	5.49e-15	MNKEV CKRFENVWKKFPDTL SNEKYQFKGD
PY07421	7	7.84e-15	MLTSKM CDQFDTIWKAFDEL NSGEYDFKGG
PY02687	6	9.35e-15	MNKEV CKRFKNVWDAFPDTL DSSGKYQFND
PY07546	6	9.35e-15	MNKEV CKRFKNVWEDFPDTL NNGDYQFNID
PY05673	6	1.11e-14	MNKEV CKRFKNVWNAFPDTL DNSKNYQFND
PY03359	48	1.85e-14	NINLYNLYRD CGEFGTIWKFFDEL TNSGEYNFRV
PY03983	6	1.85e-14	MDNRL CGRFDALRNLYLPDDL NNSATLDFHK
PY06851	6	2.18e-14	MDNRL CGRFDTLRNLYLPDLS GKNALELKT
PY00494	6	2.58e-14	MDKDV CEKFEENVWKKFPDKL TSDNEYDFKK
PY06763	6	2.58e-14	MDKDV CEKFEENVWKKFPDKL TSDNEYDFKK
PY02541	7	3.04e-14	MLTSTV CEEFDSLREKFPDEL DDPVKYMSTS
PY07080	6	3.57e-14	MDDTL CGKFDSLREYLPDDL KDSKLDIFYDN
PY01871	6	5.76e-14	MDKQV CERFKNVREWISDEL IGGKYQFKDD
PY04327	6	5.76e-14	MDDTL CGKFDFLREYLPDDL GATTKLDLND
PY04083	6	6.74e-14	MNKKV CEKFEENVWGKFPDKL TSDNKYQFKT
PY07327	5	6.74e-14	MNKK CEKFEENVWGKFPDKL TSDNKYQFKT
PY02970	6	7.87e-14	MDKEV CKRFKNIWDTFPDEL DNTENYKFKD
PY07406	6	7.87e-14	MNKEV CKRFKNIWDTFPDEL GDSGNYQFKD
PY07111	7	9.18e-14	MAISKV CRDFTFWRFFPDEL KDSGESKEYD
PY07594	6	1.07e-13	MDAEI CKKFQNVREWLPDEL IEGNYKNIDD
PY01184	6	1.07e-13	MDYKL CGRFDTLKKYLPDEL NKSLSYDFHG
PY06796	6	1.24e-13	MKDDI CSKFDLLRKYLPDEL NVNAEIDLEN
PY00493	24	1.45e-13	KVYWNKNKVI CKRFENVRKWISDEL IDGNYQFNDN
PY02298	6	1.68e-13	MDKNV CEKFEENVWKKFPDVL NNGEYEFKDN
PY07175	6	2.25e-13	MDKQV CKRFKNVREWISDEL IKGNDQFNDF
PY06567	6	2.25e-13	MDYLL CIRFGTLRNLYFPDEL GKSTDYDFHK
PY03332	36	2.61e-13	QCERDKDSIH CQKFDNFRRLFPDEL KDSKQYDFNN
PY04321	37	3.01e-13	NFYNKIIMDI CGEFESIWKIFPDDL NASGEYSVGG
PY01834	38	3.48e-13	YSFHNIFRY YGFRFNTLRAFYDEL DKSPSIKPHN
PY01595	6	3.48e-13	MDKIL CEQFDTLRNLYLPDDS SNSTTSDINK
PY02940	10	3.48e-13	MNKKVVYAF CEKFDNVWEVFSDTL TSDKKYEFKT
PY07477	59	4.01e-13	NKAIDLTTIK CGKFDLLRIYLPDEL SKDGTLELKE
PY01111	7	4.01e-13	MSISKV CGDFATFWKFFPDEL KESKYDFKST
PY05648	6	4.62e-13	MNKEV CKRFENVRGWISDEL NEGKYQFN DY
PY05688	21	4.62e-13	KMDVIINMKG CNNFDTLWKIFPDEL NNSGNYNFPN
PY05912	7	4.62e-13	MAINKV CQKFEFNRRLFPDEL KNSKQYDFNN
PY06220	7	4.62e-13	MLTSKM CGEFESIWKLPDDL NASGEYSISG

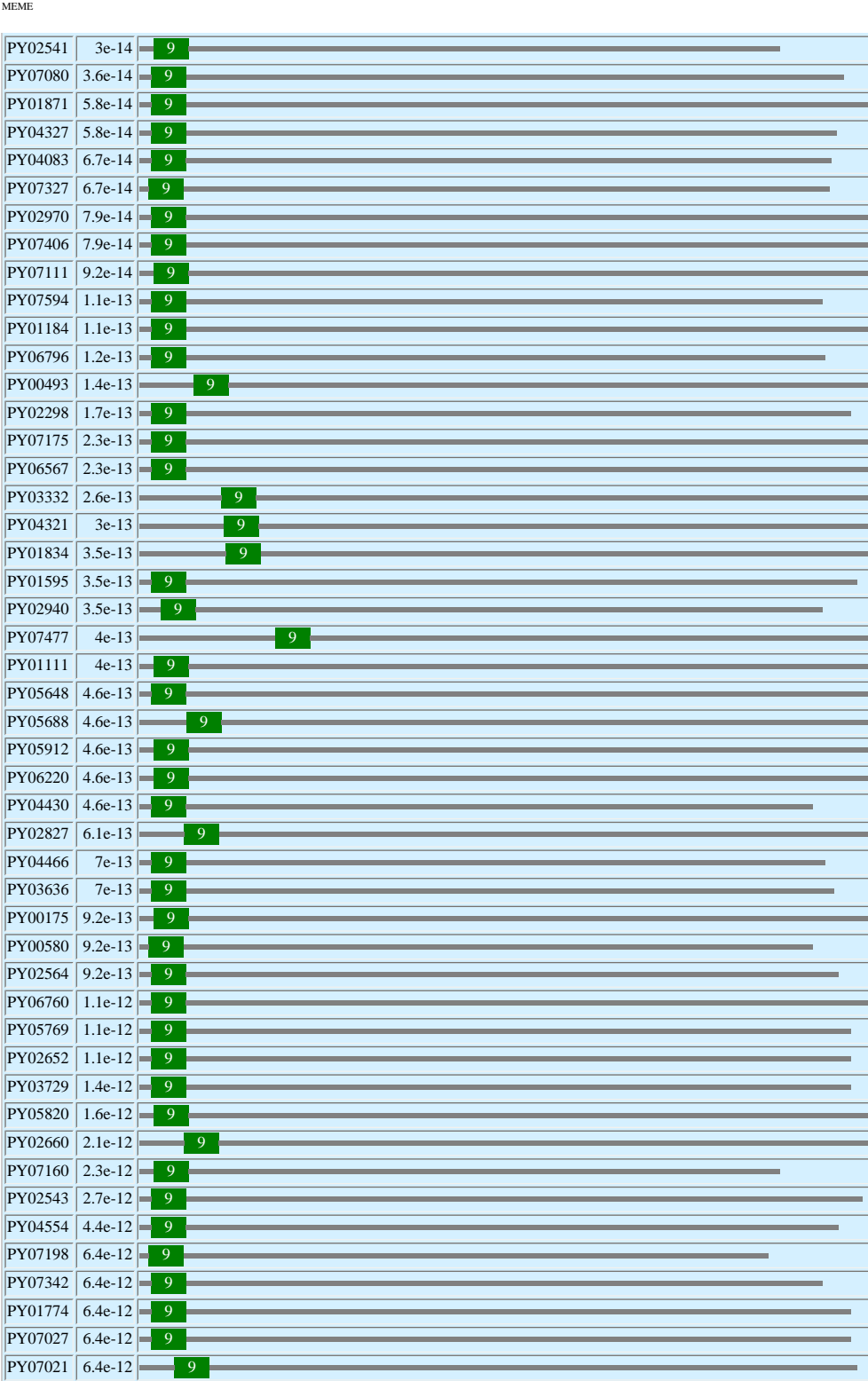
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PY02827	20	6.11e-13	MVQLCYHLLS	CIRFNTLRRYYPDGL	NISTNYDFHS
PY04466	6	7.01e-13	MNKEV	CKKFTSIWEFFPDTL	DKGEYKFNDN
PY03636	6	7.01e-13	MDDFL	CRKFALLRTYLPDEL	NTNVTSDFEE
PY00175	7	9.22e-13	MSINNV	CEEFDTFWKFFRDGL	KEYKYDFNNG
PY00580	5	9.22e-13	MDDI	CGKFVVLARNYLPDEL	DGHATLELKD
PY02564	6	9.22e-13	MNKQV	CEKFENLWNGFPDKL	ENNKYHEFKN
PY06760	6	1.06e-12	MNRQM	CEKFQEVVRNSLPDQL	NSSGYYQFKD
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PY02652	6	1.06e-12	MNKQV	CEKFRSIWDKFPDTL	DSNNNYQFKE
PY03729	6	1.38e-12	MNKEV	CKKFTSIWDDFFPDTL	DKGEYKFNDN
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PY02660	20	2.05e-12	EYFIKKDNKI	CSTFDTLRRFFPDKL	KSSGEYNFKG
PY07160	7	2.34e-12	MLTSTV	CKEFDLSLRKIPDEL	DDPVNYMSTS
PY02543	6	2.66e-12	MNKQV	CESFLSVWDAPDKL	TKTNEYHEFN
PY04554	6	4.43e-12	MDKKL	CQQFKSVLTYFPDEL	ENGENYNFVY
PY07198	5	6.44e-12	MNKE	CEKFKSIWDDFFSDTL	DEGEYKFKEK
PY07342	6	6.44e-12	MDDSI	CSNFDILRKYLDEL	NKSGELELET
PY01774	6	6.44e-12	MNKQV	CEKFENLWDKFSDKL	DSNNNYIFQK
PY07027	6	6.44e-12	MNKQV	CEKFENLWDKFSDKL	DSNNNYIFQK
PY07021	16	6.44e-12	IMFSFTFYDI	CSNFLLVARNWFPDKL	GSNGDYQFKD
PY07035	42	8.23e-12	VLNNPLFKEV	CKRFKNVWDDFADKL	DSSGKYQFND
PY06020	6	9.30e-12	MADRL	CNQFDTLRKIFRDEL	KDSKQYDFER
PY05244	6	9.30e-12	MDYRL	CARFDKLRSYLPDEL	NISTSNDIHS
PY02312	28	9.30e-12	DQNKYLEFKA	CQKFDDNFRKLFDEL	KDSKEYDFNN
PY02614	6	1.05e-11	MDKDV	SEKFENLWDDKFPDEL	KNGEYEFKDN
PY03177	6	1.05e-11	MEKDI	CPKFDDLLRTYLPDNL	GDVAKSELKE
PY03042	6	1.05e-11	MDAEI	CKNFDLLVREKFPDQL	NSDGKYTFKD
PY07090	6	1.18e-11	MDNQI	CLRFPDKLRNYLPDDL	NISKGSDIHS
PY06151	13	1.33e-11	NYIFFKFIK	CNKFFALRNWFPDQL	SRDGNVQFKS
PY07624	7	1.50e-11	MLTSTV	CEEFDLSLRKDFSDEW	DDSGNYIFTS
PY00997	7	1.50e-11	MAISKM	CDDFDTFRKFFRDEL	KSGEYDFNS
PY00924	135	1.69e-11	AKYIIKLYNK	CGKIDLLRMCLPDEL	GTPATBELNT
PY06029	32	1.69e-11	IYPTTIKVYI	CGRFDDKLSNYLPDEL	SKSTNNNDINS
PY05410	6	1.69e-11	MDDTL	CGKIDLVVKYLPDNS	ENPTTLDFYD
PY00284	13	1.69e-11	YPLVYPFFNK	CEKFDELKKSLPDEL	KRHASVDFNK
PY07405	6	1.90e-11	MNKEV	CEKFQEVVRNSISDEL	KNGGIPEFGD
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PY03010	14	2.40e-11	LNLQIKNKTP	SQ_FKSVWGYFPDEL	TNDGNYNFLF
PY02973	5	2.40e-11	MDDI	CSNFVVLARNYLPDEL	DSTPQSELKN
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PY06339	6	5.96e-11	MNKTV	CKKFQDVVRNAISDEL	DSTGNYQFIN
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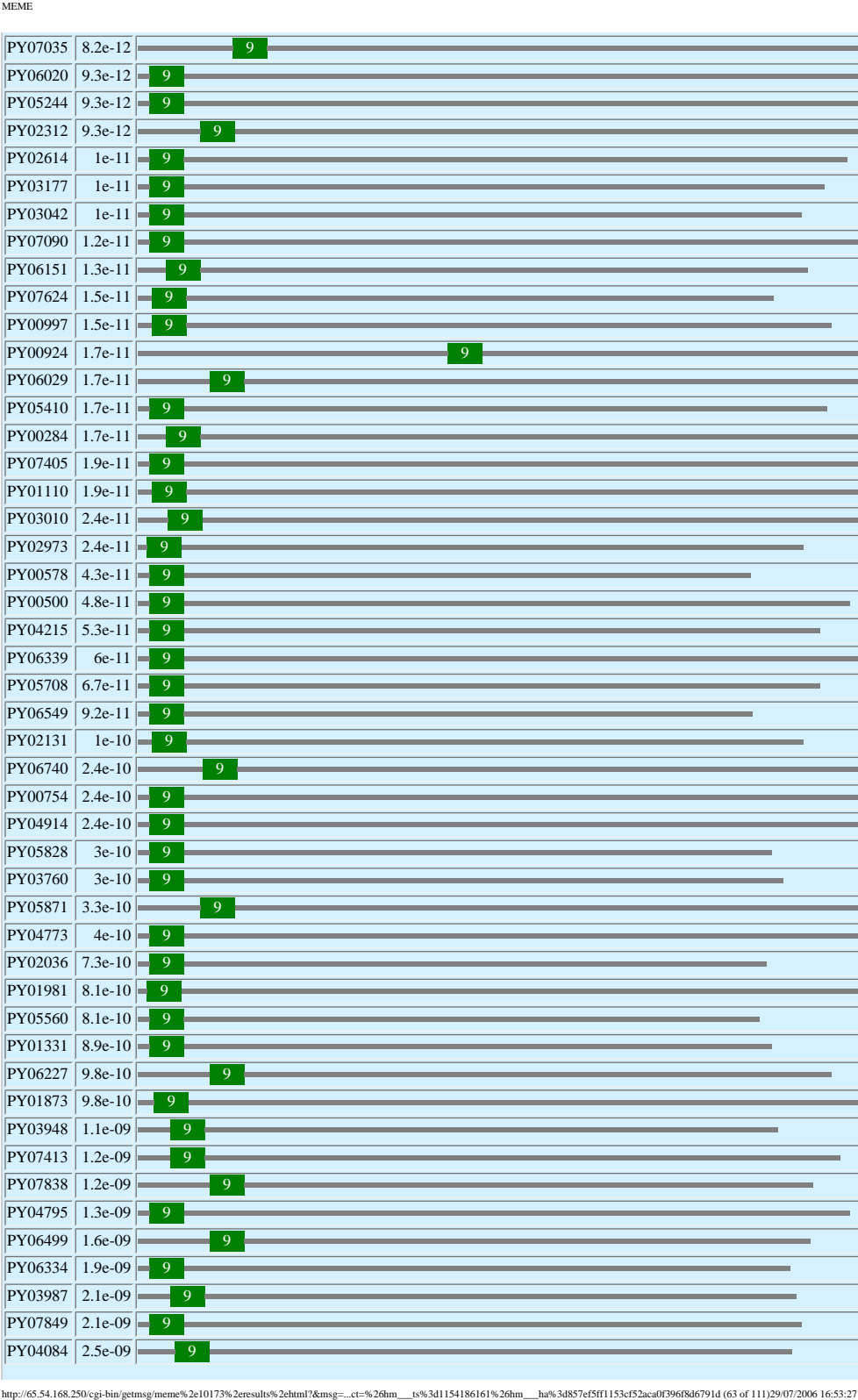
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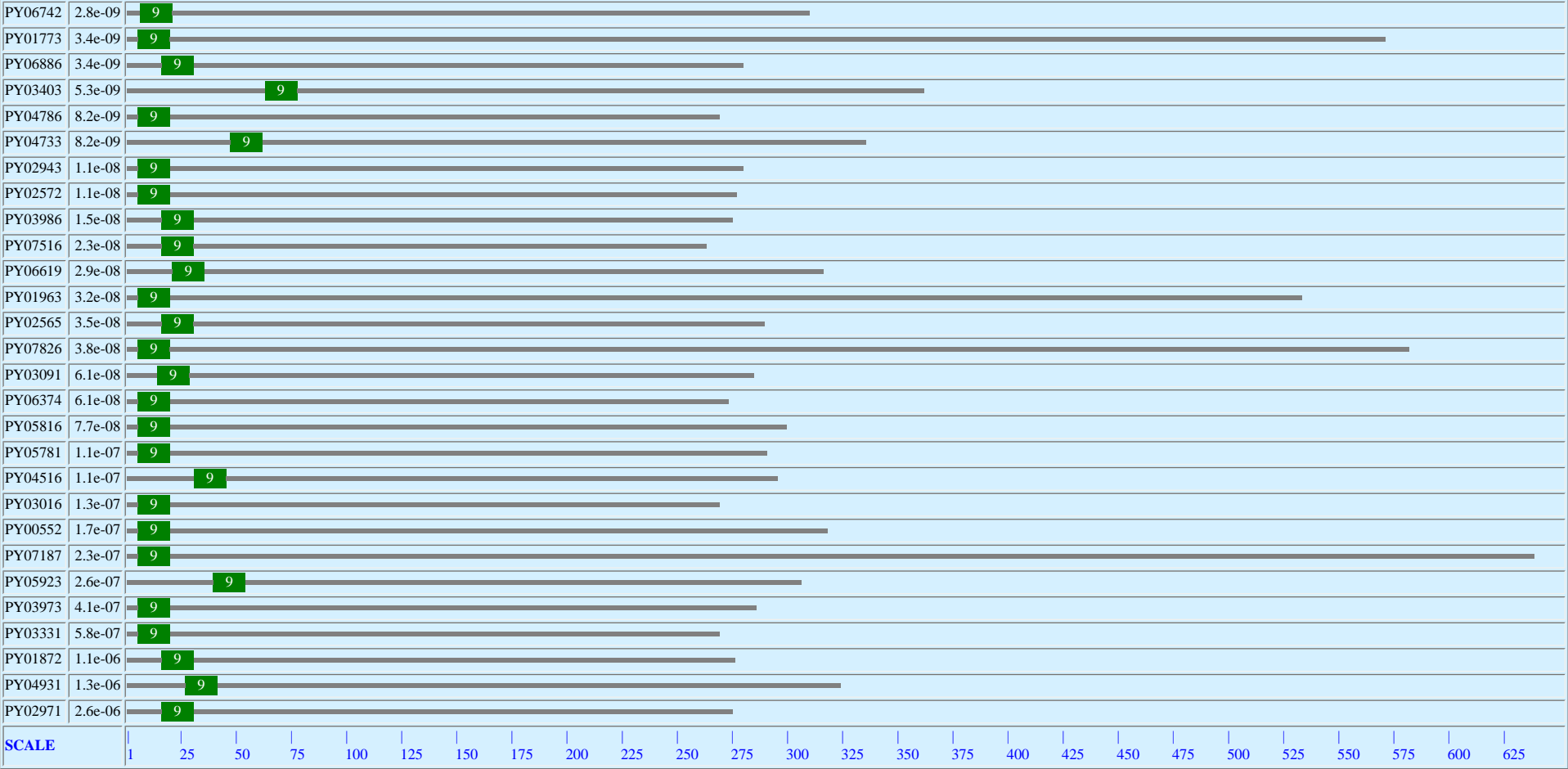
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Motif 9 block diagrams









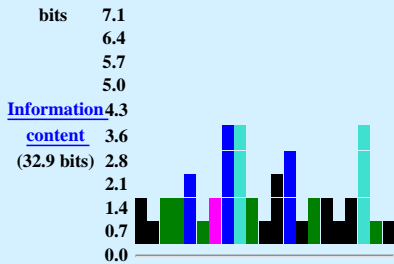
[Motif 9 in BLOCKS format](#)

to [BLOCKS multiple alignment processor](#).

[Motif 9 position-specific scoring matrix](#)

[Motif 9 position-specific probability matrix](#)

Time 1807.25 secs.

[illegible]

Multilevel
consensus
sequence

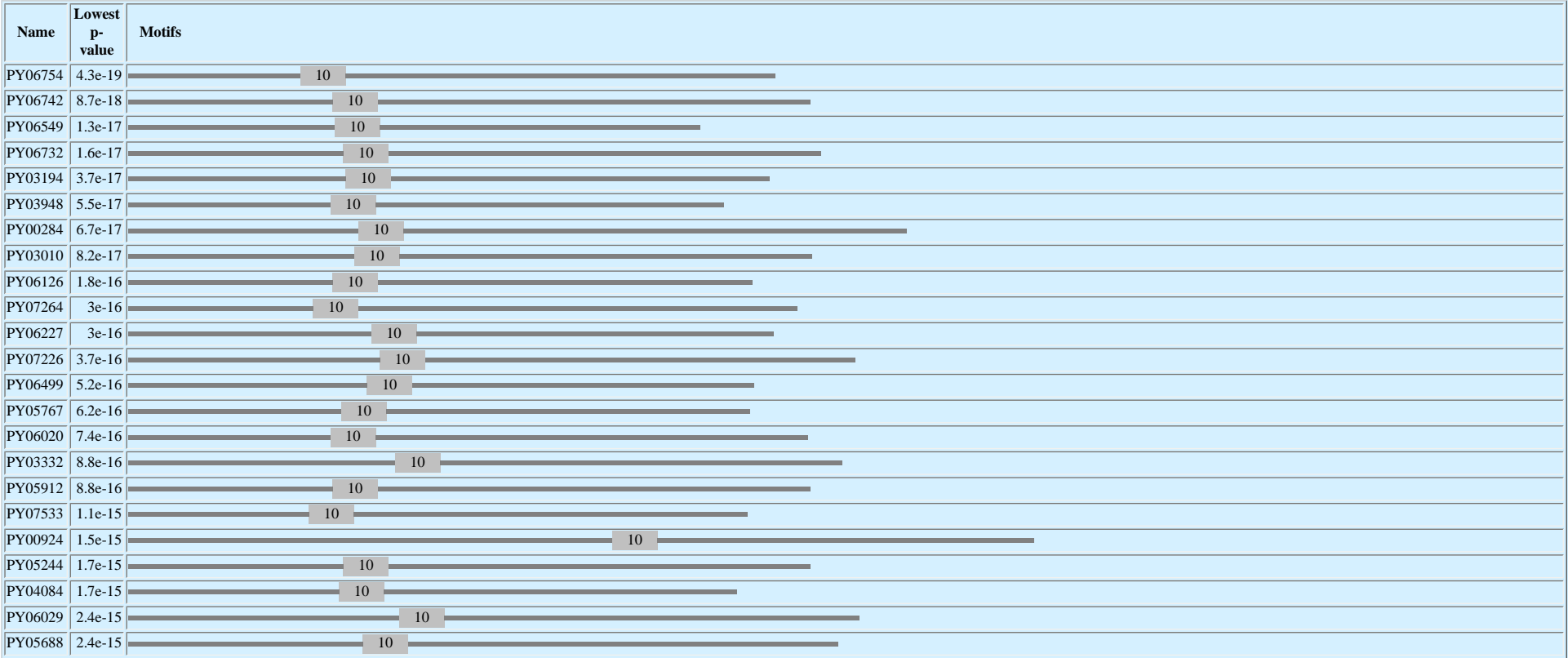
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PY06227	114	3.05e-16	SHKLNQKKQD GTTRLNDFYTN IETNSCYKD NIDKTTDSNS
PY07226	118	3.65e-16	SYKLNQKSQN GITTFNDFYSK IQNAE BYNK DIDGVDDYSS
PY06499	112	5.22e-16	SHKLNQKKQN GITRLDDFYTK IETNNCYKG NIPNNIMDD
PY05767	100	6.23e-16	SYKLNQKTQN GTTKLYDFYNN IKTNSKYKE HITAGDKINN
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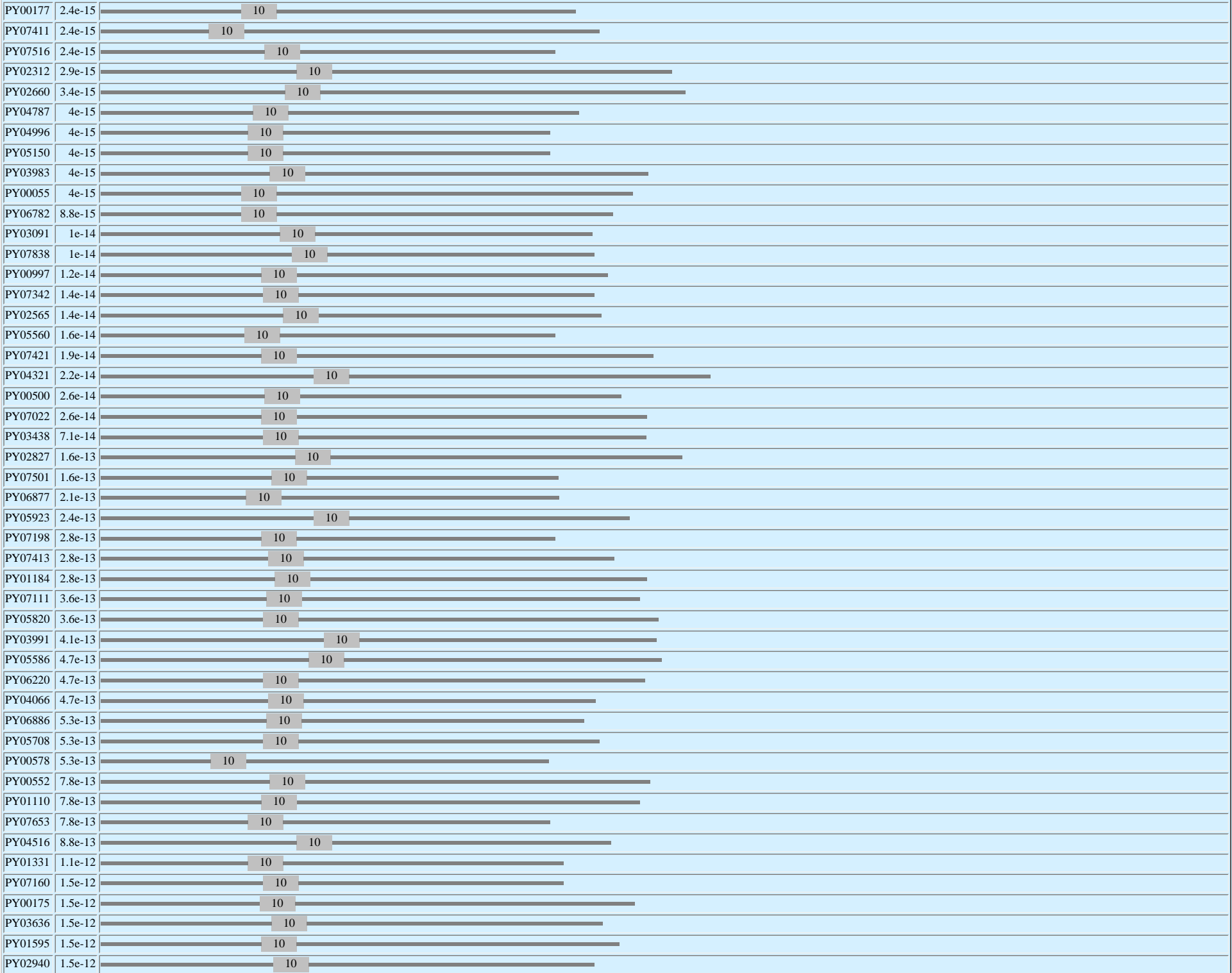
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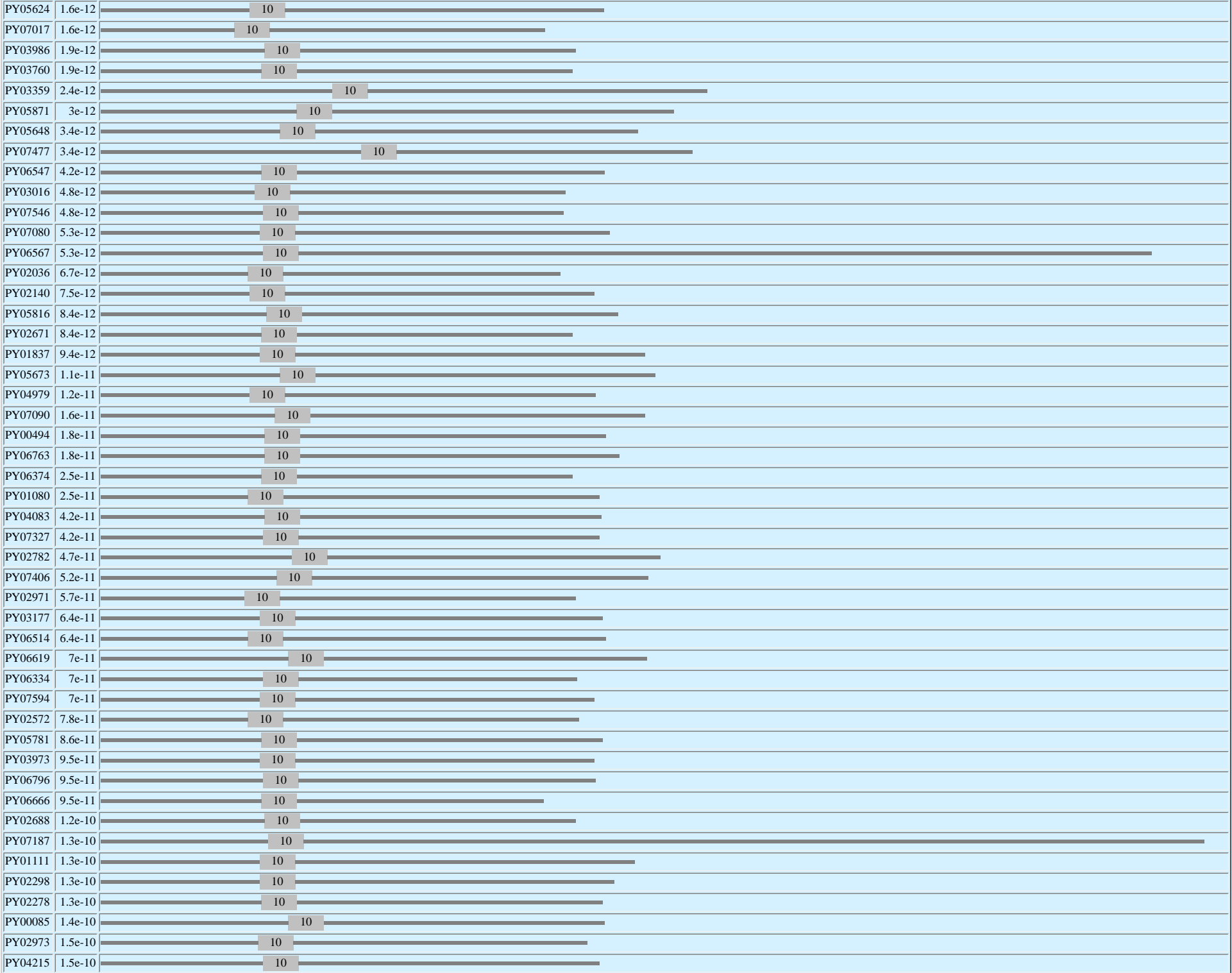
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PY01871	107	5.23e-10	SYMLNLGKSE	EEDNITGFYIEYIHDCKNYNK	KINELTDYDN
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PY02541	97	6.86e-10	GYKLNHKLNT	QFSNINEFYNTMKNNYGYAK	KIDYVDDYNS
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PY00308	110	7.50e-10	SYKLDQKQKD	KLTLNLKIFYTDHIEKNKYYN	KIKDDDTTTY
PY00493	132	8.20e-10	LSYMLNLKES	EKDNTTCFYSTCIYDCKYNT	EINKLTDYKS
PY03729	97	8.20e-10	YMLNLKEQPG	NDSNLKFFFYSTTINNDRYKNS	INGVTEYKNY
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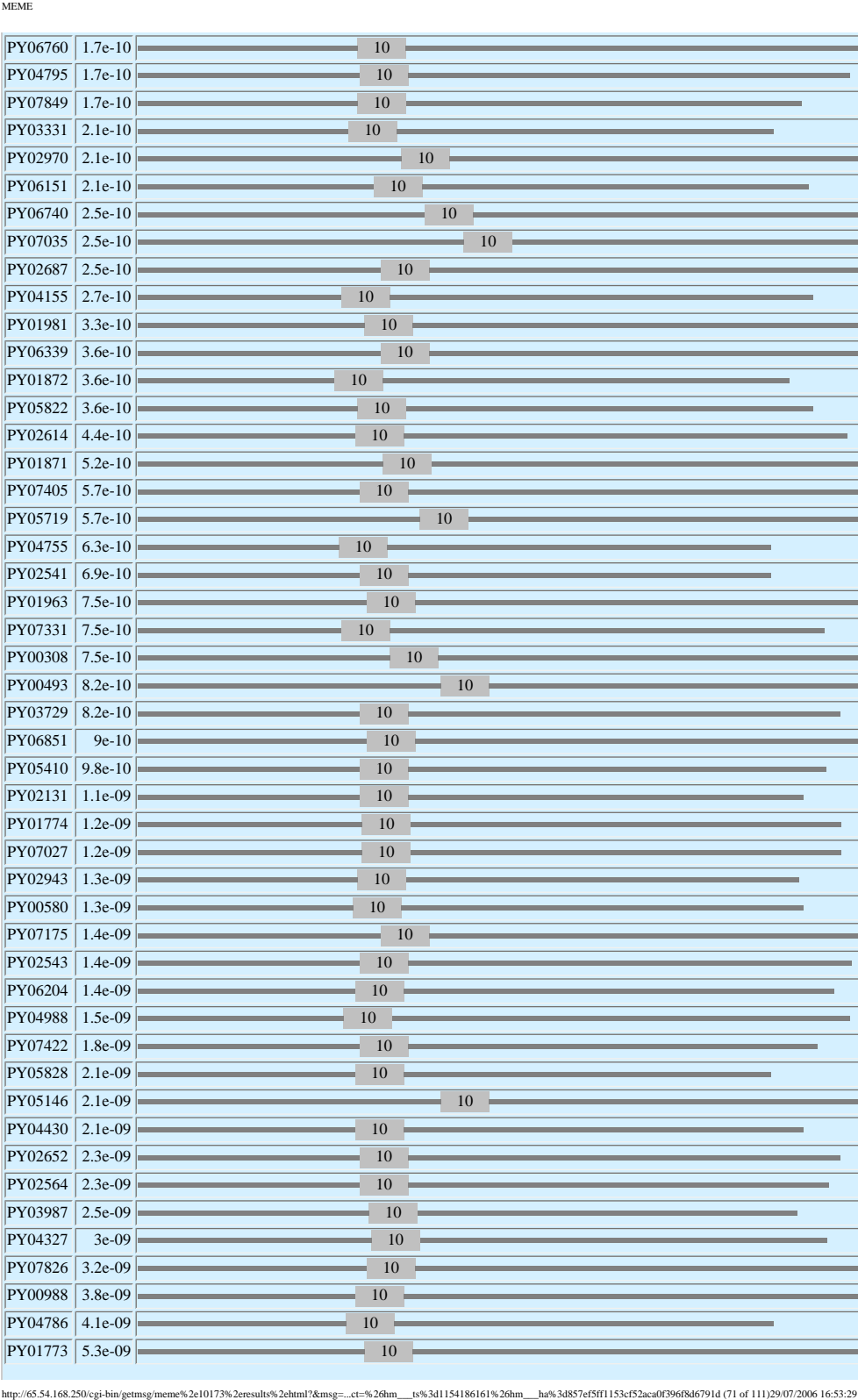
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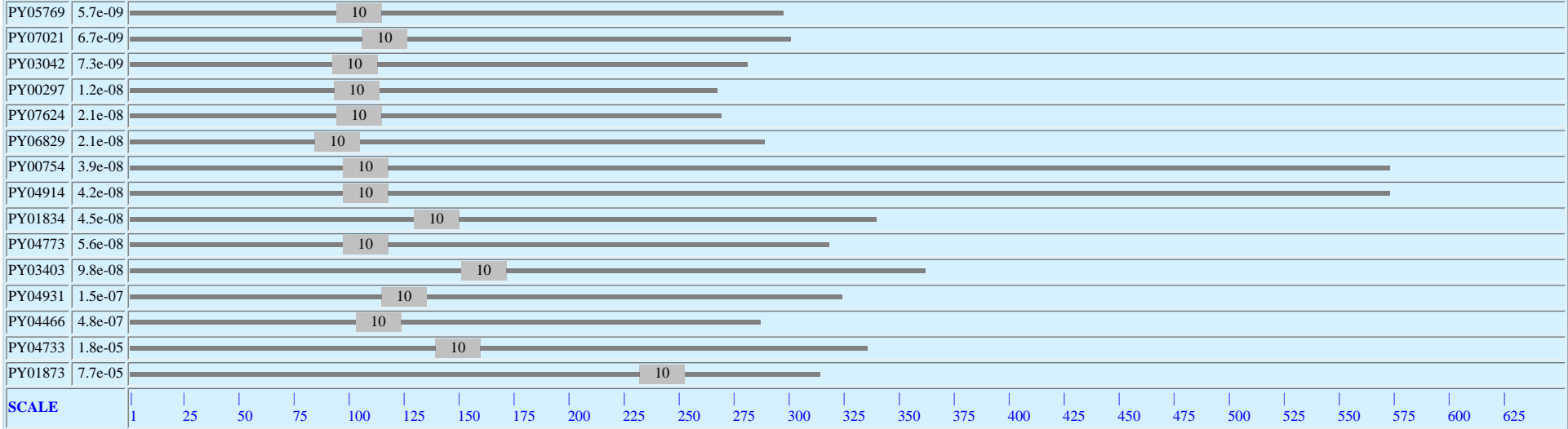
Motif 10 block diagrams











Motif 10 in BLOCKS format

to BLOCKS multiple alignment processor.

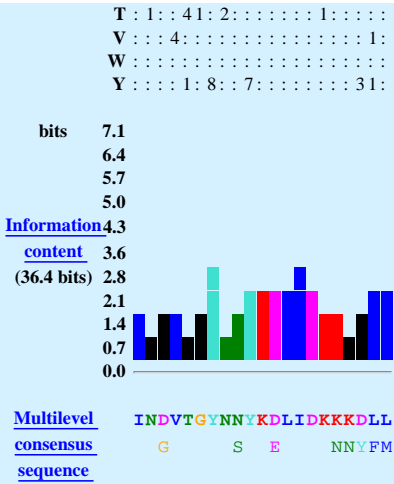
Motif 10 position-specific scoring matrix

Motif 10 position-specific probability matrix

Time 1937.66 secs.

PN MOTIF 11 width = 21 sites = 126 llr = 3175 E-value = 4.7e-688

Simplified **A** : 1: 1: 1:
pos.-
specific **C** : 1:
probability **D** : 23 112: 11: 4: 6: 3:
matrix **E** : 1: 12: 4: 11: 12:
F : 1: 1: 2: 2:
G : 3: 3: 3: 1: 1:
H : 1:
I 6: 1: 29: 11: 1
K 11: 111: 2: 71: 654:
L 1: 1: 1: 6: 54
M : 1: 4
N : 32: 24: 1: 2: 221:
P :
Q : 1:
R : 1: 1:
S : 1: 1: 23:

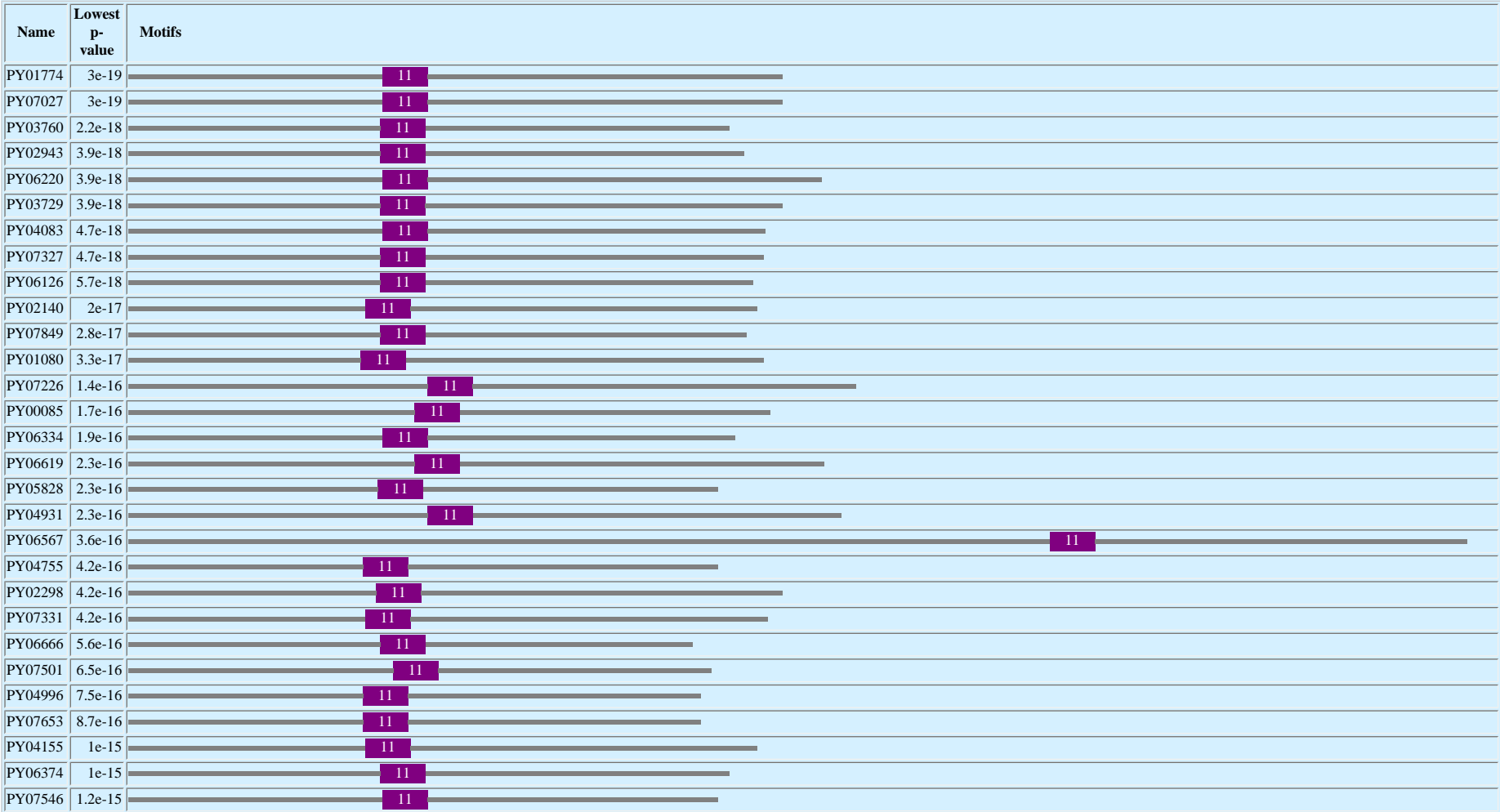


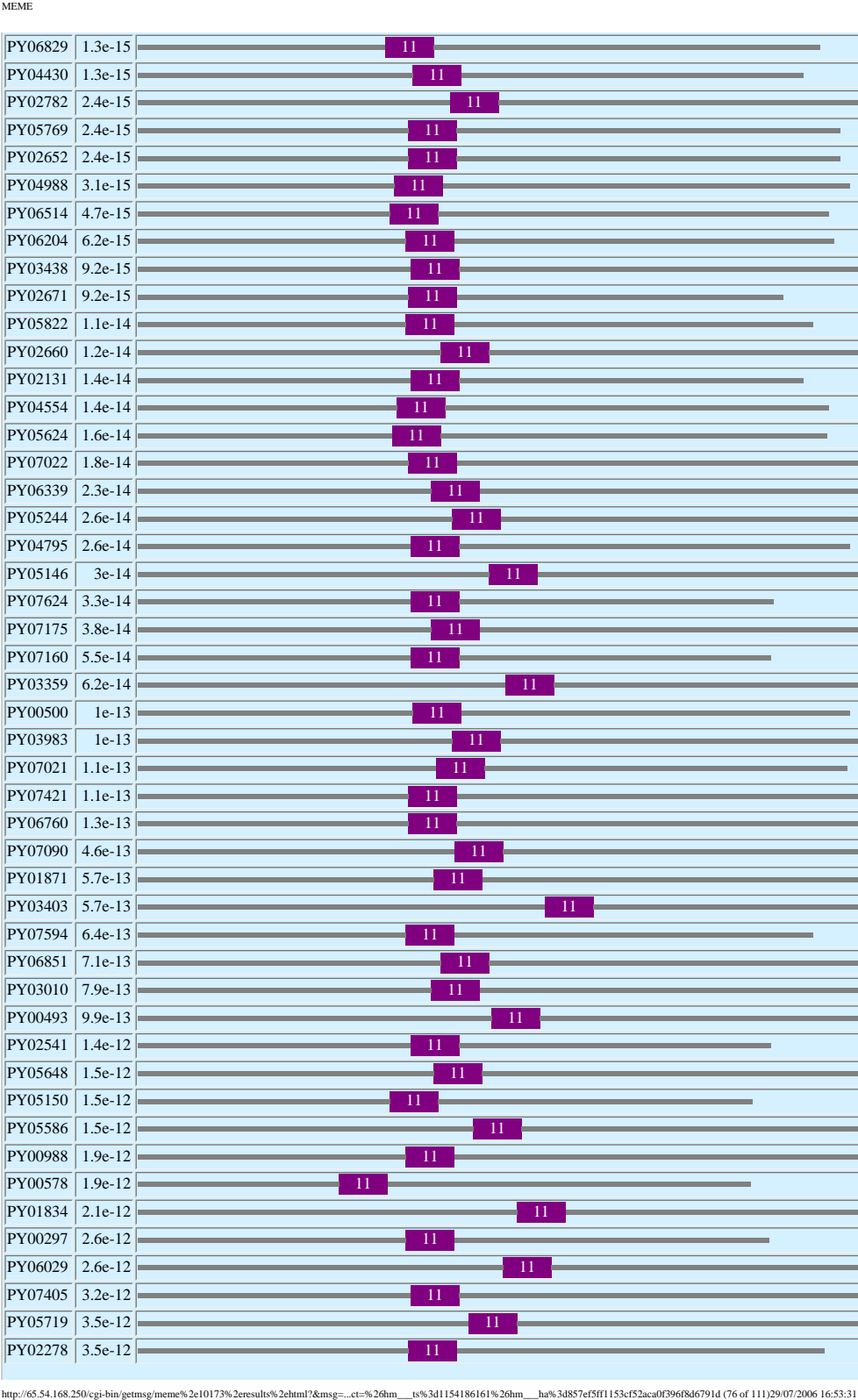
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PY03760	118	2.24e-18	INNGDKYIKA ITGVS DYKSYKDLIDKKQELMNMDMKIISKF
PY02943	118	3.93e-18	IKDCDKYNNK IDGVTAYNSYKDLIDKKEDLSIYVKDISKF
PY06220	119	3.93e-18	MQNTDEYKNH IDDVTEGTYNYIDLINQKKELMNINISVMSKF
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PY07327	118	4.73e-18	TIDNDRYKNS IADVKEYKNYKDLIDKKKEFMDISNEKITKL
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PY02140	111	1.96e-17	IENS DWYKKE ITGVTAYKNYKDLIDRNNYFLSMDKSIISKL
PY07849	118	2.76e-17	ITKDDRYIKD INNVS GYNSYKDLIDKKQNLMSIYVKDMSNF
PY01080	109	3.27e-17	TIDNDRYKKT INGVTKYSNYKDLIDQKKYLI DMDKKIISNF
PY07226	140	1.41e-16	IQNAEYKKD IDGVDDYSSYMDLINQKNELM DIDISVMSKF
PY00085	134	1.65e-16	INGDEKYNKN IDDVTA YKNYKDLIDKNNYILSMDMSIISKF
PY06334	119	1.93e-16	INN DNKYNQE INDVTAYTSYKDLIYKKENLMSISIIDMYIF
PY06619	134	2.26e-16	IEGGNNYKQA IKNVTEYTYNYKDLIDTKKYVLMKMDKNIISKL
PY05828	117	2.26e-16	INN DQKYNIK INGVTEGKYTYNELVDKKEDLMSIDIKDMSKF
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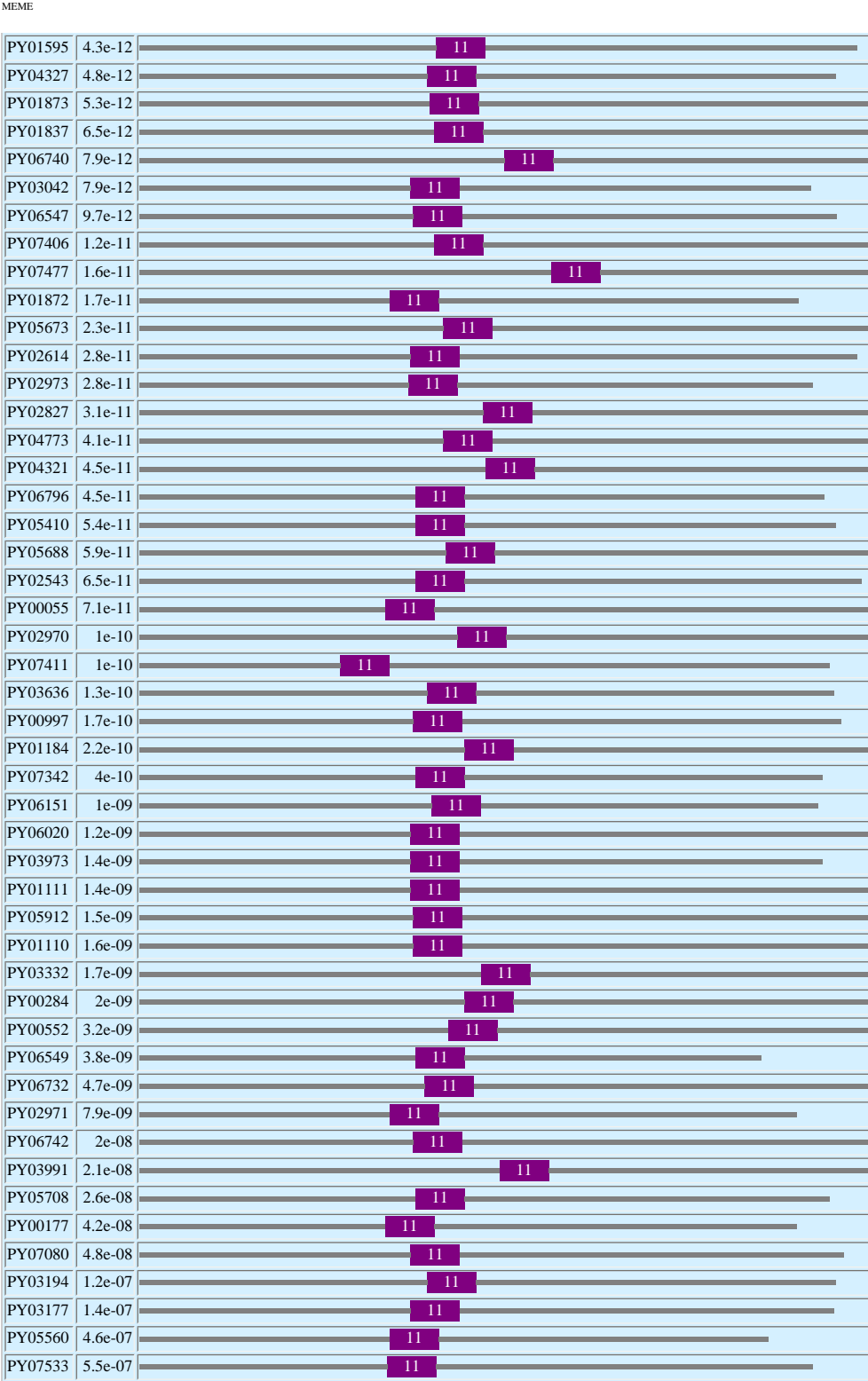
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 PY07022 118 1.77e-14 MQNVEEYKKS **IDDD**TEYTSYN**D**LIN**Q**KN**KFM** DIDISVMSEF
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PY00177	106	4.23e-08	VKNGGKYSNF	NSDSFRFTSIDEFIEGKDLL	NINIKDLSEF
PY07080	117	4.84e-08	VKNSGKYPKF	TNAANTFTNLEVDLNTKSDLL	NNNIEDLSEF
PY03194	124	1.20e-07	VKNNDKYNSF	TDPAYKISLEKKFMDDRNDLF	NINIEDLSKF
PY03177	117	1.36e-07	VISNGKYSKF	TNEAFKISDLDEFMKERTDLL	NMNIKDMSKF
PY05560	108	4.61e-07	IETNDFYK GK	ISNVSNGLINMDLIGEKIRLM	NMDIKDISNF
PY07533	107	5.49e-07	IKENSKYNED	IGTDSGSKIKKEVIDTKIKSM	DIDIKDISNF
PY03016	113	1.22e-06	NIESNSNYYE	EDIFADNNIRKDVIDKKIGSM	NIDINDISNF

Motif 11 block diagrams







PY03016	1.2e-06	<div><div></div><div>11</div></div>																								
SCALE		1	25	50	75	100	125	150	175	200	225	250	275	300	325	350	375	400	425	450	475	500	525	550	575	600

[Motif 11 in BLOCKS format](#)

to [BLOCKS multiple alignment processor](#).

[Motif 11 position-specific scoring matrix](#)

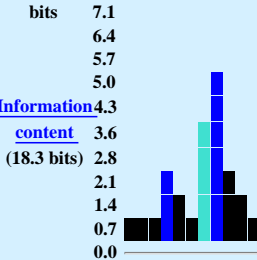
[Motif 11 position-specific probability matrix](#)

Time 2057.45 secs.

PN [MOTIF 12](#) width = 11 sites = 157 llr = 1994 E-value = 5.0e-262

[Simplified pos.-specific probability matrix](#)

A	:	:	:	:	:	:	:	:	:	:
C	:	:	:	:	:	:	:	:	a	:
D	2	1	1	:	2	1	:	:	1	2
E	1	1	:	:	1	:	:	:	1	:
F	:	:	2	3	:	:	:	:	:	:
G	1	2	:	:	1	:	:	:	1	2
H	:	1	:	:	:	:	:	:	:	:
I	1	:	1	:	:	:	:	:	:	:
K	1	1	:	:	4	2	:	:	1	1
L	:	:	1	5	:	:	:	:	:	:
M	1	:	:	:	:	:	:	:	:	:
N	2	2	1	:	2	2	:	:	1	4
P	:	:	:	:	:	:	:	:	4	:
Q	:	:	:	:	:	:	:	:	:	:
R	:	:	:	:	:	:	:	:	:	:
S	1	1	1	:	1	2	:	:	1	1
T	:	1	1	:	:	1	:	:	1	:
V	:	:	:	:	:	:	:	:	:	:
W	:	:	:	:	:	:	:	:	:	:
Y	:	:	:	1	:	9	:	:	:	1



[Multilevel](#) **xNFLKKYC** **P** **N**

consensus

F

D

sequence

NAME	START	P-VALUE	SITES
PY03332	60	2.42e-10	LKDSKQYDFN NGTFKKYCFNN KCDSDTNIVN
PY02312	52	5.99e-10	LKDSKEYDFN NGAFKKYCFNN NCDGDINKIN
PY00175	30	9.23e-10	GLKEYKYDFN NGTFKKYCFNS SCVADTDILN
PY05719	57	1.40e-09	SNNKKYQFKE DTFFKKYCTGG KCDGDLDKIN
PY03331	29	1.71e-09	DPNNSEKHKY MGMFNSYCFDN NCDTDEKKVI
PY03983	31	1.71e-09	NNSATLDFHK NDNLKKYCFNG GSGETKCNTE
PY01110	31	2.09e-09	LNDSKEYKIN PGSFKKYCPDG NCNNDIDKIN
PY03010	40	2.54e-09	NDGNYNFLFN GQFFKQYCTNN SCDSNLEQIN
PY04321	61	3.08e-09	LNASGEYSVG GGTIKNYCFNR KCDSIDINKID
PY07546	30	3.08e-09	LNNGDYQFNI DRFFKTYCTNN NCEMPLEKIN
PY06877	28	3.71e-09	GDPKKPGEQH MNILNTYCPDG NCSSDELKII
PY06619	46	4.45e-09	LIGGDYKIVN DEFLKNYCTSG CDNALDKINA
PY06732	36	4.45e-09	LKGSEYEFEK STFFNGYCFNN NCESDINKIT
PY03438	31	4.45e-09	LNESGEYYIS GGTIKKYCFNK NCDSDINKIH
PY06020	30	7.53e-09	LKDSKQYDFE RGIFKKYCFNK NCGTDTDIAN
PY05708	31	7.53e-09	GGIPKSEFNK ITNFDKYCFNN NCDTDLEKIT
PY06547	18	8.91e-09	GESAKIDFKK SSSLKKYCFNG NCDTNLDKIK
PY03359	72	1.05e-08	LTNSGEYNFR VGSLNSYCFNR KCENDIDKIN
PY02131	31	1.45e-08	WDDSGSYIFT SGTLKQYCFDK ECKNYINLVK
PY03729	30	1.45e-08	LDKGEEKFND NNFLDSYCDGN KCDSAFERID
PY07421	30	1.45e-08	ELNSGEYDFK GGSLNRYCFKN NCETNINKIH
PY07080	30	1.99e-08	LKDSKLDIFYD NNNFKNYCFDK NCNSELEKIT
PY04084	40	1.99e-08	DPNNLGIGIS MDLLKMYCPDY NCSSDELKII
PY01111	30	2.33e-08	ELKESKYDFK STFFKDYCFNK NCNNDIEKIN
PY02564	31	2.33e-08	ENNKYHEFEK NNFLNGYCDGN KCSDFEKIS
PY02940	35	2.33e-08	TSDKKYEFKT GNFLDSYCGDN NCSTDYGKIS
PY04155	24	2.71e-08	GTEGNHYFNS GNNFDKYCTNN SCDSNLGKIN
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PY00284	38	5.65e-08	KRHASVDPNK NENIKYYCFNG NSGHNECITE
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PY05560	29	6.50e-08	DPKNPGKDIS VDSLNDYCFDN NCSSDEEKVI
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PY02543	32	7.47e-08	KTNEYHEFNY GNFLNSYCFNN ECKGDLEKIN
PY06204	30	7.47e-08	LNNGEYEFKD NNFLDSYCNNG KCEGNLDKIN
PY00500	31	8.58e-08	DSDGNQIKD DEFFKKYCDKE KCDDPLEKVN
PY06220	31	8.58e-08	LNASGEYSIS GGTIKNYCFKK KCDSNVNKH
PY03042	30	8.58e-08	LNSDGKYTFK DEYFKDYCTGG CDNDFKKINA
PY00578	31	8.58e-08	DKAADFELEE ITDYKNYCFGN NCNSETTEKIT
PY00924	160	9.83e-08	GTPATTELNT IQNYKRYCFSG DCNTELEKIT
PY07022	31	9.83e-08	LNESGSYNFK KGLFTKYCFNN CENNIDKINA
PY04787	28	1.12e-07	DPKNSGGYNS ISYFKYYCFDN KCDTDEKKII
PY07624	31	1.12e-07	WDDSGNYIFT SGTLKQYCFDK ECKNYINLVK
PY02541	31	1.12e-07	LDDPVKYMST SGTLKQYCFDK ECKTYNNIVN
PY01184	31	1.12e-07	NKSLSYDFHG LGSIRNYCFNG DSKEKECKNE
PY00988	30	1.12e-07	SNNKDYKFKE DEFLKNYCISG CDNNLEKINA
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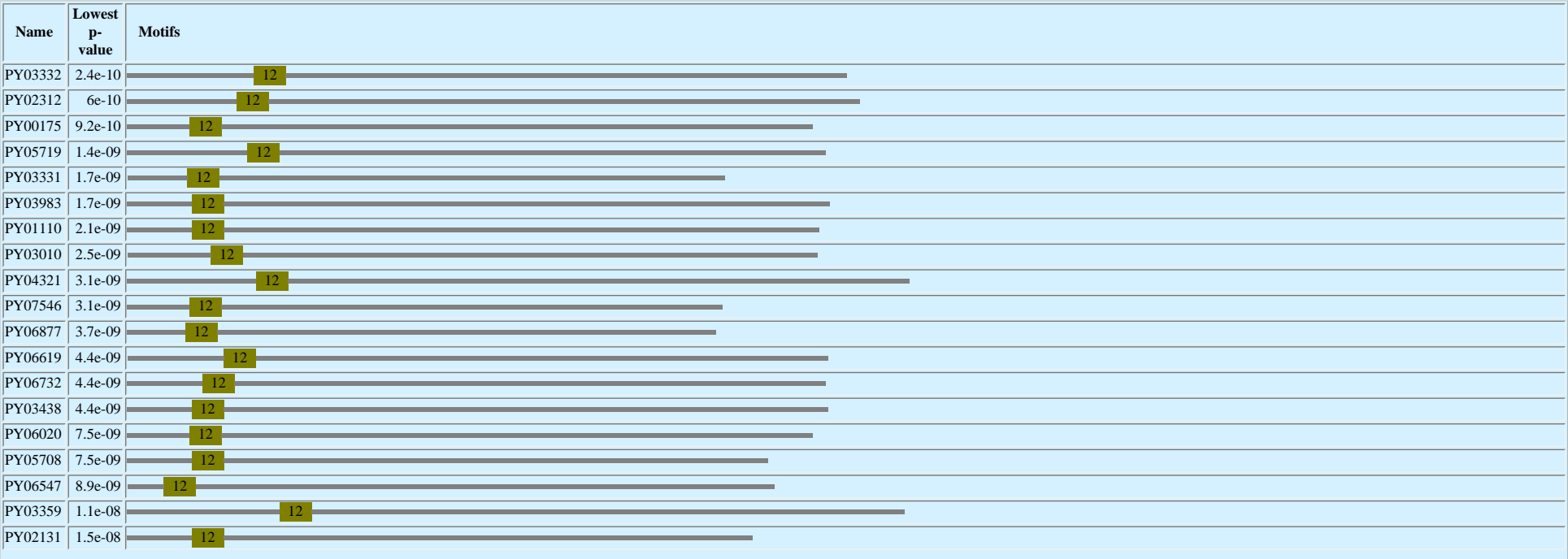
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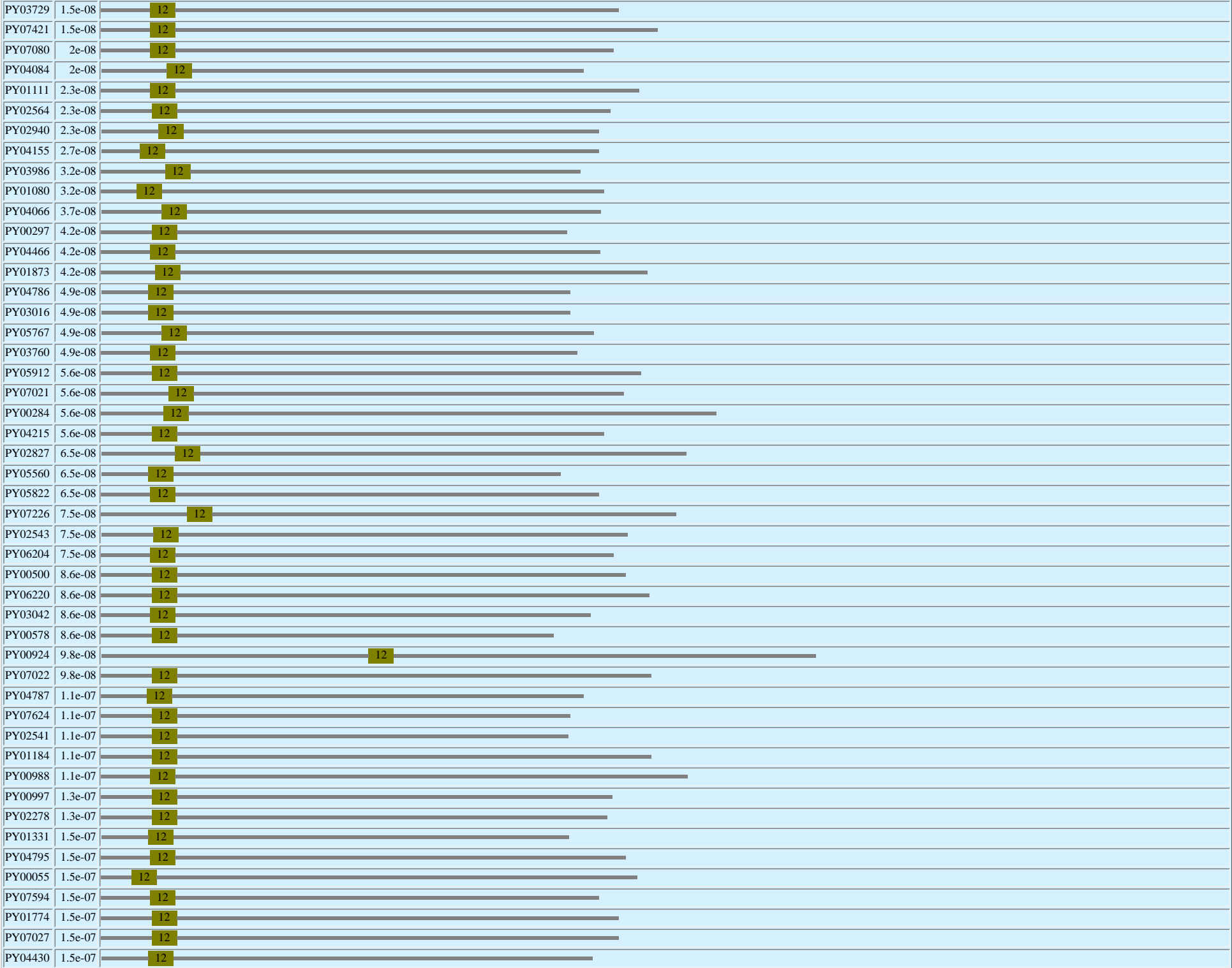
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PY00055	19	1.47e-07	LNNSGEYAFS	RGILGKYCFNE	NCNNYIDKIN
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PY01774	31	1.47e-07	DSDNNYIFQK	ENFLDGYCGSN	SCDTDFEKIN
PY07027	31	1.47e-07	DSDNNYIFQK	ENFLDGYCGSN	SCDTDFEKIN
PY04430	29	1.47e-07	GLVVGINTNI	KNLKKYCDNG	SCDDPFGKVN
PY00552	31	1.67e-07	DDSEYDIYD	IPDIDBYCFDG	ESGEGKCNTK
PY04554	32	1.67e-07	NGENYNFVYG	DQNFKKYCTNS	CDSNLEKINA
PY02973	30	1.90e-07	DSTPQSELKN	IKDFDKYCFND	NCNTELEKNT
PY02140	24	1.90e-07	DTGGNHYFNS	GRNFDKYCTND	SCDSNLGKIN
PY06334	31	2.16e-07	NASGSYEFTN	EDDFKDYCTGN	KCNDTGTKIS
PY05828	29	2.46e-07	DVVVGNNNTNI	NEKLKNYCDNG	SCDASFGKVN
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PY06760	31	3.58e-07	NSSGYYQFKD	EEFLNNYCNSN	QCQSDYDRIS
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PY06829	22	3.58e-07	TDDKQYDFKK	DNFLDSYCG\$Y	SCDGDIEKIN
PY07849	30	3.58e-07	SSNGSYKFIN	DKYFKEYCTDG	QCEEDINKIN
PY06499	55	4.04e-07	DPKKSGEFNS	LDLLKLYCFDN	TCSSDEEKIT
PY07160	31	4.04e-07	LDDPVNYMST	SGTLTLYCFDN	QCKTYNNIVN
PY05244	31	4.04e-07	NISTSNDIHS	LGNAKNYCFNR	DSGETECKTD
PY05769	31	4.04e-07	DSNNNYQFKE	KNFLDSYCD\$K	SCDTDFRRID
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PY00085	46	8.21e-07	DKGVTYQFTT	DEDYKNYCTNE	NCNDNTDKMN
PY07090	31	8.21e-07	NISKGSDIHS	LGNIKKYCSNG	ESEGTGCKTD
PY06666	30	8.21e-07	EKDESYRFID	DVDPFKEYCTNE	NCVDDTAKIN
PY07516	39	8.21e-07	DGPKLPGEQY	MNILNTYCPES	NCSSDELKII
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PY03991	67	1.15e-06	DNIKPLDFYG	YQGFKNYCFSS	SCNSELEKIT
PY07198	29	1.28e-06	LDEGEYKFKE	KNFLDSYCN\$Y	KCEGDLDKIN
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PY03973	30	1.59e-06	SNNESYKFIN	NEYFQ\$YCTGD	SCDNLDLKDIN
PY07342	31	1.59e-06	NKSGELELET	ISNY\$NYCF\$K	DCNTELEKIT
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PY03194	31	2.68e-06	SKEAEFELND	N\$SFKKYCFIT	DSGKNECNND
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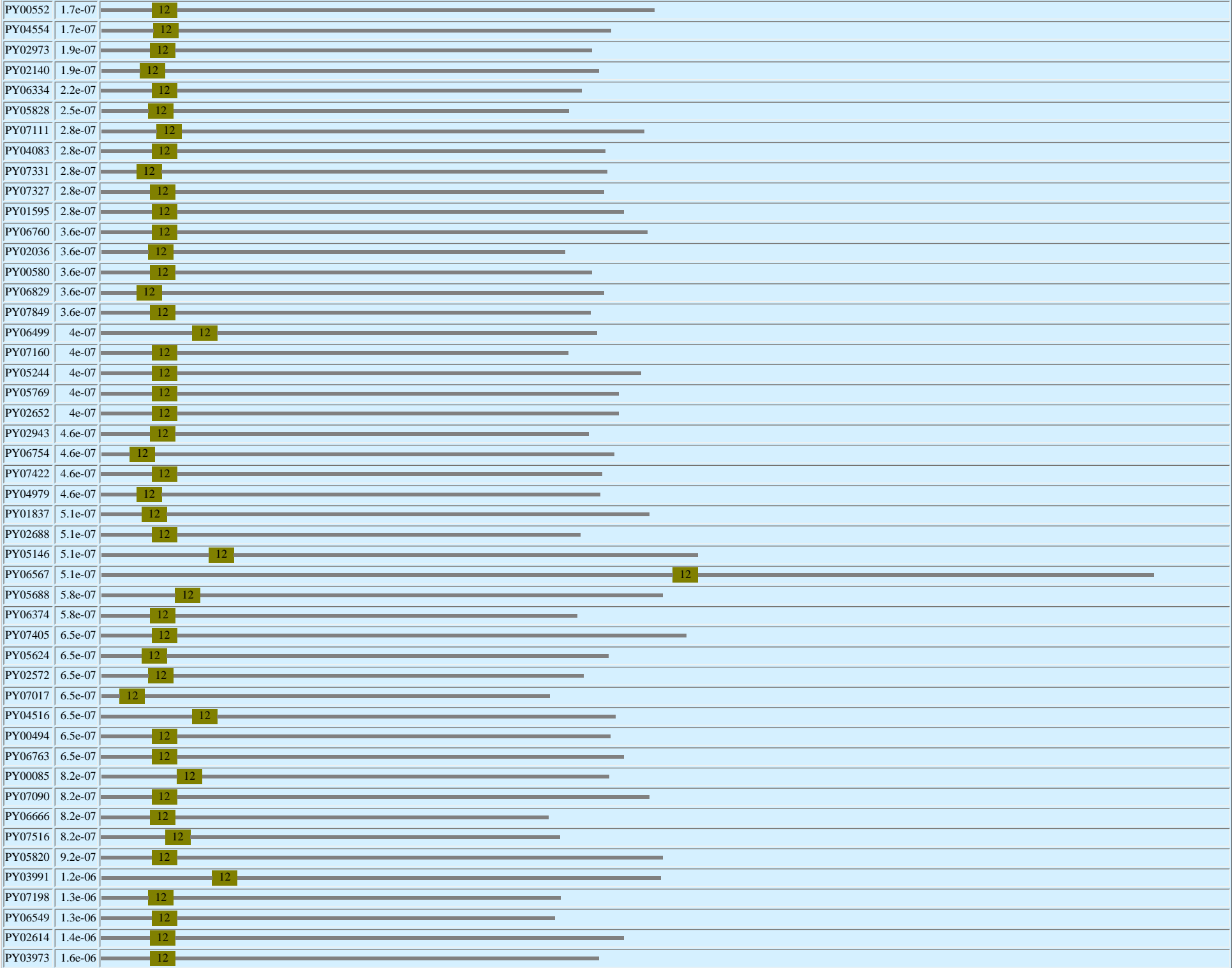
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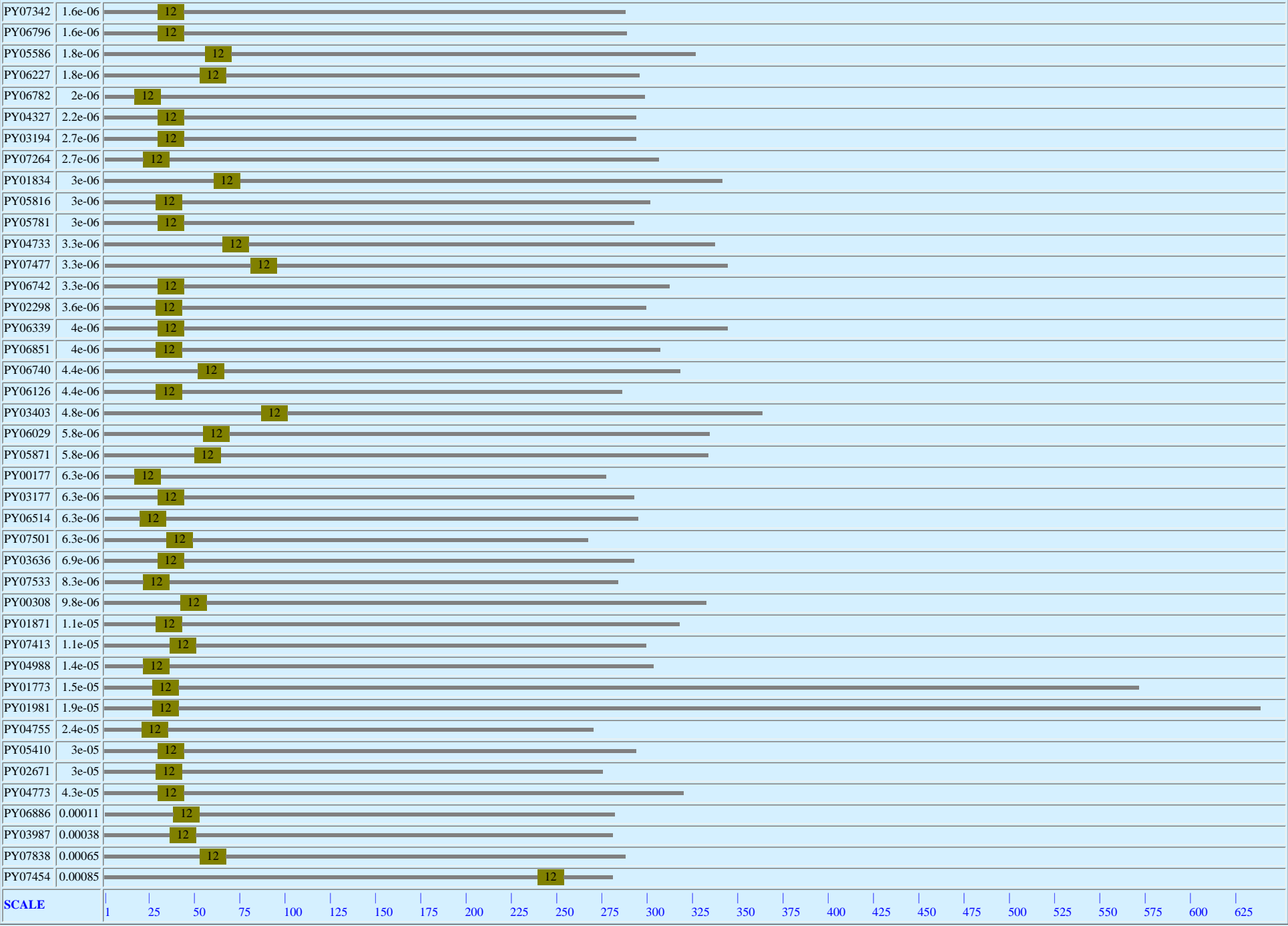
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PY07477	84	3.27e-06	SKDGTLELKE	HTDFKKNYCFVT	DSGENECDNN
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PY06029	57	5.77e-06	SKSTNNDINS	LGSIRDYCSNG	ESDGTGCKTD
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PY07838	55	6.55e-04	DLNNRGENNY	RDALSTFFPDS	DSCSGEEKII
PY07454	247	8.54e-04	IKFVDIKQNI	YSFIDIFCNTN	FLWNCIIFVI

Motif 12 block diagrams









Motif 12 in BLOCKS format

to BLOCKS multiple alignment processor.

[Motif 12 position-specific scoring matrix](#)

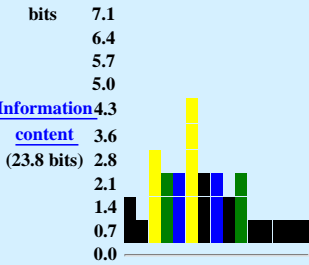
[Motif 12 position-specific probability matrix](#)

Time 2173.40 secs.

MOTIF 13 width = 15 sites = 113 llr = 1867 E-value = 5.4e-264

[Simplified pos.-specific probability matrix](#)

A	:	:	:	:	:	:	:	:	:	:	:	:	:	1	1	1	1	2	1
C	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
D	3	:	:	:	:	:	:	:	:	:	:	:	:	1	:	:	:	:	:
E	:	:	:	:	:	1	4	1	2	:	:	1	1	:	:	:	:	:	1
F	:	2	:	:	:	2	:	:	:	:	:	:	:	:	:	:	:	:	:
G	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
H	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
I	:	2	:	:	1	:	:	7	:	1	:	1	1	1	1	:	:	:	:
K	1	:	:	:	:	:	:	:	:	1	4	1	2	2	1	:	:	:	1
L	:	1	:	:	6	:	:	:	:	:	:	:	:	:	:	:	:	:	:
M	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
N	3	:	:	:	:	:	:	:	:	:	:	:	:	1	1	3	:	:	1
P	1	:	6	1	:	:	8	1	:	:	:	:	:	1	:	:	:	:	:
Q	:	:	:	:	:	:	:	:	:	1	:	2	1	:	:	:	:	:	:
R	:	1	:	:	:	:	:	:	:	1	:	:	:	:	:	:	:	:	:
S	1	1	2	6	:	1	1	:	:	1	:	1	1	1	1	:	:	:	:
T	:	:	1	1	:	3	:	1	6	2	:	:	:	:	:	:	:	:	1
V	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	1	2	:	:
W	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
Y	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	1	:



[Multilevel consensus sequence](#)

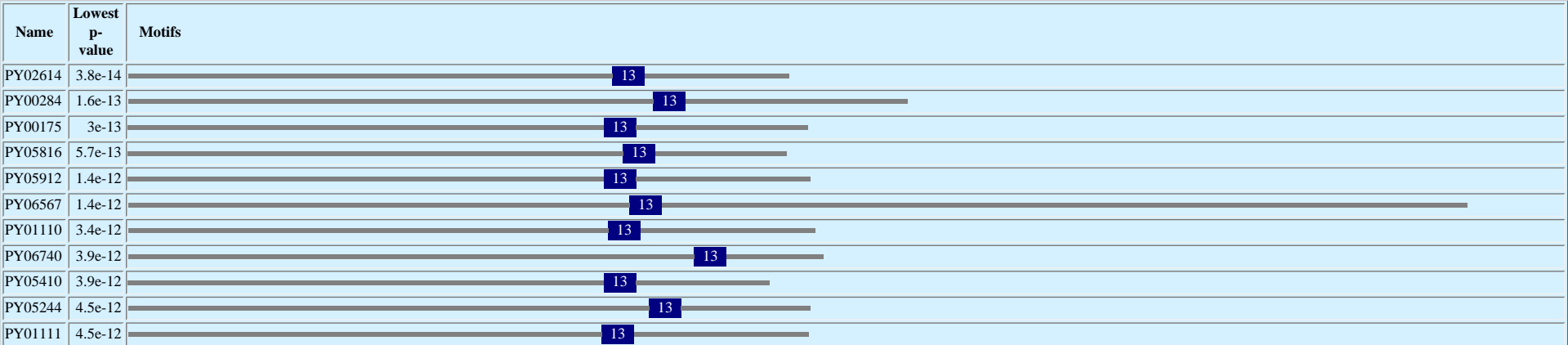
D I P S L P P I K T x K N x x
N F S T

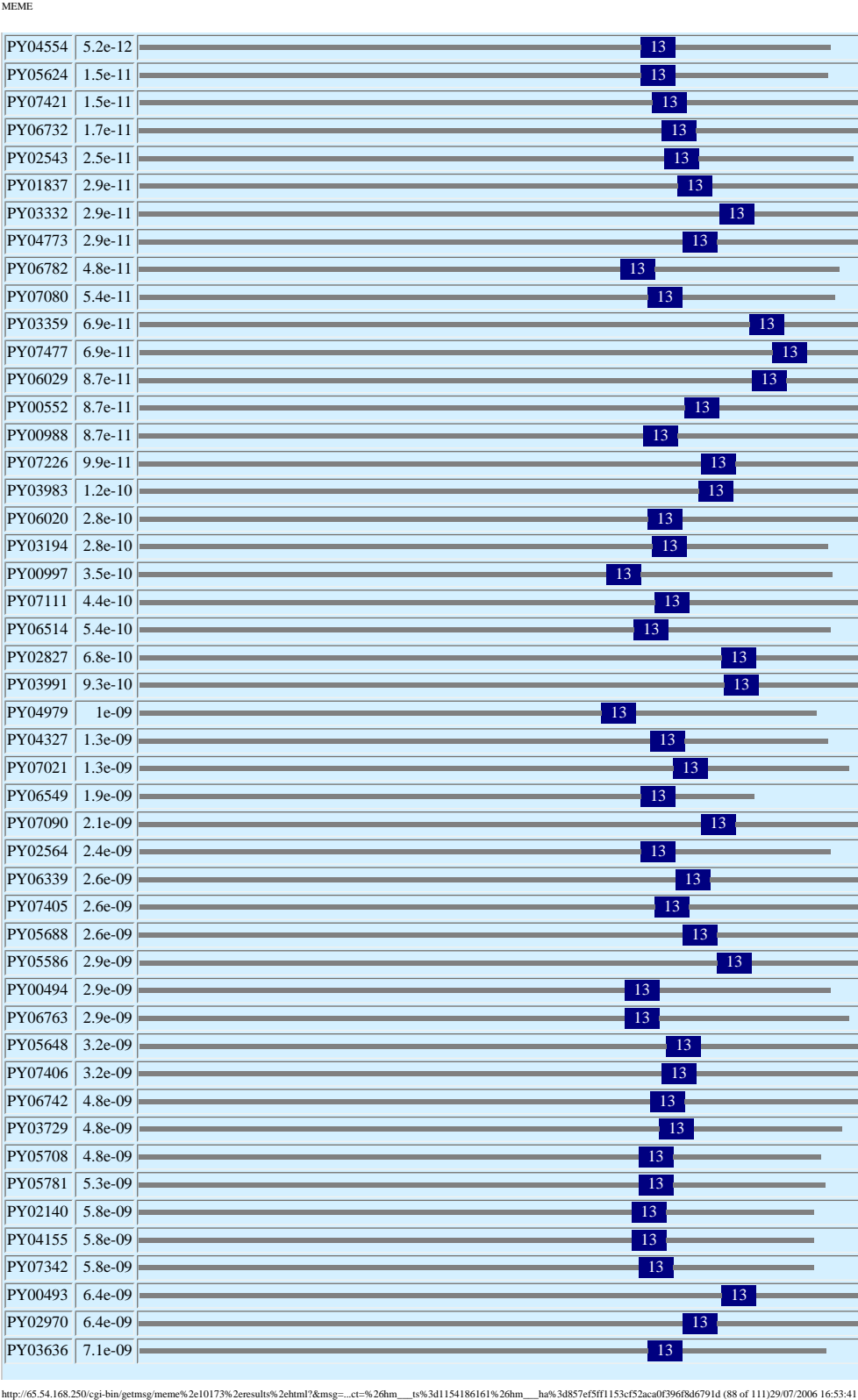
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PY00284	245	1.55e-13	KDEYDDINCV DIPSLPSIKTTQH HIQSSSEDHSEHG
PY00175	222	3.01e-13	DYTLNNTPI NRPTLP TKKTPQQVNVQEVPEIKTT
PY05816	231	5.71e-13	KNKYNGINCM NIPSPPSIKR TQQVNVQSSGVTSSSL
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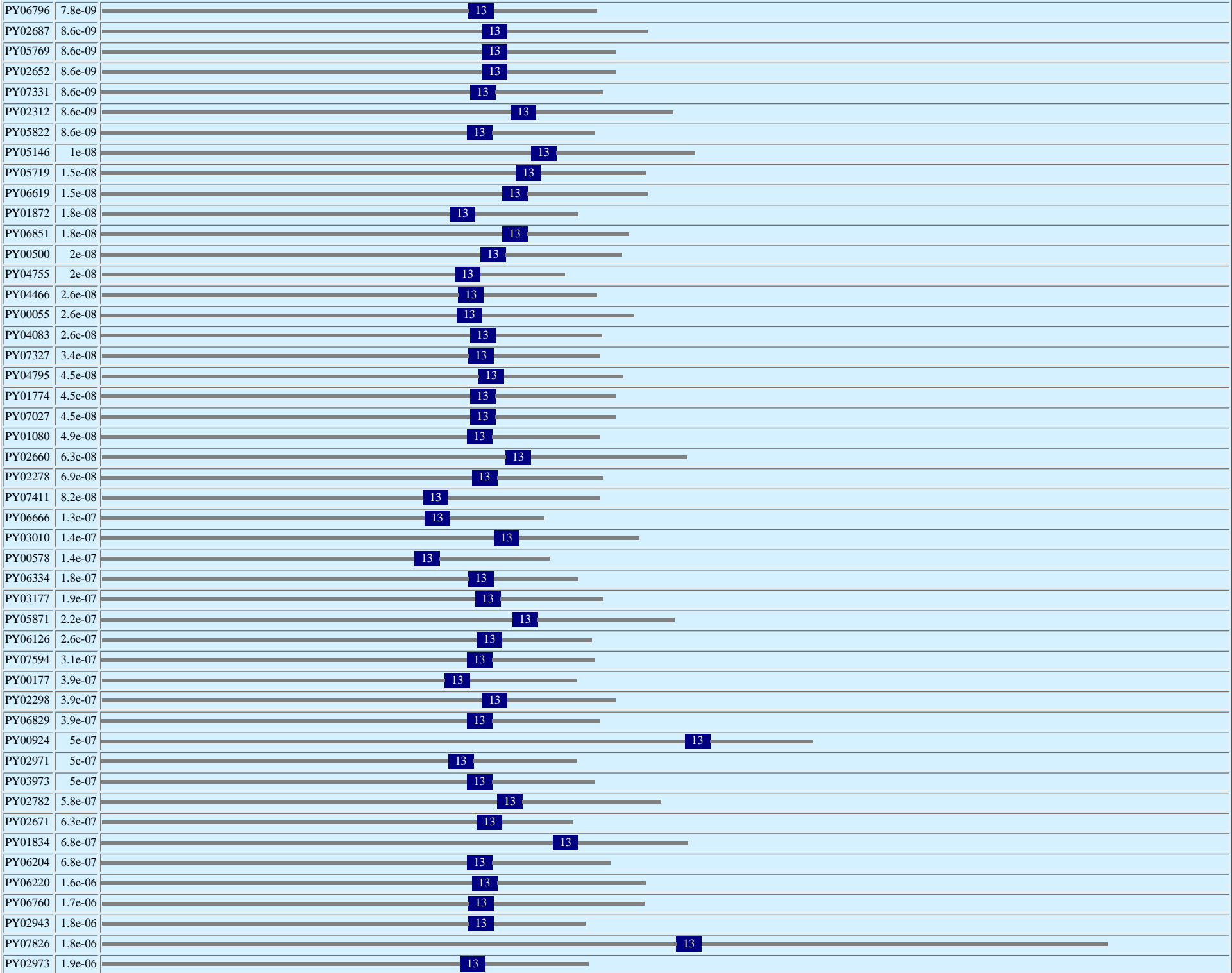
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PY01110	224	3.41e-12	KGTRFNNTSI	NRPSLPTKTPKKDN	TEGTKVTKAT
PY06740	264	3.92e-12	YCTSKGVDCN	DFPSLPMIKTKKNSV	KSSERTSVQD
PY05410	222	3.92e-12	KEKCNNVQPR	SFPFLPEIATSISAQ	MSGVTSPSLS
PY05244	243	4.51e-12	YCDDNNVDCN	DIPLLPEIKTTNNEV	QDSGQKIEAT
PY01111	221	4.51e-12	KGNKFNTTSV	DRPSLPTQKTPKKDN	PGPKVTKATD
PY04554	218	5.19e-12	KNECKDAQDV	VFPSSLPEIKTSQNTT	KIPGETSDKN
PY05624	218	1.52e-11	YYTSKGGNSK	DIPSLSPIKTEENDA	LSSGLISEDA
PY07421	223	1.52e-11	GKNKIGNTSI	NLPSLPTKTNENVG	ISDSKETITV
PY06732	227	1.73e-11	IGRSYKNISI	DRPSLPTQKTVKKVN	VEGSNGTKTP
PY02543	228	2.55e-11	YCSKKGGTCN	NFPSSLSPIKTKENDA	LSSGLFSEDA
PY01837	234	2.89e-11	YCENENKGCN	DIPSLLPIKTKENAV	QSSAHDNVQN
PY03332	252	2.89e-11	KGTRFSNISK	DRPFLPTKTKGKVE	VEGSKGNKTV
PY04773	236	2.89e-11	KKDYDDNSCM	GIPSIPTIKIKQNIV	QSYEDHSEHD
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PY07080	221	5.39e-11	YCNKKGANCK	EFSSLPEITTKFAAQ	LSGDTSSSSI
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PY07477	275	6.88e-11	DYNNLINKCK	SFTSLPEITTEFSAQ	MSGVTSSSPI
PY06029	266	8.75e-11	YCTENGVDN	DIPSLSPIKTKENDL	QSGEHISEVT
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PY07405	224	2.63e-09	IKKCNDTQCC	KSSSLPTIETEKIPE	NCSEETSEKT
PY05688	236	2.63e-09	KGTRYNNNTSI	NLTFLPTKKTTPKKDN	VESSKETKTT
PY05586	251	2.91e-09	KKNCSDVNCK	DIPPLQSIKTKKNIV	DFSKQNSEVG
PY00494	211	2.91e-09	DYDNLKSKCS	DSSSFREIKTPTNCV	KRSKQSSQLI
PY06763	211	2.91e-09	DYDNLKSKCS	DSSSFREIKTPTNCV	KRSKQSSQLI
PY05648	229	3.22e-09	DYDNFKKKCN	DNSSLPTIETEKISE	ICSEKTSKKT
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PY05781	217	5.28e-09	NYNNFKKKCN	DLPSISTIDTTDNSV	YTSGLTSEVT
PY02140	214	5.82e-09	DYDNFKKKNN	NSSSLPSIKTKIYMP	IYGFSSLIFL
PY04155	214	5.82e-09	DYDNLKKKNN	NSSSLPSIKTKIYMP	IYGFSSLIFL
PY07342	217	5.82e-09	DYNNLNEKYS	DIPFSFIESKISAL	ASEDTSSSSI
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PY05146	255	1.04e-08	NFKKNCVSKC	SISSEFPTIEKPKNYV	ETFEKGSCKT
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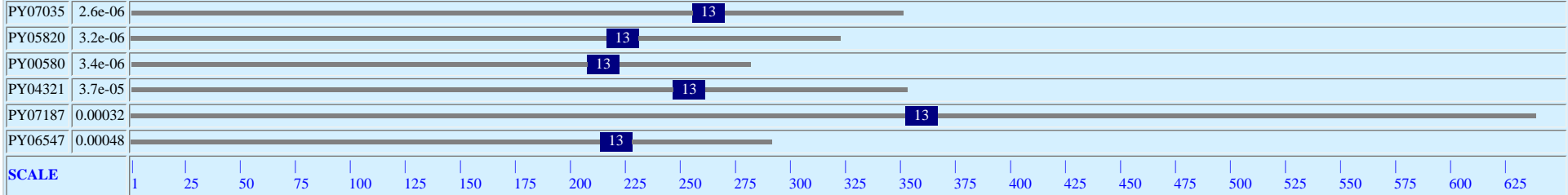
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PY04755	210	1.99e-08	DYNNLKNVCN	DFPSLPTYSRRLVIK	KTLPVPIAFIF
PY04466	212	2.61e-08	MNKYNNQTQCS	KSSFXPTIETTENFA	QQILQSSSED
PY00055	211	2.61e-08	KYRVVPYNKQM	KRPFLPTEKKAENKD	VVDSSETKID
PY04083	219	2.61e-08	DYGNLKKKCK	NSSSFPSIEITDNSA	HTSEVASSSS
PY07327	218	3.42e-08	DYGNLKKKCK	NSSFPPSIEITDNSA	HTSEVASSSS
PY04795	224	4.47e-08	KNKCKDIKCS	NYSSFPTIEKKNNSL	KCSEKTAQGS
PY01774	219	4.47e-08	DYSNFKKKCK	NSSSFPSIEATNNFI	RTSELTSTQT
PY07027	219	4.47e-08	DYSNFKKKCK	NSSSFPSIEATNNFI	RTSELTSTQT
PY01080	217	4.88e-08	YNNSQHFKSS	PIPTIEGIQTSAQQI	LQISGDTSSS
PY02660	240	6.34e-08	RTLEVEFVRK	QIPELPKEKTTQVST	IPKESEMHES
PY02278	220	6.92e-08	DYNKLKDKCN	GNSSFPSIETMQNSG	LISEDTSSSS
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PY06666	192	1.26e-07	DYDNLKKNCE	HFPSTPDIKKIISEQ	HVCEVASSSS
PY03010	233	1.36e-07	KNECKDAKDS	NFPALKEISTPQDTI	ESIGQTTEQI
PY00578	186	1.36e-07	DYNNLKNRCK	HIQSLPEITTFPSALA	STYEFTSSSS
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PY00177	204	3.93e-07	DYNNIKGKRR	DYQTLPEITTFPSALA	SKYGVTSSSS
PY02298	226	3.93e-07	SKGGNCKNYP	ELPTIEEIQASAQKT	VQISEDTSSS
PY06829	217	3.93e-07	SKGGNCKNYP	ELPTIEEIQASAQKT	VQISEDTSSS
PY00924	346	4.97e-07	DYNKLNNKCS	NIPSFSELASKISAL	ASEDTSSSSI
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PY06204	217	6.79e-07	DYDNFKKKCK	DISSFPAIDKPNITP	KCPEQNLSSA
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PY07826	341	1.80e-06	KCMSEKKETG	SGFSSPPSSSTEQTDT	HQSSSESESEK
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PY05820	222	3.20e-06	KQTIYHLHRN	KLPNLITEKTATQVS	GSSPKEPQDT
PY00580	213	3.44e-06	DYNNLKIKCK	DCTFLPDI TNISALA	SVDTSSSSSI
PY04321	253	3.67e-05	YFRNSYVKSI	KQGTIPELITEKTTO	ISVSNHEGTQ
PY07187	361	3.17e-04	PPSSQDPPGS	SGPSGSDSSDTFDS	SDTSDTSDTS
PY06547	219	4.79e-04	FTTKNASKID	NSKKFPILPTEKATK	SLIRHSSIQI

Motif 13 block diagrams









Motif 13 in BLOCKS format

to BLOCKS multiple alignment processor.

Motif 13 position-specific scoring matrix

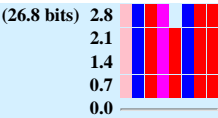
Motif 13 position-specific probability matrix

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Time 2286.34 secs.
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MOTIF 14 width = 8 sites = 65 llr = 1206 E-value = 1.2e-226

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<u>pos.-</u>	C	:	:	:	:	:	:	:	:
<u>specific</u>	D	:	:	:	:	:	:	:	:
<u>probability</u>	E	:	:	:	:	8	:	:	:
<u>matrix</u>	F	:	:	:	:	:	:	:	:
	G	:	:	:	:	:	:	:	:
	H	7	:	:	:	:	:	:	:
	I	1	:	:	:	1	:	:	:
	K	1	:	:	18	:	:	a	9
	L	:	:	9	:	:	:	9	:
	M	:	:	:	:	1	:	:	:
	N	:	:	:	:	:	:	:	:
	P	:	:	:	:	:	:	:	:
	Q	:	:	:	:	:	:	:	:
	R	:	:	:	a	:	:	:	:
	S	:	:	:	:	:	:	:	:
	T	:	:	:	:	:	:	:	:
	V	:	:	:	:	:	:	:	:
	W	:	:	:	:	:	:	:	:
	Y	1	:	:	:	:	:	:	:

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content	3.6

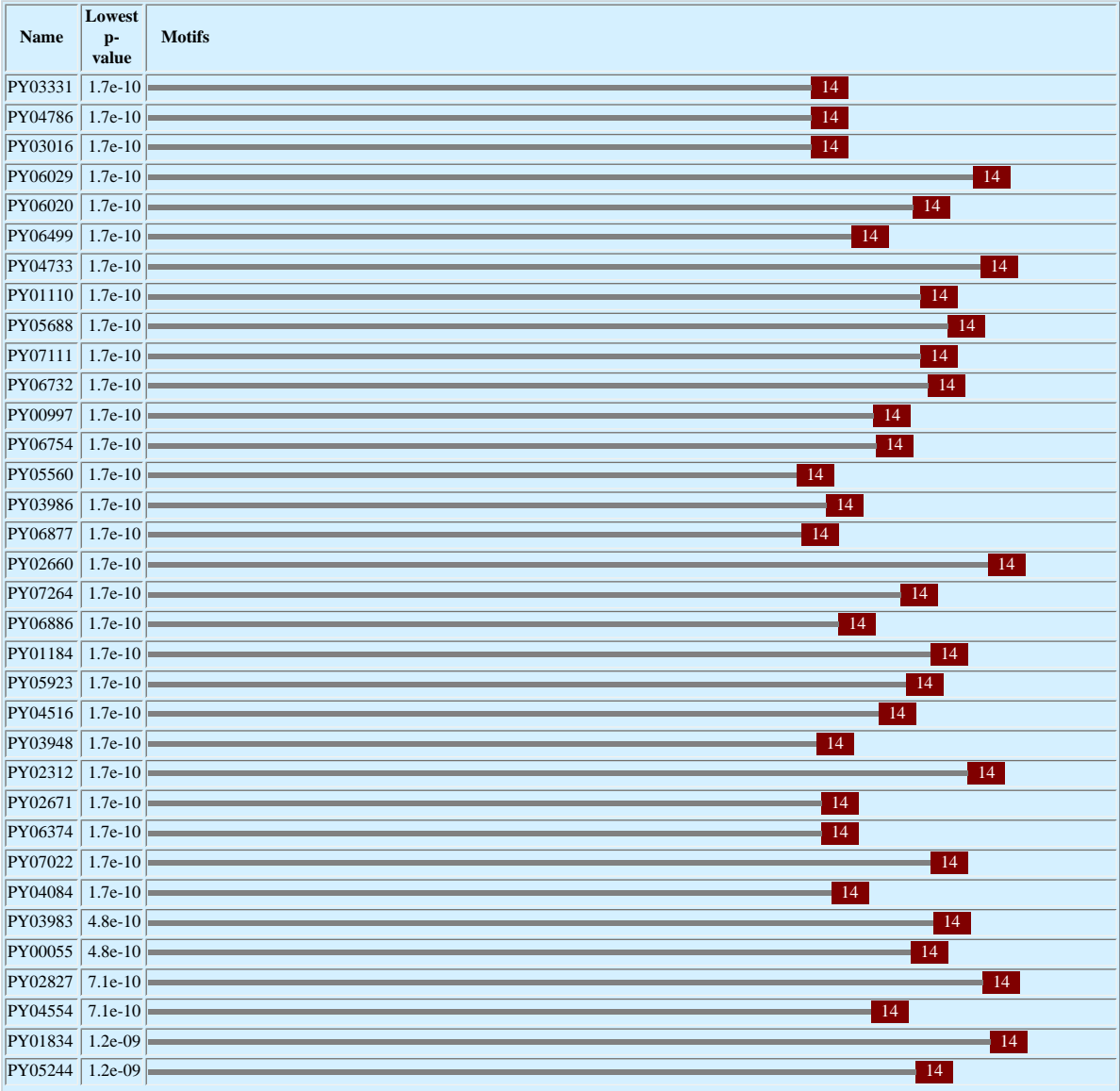


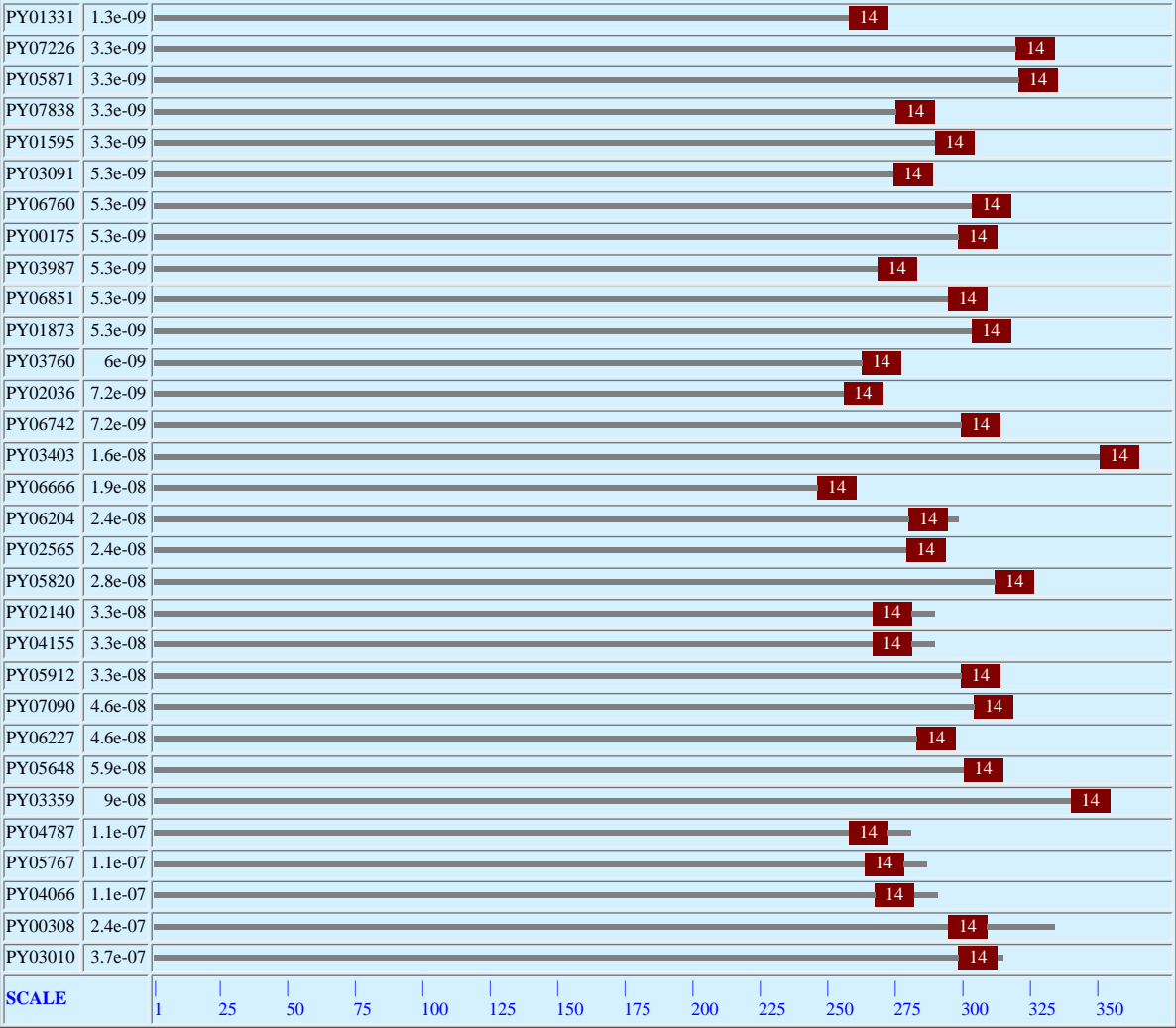
[Multilevel](#) **HLREKLKK**
[consensus](#)
[sequence](#)

NAME	START	P-VALUE	SITES
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PY04786	268	1.70e-10	FGFRKRSQKQ HLREMLKK
PY03016	268	1.70e-10	FGFRKRPEKQ HLREMLKK
PY06029	333	1.70e-10	FGSRKRSQKQ HLREKLKK
PY06020	309	1.70e-10	FGFRKRSQKQ HLREKLKK
PY06499	284	1.70e-10	FGFRKRSQKQ HLREMLKK
PY04733	336	1.70e-10	LFGFRKRVQK HLREKLKK
PY01110	312	1.70e-10	FGFRKRSKKQ HLREKLKK
PY05688	323	1.70e-10	LFGFRKRSQK HLREKLKK
PY07111	312	1.70e-10	FGFRKRVQKQ HLREKLKK
PY06732	315	1.70e-10	FGFRKRSQKQ HLREKLKK
PY00997	293	1.70e-10	FGFRKRSKKQ HLREKLKK
PY06754	294	1.70e-10	FGFRKRSQKQ HLREKLKK
PY05560	262	1.70e-10	FGFRKRSQKQ HLREMLKK
PY03986	274	1.70e-10	FGFQKRSQKQ HLREKLKK
PY06877	264	1.70e-10	FGFRKRSQKQ HLREMLKK
PY02660	339	1.70e-10	LFGFRKRAQK HLREKLKK
PY07264	304	1.70e-10	FGFRKQSQKQ HLREKLKK
PY06886	279	1.70e-10	FGFRKRSQKH HLREKLKK
PY01184	316	1.70e-10	LFGFRKQSKK HLREKLKK
PY05923	306	1.70e-10	FGFRKRSQKQ HLREMLKK
PY04516	295	1.70e-10	FGFRKRFFKQ HLREKLKK
PY03948	270	1.70e-10	FGFRKRSQKQ HLREKLKK
PY02312	331	1.70e-10	FGFRKRAQKQ HLREKLKK
PY02671	272	1.70e-10	LFGFRKRSKK HLREKLKK
PY06374	272	1.70e-10	LFGFRKRSKK HLREKLKK
PY07022	316	1.70e-10	FGFRKRSQKQ HLREKLKK
PY04084	276	1.70e-10	FGFRKRSQKQ HLREMLKK
PY03983	317	4.84e-10	FGFRKRSQKQ HLREKIKK
PY00055	308	4.84e-10	FGFRKRSQKQ HLREKIKK
PY02827	337	7.12e-10	FGFRKRTQKQ HLREKLKK
PY04554	292	7.12e-10	FGFRKRSQKQ HLREKLKK
PY01834	340	1.20e-09	FGFRKRTQKH HLRENLLK
PY05244	310	1.20e-09	FGFRKRTQKQ HLRKLLKK
PY01331	267	1.27e-09	FGFRKRSQKQ HLREKLKT
PY07226	331	3.27e-09	FGFRKRSQKQ YLRKLKK
PY05871	332	3.27e-09	FGFRKRSQKQ QLREKLKK
PY07838	285	3.27e-09	FGFRKRSQKQ YLRMLKK
PY01595	300	3.27e-09	FVLRKRAQKQ YLRKLKK
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PY06760	314	5.32e-09	FGFRKRFAQKQ KLREKLKK
PY00175	309	5.32e-09	FGFRKRFAQKQ KLREKLKK
PY03987	278	5.32e-09	LGFRRNRFQKQ KLREKLKK
PY06851	305	5.32e-09	FGFRKRSQKQ KLREKLKK
PY01873	314	5.32e-09	FGFRKRFAQKQ KLREKLKK
PY03760	272	5.98e-09	LFGFRKRFAQKQ HLRKRLKK
PY02036	265	7.22e-09	FGFRKRSQKH HLKEMLLK
PY06742	310	7.22e-09	FGFRKRSQKQ HLKEKLKK
PY03403	363	1.60e-08	LFGFRKRVQK NLRKLKK
PY06666	255	1.88e-08	FGFRKRSQKQ HLREIVKK
PY06204	290	2.40e-08	FGFRKRFAQKQ KLREKIKK IKKK
PY02565	289	2.40e-08	FGFRKRFAQKQ KLREKIKK

MEME					
PY05820	323	2.78e-08	FGFRKRSQKQ	QIREKLKK	
PY02140	276	3.29e-08	SGFRNRFKKL	YLRKKLKK	MKKEWTINI
PY04155	276	3.29e-08	SGFRNRFKKL	YLRKKLKK	MKKEWTINI
PY05912	310	3.29e-08	FGFRKRARKQ	YLRENLKK	
PY07090	315	4.57e-08	FGFRKRTKKQ	HLKEKIKK	
PY06227	293	4.57e-08	FGFRKRFQKQ	KLRENLKK	
PY05648	311	5.86e-08	LFGFRKRVQK	HLRKKLIK	
PY03359	352	8.98e-08	FGFRKRSQKQ	HLRKKIKT	
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PY04066	277	1.10e-07	LFGFRKKVKK	RLRRKLKS	LRRKWLIDI
PY00308	305	2.43e-07	FGFDKLFQRQ	YLRKKLKK	FLCCGTHIRF
PY03010	309	3.73e-07	LFGFRKRSQK	HLREKVDV	MF

Motif 14 block diagrams



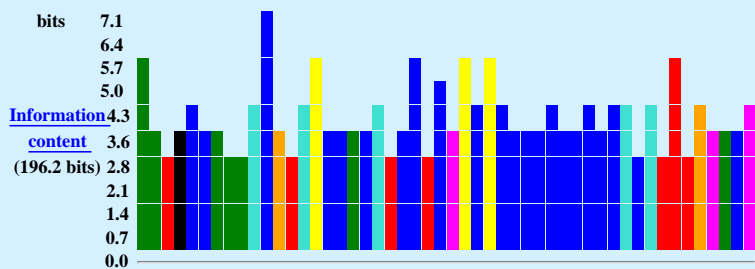


[Motif 14 in BLOCKS format](#)

to [BLOCKS multiple alignment processor](#).

[Motif 14 position-specific scoring matrix](#)

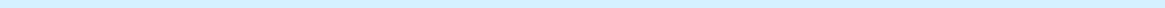
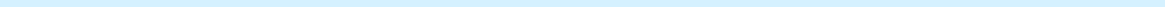
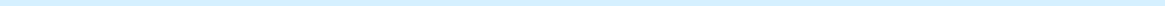
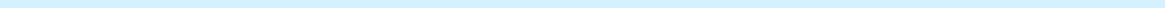
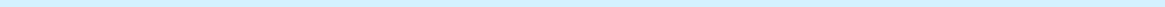
[Motif 14 position-specific probability matrix](#)

[illegible]

Multilevel
consensus
sequence

NAME	START	P-VALUE	SITES
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PY00754	537	2.63e-61	EIIINSSKKK QTK DFINSTYWGKYPLLNLYKLMKADPVFIIILFLLFIFYLYKRKGDSLE
PY04914	537	2.63e-61	EIIINSSKKK QTK DFINSTYWGKYPLLNLYKLMKADPVFIIILFLLFIFYLYKRKGDSLE
PY01773	535	2.63e-61	EIIINSSKKK QTK DFINSTYWGKYPLLNLYKLMKADPVFIIILFLLFIFYLYKRKGDSLE
PY01981	604	1.43e-60	KFIDLSTQKK QAK FINSIYWEEKYPLLNLYKLMKADPVFIIILFLLFIFYVYKRKGDSLE
PY07826	546	3.99e-60	EIIINSSKKK QTN FINSTYWGKYPLLNLYKLMKADPVFIIILFLLFIFYLYKRKGDSLE
PY07187	604	1.52e-53	IFINSYTPKK QDK NFINFIYWEEKYPLLNLYKLMKADPIFIIILFLLFIFYVYKRKDDSE

Motif 15 block diagrams

Name	Lowest p-value	Motifs
PY01963	1.5e-61	
PY00754	2.6e-61	
PY04914	2.6e-61	
PY01773	2.6e-61	
PY01981	1.4e-60	

[illegible]

Motif 15 in BLOCKS format

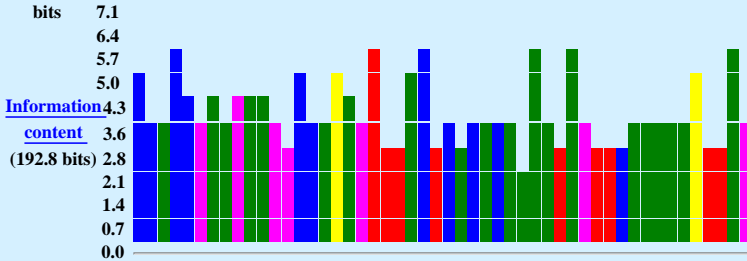
to BLOCKS multiple alignment processor.

Motif 15 position-specific scoring matrix

Motif 15 position-specific probability matrix

Time 2494.50 secs.

PN MOTIF 16 width = 50 sites = 7 llr = 936 E-value = 1.4e-178

[illegible]

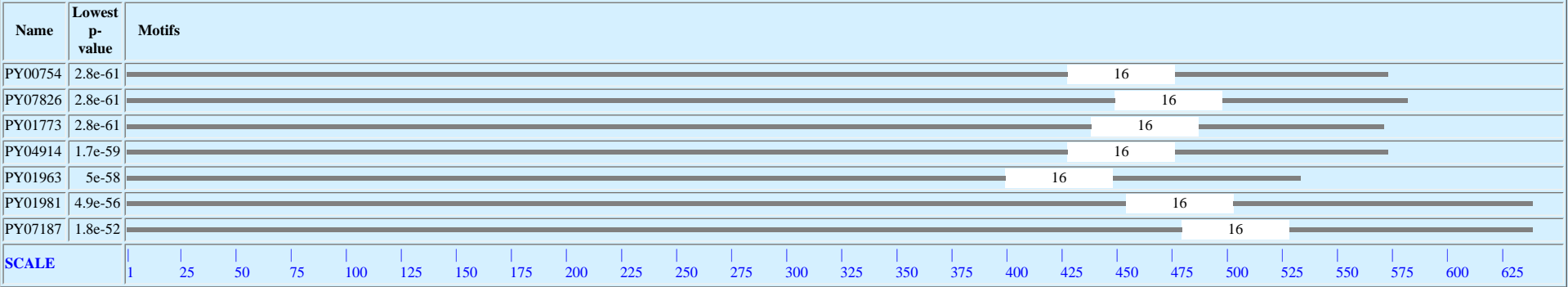
[Multilevel consensus sequence](#)

AINMFDTNETTTEEVINPTDRKKQMKITINLSSQNKQDKKLTNSSTPKKQD

Q I T G FI

NAME	START	P-VALUE	SITES
PY00754	438	2.81e-61	KSKKKKKMKK AINMFDTNETTTEEVINPTDRKKQMKITINLSSQNKQDKKLTNSSTPKKQD KQFINSSTPK
PY07826	460	2.81e-61	KSKKKKKMKK AINMFDTNETTTEEVINPTDRKKQMKITINLSSQNKQDKKLTNSSTPKKQD KQFINSSTPK
PY01773	449	2.81e-61	KSKKKQKMKK AINMFDTNETTTEEVINPTDRKKQMKITINLSSQNKQDKKLTNSSTPKKQD KQFINSSTPK
PY04914	438	1.74e-59	KSKKKKKMKK AINMFDTNETTTEEVINPTDRKKQMKITINLSNQNKQDKKLTNSSTPKKQD KQFINSSTPK
PY01963	409	4.99e-58	KSKKKKKMKK AINMFDTNETTTEEVINPTDRKKQMIIINLSSQNKQGKKLTNSSIQKKQD KKLTNSTQK
PY01981	465	4.94e-56	KSKKKKKMKK AINMFGTNETTESVINPTDRKKQMIIINLSTQNKQGKKFINSSTPKKQD KQFINSSTPK
PY07187	491	1.82e-52	KSKKKKKMKK AINMFDTNETTKRVINSTDRKKPMQIIINLSTQNKQGKKFINSSTPKKQD KKLTSYQTQK

Motif 16 block diagrams



Motif 16 in BLOCKS format

to [BLOCKS multiple alignment processor](#).

Motif 16 position-specific scoring matrix

Motif 16 position-specific probability matrix

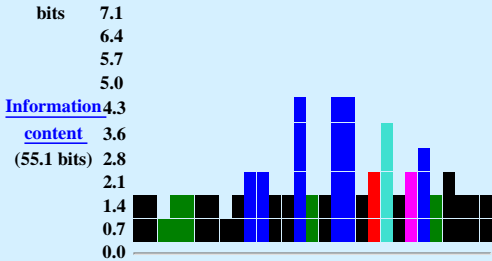
Time 2597.37 secs.

MOTIF 17 width = 29 sites = 32 llr = 1223 E-value = 1.1e-171

[Simplified pos.-specific probability matrix](#)

A 23: 11: : : : : 8: : : 1: 1: 1: : : : :
C : : : : : 3: : 2: : : : : : : : : : : : : : :
D 41: 11421: : : 12: 11: : : : : 1: : 4221
E : 311: : : 2: : : 3: : 14: : 21: 35: : 1: : :
F : : : : : : : : : : a: : : : : : : : : : :
G : : : : : 2: : : : 1: : : : : : : : : : 1: :
H : : : 1: : 1: : : : : : : : : : : : : : : : :

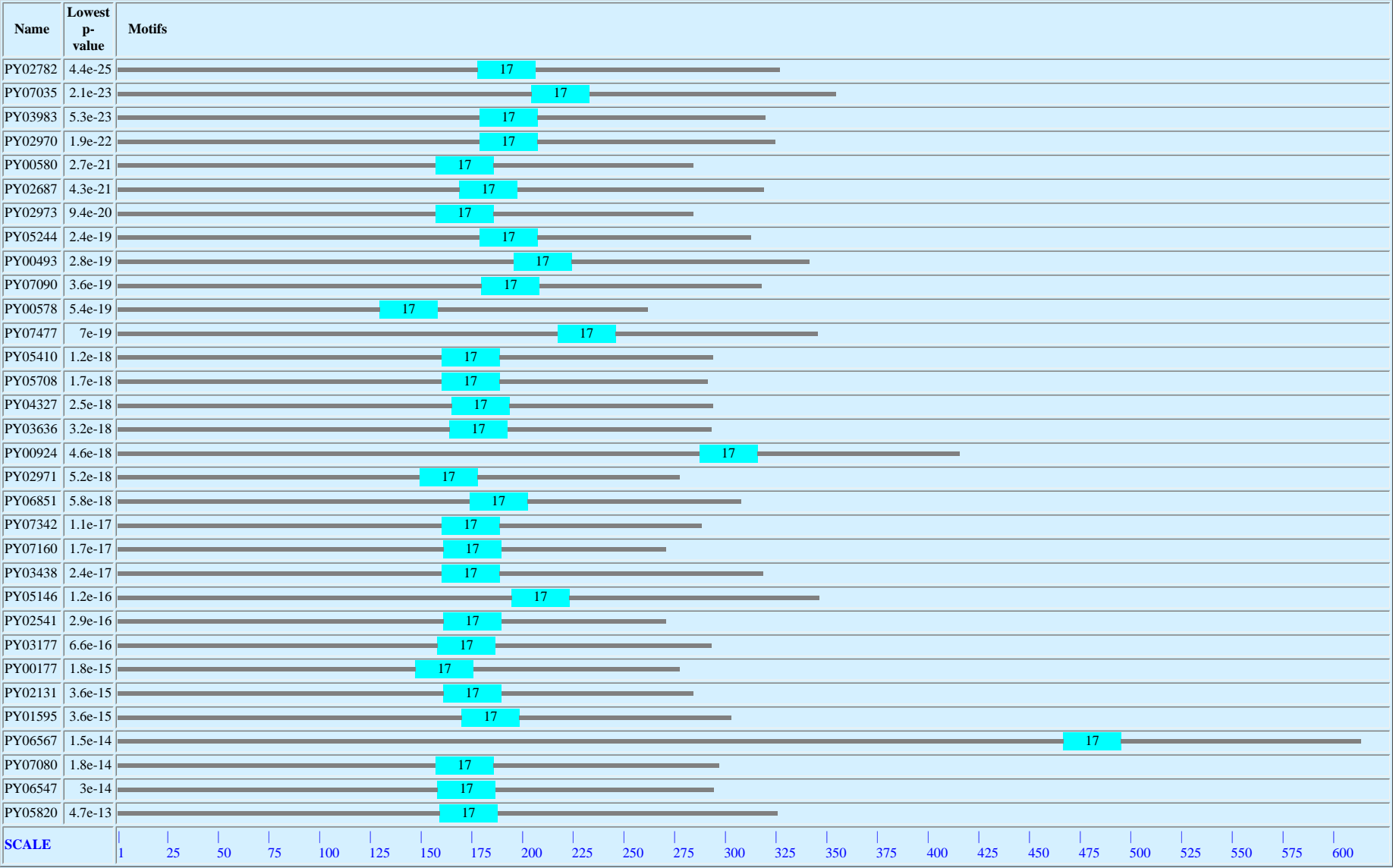
I ::::: 1::: 11::: 2
K 1: 2 122: 24:: 13: 31:: 47: 22: 3: 1: 1
L ::::: 46::: 9: 1:
M ::::: 1:
N 2: 3 31222::: 34: 31:: 1: 1: 64 135
P :::: 1::: 1::: 2:
Q :: 1: 1::: 1: 1: 11:::
R ::::: 1:
S 111131: 11: 3: 1: 1::: 22:
T :: 2221: 24::: 12::: 3: 1:
V 11::: 1:: 8::: 1:
W :::::
Y ::::: 1: 3::: a::: 13:



Multilevel DANNSDCNKLLNNAKEFVKKYTELNDxNN
consensus E K TYSNK N E KN YI
sequence C

NAME	START	P-VALUE	SITES
PY02782	181	4.37e-25	KLLCEMYTEF DENTSCKTKCLEKAKEFVKIYEELNDPNN AKYIGYCQTL
PY07035	208	2.09e-23	KLLCEMYTEF DENASNCTKCSSEKANEFVKAYEKLNDPNN AKYIGYCQAF
PY03983	182	5.31e-23	KPLCNMYTEL DANDTDNKKYLENAEEFVKKYERLNDPNN TKDSYYYQVL
PY02970	182	1.86e-22	KLLCEMYTEF DENTPNCATCSSEKADNFVKIYKELNDPNN IKYSGYCQAW
PY00580	160	2.67e-21	FKLLCNMYSE VATNKDDNTLLDNANRFVQKYTELNTYNI EDTPRSQILS
PY02687	172	4.27e-21	KLLCEMYTEF DENASNCTKCSSEKANEFVKIYKELNDSNN TKYIGYCQAF
PY02973	160	9.38e-20	FKLLCIMYNA DATNKDDNTLSDNATRFVQKYTELNTYNI EDTPRSQILS
PY05244	182	2.44e-19	KPLCNMYTEL NANDASDKRYLKNAKEFVKKYDELNNPNN TKDSAYYQVL
PY00493	199	2.79e-19	KLLCEMYTEF DEKKNCTKCLGKSEEFVKIYKELNDPNN TNYEGYCQAW
PY07090	183	3.64e-19	KPLCNMYTEL SANNPQNKKYLENAREFVEKKYEKLNVSAI SEDSPYYKVL
PY00578	132	5.40e-19	SKLICSMYGN VAQSQTGEILSNNVKFEFVKKYTELKNTYN DEGSPHSKIL
PY07477	221	7.00e-19	SKLLCSMYIN AEKTKDSTLPNEAKDFVIKYKDLNREGYN IEDTARSKIL
PY05410	163	1.17e-18	SKLLCNMYGN VEKNANDTTLSNDAKDFAKKYTGLNREGYN IESSARIKIL
PY05708	163	1.71e-18	SKLICSMYAN KATNTDNKKLLNDATSFVIKYKKLKDGSN TEGTSNNQIL
PY04327	168	2.48e-18	SKLICSMYIN AEKTKESTVPNDAKNFVIKYTDLNESYN IEDTARRKIL
PY03636	167	3.17e-18	AFKLLCSMYG NFEETNKLEQLPDNATSFVNKYTELKDDSN IKGTLHSQLL
PY00924	292	4.57e-18	SKLICSMYAN KSMNTDGNKLLNDATMFVKTYAELKDGSN AEGIPNNQIL
PY02971	152	5.15e-18	FKLLCNIYGN VTRKDDNNTLSNSATSFVNKYTELNNDSK IEGTARSKIL
PY06851	177	5.81e-18	KPLCKMYTEL NANESKCEBCLKNAKKFVEKYNELNASDI DENSPYYQVL
PY07342	163	1.05e-17	SKLICSMYGN GVQNKKGTELSNDATSFVQKYTNLNNKYK TEGASHLQIL
PY07160	164	1.67e-17	KSLCKLYTEC DDSESDYNSYLEKTQEFVKKYEQLKDLDI SENESYRQLF
PY03438	163	2.36e-17	FKILCKMIIN ADKKDDGKTYLEKANEFVIEYQKLLNDND TEDSSYNKIL
PY05146	198	1.25e-16	YALCMMHFEF NQESPDGKYLKNAQNFAEKYKKLNNVSD NKDSPYNRLL
PY02541	164	2.91e-16	KSLCKLYTEC DNIESDYNSYLEKTQEFVKKYEQLKDLDI NKNESYGKLF
PY03177	161	6.65e-16	FKLLCIMYDN YSTNKDNKTLNLSANDFVKVYASLNNDRN IEDTVRNKIL
PY00177	150	1.81e-15	SKLICNMYGN AAQNQTGNILSNNVNDFASQYTELNNKYK DKGTPHSKIL
PY02131	164	3.57e-15	KSLCKLYTEC DDSDSNYYSYLEKTQEFVNKYEQLKEDFD VSEGSYPHQLF
PY01595	173	3.57e-15	KPLCNMYTEL DGSKTISEKSLNANKFVEKYNELNVSDI DKDSPYHQVL
PY06567	474	1.46e-14	YTLCCMYLEF DEESRNCSSKNSGRAKEFVEKYEYLKKNYS ITKNSPYYKL
PY07080	160	1.75e-14	IFKLLCSMYN NVEITNSRDKLPNNANAFIEKYRELNNCN IKGTAYSKIF
PY06547	161	3.02e-14	AFKSLCNMYN SVATSKIDTLLDNAINFFNEYTEINDYYN IENSPYSQIL
PY05820	162	4.66e-13	FKILCNMINS ADKKDGGGETCLKYADQFVDAYQKFINDTD IENSSYNKIL

Motif 17 block diagrams



Motif 17 in BLOCKS format

to [BLOCKS multiple alignment processor](#).

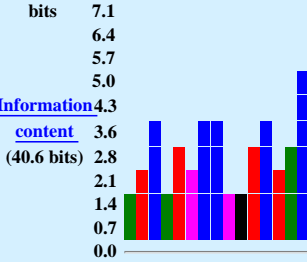
Motif 17 position-specific scoring matrix

Motif 17 position-specific probability matrix

Time 2699.16 secs.

PN **MOTIF 18** width = 15 sites = 25 llr = 703 E-value = 1.2e-097

[Simplified](#) A : : : : 1 : : 1 : : : :
[pos.-specific](#) C : : : : : : 1 : : : : : :
[probability matrix](#) D 2 : : : : 6 2 : 2 : : : : : :
E 1 : : : : : : 4 : : : 2 : :
F : : : : : : : : : : : : : :
G : : : : 1 : : 1 : : : : : :
H : : : : : : : : : : : : : :
I : : a : : : : a : : : a : : 1
K : 7 : 2 6 : : : 1 4 a : 7 : :
L : : : : : : : : : : : : : :
M : : : : 3 : : : : : : : : 9
N 4 2 : 6 : 1 : : : 3 : : : :
P : : : : : : : : : : : : : :
Q : : : : : : : : : : : : : :
R : : : : : : : : : : 1 : :
S 2 : : 1 : 1 : : : : : : a :
T : : : : : : : : 1 : : : :
V : : : : : : 8 : : : : : :
W : : : : : : : : : : : :
Y : : : : : : : : : : : : : :

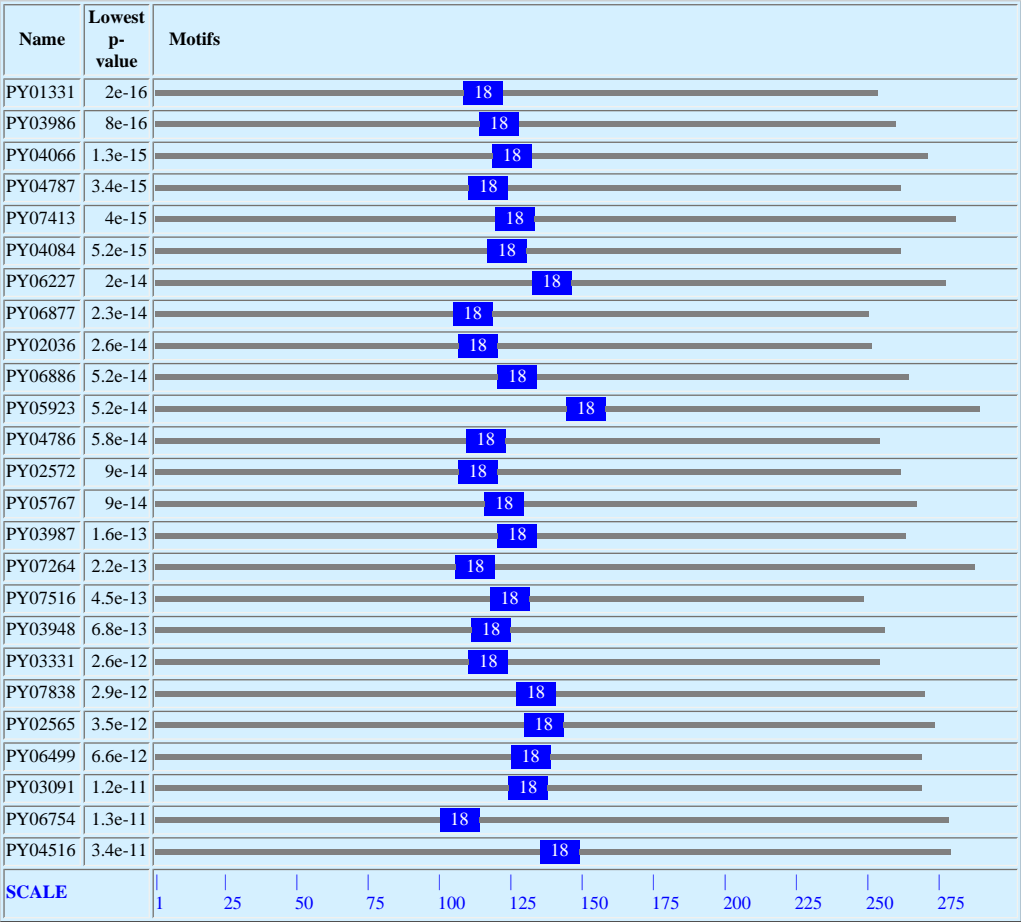


[Multilevel consensus sequence](#) **NKINKDVIEKKIKSM**
DN KM DN

NAME	START	P-VALUE	SITES
PY01331	118	2.02e-16	GHIADNSDNG DKINKDVIEKKIKSM NIDIKYISNY
PY03986	124	8.03e-16	NKYEENISTN NNINKDVIEKKIKSM NMNIKDVSNF
PY04066	129	1.28e-15	DKHITDSDGS NKINKAVIEKKIKSM NMNIKDISNF
PY04787	120	3.39e-15	DKHITDNGS NKINKAVIDKKIKSM NMNIKDISNF
PY07413	130	3.96e-15	ENISNSIDSN GKINMGVIDKKIKSM KMNIKDISNF
PY04084	127	5.24e-15	YNENIGVNSD DKIKKDVIEKKIKSM DMNIKDISNF
PY06227	144	1.99e-14	DNIDKTDSN SNINMTVIEKKIRSM DIDIKDIYNF
PY06877	114	2.28e-14	CYKEHITDSG ENINKDVIEKKMKSM NMNIKDISNF
PY02036	116	2.59e-14	YINNIDDNSD DNINKSVIEKKIKSM NMDIKDISNF
PY06886	131	5.18e-14	IAADSDSDSD SKINKNVICKKIKSM DIDIKDISNF
PY05923	157	5.18e-14	KHIASDSSSG KKI MDVIDTKIE SM NIDIKDISNF
PY04786	119	5.80e-14	YDKHITSSTS ENINKSVIEKKIKSM NMNIKDISNF

PY02572	116	9.02e-14	YKGNISADSD	DHINMEVISAKIKSM	NIDIKDISNF
PY05767	126	9.02e-14	SKYKEHITAG	DKINNDVIKNKIKSM	NMNIKDISNF
PY03987	131	1.58e-13	QKINANSDDSD	NKISKDVIKKKIISM	DIDIKDISNF
PY07264	115	2.18e-13	YNQEKIGDSN	NKIKIDVIDAKIKSM	NMNIKDISNF
PY07516	128	4.55e-13	EHIDTDNSSG	NKIYMGVIDEKKIISM	DIDIKDISNF
PY03948	121	6.78e-13	SCYKENIGTD	SKIKKDDICKKKIKSM	NIDIKDISNF
PY03331	120	2.63e-12	YEKNISTDSN	IKINMGFIDTKIISM	NMDIKDISNF
PY07838	138	2.89e-12	NNSCYKGNIP	NDINMDDIGNKIKLM	DIDIKDISNF
PY02565	141	3.47e-12	INAHNDSDSG	NKISKDVIETKIRSI	NIDIKDISNF
PY06499	136	6.60e-12	TNNCYKGNIP	NNINMDDIGNKIKSI	DIDIKDISNF
PY03091	135	1.22e-11	YKENIGVKSG	DKITKDVIKKQISSM	NIDIKDISNF
PY06754	109	1.34e-11	YNQKINTNSS	NKIKKNDIENKINSM	NIGIKDMSNF
PY04516	147	3.42e-11	EVINANSDSG	SKIKKDVIVKKIKST	NIDIKDISNF

Motif 18 block diagrams



Motif 18 in BLOCKS format

to BLOCKS multiple alignment processor.

Motif 18 position-specific scoring matrix

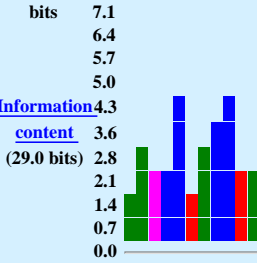
Motif 18 position-specific probability matrix

Time 2798.48 secs.

MOTIF 19 width = 11 sites = 31 llr = 622 E-value = 1.9e-067

Simplified pos.-specific probability matrix

A	:	1	:	:	:	:	9	:	:
C	:	:	:	:	:	:	:	:	:
D	3	:	3	:	:	:	1	:	:
E	:	:	3	:	:	1	:	:	1
F	:	:	:	:	:	:	:	:	:
G	:	:	1	:	:	:	:	:	1
H	:	:	:	:	:	:	:	:	:
I	:	:	:	:	:	:	:	:	:
K	:	:	:	:	5	:	:	6	:
L	:	:	:	5	:	:	:	:	:
M	:	:	:	:	:	:	:	:	:
N	2	:	:	1	:	2	:	1	:
P	:	:	:	:	:	:	:	:	:
Q	:	:	1	:	:	1	:	:	:
R	:	:	:	:	:	1	:	:	1
S	2	8	3	1	:	:	9	:	:
T	3	:	:	:	:	:	:	:	1
V	1	:	:	3	:	:	:	7	:
W	:	:	:	:	:	:	:	:	:
Y	:	:	:	:	:	:	:	1	:



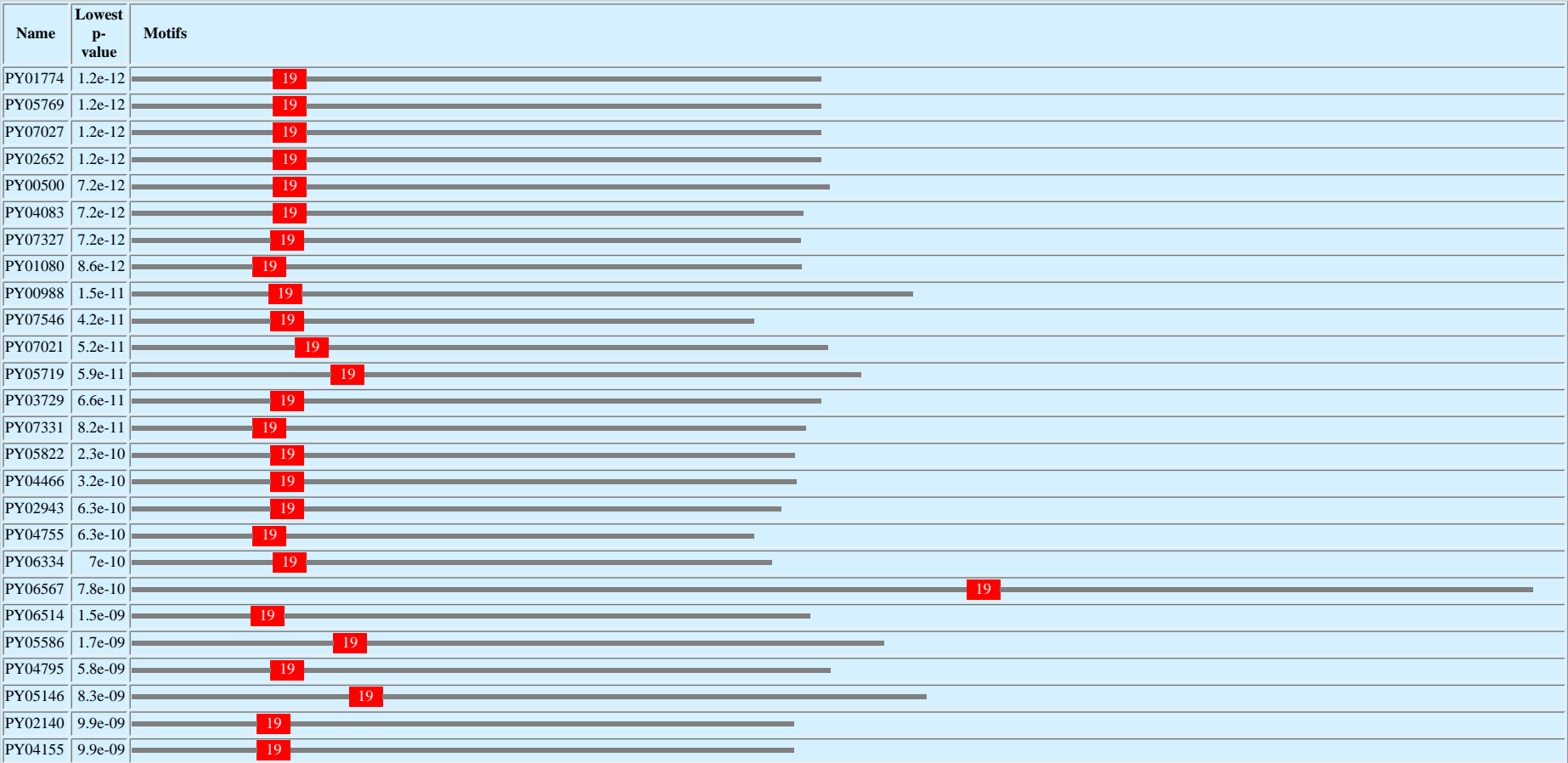
Multilevel consensus sequence

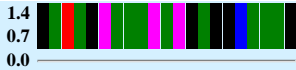
D	S	E	L	F	K	S	V	A	K	S
T	S	V			N				N	
S		D								

NAME	START	P-VALUE	SITES
PY01774	64	1.22e-12	CLYLFNKIFG TSELFKSVANS NINIVEYIMI
PY05769	64	1.22e-12	CLYLFKQIFG TSELFKSVANS NINIVDYILI
PY07027	64	1.22e-12	CLYLFNKIFG TSELFKSVANS NINIVEYIMI
PY02652	64	1.22e-12	CLYLFKQIFG TSELFKSVANS NINIVDYILI
PY00500	64	7.18e-12	CLYFFNEFFG SSDLFKSVAKS NINIAGYIMI
PY04083	64	7.18e-12	CLYLFNQIFG TSQLFKSVANS NINIVEYIMI
PY07327	63	7.18e-12	CLYLFNQIFG TSQLFKSVANS NINIVEYIMI

MEME					
PY01080	55	8.64e-12	CLYLFNKFFG	SS EL FKSVANS	NINIVDYILI
PY00988	62	1.47e-11	CLYLLYTFFG	SS DL FQSVAKS	NTNIVDYIII
PY07546	63	4.24e-11	CLYLFDGFFK	DAD LF KSVAKS	NIDIVEYIMI
PY07021	74	5.23e-11	CLYFFNEFFK	DAS VFR SVAKS	NIDIVDYIII
PY05719	90	5.88e-11	CLYLFNAFFG	SS DL FNSVAKG	NINIVDYIIL
PY03729	63	6.58e-11	CLYLFKQIFG	TS EFF KSVANS	NINIVDYILI
PY07331	55	8.17e-11	CLYLFNHFFG	SS EL FKTVANS	NINIVDYILT
PY05822	63	2.31e-10	CLYLLNEFFK	NSS VF QSVAKN	NINIVEYIMI
PY04466	63	3.19e-10	CLYLFMQIFG	TS EL FTSVANN	NINIVDYILI
PY02943	63	6.26e-10	CLFLFNELFG	SS D SFNSVAKG	NINIVEYIMI
PY04755	55	6.26e-10	CLFLFNELFG	SS D SFNSVAKG	NTNIVDYILI
PY06334	64	7.02e-10	CLYLLDAFFK	DNS VFN SVAKS	NINIVEYIII
PY06567	374	7.82e-10	CLYLLDSFFK	DSS VFR SVAKS	NTNIVEYIII
PY06514	54	1.51e-09	CLYLFDAFFK	NSS VFK SDAKS	NINIVEYIII
PY05586	91	1.67e-09	CLYLLDAFFK	NSS VFK SVAKS	NIDVVEYIII
PY04795	63	5.79e-09	CLYLFNEFFG	NSS VFE SVSKS	NVNIVEYIMI
PY05146	98	8.27e-09	CLYLFDAFFK	NSS VFM SDAKG	NTNIVEYIII
PY02140	57	9.87e-09	CLFLFDEFFK	DSD NFK SNAKS	NINIVEYIMI
PY04155	57	9.87e-09	CLFLFDEFFK	DSD NFK SNAKS	NINIVEYIMI
PY03042	62	1.53e-08	CLYFFDAFFK	DSS LF EKVAKN	NINIVDYIII
PY05828	62	1.82e-08	CLYLFDELFK	DY EK FNSVAKR	KINIVDYILI
PY04430	62	8.27e-08	CLYLFDEFFA	GFT Q FNSVAKR	KINIVDYILI
PY07017	45	1.23e-07	FLYLLNQFCG	VS GL FKSC ET S	NINVVEYTMI
PY02940	68	1.67e-07	FLYLFNGLFG	VS GL FNSR ET S	NINVVEYIMI

Motif 19 block diagrams

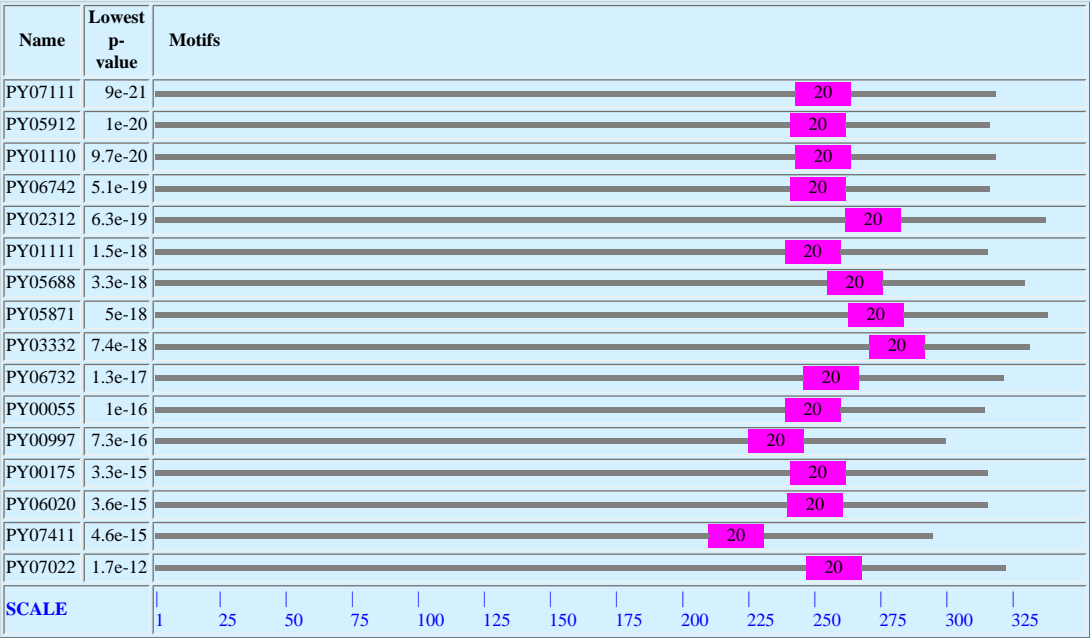




Multilevel consensus sequence
ETKTT**E**SSSETDQSD**I**ETTL
G K N V P

NAME	START	P-VALUE	SITES
PY07111	244	8.95e-21	AENGGISDSK VT K T I E S S S E T G Q S N I V T T T F SSNTTLSGSS
PY05912	242	1.01e-20	AKKVEVEGYN ET K I G E S S S E T G Q S D H E T T I P SYDTTLSGLS
PY01110	244	9.66e-20	PKKDNTEGTK VT K A T G S S S E P D R S N I A T T P Q ISNITLSESS
PY06742	242	5.08e-19	AQKVEVEISN ET K T T G S S S E T G N Q D I E T I T L IPNTALSDSS
PY02312	263	6.30e-19	SKTVDVEGSN RT K T D E S S S E T D Q T I N V M T P L SSNSALSDSS
PY01111	240	1.46e-18	TPKKDNPGBK VT K A T D I S S E T D N S D I A T A T P SSDITLSDSS
PY05688	256	3.32e-18	PKKDNVESSK ET K T E S S N E A G K S D I A T I T L SQNTALSDSS
PY05871	264	4.97e-18	AKKVSVEGSN A T Q T V G S S S G P D K S N I E T A T P ISNTTLSESS
PY03332	272	7.39e-18	GKKVEVEGSK G N K T V E S S S E T S Q S I N V S T T P IYDTILPGSS
PY06732	247	1.33e-17	VKKVNVEGSN G T K T P E S S I K T D Q S N L V T T T ISNTILPYSS
PY00055	240	1.05e-16	SETKIDGSSS ET K I D N S S S E T V Q S I N V T E T M SYNTTLAGSS
PY00997	226	7.35e-16	DNPEDPKVTK A T K G T E I S S E E D K S D I E T I Q S YDTILSGSSL
PY00175	242	3.34e-15	PQQVNQEVPK E I K T T E T S S G S D K L D T E T T L S SNITLSESSL
PY06020	241	3.63e-15	AQKVNQEVPK E I K T T E T S S E S D K L D T E M T N L SSNITLSGSS
PY07411	211	4.64e-15	SRKVIVAGSN ET K I D D S S I G I V Q S N L V T T P L SFNTILSDSS
PY07022	248	1.73e-12	SNPIEGKDVS L G E T S E S S F E T D V S R S E T E V S DSDSGSPSSL

Motif 20 block diagrams



Motif 20 in BLOCKS format

to BLOCKS multiple alignment processor.

Motif 20 position-specific scoring matrix

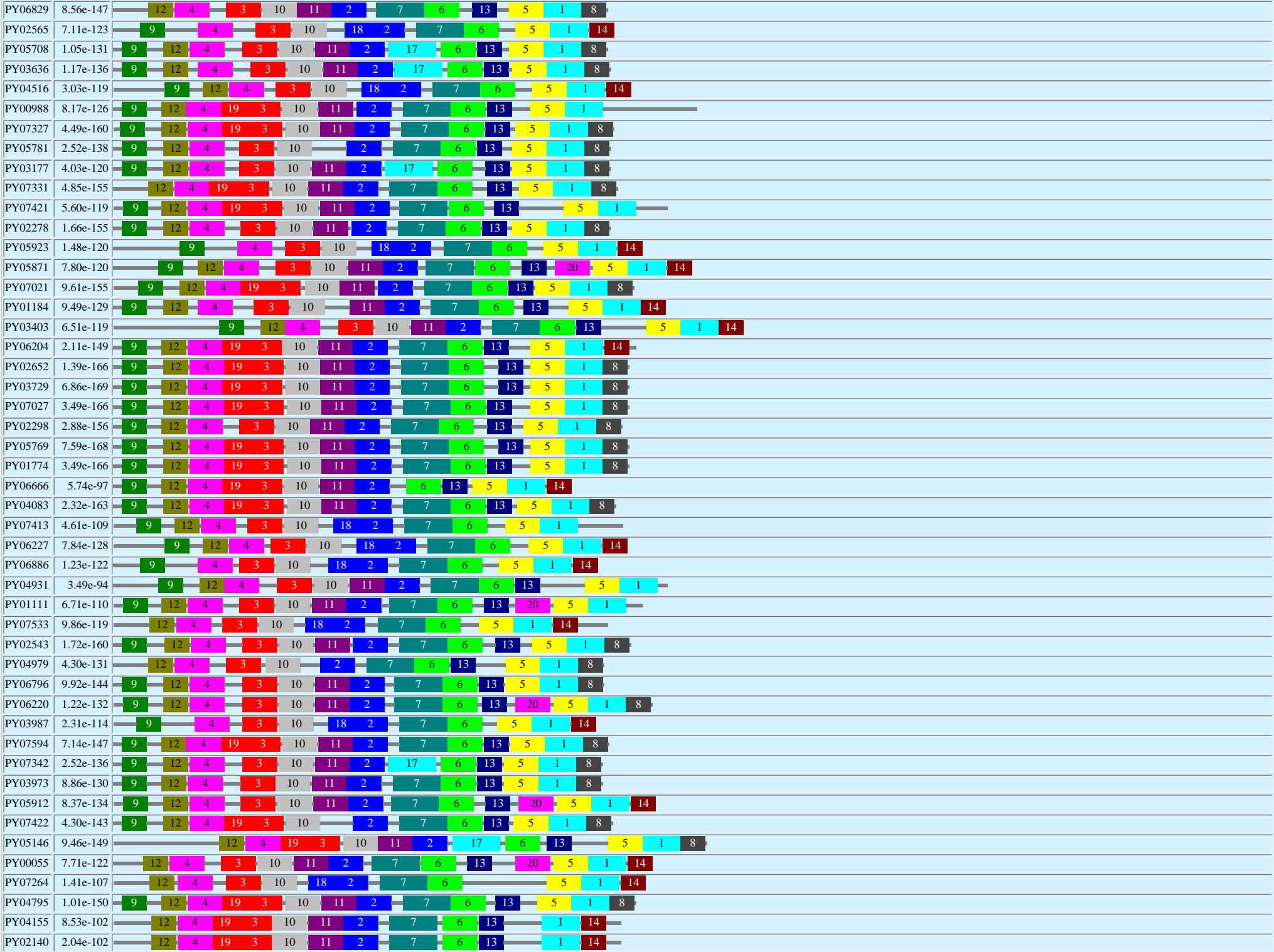
Motif 20 position-specific probability matrix

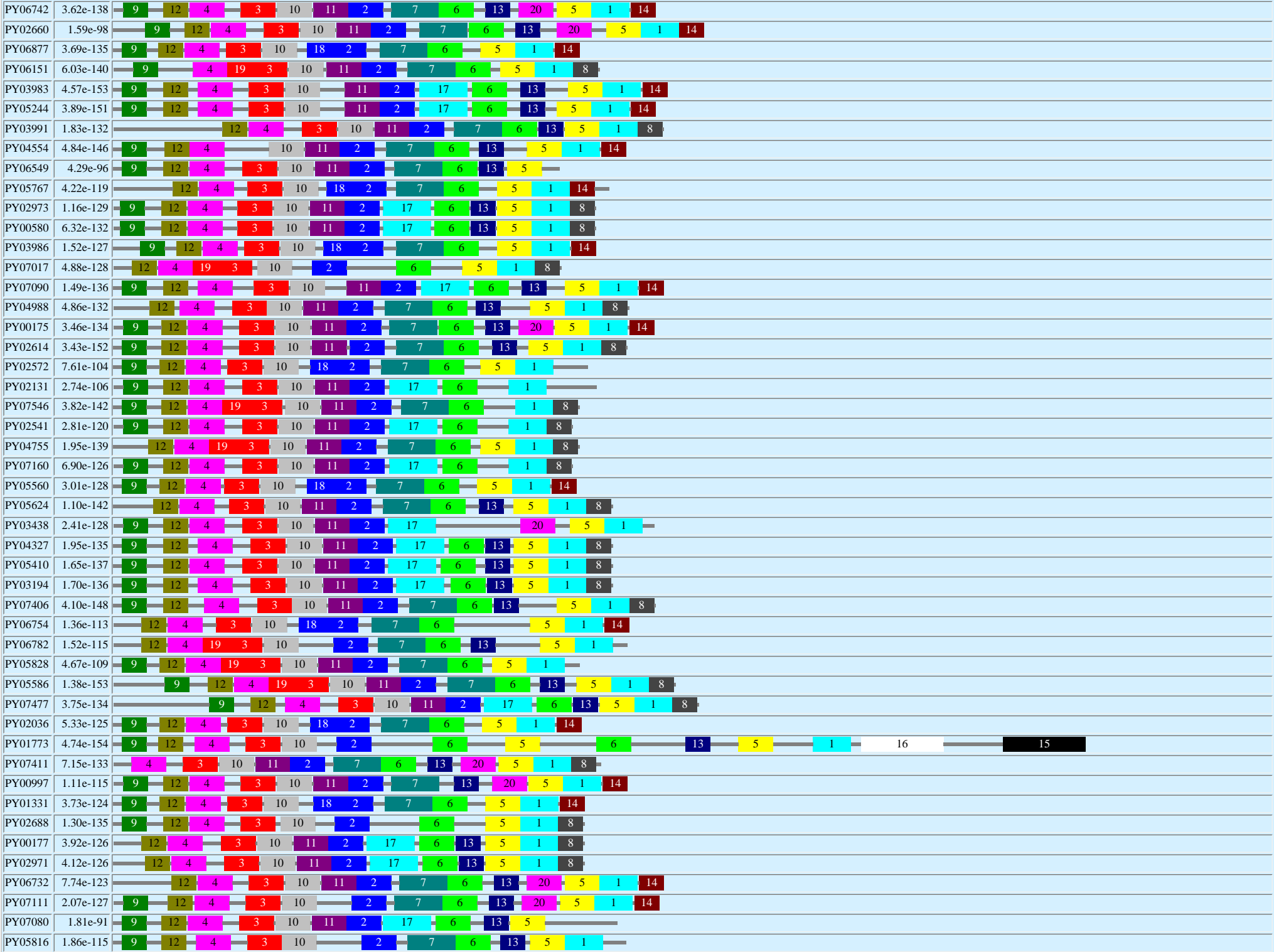
Time 2996.41 secs.

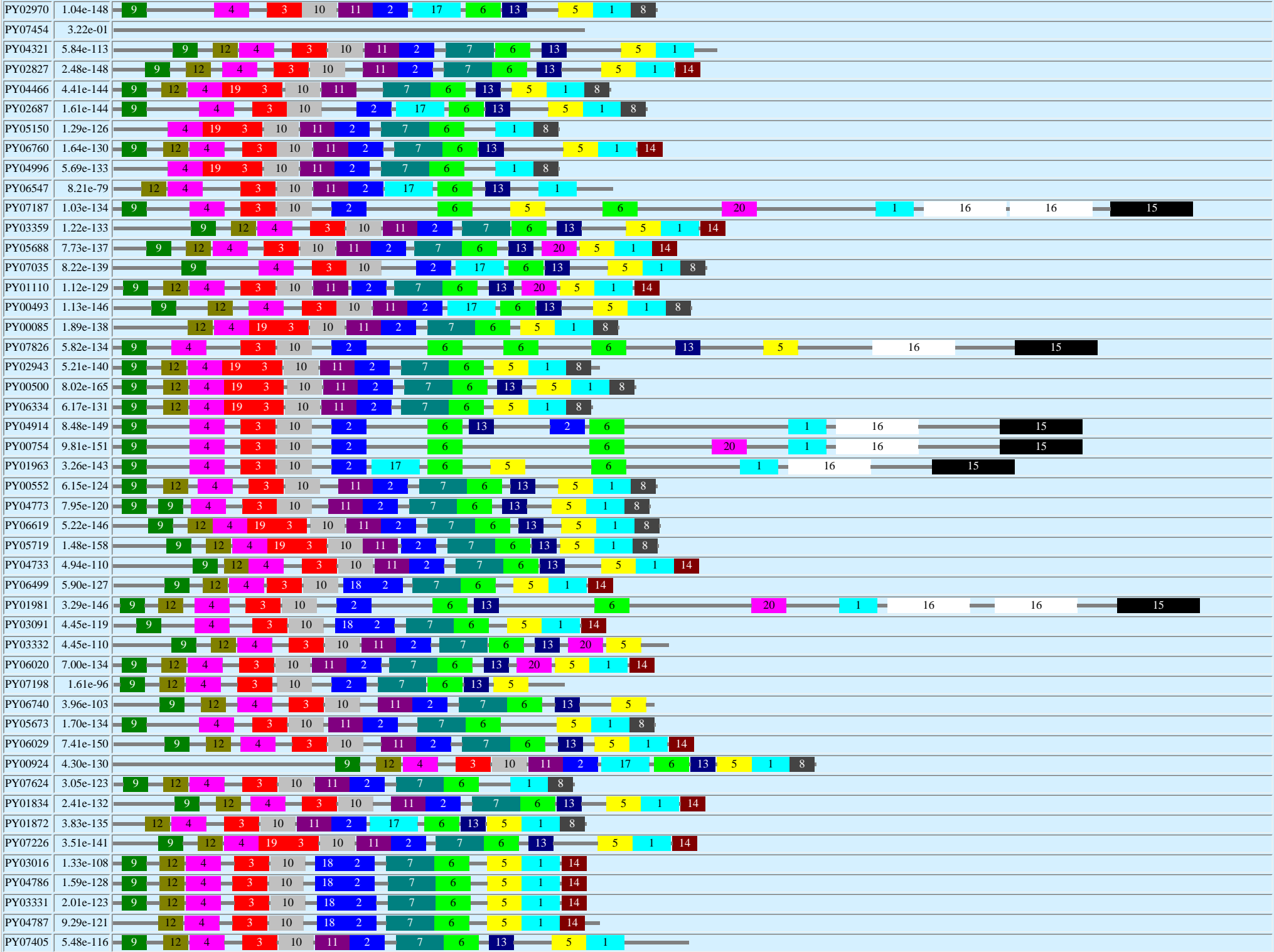
SUMMARY OF MOTIFS

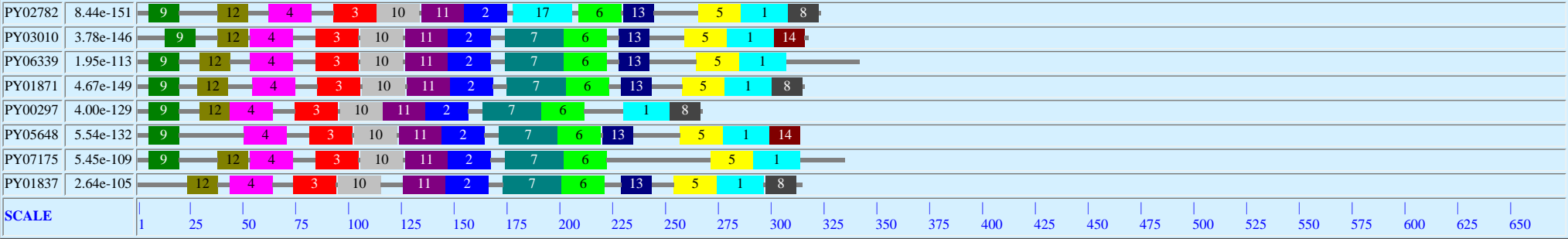
Combined block diagrams: non-overlapping sites with p-value < 0.0001

Name	Combined p-value	Motifs
PY02940	5.20e-147	<div><div>9</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>8</div></div>
PY04215	1.64e-134	<div><div>9</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>8</div></div>
PY01080	7.84e-164	<div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>13</div><div>5</div><div>1</div><div>8</div></div>
PY00578	8.93e-89	<div><div>9</div><div>12</div><div>3</div><div>10</div><div>11</div><div>2</div><div>17</div><div>6</div><div>13</div><div>5</div><div>1</div></div>
PY04066	5.31e-116	<div><div>12</div><div>4</div><div>3</div><div>10</div><div>18</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>14</div></div>
PY05822	7.70e-153	<div><div>9</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>13</div><div>5</div><div>1</div><div>8</div></div>
PY04084	4.44e-132	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>18</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>14</div></div>
PY05820	5.21e-109	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>2</div><div>17</div><div>6</div><div>13</div><div>20</div><div>5</div><div>1</div><div>14</div></div>
PY07022	4.10e-141	<div><div>9</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>13</div><div>20</div><div>5</div><div>1</div><div>14</div></div>
PY01595	3.74e-111	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>11</div><div>2</div><div>17</div><div>6</div><div>5</div><div>1</div><div>14</div></div>
PY04430	7.88e-133	<div><div>9</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>8</div></div>
PY07516	5.13e-111	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>18</div><div>2</div><div>6</div><div>5</div><div>1</div><div>8</div></div>
PY01873	2.07e-121	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>13</div><div>5</div><div>1</div><div>14</div></div>
PY07501	1.55e-79	<div><div>9</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>5</div></div>
PY06567	6.85e-184	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>13</div><div>5</div><div>1</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>13</div><div>5</div><div>1</div><div>8</div></div>
PY00308	8.55e-73	<div><div>12</div><div>4</div><div>3</div><div>10</div><div>2</div><div>7</div><div>6</div><div>13</div><div>1</div><div>14</div></div>
PY06374	1.06e-121	<div><div>9</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>14</div></div>
PY07849	1.58e-138	<div><div>9</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>8</div></div>
PY03760	4.68e-141	<div><div>9</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>14</div></div>
PY07653	1.91e-127	<div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>1</div><div>8</div></div>
PY03042	5.76e-148	<div><div>9</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>8</div></div>
PY06126	2.32e-143	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>8</div></div>
PY02671	9.51e-121	<div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>14</div></div>
PY06514	2.33e-156	<div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>13</div><div>5</div><div>1</div><div>8</div></div>
PY00284	9.32e-105	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>13</div><div>5</div></div>
PY06763	1.43e-104	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>2</div><div>7</div><div>6</div><div>13</div><div>5</div><div>1</div></div>
PY00494	1.75e-141	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>2</div><div>7</div><div>6</div><div>13</div><div>5</div><div>1</div><div>8</div></div>
PY02564	7.33e-146	<div><div>9</div><div>12</div><div>4</div><div>19</div><div>3</div><div>10</div><div>2</div><div>7</div><div>6</div><div>13</div><div>5</div><div>1</div><div>8</div></div>
PY02312	3.69e-127	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>11</div><div>2</div><div>7</div><div>6</div><div>13</div><div>20</div><div>5</div><div>1</div><div>14</div></div>
PY06851	3.76e-133	<div><div>9</div><div>12</div><div>4</div><div>3</div><div>10</div><div>11</div><div>2</div><div>17</div><div>6</div><div>13</div><div>5</div><div>1</div><div>14</div></div>
PY03948	7.99e-126	<div><div>9</div><div>4</div><div>3</div><div>10</div><div>18</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>14</div></div>
PY07838	2.34e-123	<div><div>9</div><div>4</div><div>3</div><div>10</div><div>18</div><div>2</div><div>7</div><div>6</div><div>5</div><div>1</div><div>14</div></div>









Motif summary in machine readable format.

Stopped because nmotifs = 20 reached.

CPU: unknown

EXPLANATION OF MEME RESULTS

The MEME results consist of:

- The [version](#) of MEME and the date it was released.
- The [reference](#) to cite if you use MEME in your research.
- A description of the [sequences](#) you submitted (the "training set") showing the name, "weight" and length of each sequence.
- The [command line summary](#) detailing the parameters with which you ran MEME.
- Information on each of the [motifs](#) MEME discovered, including:
 - 1. A [summary line](#) showing the width, number of occurrences, log likelihood ratio and statistical significance of the motif.
 - 2. A [simplified position-specific probability matrix](#).
 - 3. A [diagram](#) showing the degree of conservation at each motif position.
 - 4. A [multilevel consensus sequence](#) showing the most conserved letter(s) at each motif position.
 - 5. The [occurrences of the motif](#) sorted by *p*-value and aligned with each other.
 - 6. [Block diagrams](#) of the occurrences of the motif within each sequence in the training set.
 - 7. The motif in [BLOCKS or FASTA format](#).
 - 8. A [position-specific scoring matrix \(PSSM\)](#) for use by the [MAST](#) database search program.
 - 9. The [position specific probability matrix \(PSPM\)](#) describing the motif.
- A [summary of motifs](#) showing an optimized (non-overlapping) tiling of all of the motifs onto each of the sequences in the training set.
- The reason why MEME [stopped](#) and the name of the CPU on which it ran.
- This [explanation](#) of how to interpret MEME results.

MOTIFS

For each motif that it discovers in the training set, MEME prints the following information:

- [Summary Line](#)

This line gives the width (width'), number of occurrences in the training set (sites'), log likelihood ratio (llr) and *E*-value of the motif. Each motif describes a pattern of a fixed width--no gaps are allowed in MEME motifs. MEME numbers the motifs consecutively from one as it finds them. MEME usually finds the most statistically significant (low *E*-value) motifs first. The statistical significance of a motif is based on its log likelihood ratio, its width and number of occurrences, the background letter frequencies (given in the [command line summary](#)), and the size of the training set. The *E*-value is an estimate of the expected number of motifs with the given log likelihood ratio (or higher), and with the same width and number of occurrences, that one would find in a similarly sized set of random sequences. (In random sequences each position is independent with letters chosen according to the background letter frequencies.) The log likelihood ratio is the logarithm of the ratio of the probability of the occurrences of the motif given the motif model (likelihood given the motif) versus their probability given the background model (likelihood given the null model). (Normally the background model is a 0-order Markov model using the background letter frequencies, but higher order Markov models may be specified via the **-bfile** option to MEME.) Clicking on the **buttons** to the left of the motif summary line takes you to the previous motif (P) or next motif (N).

- [Simplified Position-Specific Probability Matrix](#)

MEME motifs are represented by position-specific probability matrices that specify the probability of each possible letter appearing at each possible position in an occurrence of the motif. In order to make it easier to see which letters are most likely in each of the columns of the motif, the simplified motif shows the letter probabilities multiplied by 10 rounded to the nearest integer ("a" means 10). Zeros are replaced by ":" (the colon) for readability.

• [Information Content Diagram](#)

The information content diagram provides an idea of which positions in the motif are most highly conserved. Each column (position) in a motif can be characterized by the amount of information it contains (measured in bits). Highly conserved positions in the motif have high information; positions where all letters are equally likely have low information. (The information content is relative to the background letter frequencies which are given in the [command line summary](#) section.) The diagram is printed so that each column lines up with the same column in the simplified position-specific probability matrix above it. Columns in the information content diagram are colored according to the majority category of the letters occurring in that column of the alignment. If no letter category has frequency above 0.5, the column in the diagram is colored black. For DNA sequences, the letter categories contain one letter each. For proteins, the categories are based on the biochemical properties of the various amino acids. The categories and their colors are:

NUCLEIC ACIDS	COLOR
A	RED
C	BLUE
G	ORANGE
T	GREEN

AMINO ACIDS	COLOR	PROPERTIES
A, C, F, I, L, V, W and M	BLUE	Most hydrophobic[Kyte and Doolittle, 1982]
NQST	GREEN	Polar, non-charged, non-aliphatic residues
DE	MAGENTA	Acidic
KR	RED	Positively charged
H	PINK	
G	ORANGE	
P	YELLOW	
Y	TURQUOISE	

J. Kyte and R. Doolittle, 1982. "A Simple Method for Displaying the Hydropathic Character of a Protein", J. Mol Biol. 157, 105-132.

Summing the information content for each position in the motif gives the total information content of the motif (shown in parentheses to the left of the diagram). The total information content is approximately equal to the log likelihood ratio divided by the number of occurrences times ln(2). The total information content gives a measure of the usefulness of the motif for database searches. For a motif to be useful for database searches, it must as a rule contain at least log₂(N) bits of information where N is the number of sequences in the database being searched. For example, to effectively search a database containing 100,000 sequences for occurrences of a *single* motif, the motif should have an IC of at least 16.6 bits. Motifs with lower information content are still useful when a family of sequences shares more than one motif since they can be combined in *multiple* motif searches (using MAST).

• [Multilevel Consensus Sequence](#)

The multilevel consensus sequence corresponding to the motif is an aid in remembering and understanding the motif. It is calculated from the motif position-specific probability matrix as follows. Separately for each column of the motif, the letters in the alphabet are sorted in decreasing order by the probability with which they are expected to occur in that position of motif occurrences. The sorted letters are then printed vertically with the most probable letter on top. Only letters with probabilities of 0.2 or higher at that position in the motif are printed. As an example, the multilevel consensus sequence of motif 1 in the sample output is:

```
Multilevel  TTATGTGAACGACGTCACACT
consensus  AA  T A G A GA      AA
sequence   T C TT      T
```

This multilevel consensus sequence says several things about the motif. First, the most likely form of the motif can be read from the top line as TTATGTGAACGACGTCACACT. Second, that only letter A has probability more than 0.2 in position 3 of the motif, both T and A have probability greater than 0.2 in position 1, etc. Third, a *rough approximation* of the motif can be made by converting the multilevel consensus sequence into the Prosite signature [TA]-[TA]-A-T-[GT]-[T]-[GA]-A-[AGT]-C-[GAC]-A-[CGT]-[GAT]-T-C-A-C-A-[CAT]-[TA].

• [Occurrences of the Motif](#)

MEME displays the occurrences (sites) of the motif in the training set. The sites are shown aligned with each other, and the ten sequence positions preceding and following each site are also shown. Each site is identified by the name of the sequence where it occurs, the strand (if both strands of DNA sequences are being used), and the position in the sequence where the site begins. When the DNA strand is specified, '+' means the sequence in the training set, and '-' means the reverse complement of the training set sequence. (For '-' strands, the 'start' position is actually the position on the **positive** strand where the site ends.) The sites are listed in order of increasing statistical significance (*p*-value). The *p*-value of a site is computed from the the match score of the site with the [position specific scoring matrix](#) for the motif. The *p*-value gives the probability of a random string (generated from the background letter frequencies) having the same match score or higher. (This is referred to as the **position *p*-value** by the MAST algorithm.)

• [Block Diagrams of Motif Occurrences](#)

The occurrences of the motif in the training set sequences are shown with MAST-style block diagrams. One diagram is printed for each sequence showing all the occurrences of the motif in that sequence. The sequences are sorted by the **lowest** *p*-value among all occurrences of the motif in a given sequence. (The *p*-value of an occurrence is the probability of a single random subsequence the length of the motif, generated according to the 0-order background model, having a score at least as high as the score of the occurrence.) When the DNA strand is specified, '+' means the motif appears from left to right on the sequence, and '-' means the motif appears from right to left on the complementary strand. A sequence position scale is shown at the end of each table of block diagrams. Very long sequences are shown with thick lines connecting the motifs and are **not** drawn to scale.

• [Motif in BLOCKS format or FASTA format](#)

For use with [BLOCKS tools](#), MEME prints the occurrences of the motif in BLOCKS format.

You can convert these blocks to PSSMs (position-specific scoring matrices), LOGOS (color representations of the motifs), phylogeny trees and search them against a database of other blocks by pasting everything from the "BL" line to the "/" line (inclusive) into the [Multiple Alignment Processor](#). If you include the **-print_fasta** switch on the command line, MEME prints the motif sites in FASTA format instead of BLOCKS format.

• [Position-Specific Scoring Matrix](#)

The position-specific scoring matrix corresponding to the motif is printed for use by database search programs such as MAST. This matrix is a log-odds matrix calculated by taking 100 times the log (base 2) of the ratio p/f at each position in the motif where p is the probability of a particular letter at that position in the motif, and f is the background frequency of the letter (given in the [command line summary](#) section.) This is the same matrix that is used above in computing the p -values of the occurrences of the motif in the [Occurrences of the Motif](#) and [Block Diagrams of Motif Occurrences](#) sections. The scoring matrix is printed "sideways"--columns correspond to the letters in the alphabet (in the same order as shown in the simplified motif) and rows corresponding to the positions of the motif, position one first. The scoring matrix is preceded by a line starting with "log-odds matrix:" and containing the length of the alphabet, width of the motif, number of characters in the training set, the scoring threshold (obsolete) and the motif E -value.

Note: The probability p used to compute the PSSM is *not* exactly the same as the corresponding value in the Position Specific Probability Matrix (PSPM). The values of p used to compute the PSSM take into account the motif prior, whereas the values in the PSPM are just the *observed* frequencies of letters in the motif sites.

• [Position-Specific Probability Matrix](#)

The motif itself is a position-specific probability matrix giving, for each position in the pattern, the observed frequency ("probability") of each possible letter. The probability matrix is printed "sideways"--columns correspond to the letters in the alphabet (in the same order as shown in the simplified motif) and rows corresponding to the positions of the motif, position one first. The motif is preceded by a line starting with "letter-probability matrix:" and containing the length of the alphabet, width of the motif, number of occurrences of the motif, and the E -value of the motif.

Note: Earlier versions of MEME gave the posterior probabilities--the probability after applying a prior on letter frequencies--rather than the observed frequencies. These versions of MEME also gave the number of *possible* positions for the motif rather than the actual number of occurrences. The output from these earlier versions of MEME can be distinguished by "n=" rather than "nsites=" in the line preceding the matrix.

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