
MEME - Motif discovery tool

MEME version 5.1.1 (Release date: Wed Jan 29 15:00:42 2020 -0800)

For further information on how to interpret please access <http://alternate.meme-suite.org/>.
To get a copy of the MEME software please access <http://meme-suite.org>.

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

PRIMARY SEQUENCES= All_radiation_promoters_greater_than_five.txt

CONTROL SEQUENCES= --none--

ALPHABET= ACGT

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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.

command: meme All_radiation_promoters_greater_than_five.txt -dna -oc . -nostatus -time 17929 -mod zoops -

nmotifs 10 -minw 6 -maxw 50 -objfun classic -revcomp -markov_order 0 -psp priors.psp

model: mod= zoops nmotifs= 10 evt= inf
objective function: em= E-value of product of p-values
starts= E-value of product of p-values

strands: + -
width: minw= 6 maxw= 50
nsites: minsites= 2 maxsites= 467 wnsites= 0.8
theta: spmap= uni spfuzz= 0.5
em: prior= dirichlet b= 0.01 maxiter= 50
distance= 1e-05
trim: wg= 11 ws= 1 endgaps= yes
data: n= 466858 N= 467
sample: seed= 0 hsfrac= 0
searchsize= 100000 norand= no csites= 1000

Letter frequencies in dataset:
A 0.243 C 0.257 G 0.257 T 0.243
Background letter frequencies (from file dataset with add-one prior applied):
A 0.243 C 0.257 G 0.257 T 0.243
Background model order: 0

MOTIF STTCAAGTT MEME-1 width = 9 sites = 165 llr = 1677 E-value = 8.3e-005

Motif STTCAAGTT MEME-1 Description

Simplified A 1:::aa:::
pos.-specific C 6::8:::1
probability G 3::2::a:1
matrix T :aa:::a8

bits 2.0 ** **
1.8 ** ****
1.6 ** ****
1.4 ** ****
Relative 1.2 ****
Entropy 1.0 ****
(14.7 bits) 0.8 ****
0.6 ****
0.4 ****
0.2 ****
0.0 -----

Multilevel CTTCAAGTT
consensus G G
sequence

Motif STTCAAGTT MEME-1 sites sorted by position p-value

Table with 5 columns: Sequence name, Strand, Start, P-value, Site. Lists sequence names like HMPREF1120_01601 and their corresponding strand, start position, p-value, and site sequence.

HMPREF1120_06465	+	462	3.49e-06	AAACAATCGC	CTTCAAGTT	TAGGTCCTC
HMPREF1120_07879	-	754	3.49e-06	CGGCGCGAG	CTTCAAGTT	TGCTTTATCC
HMPREF1120_00198	-	370	3.49e-06	CCTCTCCAGA	CTTCAAGTT	TTGCCAGCAC
HMPREF1120_01182	-	709	3.49e-06	AACGCATTCA	CTTCAAGTT	CAACTTGAGT
HMPREF1120_04734	+	975	3.49e-06	CTCCAACAT	CTTCAAGTT	CTCTCAACTT
HMPREF1120_03451	-	193	3.49e-06	CCGAAGCGAA	CTTCAAGTT	TGCGCCGGGC
HMPREF1120_01099	-	447	3.49e-06	GAAGCTGGGA	CTTCAAGTT	GAGGGTGTCA
HMPREF1120_00038	+	12	3.49e-06	TACGTAAGGG	CTTCAAGTT	GCCATACATG
HMPREF1120_07676	+	984	3.49e-06	TGAAGTTGTG	CTTCAAGTT	CATTATCT
HMPREF1120_01403	-	562	3.49e-06	TCCATTCTCT	CTTCAAGTT	CGGCATCTTC
HMPREF1120_04224	-	863	3.49e-06	CGAGAGAGAG	CTTCAAGTT	CCTTATACCC
HMPREF1120_06777	+	455	3.49e-06	GAGTGCTGAC	CTTCAAGTT	GATGAACGGC
HMPREF1120_00264	-	754	3.49e-06	CTCGGAGGAG	CTTCAAGTT	CGATTCTGG
HMPREF1120_06644	+	789	3.49e-06	TGGCTTGCCT	CTTCAAGTT	GTCAATATCG
HMPREF1120_09134	+	398	3.49e-06	TTGATTTGTT	CTTCAAGTT	TTACCATTTC
HMPREF1120_07623	+	503	3.49e-06	TTATCTCTGA	CTTCAAGTT	CGCCAGCAAC
HMPREF1120_09019	+	781	3.49e-06	CCTTTGCACG	CTTCAAGTT	CCCAGCGAAG
HMPREF1120_02305	+	416	3.49e-06	CCCGCTCAAG	CTTCAAGTT	CGCACTACAG
HMPREF1120_06645	-	824	3.49e-06	TGGCTTGCCT	CTTCAAGTT	GTCAATATCG
HMPREF1120_02286	-	802	3.49e-06	GATCACTGCA	CTTCAAGTT	CGCTTGGGAG
HMPREF1120_03649	-	159	3.49e-06	AATGCTGTCC	CTTCAAGTT	TCAATCGTGT
HMPREF1120_02776	+	731	3.49e-06	ATATTCCAAC	CTTCAAGTT	TCCCAAAGTT
HMPREF1120_08138	-	627	3.49e-06	CTACCAGCGC	CTTCAAGTT	TGCTAGACTG
HMPREF1120_08154	+	513	3.49e-06	CTTCTGGCCC	CTTCAAGTT	GGACGCCTAG
HMPREF1120_01375	-	340	3.49e-06	CCGCGCCCGG	CTTCAAGTT	GCCCTGACAA
HMPREF1120_01579	-	752	3.49e-06	CTCTCCCTTG	CTTCAAGTT	CTCCCTCATC
HMPREF1120_08650	+	730	3.49e-06	CAGGCTTCAA	CTTCAAGTT	TGCGACGACA
HMPREF1120_02021	-	823	3.49e-06	TGCTGCAGAC	CTTCAAGTT	CAATTTGCT
HMPREF1120_02359	-	255	3.49e-06	ACGTGTACCA	CTTCAAGTT	GAACACACGC
HMPREF1120_01968	-	980	3.49e-06	TGGTCAATGC	CTTCAAGTT	GTGGGGAACG
HMPREF1120_07996	+	509	3.49e-06	CATTGGCGGA	CTTCAAGTT	CGAGCCATGC
HMPREF1120_02634	+	19	3.49e-06	AGTCCGCTCT	CTTCAAGTT	TCTGCCATTT
HMPREF1120_00652	-	530	3.49e-06	CGATCGTCCG	CTTCAAGTT	GCTGCTGCTG
HMPREF1120_06490	-	663	3.49e-06	GAGGAGGCTG	CTTCAAGTT	GTTGCTGAC
HMPREF1120_05710	-	188	3.49e-06	AAATTTCAAT	CTTCAAGTT	GGTGATACAAA
HMPREF1120_07664	+	939	3.49e-06	AAAAGCTCT	CTTCAAGTT	TCGATCGGCG
HMPREF1120_01967	+	952	3.49e-06	TGGTCAATGC	CTTCAAGTT	GTGGGGAACG
HMPREF1120_05950	-	954	3.49e-06	ATTGCCAGT	CTTCAAGTT	CCATTACTAG
HMPREF1120_07962	-	697	3.49e-06	TGGAAGCACC	CTTCAAGTT	CCTCTGCAGA
HMPREF1120_02631	-	259	3.49e-06	AGTCCGCTCT	CTTCAAGTT	TCTGCCATTT
HMPREF1120_06129	-	937	3.49e-06	CAAAGGCTGG	CTTCAAGTT	GTACCACTGG
HMPREF1120_07528	-	486	3.49e-06	ACTCTACAAT	CTTCAAGTT	TGCTCAGATC
HMPREF1120_00418	-	806	3.49e-06	AGATTCATGT	CTTCAAGTT	GTCAGTGTTC
HMPREF1120_08476	-	949	6.99e-06	GTGTGATGGC	GTTCAAGTT	TGCTCTGCAC
HMPREF1120_05486	+	399	6.99e-06	AAAATCTCTG	GTTCAAGTT	CGCGGAGACA
HMPREF1120_07182	-	553	6.99e-06	CCAGACTAAG	GTTCAAGTT	GTAGATATGG
HMPREF1120_01818	-	229	6.99e-06	GATGCTCGTC	GTTCAAGTT	GGTGATGTGG
HMPREF1120_00523	+	304	6.99e-06	CACGCGCAGG	GTTCAAGTT	TGTCTGGGGA
HMPREF1120_06804	+	798	6.99e-06	GCGCATCGCT	GTTCAAGTT	GTCTTCGGCG
HMPREF1120_01982	-	590	6.99e-06	ACGACCTCAT	GTTCAAGTT	CAACGAATCC
HMPREF1120_05841	-	486	6.99e-06	GTGTTTGTAG	GTTCAAGTT	GTCGATTCTG
HMPREF1120_00902	+	315	6.99e-06	GAGTGAGTGA	GTTCAAGTT	GCTAGAGCCT
HMPREF1120_01020	+	102	6.99e-06	TGCCCTGCGCT	GTTCAAGTT	GCTCGATGTT
HMPREF1120_03603	-	794	6.99e-06	TGGAAGAGCA	GTTCAAGTT	CAGAGACAGA
HMPREF1120_06290	-	357	6.99e-06	GCGGTGATGC	GTTCAAGTT	GGCTGAGACG
HMPREF1120_09238	-	793	6.99e-06	ACTGTACGAC	GTTCAAGTT	TATTCAAACG
HMPREF1120_05234	+	234	6.99e-06	GGTGGGAGCC	GTTCAAGTT	AGCGACGATA
HMPREF1120_05354	-	875	6.99e-06	CTTTGCCAGC	GTTCAAGTT	CACTGCGTCT
HMPREF1120_05142	-	361	6.99e-06	TTTCAAGAGC	GTTCAAGTT	TGATGCCCCA
HMPREF1120_00375	-	958	6.99e-06	GGTCTCCAAG	GTTCAAGTT	GTGCATGAAT
HMPREF1120_06679	+	209	6.99e-06	ATGGAGCTAG	GTTCAAGTT	GGTGCTGGGT
HMPREF1120_02578	-	964	6.99e-06	TGTTCCGCG	GTTCAAGTT	CAGCCTTGCC
HMPREF1120_02698	-	626	6.99e-06	GAGGCTCGTG	GTTCAAGTT	GAAGTTATCA
HMPREF1120_03095	-	258	6.99e-06	CGGCACTACA	GTTCAAGTT	CCCGGTAACC
HMPREF1120_00041	+	523	6.99e-06	GACTAAAGTC	GTTCAAGTT	GCGGCTGATC
HMPREF1120_09262	+	724	6.99e-06	TCGACCCGGA	GTTCAAGTT	CATTGTTGTT
HMPREF1120_08308	-	432	6.99e-06	GAGTGGTGT	GTTCAAGTT	GGAAACCTCT
HMPREF1120_06188	+	885	6.99e-06	TCATCGACTT	GTTCAAGTT	GTATGGGGAA
HMPREF1120_05801	+	264	6.99e-06	TGCACCTGAG	GTTCAAGTT	CAATCCACAC

HMPREF1120_02118	+	288	6.99e-06	GCTTCTGTAT	GTTCAAGTT	TCGTTATCTA
HMPREF1120_07951	-	837	6.99e-06	GAATGTCCAC	GTTCAAGTT	TCGCGTGGAA
HMPREF1120_05644	+	917	6.99e-06	GCGTGGAGCT	GTTCAAGTT	GCGGCTGTGG
HMPREF1120_00689	+	695	6.99e-06	CCCGTTGTTT	GTTCAAGTT	AAGAGTCTAC
HMPREF1120_03835	+	45	6.99e-06	AATCCACCAG	GTTCAAGTT	CAGGGCAGGA
HMPREF1120_00627	+	950	6.99e-06	CCACTTTGCA	GTTCAAGTT	TGCGATTGAG
HMPREF1120_00342	+	137	6.99e-06	GCCAGTTCGA	GTTCAAGTT	GGATTTGGAT
HMPREF1120_01106	+	772	6.99e-06	CAATTGTGCA	GTTCAAGTT	CGCATGTCTG
HMPREF1120_04359	+	404	1.05e-05	GATGGTTCGA	CTTGAAGTT	CGACCAGCTC
HMPREF1120_03772	+	373	1.05e-05	TTGTTGTGTC	CTTGAAGTT	ACCTTTCTAA
HMPREF1120_06528	-	544	1.05e-05	AGTCCTTGGA	CTTGAAGTT	CAACGAACCT
HMPREF1120_08115	-	196	1.05e-05	GGGTTGGGTT	CTTGAAGTT	CAGTGTGAC
HMPREF1120_02454	-	176	1.05e-05	GACCACGACA	CTTGAAGTT	GGAGCGTCTT
HMPREF1120_06671	+	639	1.05e-05	ACTGGCACGA	CTTGAAGTT	GAGCTGCCAG
HMPREF1120_01817	+	203	1.05e-05	CAGATGAAGA	CTTGAAGTT	GTAAAGAGTT
HMPREF1120_08525	+	763	1.05e-05	GTGAACTGGA	CTTGAAGTT	GGGGACAGCG
HMPREF1120_06823	+	483	1.05e-05	TTGCTGAAGA	CTTGAAGTT	CTACTTTGAG
HMPREF1120_01653	-	836	1.05e-05	AGACGTTCTA	CTTGAAGTT	GTGACCCGGG
HMPREF1120_06027	+	234	1.77e-05	CTTCGCCGTT	GTTGAAGTT	GCGTCCGATG
HMPREF1120_06617	+	638	1.77e-05	CCGTTTCTGG	CTTCAAGTG	GCGACCATCT
HMPREF1120_01923	+	75	1.77e-05	GCTGCATCAG	CTTCAAGTG	ATACCTCTTC
HMPREF1120_07608	+	501	1.77e-05	TGGCGAAAA	GTTGAAGTT	CTGGATCGGA
HMPREF1120_03297	+	875	1.77e-05	AAATCAAATA	CTTCAAGTG	CCCCCAAGCA
HMPREF1120_08742	+	7	1.77e-05	GAATTG	GTTGAAGTT	TCTCGGTTTC
HMPREF1120_07560	+	293	1.77e-05	CAGAGTGTGA	CTTCAAGTG	GGAGGCTCCT
HMPREF1120_03846	-	894	1.77e-05	AGTTGGTGTG	CTTCAAGTG	CCATGGCCAA
HMPREF1120_08773	+	639	1.77e-05	TTATCAGAGA	GTTGAAGTT	TTGCCGGCAT
HMPREF1120_02653	-	455	1.77e-05	CCAGGTACGG	GTTGAAGTT	TGCCTGCGAT
HMPREF1120_07048	+	772	1.77e-05	AGTGGAAGTT	GTTGAAGTT	CCGGCACAAAC
HMPREF1120_08684	-	232	2.14e-05	ACATCTCGTC	CTTCAAGTC	TTCGATCGAT
HMPREF1120_02127	-	812	2.14e-05	TTCCCACGCA	CTTCAAGTC	ATTCTGGACT
HMPREF1120_07908	-	635	2.14e-05	ATCTGCTCTG	CTTCAAGTC	CGCTTTACCG
HMPREF1120_00898	-	444	2.14e-05	AGTCAACCCC	CTTCAAGTC	TCTGAATGTG
HMPREF1120_00585	+	369	2.14e-05	TCTTTCAATG	CTTCAAGTC	CTCCTGGTCC
HMPREF1120_03541	-	908	2.14e-05	AACCAACTTT	CTTCAAGTC	GTGCAGTTGT
HMPREF1120_01453	-	708	2.47e-05	CTTCCGATGC	ATTCAAGTT	CCCCTCACT
HMPREF1120_01523	+	805	2.47e-05	AATTTCTTCC	ATTCAAGTT	CGGCTTCCCG
HMPREF1120_00954	+	547	2.47e-05	CGGGTCGTCC	ATTCAAGTT	GTGTGTAGGA
HMPREF1120_06046	+	612	2.47e-05	ACTCAACGAC	ATTCAAGTT	TCCCACCTTT
HMPREF1120_05027	-	815	2.47e-05	ATGTAGTTGC	ATTCAAGTT	GCGAACTTGC
HMPREF1120_07372	+	628	2.47e-05	ATACTGACTG	ATTCAAGTT	CTGCGAGACA
HMPREF1120_03386	+	663	2.47e-05	ATATTATGGT	ATTCAAGTT	TGATTCTGGC
HMPREF1120_00717	-	774	2.47e-05	ATTCAAATTA	ATTCAAGTT	TACCATTGAT
HMPREF1120_04934	-	700	2.47e-05	CAGGACCGGC	ATTCAAGTT	GTAGACCTGC
HMPREF1120_04516	+	786	2.47e-05	CTGCGCCCAA	ATTCAAGTT	CCTTGCTCGA
HMPREF1120_04980	+	298	2.84e-05	TTACCGTATG	GTTCAAGTG	ACCAATGGGC
HMPREF1120_01777	+	573	2.84e-05	CAAAGCTGAG	GTTCAAGTG	GTGAGAAGAG
HMPREF1120_08448	-	858	2.84e-05	CGAGCGCCTT	GTTCAAGTG	CACTGTCTAC
HMPREF1120_03061	-	601	2.84e-05	AATGAACATA	GTTCAAGTG	GACAAAATTT
HMPREF1120_05848	-	810	3.21e-05	GTCATGCTTG	GTTCAAGTC	AATGCATACA
HMPREF1120_01149	+	499	3.21e-05	GATGGTTTGG	GTTCAAGTC	TGCGGCACTG
HMPREF1120_06363	-	827	3.21e-05	GAATTGTCCG	GTTCAAGTC	TGTTTGTGGT
HMPREF1120_02703	+	679	3.21e-05	GGCACCCACC	GTTCAAGTC	GTGCTCACTG
HMPREF1120_03411	+	268	3.54e-05	CAGAGCAGCC	TTTCAAGTT	GCCGGCGACG
HMPREF1120_03646	+	558	3.54e-05	CACCACCGTG	TTTCAAGTT	GTGAGTGCAA
HMPREF1120_04550	+	343	3.54e-05	ACACCTTTCC	TTTCAAGTT	GCGCAGTGCC
HMPREF1120_02566	-	454	3.54e-05	GTATTTCTGG	TTTCAAGTT	CTTCATGCTC
HMPREF1120_08439	+	256	3.91e-05	GACACCCGGC	CTTGAAGTG	AGGCTTAAAC
HMPREF1120_01156	+	332	3.91e-05	CTCTTGCTCC	CTTGAAGTG	AGCTTGCACG
HMPREF1120_06138	+	675	3.91e-05	GTACGTGCC	CTTGAAGTG	GTAAGGCGTG
HMPREF1120_06393	-	256	3.91e-05	GATACTCTTG	CTTGAAGTG	GATCGGATTG
HMPREF1120_04843	-	861	3.91e-05	GGATGTCCGG	CTTGAAGTG	TCTGTCCGGC
HMPREF1120_04574	+	731	3.91e-05	TATTTATGGC	CTTGAAGTG	TATAGTCACT
HMPREF1120_05635	-	400	3.91e-05	AAGCGACTGC	CTTGAAGTG	TCGCGAGGCT
HMPREF1120_04938	+	65	3.91e-05	ACCGCATCCG	CTTGAAGTG	TCGTCCGTTC
HMPREF1120_04140	+	363	4.28e-05	CAAATCGGC	CTTGAAGTC	GTCCTGCGTC
HMPREF1120_07157	-	888	4.28e-05	CCGTGTGTTT	CTTGAAGTC	GCAGGTTCCG
HMPREF1120_03399	-	967	4.28e-05	AATTGAAGTG	CTTGAAGTC	GCTTTCCCGC
HMPREF1120_07533	+	695	4.28e-05	TGGATGTGT	CTTGAAGTC	TGGATACAGA

HMPREF1120_04438	+	573	4.28e-05	ACCTTTGTCC	CTTGAAGTC	GAAGATACAC
HMPREF1120_02117	-	659	4.28e-05	TTTCCTTGGG	CTTGAAGTC	AGCGAGCATG
HMPREF1120_03745	-	857	4.98e-05	GAAGAAGAGG	GTTGAAGTG	GCCTTTAAGC
HMPREF1120_03454	+	171	4.98e-05	GAAAAGCGCA	GTTGAAGTG	CAGGATCTCA
HMPREF1120_09162	-	918	4.98e-05	AGTCGAACAG	GTTGAAGTG	GCACACAAGA
HMPREF1120_06279	+	171	4.98e-05	TGCCCAAAGG	GTTGAAGTG	ACCCCGGCCT
HMPREF1120_00149	-	484	4.98e-05	AAAACATCAT	GTTGAAGTG	GTATGCCATA
HMPREF1120_02715	-	765	4.98e-05	ACTGCACTTG	GTTGAAGTG	CAAGTGTGGT
HMPREF1120_01896	+	822	6.05e-05	TCCCGCAGTC	CTTCAAGAT	GCTTTGAAAT
HMPREF1120_06164	+	505	6.05e-05	GATCACGTGG	CTTCAAGAT	AGCTGACTAA
HMPREF1120_04784	-	379	6.05e-05	GGCACAGTAG	CTTCAAGAT	CGAGATCAAC
HMPREF1120_00621	+	220	6.38e-05	GCGTGGCTGA	TTTGAAGTT	GATCCTTGTT
HMPREF1120_04788	-	317	7.09e-05	GTACAGACTC	CTCCAAGTT	TACCGCAGCA
HMPREF1120_05260	-	279	8.86e-05	AAGGAATTTG	CTTCAACTT	GAGCGTAAGC
HMPREF1120_07526	+	592	8.86e-05	CAATCATTAT	GTCCAAGTT	GTAGGTGGTT

Motif STTCAAGTT MEME-1 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
HMPREF1120_01601		3.5e-06	613_[+1]_378
HMPREF1120_05622		3.5e-06	123_[+1]_868
HMPREF1120_02391		3.5e-06	553_-[-1]_438
HMPREF1120_02756		3.5e-06	522_[+1]_469
HMPREF1120_03417		3.5e-06	849_[+1]_142
HMPREF1120_03803		3.5e-06	898_[+1]_93
HMPREF1120_08783		3.5e-06	39_-[-1]_952
HMPREF1120_07241		3.5e-06	662_[+1]_329
HMPREF1120_05790		3.5e-06	207_[+1]_784
HMPREF1120_02792		3.5e-06	346_[+1]_645
HMPREF1120_06484		3.5e-06	359_[+1]_632
HMPREF1120_02938		3.5e-06	479_[+1]_512
HMPREF1120_06465		3.5e-06	461_[+1]_530
HMPREF1120_07879		3.5e-06	753_-[-1]_238
HMPREF1120_00198		3.5e-06	369_-[-1]_622
HMPREF1120_01182		3.5e-06	708_-[-1]_283
HMPREF1120_04734		3.5e-06	974_[+1]_17
HMPREF1120_03451		3.5e-06	192_-[-1]_799
HMPREF1120_01099		3.5e-06	446_-[-1]_545
HMPREF1120_00038		3.5e-06	11_[+1]_980
HMPREF1120_07676		3.5e-06	983_[+1]_8
HMPREF1120_01403		3.5e-06	561_-[-1]_430
HMPREF1120_04224		3.5e-06	862_-[-1]_129
HMPREF1120_06777		3.5e-06	454_[+1]_537
HMPREF1120_00264		3.5e-06	753_-[-1]_238
HMPREF1120_06644		3.5e-06	788_[+1]_203
HMPREF1120_09134		3.5e-06	397_[+1]_594
HMPREF1120_07623		3.5e-06	502_[+1]_489
HMPREF1120_09019		3.5e-06	780_[+1]_211
HMPREF1120_02305		3.5e-06	415_[+1]_576
HMPREF1120_06645		3.5e-06	823_-[-1]_168
HMPREF1120_02286		3.5e-06	801_-[-1]_190
HMPREF1120_03649		3.5e-06	158_-[-1]_833
HMPREF1120_02776		3.5e-06	730_[+1]_261
HMPREF1120_08138		3.5e-06	626_-[-1]_365
HMPREF1120_08154		3.5e-06	512_[+1]_479
HMPREF1120_01375		3.5e-06	339_-[-1]_652
HMPREF1120_01579		3.5e-06	751_-[-1]_240
HMPREF1120_08650		3.5e-06	729_[+1]_262
HMPREF1120_02021		3.5e-06	822_-[-1]_169
HMPREF1120_02359		3.5e-06	254_-[-1]_737
HMPREF1120_01968		3.5e-06	979_-[-1]_12
HMPREF1120_07996		3.5e-06	508_[+1]_483
HMPREF1120_02634		3.5e-06	18_[+1]_973
HMPREF1120_00652		3.5e-06	529_-[-1]_462
HMPREF1120_06490		3.5e-06	662_-[-1]_329
HMPREF1120_05710		3.5e-06	187_-[-1]_804

HMPREF1120_07664	3.5e-06	938	[+1]	53
HMPREF1120_01967	3.5e-06	951	[+1]	40
HMPREF1120_05950	3.5e-06	953	[-1]	38
HMPREF1120_07962	3.5e-06	696	[-1]	295
HMPREF1120_02631	3.5e-06	258	[-1]	733
HMPREF1120_06129	3.5e-06	936	[-1]	55
HMPREF1120_07528	3.5e-06	485	[-1]	506
HMPREF1120_00418	3.5e-06	805	[-1]	186
HMPREF1120_08476	7e-06	948	[-1]	43
HMPREF1120_05486	7e-06	398	[+1]	593
HMPREF1120_07182	7e-06	552	[-1]	439
HMPREF1120_01818	7e-06	228	[-1]	763
HMPREF1120_00523	7e-06	303	[+1]	688
HMPREF1120_06804	7e-06	797	[+1]	194
HMPREF1120_01982	7e-06	589	[-1]	402
HMPREF1120_05841	7e-06	485	[-1]	506
HMPREF1120_00902	7e-06	314	[+1]	677
HMPREF1120_01020	7e-06	101	[+1]	890
HMPREF1120_03603	7e-06	793	[-1]	198
HMPREF1120_06290	7e-06	356	[-1]	635
HMPREF1120_09238	7e-06	792	[-1]	199
HMPREF1120_05234	7e-06	233	[+1]	758
HMPREF1120_05354	7e-06	874	[-1]	117
HMPREF1120_05142	7e-06	360	[-1]	631
HMPREF1120_00375	7e-06	957	[-1]	34
HMPREF1120_06679	7e-06	208	[+1]	783
HMPREF1120_02578	7e-06	963	[-1]	28
HMPREF1120_02698	7e-06	625	[-1]	366
HMPREF1120_03095	7e-06	257	[-1]	734
HMPREF1120_00041	7e-06	522	[+1]	469
HMPREF1120_09262	7e-06	723	[+1]	268
HMPREF1120_08308	7e-06	431	[-1]	560
HMPREF1120_06188	7e-06	884	[+1]	107
HMPREF1120_05801	7e-06	263	[+1]	728
HMPREF1120_02118	7e-06	287	[+1]	704
HMPREF1120_07951	7e-06	836	[-1]	155
HMPREF1120_05644	7e-06	916	[+1]	75
HMPREF1120_00689	7e-06	694	[+1]	297
HMPREF1120_03835	7e-06	44	[+1]	947
HMPREF1120_00627	7e-06	949	[+1]	42
HMPREF1120_00342	7e-06	136	[+1]	855
HMPREF1120_01106	7e-06	771	[+1]	220
HMPREF1120_04359	1e-05	403	[+1]	588
HMPREF1120_03772	1e-05	372	[+1]	619
HMPREF1120_06528	1e-05	543	[-1]	448
HMPREF1120_08115	1e-05	195	[-1]	796
HMPREF1120_02454	1e-05	175	[-1]	816
HMPREF1120_06671	1e-05	638	[+1]	353
HMPREF1120_01817	1e-05	202	[+1]	789
HMPREF1120_08525	1e-05	762	[+1]	229
HMPREF1120_06823	1e-05	482	[+1]	509
HMPREF1120_01653	1e-05	835	[-1]	156
HMPREF1120_06027	1.8e-05	233	[+1]	758
HMPREF1120_06617	1.8e-05	637	[+1]	354
HMPREF1120_01923	1.8e-05	74	[+1]	917
HMPREF1120_07608	1.8e-05	500	[+1]	491
HMPREF1120_03297	1.8e-05	874	[+1]	117
HMPREF1120_08742	1.8e-05	6	[+1]	985
HMPREF1120_07560	1.8e-05	292	[+1]	699
HMPREF1120_03846	1.8e-05	893	[-1]	98
HMPREF1120_08773	1.8e-05	638	[+1]	353
HMPREF1120_02653	1.8e-05	454	[-1]	537
HMPREF1120_07048	1.8e-05	771	[+1]	220
HMPREF1120_08684	2.1e-05	231	[-1]	760
HMPREF1120_02127	2.1e-05	811	[-1]	180
HMPREF1120_07908	2.1e-05	634	[-1]	357
HMPREF1120_00898	2.1e-05	443	[-1]	548
HMPREF1120_00585	2.1e-05	368	[+1]	623
HMPREF1120_03541	2.1e-05	907	[-1]	84

HMPREF1120_01453	2.5e-05	707	[-1]	284
HMPREF1120_01523	2.5e-05	804	[+1]	187
HMPREF1120_00954	2.5e-05	546	[+1]	445
HMPREF1120_06046	2.5e-05	611	[+1]	380
HMPREF1120_05027	2.5e-05	814	[-1]	177
HMPREF1120_07372	2.5e-05	627	[+1]	364
HMPREF1120_03386	2.5e-05	662	[+1]	329
HMPREF1120_00717	2.5e-05	773	[-1]	218
HMPREF1120_04934	2.5e-05	699	[-1]	292
HMPREF1120_04516	2.5e-05	785	[+1]	206
HMPREF1120_04980	2.8e-05	297	[+1]	694
HMPREF1120_01777	2.8e-05	572	[+1]	419
HMPREF1120_08448	2.8e-05	857	[-1]	134
HMPREF1120_03061	2.8e-05	600	[-1]	391
HMPREF1120_05848	3.2e-05	809	[-1]	182
HMPREF1120_01149	3.2e-05	498	[+1]	493
HMPREF1120_06363	3.2e-05	826	[-1]	165
HMPREF1120_02703	3.2e-05	678	[+1]	313
HMPREF1120_03411	3.5e-05	267	[+1]	724
HMPREF1120_03646	3.5e-05	557	[+1]	434
HMPREF1120_04550	3.5e-05	342	[+1]	649
HMPREF1120_02566	3.5e-05	453	[-1]	538
HMPREF1120_08439	3.9e-05	255	[+1]	736
HMPREF1120_01156	3.9e-05	331	[+1]	660
HMPREF1120_06138	3.9e-05	674	[+1]	317
HMPREF1120_06393	3.9e-05	255	[-1]	736
HMPREF1120_04843	3.9e-05	860	[-1]	131
HMPREF1120_04574	3.9e-05	730	[+1]	261
HMPREF1120_05635	3.9e-05	399	[-1]	592
HMPREF1120_04938	3.9e-05	64	[+1]	927
HMPREF1120_04140	4.3e-05	362	[+1]	629
HMPREF1120_07157	4.3e-05	887	[-1]	104
HMPREF1120_03399	4.3e-05	966	[-1]	25
HMPREF1120_07533	4.3e-05	694	[+1]	297
HMPREF1120_04438	4.3e-05	572	[+1]	419
HMPREF1120_02117	4.3e-05	658	[-1]	333
HMPREF1120_03745	5e-05	856	[-1]	135
HMPREF1120_03454	5e-05	170	[+1]	821
HMPREF1120_09162	5e-05	917	[-1]	74
HMPREF1120_06279	5e-05	170	[+1]	821
HMPREF1120_00149	5e-05	483	[-1]	508
HMPREF1120_02715	5e-05	764	[-1]	227
HMPREF1120_01896	6e-05	821	[+1]	170
HMPREF1120_06164	6e-05	504	[+1]	487
HMPREF1120_04784	6e-05	378	[-1]	613
HMPREF1120_00621	6.4e-05	219	[+1]	772
HMPREF1120_04788	7.1e-05	316	[-1]	675
HMPREF1120_05260	8.9e-05	278	[-1]	713
HMPREF1120_07526	8.9e-05	591	[+1]	400

 Motif STTCAAGTT MEME-1 in BLOCKS format

BL MOTIF STTCAAGTT width=9 seqs=165

HMPREF1120_01601	(614)	CTTCAAGTT	1
HMPREF1120_05622	(124)	CTTCAAGTT	1
HMPREF1120_02391	(554)	CTTCAAGTT	1
HMPREF1120_02756	(523)	CTTCAAGTT	1
HMPREF1120_03417	(850)	CTTCAAGTT	1
HMPREF1120_03803	(899)	CTTCAAGTT	1
HMPREF1120_08783	(40)	CTTCAAGTT	1
HMPREF1120_07241	(663)	CTTCAAGTT	1
HMPREF1120_05790	(208)	CTTCAAGTT	1
HMPREF1120_02792	(347)	CTTCAAGTT	1
HMPREF1120_06484	(360)	CTTCAAGTT	1
HMPREF1120_02938	(480)	CTTCAAGTT	1
HMPREF1120_06465	(462)	CTTCAAGTT	1
HMPREF1120_07879	(754)	CTTCAAGTT	1

HMPREF1120_00198	(370)	CTTCAAGTT	1
HMPREF1120_01182	(709)	CTTCAAGTT	1
HMPREF1120_04734	(975)	CTTCAAGTT	1
HMPREF1120_03451	(193)	CTTCAAGTT	1
HMPREF1120_01099	(447)	CTTCAAGTT	1
HMPREF1120_00038	(12)	CTTCAAGTT	1
HMPREF1120_07676	(984)	CTTCAAGTT	1
HMPREF1120_01403	(562)	CTTCAAGTT	1
HMPREF1120_04224	(863)	CTTCAAGTT	1
HMPREF1120_06777	(455)	CTTCAAGTT	1
HMPREF1120_00264	(754)	CTTCAAGTT	1
HMPREF1120_06644	(789)	CTTCAAGTT	1
HMPREF1120_09134	(398)	CTTCAAGTT	1
HMPREF1120_07623	(503)	CTTCAAGTT	1
HMPREF1120_09019	(781)	CTTCAAGTT	1
HMPREF1120_02305	(416)	CTTCAAGTT	1
HMPREF1120_06645	(824)	CTTCAAGTT	1
HMPREF1120_02286	(802)	CTTCAAGTT	1
HMPREF1120_03649	(159)	CTTCAAGTT	1
HMPREF1120_02776	(731)	CTTCAAGTT	1
HMPREF1120_08138	(627)	CTTCAAGTT	1
HMPREF1120_08154	(513)	CTTCAAGTT	1
HMPREF1120_01375	(340)	CTTCAAGTT	1
HMPREF1120_01579	(752)	CTTCAAGTT	1
HMPREF1120_08650	(730)	CTTCAAGTT	1
HMPREF1120_02021	(823)	CTTCAAGTT	1
HMPREF1120_02359	(255)	CTTCAAGTT	1
HMPREF1120_01968	(980)	CTTCAAGTT	1
HMPREF1120_07996	(509)	CTTCAAGTT	1
HMPREF1120_02634	(19)	CTTCAAGTT	1
HMPREF1120_00652	(530)	CTTCAAGTT	1
HMPREF1120_06490	(663)	CTTCAAGTT	1
HMPREF1120_05710	(188)	CTTCAAGTT	1
HMPREF1120_07664	(939)	CTTCAAGTT	1
HMPREF1120_01967	(952)	CTTCAAGTT	1
HMPREF1120_05950	(954)	CTTCAAGTT	1
HMPREF1120_07962	(697)	CTTCAAGTT	1
HMPREF1120_02631	(259)	CTTCAAGTT	1
HMPREF1120_06129	(937)	CTTCAAGTT	1
HMPREF1120_07528	(486)	CTTCAAGTT	1
HMPREF1120_00418	(806)	CTTCAAGTT	1
HMPREF1120_08476	(949)	GTTCAAGTT	1
HMPREF1120_05486	(399)	GTTCAAGTT	1
HMPREF1120_07182	(553)	GTTCAAGTT	1
HMPREF1120_01818	(229)	GTTCAAGTT	1
HMPREF1120_00523	(304)	GTTCAAGTT	1
HMPREF1120_06804	(798)	GTTCAAGTT	1
HMPREF1120_01982	(590)	GTTCAAGTT	1
HMPREF1120_05841	(486)	GTTCAAGTT	1
HMPREF1120_00902	(315)	GTTCAAGTT	1
HMPREF1120_01020	(102)	GTTCAAGTT	1
HMPREF1120_03603	(794)	GTTCAAGTT	1
HMPREF1120_06290	(357)	GTTCAAGTT	1
HMPREF1120_09238	(793)	GTTCAAGTT	1
HMPREF1120_05234	(234)	GTTCAAGTT	1
HMPREF1120_05354	(875)	GTTCAAGTT	1
HMPREF1120_05142	(361)	GTTCAAGTT	1
HMPREF1120_00375	(958)	GTTCAAGTT	1
HMPREF1120_06679	(209)	GTTCAAGTT	1
HMPREF1120_02578	(964)	GTTCAAGTT	1
HMPREF1120_02698	(626)	GTTCAAGTT	1
HMPREF1120_03095	(258)	GTTCAAGTT	1
HMPREF1120_00041	(523)	GTTCAAGTT	1
HMPREF1120_09262	(724)	GTTCAAGTT	1
HMPREF1120_08308	(432)	GTTCAAGTT	1
HMPREF1120_06188	(885)	GTTCAAGTT	1
HMPREF1120_05801	(264)	GTTCAAGTT	1
HMPREF1120_02118	(288)	GTTCAAGTT	1
HMPREF1120_07951	(837)	GTTCAAGTT	1

HMPREF1120_05644	(917)	GTTCAAGTT	1
HMPREF1120_00689	(695)	GTTCAAGTT	1
HMPREF1120_03835	(45)	GTTCAAGTT	1
HMPREF1120_00627	(950)	GTTCAAGTT	1
HMPREF1120_00342	(137)	GTTCAAGTT	1
HMPREF1120_01106	(772)	GTTCAAGTT	1
HMPREF1120_04359	(404)	CTTGAAGTT	1
HMPREF1120_03772	(373)	CTTGAAGTT	1
HMPREF1120_06528	(544)	CTTGAAGTT	1
HMPREF1120_08115	(196)	CTTGAAGTT	1
HMPREF1120_02454	(176)	CTTGAAGTT	1
HMPREF1120_06671	(639)	CTTGAAGTT	1
HMPREF1120_01817	(203)	CTTGAAGTT	1
HMPREF1120_08525	(763)	CTTGAAGTT	1
HMPREF1120_06823	(483)	CTTGAAGTT	1
HMPREF1120_01653	(836)	CTTGAAGTT	1
HMPREF1120_06027	(234)	GTTGAAGTT	1
HMPREF1120_06617	(638)	CTTCAAGTG	1
HMPREF1120_01923	(75)	CTTCAAGTG	1
HMPREF1120_07608	(501)	GTTGAAGTT	1
HMPREF1120_03297	(875)	CTTCAAGTG	1
HMPREF1120_08742	(7)	GTTGAAGTT	1
HMPREF1120_07560	(293)	CTTCAAGTG	1
HMPREF1120_03846	(894)	CTTCAAGTG	1
HMPREF1120_08773	(639)	GTTGAAGTT	1
HMPREF1120_02653	(455)	GTTGAAGTT	1
HMPREF1120_07048	(772)	GTTGAAGTT	1
HMPREF1120_08684	(232)	CTTCAAGTC	1
HMPREF1120_02127	(812)	CTTCAAGTC	1
HMPREF1120_07908	(635)	CTTCAAGTC	1
HMPREF1120_00898	(444)	CTTCAAGTC	1
HMPREF1120_00585	(369)	CTTCAAGTC	1
HMPREF1120_03541	(908)	CTTCAAGTC	1
HMPREF1120_01453	(708)	ATTCAAGTT	1
HMPREF1120_01523	(805)	ATTCAAGTT	1
HMPREF1120_00954	(547)	ATTCAAGTT	1
HMPREF1120_06046	(612)	ATTCAAGTT	1
HMPREF1120_05027	(815)	ATTCAAGTT	1
HMPREF1120_07372	(628)	ATTCAAGTT	1
HMPREF1120_03386	(663)	ATTCAAGTT	1
HMPREF1120_00717	(774)	ATTCAAGTT	1
HMPREF1120_04934	(700)	ATTCAAGTT	1
HMPREF1120_04516	(786)	ATTCAAGTT	1
HMPREF1120_04980	(298)	GTTCAAGTG	1
HMPREF1120_01777	(573)	GTTCAAGTG	1
HMPREF1120_08448	(858)	GTTCAAGTG	1
HMPREF1120_03061	(601)	GTTCAAGTG	1
HMPREF1120_05848	(810)	GTTCAAGTC	1
HMPREF1120_01149	(499)	GTTCAAGTC	1
HMPREF1120_06363	(827)	GTTCAAGTC	1
HMPREF1120_02703	(679)	GTTCAAGTC	1
HMPREF1120_03411	(268)	TTTCAAGTT	1
HMPREF1120_03646	(558)	TTTCAAGTT	1
HMPREF1120_04550	(343)	TTTCAAGTT	1
HMPREF1120_02566	(454)	TTTCAAGTT	1
HMPREF1120_08439	(256)	CTTGAAGTG	1
HMPREF1120_01156	(332)	CTTGAAGTG	1
HMPREF1120_06138	(675)	CTTGAAGTG	1
HMPREF1120_06393	(256)	CTTGAAGTG	1
HMPREF1120_04843	(861)	CTTGAAGTG	1
HMPREF1120_04574	(731)	CTTGAAGTG	1
HMPREF1120_05635	(400)	CTTGAAGTG	1
HMPREF1120_04938	(65)	CTTGAAGTG	1
HMPREF1120_04140	(363)	CTTGAAGTC	1
HMPREF1120_07157	(888)	CTTGAAGTC	1
HMPREF1120_03399	(967)	CTTGAAGTC	1
HMPREF1120_07533	(695)	CTTGAAGTC	1
HMPREF1120_04438	(573)	CTTGAAGTC	1
HMPREF1120_02117	(659)	CTTGAAGTC	1

```

HMPREF1120_03745      ( 857) GTTGAAGTG  1
HMPREF1120_03454      ( 171) GTTGAAGTG  1
HMPREF1120_09162      ( 918) GTTGAAGTG  1
HMPREF1120_06279      ( 171) GTTGAAGTG  1
HMPREF1120_00149      ( 484) GTTGAAGTG  1
HMPREF1120_02715      ( 765) GTTGAAGTG  1
HMPREF1120_01896      ( 822) CTTCAAGAT  1
HMPREF1120_06164      ( 505) CTTCAAGAT  1
HMPREF1120_04784      ( 379) CTTCAAGAT  1
HMPREF1120_00621      ( 220) TTTGAAGTT  1
HMPREF1120_04788      ( 317) CTCCAAGTT  1
HMPREF1120_05260      ( 279) CTTCAACTT  1
HMPREF1120_07526      ( 592) GTCCAAGTT  1
//

```


Motif STTCAAGTT MEME-1 position-specific scoring matrix

```

log-odds matrix: alength= 4 w= 9 n= 463042 bayes= 12.9478 E= 8.3e-005
-200   116    37   -300
-1401 -1401 -1401   204
-1401 -441  -1401   203
-1401  159   -20  -1401
 204  -1401 -1401 -1401
 204  -1401 -1401 -1401
-1401 -540   195 -1401
 -374 -1401 -1401   202
-1401 -141   -88   165

```


Motif STTCAAGTT MEME-1 position-specific probability matrix

```

letter-probability matrix: alength= 4 w= 9 nsites= 165 E= 8.3e-005
0.060606 0.575758 0.333333 0.030303
0.000000 0.000000 0.000000 1.000000
0.000000 0.012121 0.000000 0.987879
0.000000 0.775758 0.224242 0.000000
1.000000 0.000000 0.000000 0.000000
1.000000 0.000000 0.000000 0.000000
0.000000 0.006061 0.993939 0.000000
0.018182 0.000000 0.000000 0.981818
0.000000 0.096970 0.139394 0.763636

```


Motif STTCAAGTT MEME-1 regular expression

```

[CG]TT[CG]AAGTT
-----
```

Time 506.75 secs.

```

*****
MOTIF ACTACTACTACTRNTACT MEME-2      width = 21 sites = 32 llr = 480 E-value = 8.2e+001
*****

```


Motif ACTACTACTACTRNTACT MEME-2 Description

```

Simplified      A 8::72:8:17:27:2621822
pos.-specific   C 27:16328::722a1:32:81

```

probability G :1:21::2:22:1::43:3::
matrix T :2a:17::9126::8:27::7

bits 2.0 *
1.8 * *
1.6 * *
1.4 * * * *
Relative Entropy (21.6 bits) 1.2 * * ** * **
1.0 * * **** ** ***
0.8 **** * ** ** *
0.6 **** * ** *
0.4 * ** *
0.2 * ** *
0.0 -----

Multilevel consensus sequence ACTACTACTACTAGTACT
G C G C GCCG
T

Motif ACTACTACTACTRNTACT MEME-2 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
HMPREF1120_04934	+	59	3.71e-13	TACTACTACT ACTACTACTACTACTACTACT ACTACTACTACTACTACTACTACT ACTACTACTACTACTACTACTACT
HMPREF1120_08377	+	666	8.15e-11	GTAGGCTACG AGTACTACTACTACTACTACTACT GTTCTTTCGTT
HMPREF1120_01833	+	751	1.04e-10	CACAACCTCG ACTACTCCTACCCTACTACTACTACT CCTCGTGATT
HMPREF1120_03941	+	760	2.52e-10	ACTAATTAGT ATTGCTACTACTACTGATACT TGC GCGTTGG
HMPREF1120_07793	-	381	1.08e-09	ACTCGGATAT ACTACTACTAGTACTATCGCT ATTA ACTACT
HMPREF1120_06748	-	701	1.45e-09	GTAGGTACCT ACTACTAGTAGTACTGGCACT GCAGTGCGAC
HMPREF1120_07658	+	784	1.65e-09	CGCGAGTGAT ACTACCACCCTACTACTACTACT GTGATACCAC
HMPREF1120_03151	-	205	1.14e-08	ACGCCGCTAT ACTATTACTTCTCCTAATACT CCGTAAGCGC
HMPREF1120_07182	-	660	1.55e-08	GTGCCAGAAC ACTGCCACTGCCACTGCCACT GATGCTCCAC
HMPREF1120_01156	+	747	1.73e-08	TTCGGCTCAA ATTAACCGTACTACTATTACT GAACAGGCCG
HMPREF1120_05123	-	781	2.41e-08	AGGACTTCCT ACTCCCACTACACCAACTACT GCAGTGTGCT
HMPREF1120_00038	+	943	2.99e-08	AAATATAGGT ACTAATACTACCACCATTACC ACATTCACCT
HMPREF1120_07951	-	807	2.99e-08	TTCGCGTGGG AGTAATACTACTACTAATGAT AATTGATGAT
HMPREF1120_08663	+	198	3.32e-08	TACCCAGCG ACTACTACTGTACCAGGTACT TGTATTCTGG
HMPREF1120_06308	+	453	6.46e-08	GGTCTTGCCC ATTGGTACTACCCTGCCACT AAAATCATAG
HMPREF1120_04563	+	327	6.46e-08	TGTCCATTTG ATTGCTACTACTACTATTGCA GCCGTAGGTT
HMPREF1120_07608	-	644	7.10e-08	ACTCCTTCTT ATTATTACTCCTACTATCACT GTACAGTGT
HMPREF1120_03603	+	749	7.80e-08	CGTCATCTCT ACGACTACTACTACTACCGCC TTATCGACCG
HMPREF1120_07996	-	750	7.80e-08	AATATTGCTT ACTCACACTATTACTAACACA ACGCCAACCTA
HMPREF1120_05939	-	635	8.57e-08	GCAAACCTCT CCTCCTCCTACTACAAGTACC CGGACGGCGG
HMPREF1120_06645	-	461	9.41e-08	CTTGCGTTCC ACTGCCAGTGGAACTGTTACT GTAGGTGTTG
HMPREF1120_06393	-	664	1.47e-07	AGATAGCTGG ACTACTACAATACCTGGTAAAT GTTGGGCGAA
HMPREF1120_00924	+	565	1.60e-07	CTTTCAAGCC CATACTAGTACTACA ACTACTACA CACTGTGCGG
HMPREF1120_05354	-	898	1.89e-07	TGGCACTGGC ACTGGCACTGGCACTGGTACT GGCGCTTTGC
HMPREF1120_08480	-	170	3.33e-07	TGCTTTTTCG CTTCTTAGTACTACTAATAAT ATGGCTGACG
HMPREF1120_07322	-	289	3.60e-07	TACCCTGATA CCTACTACTGTACCTGGTGCA GCTCGTCAGC
HMPREF1120_07633	+	93	4.20e-07	ACGAGCGGAT ACTAACCCTACTGCTGGAGCT CCTCTGCGCT
HMPREF1120_07632	-	827	4.20e-07	ACGAGCGGAT ACTAACCCTACTGCTGGAGCT CCTCTGCGCT
HMPREF1120_07533	-	119	4.20e-07	CGTCTCCCG CCTACTACAGGTACAAGTACA AGTCCAACCA
HMPREF1120_09262	-	540	4.87e-07	AACGGGTACT ACTACTCGTACTACTGGTAC ATCAACATGA
HMPREF1120_02776	+	894	6.99e-07	ACTCCACCAC ACTACTAGTACAGCATATACA CAATCGTCTT
HMPREF1120_08344	+	717	5.74e-06	CACTATCAGG CCTGCTACTTCCCGGTTAAAT ATATACACAA

Motif ACTACTACTACTRNTACT MEME-2 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
HMPREF1120_04934		3.7e-13	58_[+2]_921
HMPREF1120_08377		8.2e-11	665_[+2]_314
HMPREF1120_01833		1e-10	750_[+2]_229
HMPREF1120_03941		2.5e-10	759_[+2]_220

HMPREF1120_07793	1.1e-09	380	[-2]	599
HMPREF1120_06748	1.4e-09	700	[-2]	279
HMPREF1120_07658	1.7e-09	783	[+2]	196
HMPREF1120_03151	1.1e-08	204	[-2]	775
HMPREF1120_07182	1.6e-08	659	[-2]	320
HMPREF1120_01156	1.7e-08	746	[+2]	233
HMPREF1120_05123	2.4e-08	780	[-2]	199
HMPREF1120_00038	3e-08	942	[+2]	37
HMPREF1120_07951	3e-08	806	[-2]	173
HMPREF1120_08663	3.3e-08	197	[+2]	782
HMPREF1120_06308	6.5e-08	452	[+2]	527
HMPREF1120_04563	6.5e-08	326	[+2]	653
HMPREF1120_07608	7.1e-08	643	[-2]	336
HMPREF1120_03603	7.8e-08	748	[+2]	231
HMPREF1120_07996	7.8e-08	749	[-2]	230
HMPREF1120_05939	8.6e-08	634	[-2]	345
HMPREF1120_06645	9.4e-08	460	[-2]	519
HMPREF1120_06393	1.5e-07	663	[-2]	316
HMPREF1120_00924	1.6e-07	564	[+2]	415
HMPREF1120_05354	1.9e-07	897	[-2]	82
HMPREF1120_08480	3.3e-07	169	[-2]	810
HMPREF1120_07322	3.6e-07	288	[-2]	691
HMPREF1120_07633	4.2e-07	92	[+2]	887
HMPREF1120_07632	4.2e-07	826	[-2]	153
HMPREF1120_07533	4.2e-07	118	[-2]	861
HMPREF1120_09262	4.9e-07	539	[-2]	440
HMPREF1120_02776	7e-07	893	[+2]	86
HMPREF1120_08344	5.7e-06	716	[+2]	263

 Motif ACTACTACTACTRNTACT MEME-2 in BLOCKS format

BL	MOTIF	ACTACTACTACTRNTACT	width=21	seqs=32
HMPREF1120_04934	(59)	ACTACTACTACTACTACTACT	1	
HMPREF1120_08377	(666)	AGTACTACTACTACTACTACT	1	
HMPREF1120_01833	(751)	ACTACTCCTACCACTACTACT	1	
HMPREF1120_03941	(760)	ATTGCTACTACTACTGATACT	1	
HMPREF1120_07793	(381)	ACTACTACTAGTACTATCGCT	1	
HMPREF1120_06748	(701)	ACTACTAGTAGTACTGGCACT	1	
HMPREF1120_07658	(784)	ACTACCACCACTACTACTACT	1	
HMPREF1120_03151	(205)	ACTATTACTTCTCCTAATACT	1	
HMPREF1120_07182	(660)	ACTGCCACTGCCACTGCCACT	1	
HMPREF1120_01156	(747)	ATTAACCGTACTACTATTACT	1	
HMPREF1120_05123	(781)	ACTCCCACTACACCAACTACT	1	
HMPREF1120_00038	(943)	ACTAATACTACCACCATTACC	1	
HMPREF1120_07951	(807)	AGTAATACTACTACTAATGAT	1	
HMPREF1120_08663	(198)	ACTACTACTGTACCAGGTACT	1	
HMPREF1120_06308	(453)	ATTGGTACTACCACTGCCACT	1	
HMPREF1120_04563	(327)	ATTGTCACTACTACTATTGCA	1	
HMPREF1120_07608	(644)	ATTATTACTCCTACTATCACT	1	
HMPREF1120_03603	(749)	ACGACTACTACTACTACCGCC	1	
HMPREF1120_07996	(750)	ACTCACACTATTACTAACACA	1	
HMPREF1120_05939	(635)	CCTCCTCTACTACAAGTACC	1	
HMPREF1120_06645	(461)	ACTGCCAGTGGAAGTGTACT	1	
HMPREF1120_06393	(664)	ACTACTACAATACCTGGTAAT	1	
HMPREF1120_00924	(565)	CATACTAGTACTACAACTACA	1	
HMPREF1120_05354	(898)	ACTGGCACTGGCACTGGTACT	1	
HMPREF1120_08480	(170)	CTTCTTAGTACTACTAATAAT	1	
HMPREF1120_07322	(289)	CCTACTACTGTACCTGGTGCA	1	
HMPREF1120_07633	(93)	ACTAACCCCTACTGCTGGAGCT	1	
HMPREF1120_07632	(827)	ACTAACCCCTACTGCTGGAGCT	1	
HMPREF1120_07533	(119)	CCTACTACAGGTACAAGTACA	1	
HMPREF1120_09262	(540)	ACTACTCGTACTACTGGTGAC	1	
HMPREF1120_02776	(894)	ACTACTAGTACAGCATATACA	1	
HMPREF1120_08344	(717)	CCTGCTACTTTCCCGTTAAT	1	

//

Motif ACTACTACTACTACTRNTACT MEME-2 position-specific scoring matrix

log-odds matrix: alength= 4 w= 21 n= 457438 bayes= 15.8032 E= 8.2e+001

Table of log-odds matrix values for motif ACTACTACTACTACTRNTACT. The table is a 21x4 grid of integers ranging from -1164 to 174.

Motif ACTACTACTACTACTRNTACT MEME-2 position-specific probability matrix

letter-probability matrix: alength= 4 w= 21 nsites= 32 E= 8.2e+001

Table of letter-probability matrix values for motif ACTACTACTACTACTRNTACT. The table is a 21x4 grid of floating-point numbers between 0.000000 and 0.812500.

Motif ACTACTACTACTACTRNTACT MEME-2 regular expression

ACT[AG]C[TC]A[CG]TAC[TC]ACT[AG][GCT][TC][AG]CT

Time 1011.74 secs.

MOTIF TYTBKTTKBTTKBTTBNYY MEME-3 width = 21 sites = 157 llr = 1588 E-value = 1.4e+000

Motif TYTBKTTKBTTKBTTBNYY MEME-3 Description

Simplified pos.-specific probability matrix A 1:::111:::2:::1:::2:1 C 1413:22214:2:342:3333 G 2123:5:::4322423:142:1 T 757393885266643893365

bits 2.0 1.8 1.6 * 1.4 * * * 1.2 * * * 1.0 * * * ** 0.8 * * ** * ** * 0.6 *** * ** *** ** * 0.4 *** * *** **** ** * 0.2 ***** ** 0.0 -----

Multilevel consensus sequence TTTGTGTTTCTTTCTTGCTT C T T GGACGCTC CTCC C T GG TA G

Motif TYTBKTTKBTTKBTTBNYY MEME-3 sites sorted by position p-value

Table with 5 columns: Sequence name, Strand, Start, P-value, Site. Lists genomic sites with their coordinates and p-values.

HMPREF1120_00196	-	259	1.76e-06	GTGCAATTG	TCGTTGTTGGTTTCATTCTCT	TCCTCAACCC
HMPREF1120_05842	-	289	1.76e-06	AATGAATTTG	TTTGACTTTTGGTTTTGCTC	TTGCTCAAAT
HMPREF1120_03649	-	725	1.76e-06	GAAGCGGAGA	TTTGTATTTTGTGTTTGCTA	CCGTACATAC
HMPREF1120_02703	+	808	1.76e-06	CGCAAACGGA	TTCTTCTTTGTCGTGTTTCT	TTGTCACAAA
HMPREF1120_00717	+	373	2.01e-06	GTTTCGTCTG	GCGGTGTTTCTGTTGTTCCCT	ACTGTGCTTT
HMPREF1120_03202	+	81	2.29e-06	GAGCTGAGGT	TCTTTTTTGTGGGCTTGCCA	ATCGGACAAT
HMPREF1120_07792	-	381	2.61e-06	TGCCGTTGTT	TCGCTGTTGCTGGCTCTGCTT	GACTGGAATA
HMPREF1120_05260	-	680	2.96e-06	AAGCTGTCCG	TCTGTCTCTGGTTTTCTCTTT	CCATGCCTCC
HMPREF1120_06393	+	226	2.96e-06	GTTCGAAGCG	GCTGTGTTTGTGGATTATC	AATCCGATCC
HMPREF1120_05935	+	122	2.96e-06	CGCCACATCG	TCTTTGCTTTTCTTCTTTTCG	GTCCTGCGACC
HMPREF1120_06465	+	858	3.35e-06	TTTTGTTCGAT	TGTTTGCTGCATTGTTTGTG	CTCACTTCTT
HMPREF1120_02566	-	402	3.35e-06	GCCTATGCTC	GCTTTCCTGCTTCTTTGTCC	CCAGCGAAAA
HMPREF1120_07971	+	977	3.78e-06	TCTTGATCTT	TTTGTCTCTTCTCCTTTCTC	GAC
HMPREF1120_02510	-	663	3.78e-06	AGGTTATGCT	TTCTCTTTGGTGGCTTGATC	GGGGGGACGA
HMPREF1120_02072	+	503	3.78e-06	CAACGGCTGA	GTTCTCTTCGTTTGCTTCTC	CTCTGTGCAT
HMPREF1120_02634	+	507	3.78e-06	TCCTGGCACC	TCGTTCTTGTTCCTTCTCT	TCACCATCGT
HMPREF1120_03622	-	180	4.27e-06	TACTGACCGC	GCGCTTTTGTTCCTTTCTC	AGGGTCAACC
HMPREF1120_06441	+	959	4.27e-06	GCCGCCGCTG	TTCGTGTTTCGTTGTTCTCC	GACCCCTGAG
HMPREF1120_07658	+	83	4.27e-06	TTTGGCTGTG	CTTGTGTTTCTTGGCTGCTTC	CTGCGCGGCT
HMPREF1120_02509	-	778	4.81e-06	ATGACCTTCC	TCTTTGCTGTTTGGCCTTGTC	TCGCCACAAA
HMPREF1120_08154	-	472	4.81e-06	AAGTGATTGG	TCTATGATGGTTGTTTCGTT	CTAGCGCGGC
HMPREF1120_07674	+	675	4.81e-06	GCTTGAACAC	TTCTGTTTGTGGCTGTTCT	ATTTCAATGG
HMPREF1120_03503	+	475	4.81e-06	ATAGAAGCGG	GCTGTTTCTCGCTTTTGTCT	TGTGTTGAGC
HMPREF1120_06777	+	919	5.41e-06	TTCAATATAA	GCCCTTTTGTTCCTTGCTC	CTTAAAGGCG
HMPREF1120_07793	-	302	5.41e-06	CTACCTAGCT	TCTTTATCTATTTTCTTCTT	ATAATCGCCT
HMPREF1120_08679	+	332	5.41e-06	TGGACTCCAA	TTTTTTTTGGCGGGTTCTG	GACTGAGATA
HMPREF1120_04831	+	8	5.41e-06	CTCTTCT	TCTCTGCTCTTCGGCTTGTTT	GACGGGGTGG
HMPREF1120_04902	-	930	5.41e-06	TTTATGGGAT	TCTATCTTTGGTTCTTTTTC	ATGAATTCAC
HMPREF1120_08078	+	65	6.80e-06	ATGTGCTGCT	TTTGTCTCCTATGTCTTTGTT	TTCTGGTCAT
HMPREF1120_04947	+	499	6.80e-06	CCAGGGCCGG	TGGCTGTTGGGTTCTTTCATC	TTGCTGACCC
HMPREF1120_07049	+	173	7.61e-06	GCGCCAGACG	TCTGTCTTGGATGTCTGGACC	AACAGCACAG
HMPREF1120_04834	+	321	7.61e-06	AGGAACAAAA	GTTGTTTTTTTTGTTGCTGTTG	GTTCTATGCG
HMPREF1120_06537	-	812	7.61e-06	TGAGAAGCTG	TTTATTTTGTGGTGTGATA	TTGAGGTACT
HMPREF1120_07050	-	468	7.61e-06	GCGCCAGACG	TCTGTCTTGGATGTCTGGACC	AACAGCACAG
HMPREF1120_07951	+	458	7.61e-06	CGAAAACACTAG	TCCTAGTTGGATTTGTTCTTC	AATGCCGGCA
HMPREF1120_03835	+	656	7.61e-06	CGAAAACGCC	GTTTCATTTTGTCTCGTTGCC	GCGGAGAGCT
HMPREF1120_03195	+	251	8.51e-06	GTTTCTGTCT	TTTCTGTTCTCTTCTGTATG	CCAGCTTATT
HMPREF1120_05790	+	876	8.51e-06	AGCGGCTTTC	TTCTTTTTGACTGCCTTCTC	CTCTAACC GC
HMPREF1120_04140	+	232	8.51e-06	TAGCAAGACC	TTTATCTTTGTCTCTTTGGCG	GCAGCCAAGA
HMPREF1120_00374	-	244	8.51e-06	CGATGGTTGC	GTTGTGCTTTTTCGGTTTTGCT	CTTTTCGACG
HMPREF1120_02373	-	944	8.51e-06	GGTGGTTTTG	TCTGTGTTGGATGGTCTTGCA	AATATAGCAA
HMPREF1120_01523	+	962	9.49e-06	TCAGAGCTCG	TCTCTGTTTCTCTTGTGGCAC	GATTATCATT
HMPREF1120_04550	-	315	9.49e-06	AAAGAAAAGG	TGTTTGTTCGGTTCTTTTCG	TCCAATATGC
HMPREF1120_04359	-	259	1.06e-05	GCCGGGGACA	TTGTTGATCCTTTCTTGTCTG	TACCCCTTCTA
HMPREF1120_04430	-	420	1.06e-05	CTTACTTCTC	TTCTTCTTACTTTCTTTTATA	CCTCTTTCTA
HMPREF1120_03772	+	653	1.06e-05	CGTGATGAAC	TGCTGTGTCAGTGCCTTGTT	TCATCTCGGC
HMPREF1120_06138	-	286	1.06e-05	TGCTCTCTCT	TTTCTCTTGATTTTCTCGTA	CTCTACTTTT
HMPREF1120_00546	-	633	1.06e-05	TCATATCCCG	ATTTTGCTTTCGTTTCGTTATC	ATGCATAAAT
HMPREF1120_01435	-	179	1.06e-05	TCTGTGAGCA	TCTGTGTCAATTTCTCTGTCT	GACAAAAATA
HMPREF1120_03541	-	583	1.06e-05	CCATCTCATC	CCTCTGTTTATCTCTTTGCTC	TCTCCATCTC
HMPREF1120_07322	+	963	1.18e-05	TATGCTTTTA	CTTTTCTGCTGTGTTTCTCT	CTGTTATCTC
HMPREF1120_08783	-	773	1.18e-05	ACACGCGATC	TCGCTGTTTCACTGCTTGAAT	TAGCATGTG
HMPREF1120_05987	-	665	1.18e-05	GACACTTACA	TCTTCTTGCTCTGGCTTTCA	CCACACAATT
HMPREF1120_06548	+	643	1.18e-05	TATATTGATA	CTTCTCTGTTTTGGCTCGTC	AACAGAGATG
HMPREF1120_06617	+	63	1.31e-05	GGGTGGACGG	ACTGTCTTGCTTTCTCTCTG	CTGAGCGTGT
HMPREF1120_01909	+	874	1.31e-05	CAGGCATCAA	TCTATGCTTGTGCCCCTGATC	ACTCCATCTC
HMPREF1120_02791	+	920	1.31e-05	TTGTGCTGCG	GTTCTTCTGACTCCTTTTCT	CTATGCCTTT
HMPREF1120_01547	+	568	1.31e-05	CTTCGTTTAC	TCGGTGTGCTTGGATTGCTA	GGAAATGCGGA
HMPREF1120_08523	+	94	1.31e-05	CCAAATGGTA	GTTTTTATACATTTCTTCTCT	GCTCAACTCC
HMPREF1120_02139	-	865	1.31e-05	CTTGTTCTTT	TTTCTTTTGATTTCTCTCTCA	CAATCATGTT
HMPREF1120_08476	-	844	1.45e-05	TTCGATGCCT	GTCCTGTTTGATGCTTCTCT	GATATCAGTG
HMPREF1120_05486	+	955	1.45e-05	TGTGTGGATG	CCTTTGTGCGGGCTCTTTGCT	AAGCGTTCGC
HMPREF1120_07879	+	794	1.45e-05	GTTCTCTTCG	TCGTTGTTGCTGGTATTGTTA	CTGCTGCTTG
HMPREF1120_01764	+	311	1.45e-05	ATTTTTCGTA	GCTGTGTCGTTCTGTTCTGGT	ATGTCAAAAT
HMPREF1120_06580	+	784	1.45e-05	CAAAAGGTGT	TTTGTCTCGCAGTGTGGTG	GATCCGCCGC
HMPREF1120_04393	+	829	1.45e-05	TGATGCGGAA	TCCCTGTTTGGAGGCGCTCTT	ATGCCCGGCT
HMPREF1120_07128	-	446	1.45e-05	ACCATTTTGA	TTGCAGTTGTGTTGTTTACT	GGAGTAGACT
HMPREF1120_06758	+	28	1.45e-05	TTGGATCTTA	GTTTCATTTGCGTTTGTCTTA	CTTGAGCAGT
HMPREF1120_06581	-	459	1.45e-05	CAAAAGGTGT	TTTGTCTCGCAGTGTGGTG	GATCCGCCGC

HMPREF1120_01967	+	352	1.45e-05	GATTGTATAC	TCTCATTCTCTTTGGTCTTG	AAGTGCTCT
HMPREF1120_07528	+	719	1.45e-05	GTCAAATCTT	GTTTTAGTTCCTTCTTT	CTTACCGCTT
HMPREF1120_04424	+	692	1.60e-05	ACACCTTGTC	TCGTTGCTGCACTCTTCTCC	GACGGGATTT
HMPREF1120_01923	-	777	1.60e-05	TCCTCGACCT	TCTCAGTTTCACTCATTCTCT	CCCTTGACCT
HMPREF1120_06047	+	425	1.60e-05	ATCTAACGCC	TCTCTGTTGTGTTGTAGCTC	AGGTGGATGT
HMPREF1120_03688	-	711	1.60e-05	CCCTATCTCG	TTTCATTTGGTCGTGCTTGTC	TGTGCCTCCT
HMPREF1120_01817	+	220	1.60e-05	TTGTAAAGAG	TTGTTGATGGGTTTGTGATG	AAAGGTGGGA
HMPREF1120_08663	+	543	1.60e-05	CAAACGTCGG	GTTGAGTTGCATGTTCTGACT	GGTTGTCGGT
HMPREF1120_00104	+	946	1.60e-05	AGCTAATAAG	GTCCTCTTGTTTTGTGTCTT	GTAGGTAGC
HMPREF1120_07677	-	83	1.77e-05	GAAGAACGGC	TGCCTCTTCTCTCTCTCTT	GAGCAGAAAT
HMPREF1120_00924	+	824	1.77e-05	CTCCGTGCGA	TCTGTTATTCTGGTGCTCATC	TGAACGTTC
HMPREF1120_05665	-	913	1.77e-05	TGACGTCATA	GTGTTGATTTGTTCTTTGCTC	AGCTGCCAGT
HMPREF1120_07908	+	202	1.77e-05	TCAATGTGCT	CTGCTTCTGCATTCGTTGGT	TCTCCATTGT
HMPREF1120_03953	+	257	1.77e-05	GCATAATGAC	CCTGTGTTACGTGCTTGCTA	CCCATTCTCT
HMPREF1120_09162	+	498	1.96e-05	TGAGATTGCA	GTTCTCTTCTTTGCCCTTGACG	TGATTGTCTT
HMPREF1120_04224	+	207	1.96e-05	GAAGCTCTCA	TCTCTATCTCAGTTCCTTATT	GCATAATTTG
HMPREF1120_02454	-	567	1.96e-05	AGTGCCAATC	TTTTCTTTTCGTTGGGTGGATA	ACATTGCACC
HMPREF1120_01082	+	605	1.96e-05	CCGCGACCTT	TCTGTATCTGTTTCTTTGAC	CAAAGCTTCC
HMPREF1120_06790	-	562	1.96e-05	TGGCCGCGCT	CTTCATCTTTTTTTTTTTCATC	TCACTCACC
HMPREF1120_00797	-	835	1.96e-05	CGAAACCACC	TGCTTGTTTCATTTTCTGGTA	CACCAGTACG
HMPREF1120_04804	+	701	2.16e-05	TTCAGATAGG	GGTTTCTTGGGCTCTTTTCTC	CTTTCCCAT
HMPREF1120_06146	+	129	2.16e-05	AATTGAAAGT	TCTCTTCTGCGTTTCTTCGAC	AGCACAGTCC
HMPREF1120_08742	-	651	2.16e-05	ACGCTCGTCC	TTCTGTTTTCATTCACTCCTG	GCTCGCGTCT
HMPREF1120_06329	-	150	2.16e-05	AGTGAAGGCA	CCCTTCTTCTTTTGTGCTT	CCCTTCTTAC
HMPREF1120_07479	+	604	2.16e-05	TACAACATTG	TGGTTGCTTTGTCTTTGCTT	TGAGCCCAGG
HMPREF1120_03417	-	63	2.38e-05	AACGACTACT	TCTTCTCTGTGGCCTGCTT	GGGTACCCGA
HMPREF1120_04574	+	500	2.38e-05	CTCTTGGTTC	TTGTTATCGTATTTCTTCGCT	TCTACCTCCG
HMPREF1120_01052	-	670	2.38e-05	CGCGCGTGTG	TTTGTGCTTCATGTGCTCAAT	CGGCGGCTCA
HMPREF1120_04126	-	340	2.38e-05	CTCGTCAAAT	CCTGTTCTCGTTTGTGCTG	CCTCTTCTC
HMPREF1120_02172	+	592	2.38e-05	CATTCTTAC	TTTGTCTGTACTGGCTCCCT	TTTGCCTATT
HMPREF1120_01106	+	88	2.38e-05	TGACATAGCG	TTCTGTTGTCAGGTTTGGGTC	TTTGAAGTCT
HMPREF1120_01896	+	663	2.61e-05	TAAGCCCAGT	TCCGTGTCGCATGCGCTGCTT	TCCGGCAAGA
HMPREF1120_07937	-	464	2.61e-05	CGGAGCTGAT	TCTCTTGTGTGGGTTTGT	GGGCGATGCG
HMPREF1120_05100	-	135	2.61e-05	TATAACAAGG	TTGGTGATGCTTGTGTTCAAT	ATACGCTAC
HMPREF1120_02305	+	958	2.61e-05	CGCATCTTCC	CGTTTTTCTCTGTTTGTGCT	TTCTCATCAT
HMPREF1120_03745	+	801	2.87e-05	GTTACCACCT	GCTCTGATTGATTGATTGACT	GCCCGCCTTG
HMPREF1120_06583	-	957	2.87e-05	GATGCTCGGC	CCTCAGTTCGATTGTTTTGT	CCTTCTTCTT
HMPREF1120_07533	+	610	2.87e-05	GTTGCTTCTT	TCTTTGACTTTTTTGTGGACT	CGTGTTAACT
HMPREF1120_02714	+	665	2.87e-05	GTAATCAGA	ATTGTGTTAGTTTTCTGTACT	CGTGTTTTCA
HMPREF1120_04575	-	380	3.15e-05	GGAGCGAACA	CTTGTGCTGTCGGGTTGCTT	TAGATCAGCA
HMPREF1120_06922	+	876	3.45e-05	ATAAAGACAT	TTTGTTTTCATGGGGTTCATC	AAAGTTCGGC
HMPREF1120_01315	+	623	3.45e-05	CCTGCTTCTC	TCTGTATCACTCTGCTTCCCT	GCTTACTGCT
HMPREF1120_00405	+	440	3.45e-05	GCCCGTGGCG	ACTTTGCTGTCTTCTTGAAT	TCTGATCTAA
HMPREF1120_04938	+	443	3.45e-05	TCCGCAACCA	TTCTTCTTCTTTTGTGCATA	TTTGGCAACC
HMPREF1120_00689	-	729	3.45e-05	CAGAAGTAGT	TTTTTAGTTCATTGTTGTTA	GCTAGAATCC
HMPREF1120_05503	-	435	3.45e-05	CGGCTTCTTT	TTCTTTTTTCCACTTCTTCCC	TTTGCCTTTT
HMPREF1120_07676	-	515	3.78e-05	AGAGATTGTG	GCTGTATCACTTGCTTTGGT	CGTCTTCTTA
HMPREF1120_02138	-	122	3.78e-05	GGTGCTTCAT	CTTGAATTTGTTTTCTTCGCA	ACAGATTAGT
HMPREF1120_08389	+	152	4.50e-05	TTGCATCAGC	ATGATGTTGGGTTTCTTGGTC	GCGTGTGAG
HMPREF1120_05234	-	76	4.91e-05	TGAGAGCAAG	TCTGTTACGCGTGCCTTACC	ATTTCCCACG
HMPREF1120_07962	-	946	4.91e-05	TATGGAGTAT	GGGGTGTGTTGGTGTGATG	CCCAGGACGA
HMPREF1120_05841	-	500	5.35e-05	TATTATTGCT	GTGTAGTTGGTTGTCTGTGTT	TGTAGGTTCA
HMPREF1120_00375	+	686	8.05e-05	CTTATTGAGA	TTTTCTTTCGTGTTGCTGCTG	GGAATAAGCT

Motif TYTBKTKBTKBBTBNYY MEME-3 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
HMPREF1120_03803		1.7e-11	405_[+3]_574
HMPREF1120_02117		2.3e-08	945_[+3]_34
HMPREF1120_07633		2.9e-08	127_-[-3]_852
HMPREF1120_07632		2.9e-08	791_[+3]_188
HMPREF1120_06027		3.5e-08	527_[+3]_452
HMPREF1120_06028		3.5e-08	922_-[-3]_57
HMPREF1120_07062		6.3e-08	742_[+3]_237
HMPREF1120_02776		7.6e-08	969_[+3]_10
HMPREF1120_07880		1.1e-07	752_-[-3]_227

HMPREF1120_09134	1.6e-07	656_[+3]_323
HMPREF1120_07560	1.6e-07	508_-[-3]_471
HMPREF1120_05354	1.9e-07	387_[+3]_592
HMPREF1120_00523	2.6e-07	692_[+3]_287
HMPREF1120_03061	2.6e-07	617_[+3]_362
HMPREF1120_02274	3.6e-07	344_[+3]_635
HMPREF1120_02275	3.6e-07	979_-[-3]
HMPREF1120_04563	4.9e-07	32_[+3]_947
HMPREF1120_07074	4.9e-07	211_[+3]_768
HMPREF1120_05142	5.7e-07	558_[+3]_421
HMPREF1120_03399	5.7e-07	840_[+3]_139
HMPREF1120_06528	6.6e-07	919_[+3]_60
HMPREF1120_08344	6.6e-07	778_[+3]_201
HMPREF1120_03768	6.6e-07	717_[+3]_262
HMPREF1120_06363	8.8e-07	658_[+3]_321
HMPREF1120_07003	1e-06	457_[+3]_522
HMPREF1120_08211	1e-06	309_[+3]_670
HMPREF1120_00244	1e-06	456_[+3]_523
HMPREF1120_05123	1e-06	148_[+3]_831
HMPREF1120_00243	1e-06	444_-[-3]_535
HMPREF1120_05622	1.2e-06	599_-[-3]_380
HMPREF1120_06279	1.2e-06	648_-[-3]_331
HMPREF1120_00627	1.2e-06	975_-[-3]_4
HMPREF1120_02225	1.3e-06	703_[+3]_276
HMPREF1120_00041	1.3e-06	943_[+3]_36
HMPREF1120_04377	1.5e-06	185_-[-3]_794
HMPREF1120_00196	1.8e-06	258_-[-3]_721
HMPREF1120_05842	1.8e-06	288_-[-3]_691
HMPREF1120_03649	1.8e-06	724_-[-3]_255
HMPREF1120_02703	1.8e-06	807_[+3]_172
HMPREF1120_00717	2e-06	372_[+3]_607
HMPREF1120_03202	2.3e-06	80_[+3]_899
HMPREF1120_07792	2.6e-06	380_-[-3]_599
HMPREF1120_05260	3e-06	679_-[-3]_300
HMPREF1120_06393	3e-06	225_[+3]_754
HMPREF1120_05935	3e-06	121_[+3]_858
HMPREF1120_06465	3.3e-06	857_[+3]_122
HMPREF1120_02566	3.3e-06	401_-[-3]_578
HMPREF1120_07971	3.8e-06	976_[+3]_3
HMPREF1120_02510	3.8e-06	662_-[-3]_317
HMPREF1120_02072	3.8e-06	502_[+3]_477
HMPREF1120_02634	3.8e-06	506_[+3]_473
HMPREF1120_03622	4.3e-06	179_-[-3]_800
HMPREF1120_06441	4.3e-06	958_[+3]_21
HMPREF1120_07658	4.3e-06	82_[+3]_897
HMPREF1120_02509	4.8e-06	777_-[-3]_202
HMPREF1120_08154	4.8e-06	471_-[-3]_508
HMPREF1120_07674	4.8e-06	674_[+3]_305
HMPREF1120_03503	4.8e-06	474_[+3]_505
HMPREF1120_06777	5.4e-06	918_[+3]_61
HMPREF1120_07793	5.4e-06	301_-[-3]_678
HMPREF1120_08679	5.4e-06	331_[+3]_648
HMPREF1120_04831	5.4e-06	7_[+3]_972
HMPREF1120_04902	5.4e-06	929_-[-3]_50
HMPREF1120_08078	6.8e-06	64_[+3]_915
HMPREF1120_04947	6.8e-06	498_[+3]_481
HMPREF1120_07049	7.6e-06	172_[+3]_807
HMPREF1120_04834	7.6e-06	320_[+3]_659
HMPREF1120_06537	7.6e-06	811_-[-3]_168
HMPREF1120_07050	7.6e-06	467_-[-3]_512
HMPREF1120_07951	7.6e-06	457_[+3]_522
HMPREF1120_03835	7.6e-06	655_[+3]_324
HMPREF1120_03195	8.5e-06	250_[+3]_729
HMPREF1120_05790	8.5e-06	875_[+3]_104
HMPREF1120_04140	8.5e-06	231_[+3]_748
HMPREF1120_00374	8.5e-06	243_-[-3]_736
HMPREF1120_02373	8.5e-06	943_-[-3]_36
HMPREF1120_01523	9.5e-06	961_[+3]_18
HMPREF1120_04550	9.5e-06	314_-[-3]_665

HMPREF1120_04359	1.1e-05	258	[-3]	721
HMPREF1120_04430	1.1e-05	419	[-3]	560
HMPREF1120_03772	1.1e-05	652	[+3]	327
HMPREF1120_06138	1.1e-05	285	[-3]	694
HMPREF1120_00546	1.1e-05	632	[-3]	347
HMPREF1120_01435	1.1e-05	178	[-3]	801
HMPREF1120_03541	1.1e-05	582	[-3]	397
HMPREF1120_07322	1.2e-05	962	[+3]	17
HMPREF1120_08783	1.2e-05	772	[-3]	207
HMPREF1120_05987	1.2e-05	664	[-3]	315
HMPREF1120_06548	1.2e-05	642	[+3]	337
HMPREF1120_06617	1.3e-05	62	[+3]	917
HMPREF1120_01909	1.3e-05	873	[+3]	106
HMPREF1120_02791	1.3e-05	919	[+3]	60
HMPREF1120_01547	1.3e-05	567	[+3]	412
HMPREF1120_08523	1.3e-05	93	[+3]	886
HMPREF1120_02139	1.3e-05	864	[-3]	115
HMPREF1120_08476	1.4e-05	843	[-3]	136
HMPREF1120_05486	1.4e-05	954	[+3]	25
HMPREF1120_07879	1.4e-05	793	[+3]	186
HMPREF1120_01764	1.4e-05	310	[+3]	669
HMPREF1120_06580	1.4e-05	783	[+3]	196
HMPREF1120_04393	1.4e-05	828	[+3]	151
HMPREF1120_07128	1.4e-05	445	[-3]	534
HMPREF1120_06758	1.4e-05	27	[+3]	952
HMPREF1120_06581	1.4e-05	458	[-3]	521
HMPREF1120_01967	1.4e-05	351	[+3]	628
HMPREF1120_07528	1.4e-05	718	[+3]	261
HMPREF1120_04424	1.6e-05	691	[+3]	288
HMPREF1120_01923	1.6e-05	776	[-3]	203
HMPREF1120_06047	1.6e-05	424	[+3]	555
HMPREF1120_03688	1.6e-05	710	[-3]	269
HMPREF1120_01817	1.6e-05	219	[+3]	760
HMPREF1120_08663	1.6e-05	542	[+3]	437
HMPREF1120_00104	1.6e-05	945	[+3]	34
HMPREF1120_07677	1.8e-05	82	[-3]	897
HMPREF1120_00924	1.8e-05	823	[+3]	156
HMPREF1120_05665	1.8e-05	912	[-3]	67
HMPREF1120_07908	1.8e-05	201	[+3]	778
HMPREF1120_03953	1.8e-05	256	[+3]	723
HMPREF1120_09162	2e-05	497	[+3]	482
HMPREF1120_04224	2e-05	206	[+3]	773
HMPREF1120_02454	2e-05	566	[-3]	413
HMPREF1120_01082	2e-05	604	[+3]	375
HMPREF1120_06790	2e-05	561	[-3]	418
HMPREF1120_00797	2e-05	834	[-3]	145
HMPREF1120_04804	2.2e-05	700	[+3]	279
HMPREF1120_06146	2.2e-05	128	[+3]	851
HMPREF1120_08742	2.2e-05	650	[-3]	329
HMPREF1120_06329	2.2e-05	149	[-3]	830
HMPREF1120_07479	2.2e-05	603	[+3]	376
HMPREF1120_03417	2.4e-05	62	[-3]	917
HMPREF1120_04574	2.4e-05	499	[+3]	480
HMPREF1120_01052	2.4e-05	669	[-3]	310
HMPREF1120_04126	2.4e-05	339	[-3]	640
HMPREF1120_02172	2.4e-05	591	[+3]	388
HMPREF1120_01106	2.4e-05	87	[+3]	892
HMPREF1120_01896	2.6e-05	662	[+3]	317
HMPREF1120_07937	2.6e-05	463	[-3]	516
HMPREF1120_05100	2.6e-05	134	[-3]	845
HMPREF1120_02305	2.6e-05	957	[+3]	22
HMPREF1120_03745	2.9e-05	800	[+3]	179
HMPREF1120_06583	2.9e-05	956	[-3]	23
HMPREF1120_07533	2.9e-05	609	[+3]	370
HMPREF1120_02714	2.9e-05	664	[+3]	315
HMPREF1120_04575	3.1e-05	379	[-3]	600
HMPREF1120_06922	3.5e-05	875	[+3]	104
HMPREF1120_01315	3.5e-05	622	[+3]	357
HMPREF1120_00405	3.5e-05	439	[+3]	540

HMPREF1120_04938	3.5e-05	442_ [+3]_537
HMPREF1120_00689	3.5e-05	728_ [-3]_251
HMPREF1120_05503	3.5e-05	434_ [-3]_545
HMPREF1120_07676	3.8e-05	514_ [-3]_465
HMPREF1120_02138	3.8e-05	121_ [-3]_858
HMPREF1120_08389	4.5e-05	151_ [+3]_828
HMPREF1120_05234	4.9e-05	75_ [-3]_904
HMPREF1120_07962	4.9e-05	945_ [-3]_34
HMPREF1120_05841	5.3e-05	499_ [-3]_480
HMPREF1120_00375	8.1e-05	685_ [+3]_294

 Motif TYTBKTKTKBTTKBTTBNYY MEME-3 in BLOCKS format

BL	MOTIF	TYTBKTKTKBTTKBTTBNYY	width=21	seqs=157	
HMPREF1120_03803	(406)	TTTGTGTTTGTTCCTTGCTT	1		1
HMPREF1120_02117	(946)	TTTCTCTCTTTGTTTGCTT	1		1
HMPREF1120_07633	(128)	TTGTTGTTTGTGCTTTATT	1		1
HMPREF1120_07632	(792)	TTGTTGTTTGTGCTTTATT	1		1
HMPREF1120_06027	(528)	TCTGTGTTTGTGTTTTGTCC	1		1
HMPREF1120_06028	(923)	TCTGTGTTTGTGTTTTGTCC	1		1
HMPREF1120_07062	(743)	TCTCTCTTTGTTCTCTCTT	1		1
HMPREF1120_02776	(970)	TTTTGTTTCTGTTTCTCATT	1		1
HMPREF1120_07880	(753)	TCTGTTTTGCTTGTGCTTCTT	1		1
HMPREF1120_09134	(657)	CTTCTGCTTCTTTCTTCTT	1		1
HMPREF1120_07560	(509)	TCTTCTTTTCTTCTTGCTT	1		1
HMPREF1120_05354	(388)	TTGTTGTTGTTGTTTTCTT	1		1
HMPREF1120_00523	(693)	TTTGTGTTTGCCTTTGCTT	1		1
HMPREF1120_03061	(618)	TTTTCTTTTTTCTTTTCA	1		1
HMPREF1120_02274	(345)	TTTGATTTGGTTGTTGTTT	1		1
HMPREF1120_02275	(980)	TTTGATTTGGTTGTTGTTT	1		1
HMPREF1120_04563	(33)	TTTCTTTTGTGTTTGCTTT	1		1
HMPREF1120_07074	(212)	TTTGATTTTGATTGTTTCTT	1		1
HMPREF1120_05142	(559)	TTTTTCTTCTGGCTTCTCTT	1		1
HMPREF1120_03399	(841)	GCTGTGTTGGGTGTTTCGTT	1		1
HMPREF1120_06528	(920)	TGTGTATTGTTTTGTTGCTT	1		1
HMPREF1120_08344	(779)	TGTTTGCTGTTTTCTTCTCTT	1		1
HMPREF1120_03768	(718)	GTTGTGCTGTTTCTCTCTT	1		1
HMPREF1120_06363	(659)	TTTCTGATTCTTGCCTCCCT	1		1
HMPREF1120_07003	(458)	CTTCTTCTCATTTTTGATT	1		1
HMPREF1120_08211	(310)	TTTGTGATTGATTGCTTTCCCT	1		1
HMPREF1120_00244	(457)	ATTCTTTTGCATTCCTTTGTT	1		1
HMPREF1120_05123	(149)	CTTTTTTTTCTCGGTTTGCTC	1		1
HMPREF1120_00243	(445)	ATTCTTTTGCATTCCTTTGTT	1		1
HMPREF1120_05622	(600)	TCCTTTTTTCTCGCTTTTCTC	1		1
HMPREF1120_06279	(649)	TTTGTGCTGCTTGGATTCTT	1		1
HMPREF1120_00627	(976)	GTGGTCTTCTTCTTTGCTT	1		1
HMPREF1120_02225	(704)	ATTCTTTTGGTGTTTGATT	1		1
HMPREF1120_00041	(944)	GCTTTGTTTCACTCCTTTTCC	1		1
HMPREF1120_04377	(186)	TTTCTTCTCTTGCCTTTCTT	1		1
HMPREF1120_00196	(259)	TCGTTGTTGGTTTCACTTCT	1		1
HMPREF1120_05842	(289)	TTTGACTTTGTGGTTTGCTC	1		1
HMPREF1120_03649	(725)	TTTGTATTTGTGTTTGCTA	1		1
HMPREF1120_02703	(808)	TTCTTCTTTGCTGTTTCTCT	1		1
HMPREF1120_00717	(373)	GCGGTGTTTCTGTTGTTCCCT	1		1
HMPREF1120_03202	(81)	TCTTTTTTGTGGCTTGCCA	1		1
HMPREF1120_07792	(381)	TCGCTGTTGCTGGCTCTGCTT	1		1
HMPREF1120_05260	(680)	TCTGTCTCTGGTTTTCTCTT	1		1
HMPREF1120_06393	(226)	GCTGTGTTTGTGATTGATC	1		1
HMPREF1120_05935	(122)	TCTTTGCTTTTCTTCTTTG	1		1
HMPREF1120_06465	(858)	TGTTTGCTGCATTCGTTGTT	1		1
HMPREF1120_02566	(402)	GCTTCTCTGCTTTCTTTGCTT	1		1
HMPREF1120_07971	(977)	TTTGTCTCTTCTCTTTCTC	1		1
HMPREF1120_02510	(663)	TTCCTCTTGGTGGCTTGATC	1		1
HMPREF1120_02072	(503)	GTTCTCTCGTTTGTCTCTCC	1		1
HMPREF1120_02634	(507)	TCGTTCTGTTTTCCCTTCT	1		1
HMPREF1120_03622	(180)	GCGCTTTGTTTTGTTTTCT	1		1
HMPREF1120_06441	(959)	TTCGTGTTGCTTGTCTCTCC	1		1

HMPREF1120_07658 (83) CTTGTGTTTCTTGCGCTGCTTC 1
HMPREF1120_02509 (778) TCTTTGCTGTTTGCCTTGTC 1
HMPREF1120_08154 (472) TCTATGATGGTTGTTTCGTT 1
HMPREF1120_07674 (675) TTCCTGTTTGTGGCTGTTCT 1
HMPREF1120_03503 (475) GCTGTTTCTCGCTTTTGTGTC 1
HMPREF1120_06777 (919) GCCCTTTTGTTCCTTGCTC 1
HMPREF1120_07793 (302) TCTTTATCTATTTTCTTCTTT 1
HMPREF1120_08679 (332) TTTTTTTTGGCGGGTTTCTG 1
HMPREF1120_04831 (8) TCTCTGCTCTTCGGCTTGTTT 1
HMPREF1120_04902 (930) TCTATCTTTGGTTCTTTTCC 1
HMPREF1120_08078 (65) TTTGTCTCCTATGTCTTTGTT 1
HMPREF1120_04947 (499) TGGCTGTTGGGTTCCCTTCATC 1
HMPREF1120_07049 (173) TCTGTCTTGGATGTCTGGACC 1
HMPREF1120_04834 (321) GTTGTTTTTTTGTGCTGTTG 1
HMPREF1120_06537 (812) TTTATTTTGTGCTGGTGTGATA 1
HMPREF1120_07050 (468) TCTGTCTTGGATGTCTGGACC 1
HMPREF1120_07951 (458) TCCTAGTTGGATTTGTTCTTC 1
HMPREF1120_03835 (656) GTTCATTTTGTCTCGTTGCC 1
HMPREF1120_03195 (251) TTTCTGTTCTCTTCTGTATG 1
HMPREF1120_05790 (876) TTCCTTTTGTACTGCCTTCTC 1
HMPREF1120_04140 (232) TTTATCTTTGTCTCTTTGGCG 1
HMPREF1120_00374 (244) GTTGTGCTTTTTCGGTTTTGCT 1
HMPREF1120_02373 (944) TCTGTGTTGGATGGTCTTGCA 1
HMPREF1120_01523 (962) TCTCTGTTTCTCTGTGGCAC 1
HMPREF1120_04550 (315) TGTTTGTTCGGTTCTTTTCG 1
HMPREF1120_04359 (259) TTGTTGATCCTTTCCTTGCTG 1
HMPREF1120_04430 (420) TTCTTCTACTTTCTTTTATA 1
HMPREF1120_03772 (653) TGTCTGTTGCAGTGCCTTGTT 1
HMPREF1120_06138 (286) TTTCTCTGATTTTCTCGTA 1
HMPREF1120_00546 (633) ATTTTGCTTCGTTTCGTTTATC 1
HMPREF1120_01435 (179) TCTGTGTCATTTTCTCTGTCT 1
HMPREF1120_03541 (583) CCTCTGTTTATCTCTTTCGTC 1
HMPREF1120_07322 (963) CTTTTTCTGCTGTGTTTCTCT 1
HMPREF1120_08783 (773) TCGTGTTCCTACTGCTTGAAT 1
HMPREF1120_05987 (665) TCTTTCTGCTCTGGCTTCA 1
HMPREF1120_06548 (643) CTTCTCTGTTTGGCTCGTC 1
HMPREF1120_06617 (63) ACTGTCTTGCTTCTCTCTG 1
HMPREF1120_01909 (874) TCTATGCTTGTGCCCTGATC 1
HMPREF1120_02791 (920) GTTCTTCTGTACTCCTTTTCT 1
HMPREF1120_01547 (568) TCGGTGTTGCTTGGATTCGTA 1
HMPREF1120_08523 (94) GTTTTTATACATTTCTTCCCT 1
HMPREF1120_02139 (865) TTTCTTTTGATTTCTCTCTCA 1
HMPREF1120_08476 (844) GTCTTGTGTTGATGCCTGCTT 1
HMPREF1120_05486 (955) CCTTTGTCGGGCTCTTTGCCT 1
HMPREF1120_07879 (794) TCGTTGTTGCTGGTATTGTTA 1
HMPREF1120_01764 (311) GCTGTGTCGTTCTGTTCTGGTT 1
HMPREF1120_06580 (784) TTTGTCTCGCAGTGTGTTGGTG 1
HMPREF1120_04393 (829) TCCCTGTTTGGAGCGCTCTTT 1
HMPREF1120_07128 (446) TTGCAGTTGTGTTGTTGACT 1
HMPREF1120_06758 (28) GTTCATTTGCGTTTGTCTTA 1
HMPREF1120_06581 (459) TTTGTCTCGCAGTGTGTTGGTG 1
HMPREF1120_01967 (352) TCTCATCTCTTTGGTTCTTG 1
HMPREF1120_07528 (719) GTTTTAGTTCTTCTCTTCTTT 1
HMPREF1120_04424 (692) TCGTTGCTGCACTCTTCTCC 1
HMPREF1120_01923 (777) TCTCAGTTTCACTCATTCTCT 1
HMPREF1120_06047 (425) TCTCTGTTGTGTTGTAGCTC 1
HMPREF1120_03688 (711) TTTCATTTGGTCGTGCTTGTC 1
HMPREF1120_01817 (220) TTGTTGATGGGTTTGTGATG 1
HMPREF1120_08663 (543) GTTGAGTTGCATGTTCTGACT 1
HMPREF1120_00104 (946) GTCCTTGTGTTTTGTGCTTT 1
HMPREF1120_07677 (83) TGCCCTTTTCTCTCTCTTTT 1
HMPREF1120_00924 (824) TCTGTTATTCTGGTGCTCATC 1
HMPREF1120_05665 (913) GTGTTGATTTGTTCTTTGCTC 1
HMPREF1120_07908 (202) CTGCTTCTGCATTGTTGGTT 1
HMPREF1120_03953 (257) CCTGTGTTACGTGCTTGCTA 1
HMPREF1120_09162 (498) GTTCTCTTCTTTCCTTGACG 1
HMPREF1120_04224 (207) TCTCTATCTCAGTTCTTATT 1
HMPREF1120_02454 (567) TTTCTTTTTCGTTGGTGGATA 1
HMPREF1120_01082 (605) TCTGTATCTGTTTCTTTGAC 1

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HMPREF1120_06790      ( 562) CTTTCATCTTTTTTTTTTTCATC  1
HMPREF1120_00797      ( 835) TGCTTGTTTCATTTTCTGGTA  1
HMPREF1120_04804      ( 701) GGTTTCTTGGGCTCTTTTCTC  1
HMPREF1120_06146      ( 129) TCTCTCTGCGTTTCTTCGAC  1
HMPREF1120_08742      ( 651) TTCGTGTTTCATTCACCTCTG  1
HMPREF1120_06329      ( 150) CCCTTCTCTTTTTGTTGCCT  1
HMPREF1120_07479      ( 604) TGGTTGTCTTTGTCTTTGCCT  1
HMPREF1120_03417      ( 63) TCTTTCTCTTGTGGCCTGCCT  1
HMPREF1120_04574      ( 500) TTGTTATCGTATTCTTCGCT  1
HMPREF1120_01052      ( 670) TTTGTGCTTCATGTGCTCAAT  1
HMPREF1120_04126      ( 340) CCTGTTCTCGTTTGCTTGCTG  1
HMPREF1120_02172      ( 592) TTTGTTCTGTACTGGCTCCCT  1
HMPREF1120_01106      ( 88) TTCGTGTTGCAGGTTGGGTC  1
HMPREF1120_01896      ( 663) TCCGTGTCGCATGCGCTGCCT  1
HMPREF1120_07937      ( 464) TCTCTTGTTGTGGGGTTTGTT  1
HMPREF1120_05100      ( 135) TTGGTGATGCTTGTGTTCAAT  1
HMPREF1120_02305      ( 958) CGTTTTTCTCTGTTTGTTC  1
HMPREF1120_03745      ( 801) GCTCTGATTGATTGATTGACT  1
HMPREF1120_06583      ( 957) CCTCAGTTCGATTGTTTGTGTT  1
HMPREF1120_07533      ( 610) TCTTTGACTTTTTTGTGGACT  1
HMPREF1120_02714      ( 665) ATTGTGTTAGTTTCTGTACT  1
HMPREF1120_04575      ( 380) CTTGTGCTGTCGGGTTGCCT  1
HMPREF1120_06922      ( 876) TTTGTTTTTCATGGGGTTCATC  1
HMPREF1120_01315      ( 623) TCTGTATCACTCTGCTCCCT  1
HMPREF1120_00405      ( 440) ACTTTGTCTGTCTTCTTGAAT  1
HMPREF1120_04938      ( 443) TTCCTTCTCTTTGTGCATA  1
HMPREF1120_00689      ( 729) TTTTTAGTTCATTCGTTGTTA  1
HMPREF1120_05503      ( 435) TTCTTTTCCACTTCCTTCCC  1
HMPREF1120_07676      ( 515) GCTGTATCACTTGCTTTGGTT  1
HMPREF1120_02138      ( 122) CTTGAATTTGTTTCTTCGCA  1
HMPREF1120_08389      ( 152) ATGATGTTGGGTTCTTGCTC  1
HMPREF1120_05234      ( 76) TCTGTTACGCGTGCCTTACC  1
HMPREF1120_07962      ( 946) GGGGTGTTTGTGGTGTGATG  1
HMPREF1120_05841      ( 500) GTGTAGTTGGTGTCTGTGTT  1
HMPREF1120_00375      ( 686) TTTTCTTTCGTGGTTACCTG  1
//

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Motif TYTBTKTKBTTKBTTBNYY MEME-3 position-specific scoring matrix

log-odds matrix: alength= 4 w= 21 n= 457438 bayes= 12.9701 E= 1.4e+000

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-225  -125  -48  143
-1394  62  -175  112
-1394  -101  -69  156
-267  25  42  36
-125  -1394  -1394  189
-179  -43  83  21
-167  -75  -375  163
-1394  -58  -1394  177
-244  -143  52  101
-293  66  42  -16
-4  -1394  -58  129
-1394  -17  -64  132
-1394  -1394  47  141
-1394  31  -9  86
-225  47  2  45
-1394  -29  -1394  170
-425  -1394  -143  188
-1394  22  64  30
-16  34  -34  7
-244  39  -1394  135
-108  22  -125  98

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Motif TYTBTKTKBTTKBTTBNYY MEME-3 position-specific probability matrix

letter-probability matrix: alength= 4 w= 21 nsites= 157 E= 1.4e+000

0.050955	0.108280	0.184713	0.656051
0.000000	0.394904	0.076433	0.528662
0.000000	0.127389	0.159236	0.713376
0.038217	0.305732	0.343949	0.312102
0.101911	0.000000	0.000000	0.898089
0.070064	0.191083	0.458599	0.280255
0.076433	0.152866	0.019108	0.751592
0.000000	0.171975	0.000000	0.828025
0.044586	0.095541	0.369427	0.490446
0.031847	0.407643	0.343949	0.216561
0.235669	0.000000	0.171975	0.592357
0.000000	0.229299	0.165605	0.605096
0.000000	0.000000	0.356688	0.643312
0.000000	0.318471	0.242038	0.439490
0.050955	0.356688	0.261146	0.331210
0.000000	0.210191	0.000000	0.789809
0.012739	0.000000	0.095541	0.891720
0.000000	0.299363	0.401274	0.299363
0.216561	0.324841	0.203822	0.254777
0.044586	0.337580	0.000000	0.617834
0.114650	0.299363	0.108280	0.477707

Motif TYTBTkTKBTkBBTTBNYY MEME-3 regular expression

T[TC]T[GTC]T[GT]TT[TG][CGT][TA][TC][TG][TCG][CTG][TC]T[GCT][CTAG][TC][TC]

Time 1513.35 secs.

MOTIF CCAWAKGTASSTAGGTARGY MEME-4 width = 20 sites = 9 llr = 165 E-value = 2.8e+002

Motif CCAWAKGTASSTAGGTARGY MEME-4 Description

Simplified A 118671::a::a1::93::
pos.-specific C 781:111::33:::14
probability G 111::39::77::8a::79:
matrix T 1::424:a::a:1:a1::6

bits 2.0 ** ** **
1.8 ** ** **
1.6 ** ** **
1.4 *** ** ** *
Relative 1.2 *** ** ** *
Entropy 1.0 *** *****
(26.4 bits) 0.8 **** *****
0.6 ***** *****
0.4 ***** *****
0.2 ***** *****
0.0 -----

Multilevel CCAAATGTAGGTAGGTAGGT
consensus TTG CC A C
sequence

Motif CCAWAKGTASSTAGGTARGY MEME-4 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
HMPREF1120_04947	+	676	8.78e-12	GTATACGGAC CCAAAGGTAGGTAGGTAGGC AGGCAGAAGC
HMPREF1120_02531	+	687	8.12e-11	AGTAAGCCTC CCATAAGTAGGTAGGTAGGC ATCCAGCTTG
HMPREF1120_02776	+	388	1.20e-10	TATTGTTCTGA CCAAATGTACCTAGGTAAGC AATTCACTAC
HMPREF1120_02904	+	521	1.12e-09	GTCTTAGCTA CCCTAGGTACCTAGGTAGGT ACAGGCACCA
HMPREF1120_06974	-	669	1.49e-09	AGCCTGTACT ACAATTGTACCTAGGTAGGT ACCTTAGTTA
HMPREF1120_06129	-	5	4.92e-09	CGAGAGGTAC GCAATTGTAGGTAAGTAAGT ATGC
HMPREF1120_06148	-	863	6.49e-09	ATGTCTTTAG CAATACCTAGGTAGGTAGGT ACTGTACAGC
HMPREF1120_07017	+	513	1.04e-08	AAGGCAGTCC TGGTAGGTAGGTAGGTAGGT TCGGATATTC
HMPREF1120_06047	+	719	5.63e-08	ATTGAAATCA CCAACTGTAGGTATGTTACC ACGATGTCGT

Motif CCAWAKGTASSTAGGTARGY MEME-4 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
HMPREF1120_04947		8.8e-12	675_[+4]_305
HMPREF1120_02531		8.1e-11	686_[+4]_294
HMPREF1120_02776		1.2e-10	387_[+4]_593
HMPREF1120_02904		1.1e-09	520_[+4]_460
HMPREF1120_06974		1.5e-09	668_-4]_312
HMPREF1120_06129		4.9e-09	4_-4]_976
HMPREF1120_06148		6.5e-09	862_-4]_118
HMPREF1120_07017		1e-08	512_[+4]_468
HMPREF1120_06047		5.6e-08	718_[+4]_262

Motif CCAWAKGTASSTAGGTARGY MEME-4 in BLOCKS format

```
BL MOTIF CCAWAKGTASSTAGGTARGY width=20 seqs=9
HMPREF1120_04947 ( 676) CCAAAGGTAGGTAGGTAGGC 1
HMPREF1120_02531 ( 687) CCATAAGTAGGTAGGTAGGC 1
HMPREF1120_02776 ( 388) CCAAATGTACCTAGGTAAGC 1
HMPREF1120_02904 ( 521) CCCTAGGTACCTAGGTAGGT 1
HMPREF1120_06974 ( 669) ACAATTGTACCTAGGTAGGT 1
HMPREF1120_06129 ( 5) GCAATTGTAGGTAAGTAAGT 1
HMPREF1120_06148 ( 863) CAATACCTAGGTAGGTAGGT 1
HMPREF1120_07017 ( 513) TGGTAGGTAGGTAGGTAGGT 1
HMPREF1120_06047 ( 719) CCAACTGTAGGTATGTTACC 1
//
```

Motif CCAWAKGTASSTAGGTARGY MEME-4 position-specific scoring matrix

log-odds matrix: alength= 4 w= 20 n= 457905 bayes= 16.4827 E= 2.8e+002

-113	137	-121	-113
-113	159	-121	-982
168	-121	-121	-982
119	-982	-982	87
146	-121	-982	-13
-113	-121	37	87
-982	-121	179	-982
-982	-982	-982	204
204	-982	-982	-982
-982	37	137	-982
-982	37	137	-982
-982	-982	-982	204
204	-982	-982	-982
-113	-982	159	-113
-982	-982	196	-982
-982	-982	-982	204
187	-982	-982	-113
46	-982	137	-982

-982 -121 179 -982
-982 79 -982 119

Motif CCAWAKGTASSTAGGTARGY MEME-4 position-specific probability matrix

letter-probability matrix: alength= 4 w= 20 nsites= 9 E= 2.8e+002

Table with 4 columns of probabilities for each position (0.111111, 0.666667, 0.111111, 0.111111) across 20 sites.

Motif CCAWAKGTASSTAGGTARGY MEME-4 regular expression

CCA[AT][AT][TG]GTA[GC][GC]TAGGTA[GA]G[TC]

Time 2001.74 secs.

MOTIF DRGSWHGHMGDRAKSGATGADYTTGGVNSADBAMGWCSVYS MEME-5 width = 40 sites = 17 llr = 333 E-value = 1.3e+003

Motif DRGSWHGHMGDRAKSGATGADYTTGGVNSADBAMGWCSVYS MEME-5 Description

Simplified pos.-specific probability matrix A 343234155:5492:271:94:11:44:72:65:5:14:: C 1:14131242::16::22:152:1326312:5::55265 G 4564118::8361446:18132169424:451:91243:4 T 32::52:3112::4:2351:2363::21:432:152:142

Table showing Relative Entropy (28.2 bits) for each position, with values ranging from 0.0 to 2.0.

Multilevel GGGCTAGAAGAGCGATGAACTGGAACAGGACGACCACC

consensus AAAGAC TC GA TGTC GT T GCGCTTTA TGGGTG
sequence T T C T T CG C T C

Motif DRGSWHGHMGDRAKSGATGADYTGGVNSADBAMGWCSVYS MEME-5 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
HMPREF1120_07049 TATAAGAAGA	+	474	6.15e-15	CGGGAAACCC TGGATAGCCGGGAGGGATGAATTGGAACAAGAAGTCCATC
HMPREF1120_07050 TATAAGAAGA	-	148	6.15e-15	CGGGAAACCC TGGATAGCCGGGAGGGATGAATTGGAACAAGAAGTCCATC
HMPREF1120_03846 TGGGGATGGG	+	340	1.89e-13	AGCACCTGAA TGGGTTGAAGTGAGCGAAGAAGTGGCGCCTGAAGATGCTC
HMPREF1120_07560 AACCATCTCA	-	41	1.07e-11	CACATCCCAA GAGGATGCACAGATCAATGAACTGGCCCAGTAAGTGAGTC
HMPREF1120_06441 ATCCAGACGC	-	405	1.21e-11	CCAGCCGGAC GAGGTCGACGAGAACGACGAACCTGCCGACGACGATGCCG
HMPREF1120_02117 CTTTAAAGTA	-	861	4.25e-11	AGTGAAAGG GGAAGAGAAGAGAGCTTTGAGCTTGCGGCTACGACCCTT
HMPREF1120_06770 TTGACGAAAC	-	16	8.91e-11	TACCGTGAGG ATGCTCACCGTGAGGGATCAGTCGGAACAGGTCGACCACG
HMPREF1120_00038 CTTGATCGGC	-	426	1.97e-10	TGCCTGTGCC TGGCTAATAGTAAGCTTGGATCTGGGTCTCAAGTTCGTC
HMPREF1120_06902 TCGCGAAGCA	+	551	3.16e-10	ACGGGTGGAT GGACTGGAATGGATGGATGAGGTTGAAGAGTTCGTCCTCC
HMPREF1120_02623 CGCTCTCAAA	-	483	2.57e-09	AATTGATGGG AAAGTCGTCCAGGACGACGAAGAGGAAGAGGAAGACATCG
HMPREF1120_07664 CCCATCAATC	-	452	4.01e-09	TACGGATACC AAGCTTGATGAAATCATCTATCTGCGAGAACAAGTCCGCG
HMPREF1120_05439 CCAGATCCCT	+	626	7.04e-09	CAAACGCCGC GTGCACGTCGGAATCGATCGTCCGCCCATGGCGTCCGCT
HMPREF1120_02127 GGGTCAAAG	-	572	8.05e-09	TCCAGGCCAC CAAGGTGAAGAAAGCGATGGACTAGGTTATTACGAGGATG
HMPREF1120_05435 CCGGCACAGG	+	785	8.05e-09	AATCGATGAC ATGCAAGTAGTGATGAAAGAGGGTGGTCTCGCGACGGCC
HMPREF1120_05843 TGATTGGAGA	-	453	1.96e-08	CAATGAAAAC GACGACCTAGAAGACGACGACCTGGGCCCGAAGACGATC
HMPREF1120_01106 GGGTACGGCT	+	279	2.21e-08	TATCGTCGCT TGACAAGATCAGACGTTTCAGTAGGGGCATTTTCGTTCCCT
HMPREF1120_05715 TTGCTTCTTT	+	25	6.27e-08	TGTCCGGTGC AGGGCAGAAGGAATGTTGGATTTTGGAGAGCTCTGGGACG

Motif DRGSWHGHMGDRAKSGATGADYTGGVNSADBAMGWCSVYS MEME-5 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
HMPREF1120_07049		6.2e-15	473_[+5]_487
HMPREF1120_07050		6.2e-15	147_-5]_813
HMPREF1120_03846		1.9e-13	339_[+5]_621
HMPREF1120_07560		1.1e-11	40_-5]_920
HMPREF1120_06441		1.2e-11	404_-5]_556
HMPREF1120_02117		4.2e-11	860_-5]_100
HMPREF1120_06770		8.9e-11	15_-5]_945
HMPREF1120_00038		2e-10	425_-5]_535
HMPREF1120_06902		3.2e-10	550_[+5]_410
HMPREF1120_02623		2.6e-09	482_-5]_478
HMPREF1120_07664		4e-09	451_-5]_509
HMPREF1120_05439		7e-09	625_[+5]_335
HMPREF1120_02127		8.1e-09	571_-5]_389
HMPREF1120_05435		8.1e-09	784_[+5]_176
HMPREF1120_05843		2e-08	452_-5]_508
HMPREF1120_01106		2.2e-08	278_[+5]_682
HMPREF1120_05715		6.3e-08	24_[+5]_936

 Motif DRGSWHGHMGDRAKSGATGADYTGGVNSADBAMGWCSVYS MEME-5 in BLOCKS format

```
BL MOTIF DRGSWHGHMGDRAKSGATGADYTGGVNSADBAMGWCSVYS width=40 seqs=17
HMPREF1120_07049 ( 474) TGGATAGCCGGGAGGGATGAATTGGAACAAGAAGTCCATC 1
HMPREF1120_07050 ( 148) TGGATAGCCGGGAGGGATGAATTGGAACAAGAAGTCCATC 1
HMPREF1120_03846 ( 340) TGGGTTGAAGTGAGCGAAGAAGTGGCGCCTGAAGATGCTC 1
HMPREF1120_07560 ( 41) GAGGATGCACAGATCAATGAACTGGCCCAGTAAGTGAGTC 1
HMPREF1120_06441 ( 405) GAGGTCGACGAGAACGACGAACCTGCCGACGACGATGCCG 1
HMPREF1120_02117 ( 861) GGAAGAGAAGAGAGCTTTGAGCTTGCGGCGTACGACCCCT 1
HMPREF1120_06770 ( 16) ATGCTCACCGTGAGGGATCAGTCGGAACAGGTCGACCACG 1
HMPREF1120_00038 ( 426) TGGCTAATAGTAAGCTTGGATCTGGGTCTCAAGTTCGTC 1
HMPREF1120_06902 ( 551) GGACTGGAATGGATGGATGAGGTTGAAGAGTTCGTCTCTCC 1
HMPREF1120_02623 ( 483) AAAGTCGTCCAGGACGACGAAGAGGAAGAGGACATCG 1
HMPREF1120_07664 ( 452) AAGCTTGATGAAATCATCTATCTGCGAGAACAAGTGC GCG 1
HMPREF1120_05439 ( 626) GTGCACGTCGGAATCGATCGTCCGCCCCATGGCGTCCGCT 1
HMPREF1120_02127 ( 572) CAAGGTGAAGAAAGCGATGGACTAGGTTATTACGAGGATG 1
HMPREF1120_05435 ( 785) ATGCAAGTAGTGATGAAAGAGGGTGGTCTCGCGACGGCC 1
HMPREF1120_05843 ( 453) GACGACCTAGAAGACGACGACCTGGGCCCCGAAGACGATC 1
HMPREF1120_01106 ( 279) TGACAAGATCAGACGTTTCAGTAGGGGCATTTTCGTTCCCT 1
HMPREF1120_05715 ( 25) AGGGCAGAAGGAATGTTGGATTTTGAGGAGCTCTGGGACG 1
//
```

 Motif DRGSWHGHMGDRAKSGATGADYTGGVNSADBAMGWCSVYS MEME-5 position-specific scoring matrix

log-odds matrix: alength= 4 w= 40 n= 448565 bayes= 16.0525 E= 1.3e+003

28	-213	46	28
54	-1073	87	-46
28	-213	133	-1073
-46	68	68	-1073
28	-213	-113	112
76	19	-213	-4
-104	-213	168	-1073
95	-13	-1073	28
112	46	-1073	-104
-1073	-54	157	-204
95	-1073	19	-4
54	-1073	133	-1073
186	-1073	-113	-1073
-46	-213	68	54
-1073	119	68	-1073
-46	-1073	119	-4
154	-1073	-1073	28
-104	-13	-113	112
-1073	-54	157	-204
186	-1073	-113	-1073
76	-213	19	-4
-1073	104	-54	28
-104	-54	-213	141
-204	-1073	133	28
-1073	-113	178	-1073
54	19	46	-1073
54	-13	-13	-46
-1073	119	46	-204
154	19	-1073	-1073
-46	-113	46	54
-1073	-13	87	28
141	-1073	-113	-4
95	104	-1073	-1073
-1073	-1073	187	-204
95	-1073	-213	95
-1073	104	-13	-4
-104	104	46	-1073
54	-13	19	-104
-1073	119	-1073	76

-1073 87 46 -46

Motif DRGSWHGHMGDRAKSGATGADYTGGVNSADBAMGWCSVYS MEME-5 position-specific probability matrix

letter-probability matrix: alength= 4 w= 40 nsites= 17 E= 1.3e+003

0.294118	0.058824	0.352941	0.294118
0.352941	0.000000	0.470588	0.176471
0.294118	0.058824	0.647059	0.000000
0.176471	0.411765	0.411765	0.000000
0.294118	0.058824	0.117647	0.529412
0.411765	0.294118	0.058824	0.235294
0.117647	0.058824	0.823529	0.000000
0.470588	0.235294	0.000000	0.294118
0.529412	0.352941	0.000000	0.117647
0.000000	0.176471	0.764706	0.058824
0.470588	0.000000	0.294118	0.235294
0.352941	0.000000	0.647059	0.000000
0.882353	0.000000	0.117647	0.000000
0.176471	0.058824	0.411765	0.352941
0.000000	0.588235	0.411765	0.000000
0.176471	0.000000	0.588235	0.235294
0.705882	0.000000	0.000000	0.294118
0.117647	0.235294	0.117647	0.529412
0.000000	0.176471	0.764706	0.058824
0.882353	0.000000	0.117647	0.000000
0.411765	0.058824	0.294118	0.235294
0.000000	0.529412	0.176471	0.294118
0.117647	0.176471	0.058824	0.647059
0.058824	0.000000	0.647059	0.294118
0.000000	0.117647	0.882353	0.000000
0.352941	0.294118	0.352941	0.000000
0.352941	0.235294	0.235294	0.176471
0.000000	0.588235	0.352941	0.058824
0.705882	0.294118	0.000000	0.000000
0.176471	0.117647	0.352941	0.352941
0.000000	0.235294	0.470588	0.294118
0.647059	0.000000	0.117647	0.235294
0.470588	0.529412	0.000000	0.000000
0.000000	0.000000	0.941176	0.058824
0.470588	0.000000	0.058824	0.470588
0.000000	0.529412	0.235294	0.235294
0.117647	0.529412	0.352941	0.000000
0.352941	0.235294	0.294118	0.117647
0.000000	0.588235	0.000000	0.411765
0.000000	0.470588	0.352941	0.176471

Motif DRGSWHGHMGDRAKSGATGADYTGGVNSADBAMGWCSVYS MEME-5 regular expression

[GAT][GA][GA][CG][TA][ACT]G[ATC][AC]G[AGT][GA]A[GT][CG][GT][AT][TC]GA[AGT][CT]T[GT]G[AGC][ACG][CG][AC][GT][GTC][AT][CA]G[AT][CGT][CG][AGC][CT][CG]

Time 2492.86 secs.

MOTIF TATMCCATGMMAYSWRCCAMWKYNRASRGKRTKMGYSRKTBCWMTGK MEME-6 width = 50 sites = 6 llr = 238 E-value = 6.0e+004

Motif TATMCCATGMMAYSWRCCAMWKYNRASRGKRTKMGYSRKCTBCWMTGK MEME-6 Description

Simplified A 27:72:8::53a2:332::873::358:3::5::3::227:::75:2:
 pos.-specific C :2238a22237:35::8aa:3::53::7222:::5a:55:2a:38:52::
 probability G :::::72:::5:7:::3225235835272:a:333::32:::87
 matrix T 828:::82:::5:7:::2:7732:::5:83:::3::5:a3:3:8:3

bits 2.0 * * ** ** **
 1.8 * * ** ** **
 1.6 * * ** ** **
 1.4 * * *** * *** * * ** ** *
 Relative Entropy 1.2 * * **** * * **** * * * * ** ** **
 (57.3 bits) 1.0 * * **** ** **** * * * * ** * * **
 0.8 * * **** ** **** * * * * ** * * **
 0.6 * * **** ** **** * * * * ** * * **
 0.4 * * **** ** **** * * * * ** * * **
 0.2 * * **** ** **** * * * * ** * * **
 0.0 -----

Multilevel TATACCATGACATCTGCCCAATTCAAACGGTATGCCGCCATCTCCAATGG
 consensus C CA CGAA CAGTCG GA GG TA TGGG G TC T
 sequence T

Motif TATMCCATGMMAYSWRCCAMWKYNRASRGKRTKMGYSRKCTBCWMTGK MEME-6 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
HMPREF1120_07049	-	399	1.40e-24	TGAAGCTTGG
TATACCATGACATGTGCCCAATGTCGAGGGTATGCCGTCAGCTTCAATGG				TAAGGGAGAG
HMPREF1120_07050	+	213	1.40e-24	TGAAGCTTGG
TATACCATGACATGTGCCCAATGTCGAGGGTATGCCGTCAGCTTCAATGG				TAAGGGAGAG
HMPREF1120_02510	+	936	1.48e-20	CCTCTTTGAA
TATACCATGCAACCAACCAAAATCAAACAGGGTGACGCGGTCTCCTCTGT				GGATCCATTA
HMPREF1120_02509	-	686	1.48e-20	CCTCTTTGAA
TATACCATGCAACCAACCAAAATCAAACAGGGTGACGCGGTCTCCTCTGT				GGATCCATTA
HMPREF1120_06441	-	193	1.31e-15	GAAGTGGCGG
ACTCACCTACATCTGCCCTTTCTGACGGCATTCCGACATCTGGACCAG				GTTGTGGCGG
HMPREF1120_06490	-	426	1.93e-15	GAAGATACAA
TTCCCCATCGCAAGTGACCACTTGGAGCCCTGGTGCACAACCTGCAATGG				CTGAATCCTA

Motif TATMCCATGMMAYSWRCCAMWKYNRASRGKRTKMGYSRKCTBCWMTGK MEME-6 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
HMPREF1120_07049		1.4e-24	398_[-6]_552
HMPREF1120_07050		1.4e-24	212_[+6]_738
HMPREF1120_02510		1.5e-20	935_[+6]_15
HMPREF1120_02509		1.5e-20	685_[-6]_265
HMPREF1120_06441		1.3e-15	192_[-6]_758
HMPREF1120_06490		1.9e-15	425_[-6]_525

Motif TATMCCATGMMAYSWRCCAMWKYNRASRGKRTKMGYSRKCTBCWMTGK MEME-6 in BLOCKS format

BL	MOTIF	TATMCCATGMMAYSWRCCAMWKYNRASRGKRTKMGYSRKCTBCWMTGK	width=50	seqs=6
HMPREF1120_07049	(399)	TATACCATGACATGTGCCCAATGTCGAGGGTATGCCGTCAGCTTCAATGG		1
HMPREF1120_07050	(213)	TATACCATGACATGTGCCCAATGTCGAGGGTATGCCGTCAGCTTCAATGG		1
HMPREF1120_02510	(936)	TATACCATGCAACCAACCAAAATCAAACAGGGTGACGCGGTCTCCTCTGT		1
HMPREF1120_02509	(686)	TATACCATGCAACCAACCAAAATCAAACAGGGTGACGCGGTCTCCTCTGT		1
HMPREF1120_06441	(193)	ACTCACCTACATCTGCCCTTTCTGACGGCATTCCGACATCTGGACCAG		1
HMPREF1120_06490	(426)	TTCCCCATCGCAAGTGACCACTTGGAGCCCTGGTGCACAACCTGCAATGG		1

 Motif TATMCCATGMMAYSWRCCCAMWKYNRASRGKRTKMGYSRKCTBCWMTGK MEME-6 position-specific scoring matrix

log-odds matrix: alength= 4 w= 50 n= 443895 bayes= 15.8338 E= 6.0e+004

-54	-923	-923	178
146	-63	-923	-54
-923	-63	-923	178
146	37	-923	-923
-54	169	-923	-923
-923	196	-923	-923
178	-63	-923	-923
-923	-63	-923	178
-923	-63	137	-54
104	37	-63	-923
46	137	-923	-923
204	-923	-923	-923
-54	37	-923	104
-923	96	96	-923
46	-923	-923	146
46	-923	137	-923
-54	169	-923	-923
-923	196	-923	-923
-923	196	-923	-923
178	-923	-923	-54
146	37	-923	-923
46	-923	-923	146
-923	-923	37	146
-923	96	-63	46
46	37	-63	-54
104	-923	96	-923
178	-923	-63	-923
-923	137	37	-923
46	-63	96	-923
-923	-63	169	-923
-923	-63	37	104
104	-923	96	-923
-923	-923	-63	178
-923	-923	137	46
46	96	-63	-923
-923	196	-923	-923
-923	-923	196	-923
-54	96	-923	46
-54	96	37	-923
146	-923	37	-923
-923	-63	37	104
-923	196	-923	-923
-923	-923	-923	204
-923	37	37	46
-923	169	-63	-923
146	-923	-923	46
104	96	-923	-923
-923	-63	-923	178
-54	-923	169	-923
-923	-923	137	46

 Motif TATMCCATGMMAYSWRCCCAMWKYNRASRGKRTKMGYSRKCTBCWMTGK MEME-6 position-specific probability matrix

letter-probability matrix: alength= 4 w= 50 nsites= 6 E= 6.0e+004

0.166667	0.000000	0.000000	0.833333
0.666667	0.166667	0.000000	0.166667
0.000000	0.166667	0.000000	0.833333
0.666667	0.333333	0.000000	0.000000
0.166667	0.833333	0.000000	0.000000

0.000000	1.000000	0.000000	0.000000
0.833333	0.166667	0.000000	0.000000
0.000000	0.166667	0.000000	0.833333
0.000000	0.166667	0.666667	0.166667
0.500000	0.333333	0.166667	0.000000
0.333333	0.666667	0.000000	0.000000
1.000000	0.000000	0.000000	0.000000
0.166667	0.333333	0.000000	0.500000
0.000000	0.500000	0.500000	0.000000
0.333333	0.000000	0.000000	0.666667
0.333333	0.000000	0.666667	0.000000
0.166667	0.833333	0.000000	0.000000
0.000000	1.000000	0.000000	0.000000
0.000000	1.000000	0.000000	0.000000
0.833333	0.000000	0.000000	0.166667
0.666667	0.333333	0.000000	0.000000
0.333333	0.000000	0.000000	0.666667
0.000000	0.000000	0.333333	0.666667
0.000000	0.500000	0.166667	0.333333
0.333333	0.333333	0.166667	0.166667
0.500000	0.000000	0.500000	0.000000
0.833333	0.000000	0.166667	0.000000
0.000000	0.666667	0.333333	0.000000
0.333333	0.166667	0.500000	0.000000
0.000000	0.166667	0.833333	0.000000
0.000000	0.166667	0.333333	0.500000
0.500000	0.000000	0.500000	0.000000
0.000000	0.000000	0.166667	0.833333
0.000000	0.000000	0.666667	0.333333
0.333333	0.500000	0.166667	0.000000
0.000000	1.000000	0.000000	0.000000
0.000000	0.000000	1.000000	0.000000
0.166667	0.500000	0.000000	0.333333
0.166667	0.500000	0.333333	0.000000
0.666667	0.000000	0.333333	0.000000
0.000000	0.166667	0.333333	0.500000
0.000000	1.000000	0.000000	0.000000
0.000000	0.000000	0.000000	1.000000
0.000000	0.333333	0.333333	0.333333
0.000000	0.833333	0.166667	0.000000
0.666667	0.000000	0.000000	0.333333
0.500000	0.500000	0.000000	0.000000
0.000000	0.166667	0.000000	0.833333
0.166667	0.000000	0.833333	0.000000
0.000000	0.000000	0.666667	0.333333

 Motif TATMCCATGMMAYSWRCCCAMWKYNRASRGKRTKMGYSRKCTBCWMTGK MEME-6 regular expression

TAT[AC]CCATG[AC][CA]A[TC][CG][TA][GA]CCCA[AC][TA][TG][CT][AC][AG]A[CG][GA]G[TG][AG]T[GT][CA]CG[CT][CG][AG]
 [TG]CT[CGT]C[AT][AC]TG[GT]

Time 2983.61 secs.

MOTIF CDCTTGCTBTCRATNTYGKMYTCTTSAWCWKKTTYVAAMYTSRACTTC MEME-7 width = 50 sites = 7 llr = 245 E-
 value = 5.9e-001

 Motif CDCTTGCTBTCRATNTYGKMYTCTTSAWCWKKTTYVAAMYTSRACTTC MEME-7 Description

Simplified A 33::1:::69:3::114:::3:::73:3::1:1:46741:149:::
 pos.-specific C 7:7:117:4:9:::13:6:::4437:::143:9:1:1:3631344361:a3:7
 probability G :431:7::3113111::96:::3:::6:1:146:3::31:11:331::1:
 matrix T :3:9713a39:1:73a4:3167:7a9::616447764:1::37:1:::793

bits 2.0 * * * *
 1.8 * * * *
 1.6 * * * *
 1.4 * * * * * * * * * *
 Relative Entropy (50.5 bits) 1.2 * * * * * * * * * * * * * * * *
 1.0 * * * * * * * * * * * * * * * * * * * * * *
 0.8 * * * * * * * * * * * * * * * * * * * * * *
 0.6 * * * * * * * * * * * * * * * * * * * * * *
 0.4 * * * * * * * * * * * * * * * * * * * * * *
 0.2 * * * * * * * * * * * * * * * * * * * * * *
 0.0 -----

Multilevel consensus sequence CGTTGCTCTCAATATCGGATTCTTTGATCTGGTTTCAAACCTCAACTC
 AAG T G G C T TCCCGA CCA ATT GCTC CCTCGG C T
 T T T G

Motif CDCTTGCTBTCRATNTYGKMYTCTTTSAWCWKTTYVAAMYTSRACTTC MEME-7 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
HMPREF1120_07049	-	327	5.12e-25	AAAGACTCTT
CGTTGCTCTCAATTTCCGACTGTTTGATCAGGTTTCAAACCTCGACTTC				CGACGAGGTT
HMPREF1120_07050	+	285	5.12e-25	AAAGACTCTT
CGTTGCTCTCAATTTCCGACTGTTTGATCAGGTTTCAAACCTCGACTTC				CGACGAGGTT
HMPREF1120_07397	+	288	3.85e-17	ATGATGCTCC
AAGTTGTTGTCAATGTTGACTTCTTTCCACTTTTGCCAGACTTCAACCTC				CCTTCTTCGA
HMPREF1120_09019	+	14	4.52e-15	CTGCTCAGCG
AACTTGCTTGCAGATCGTCTCCTTTGAGCTGGATATGTAGATGAACTTT				CGCCAATGCG
HMPREF1120_04574	+	879	7.94e-15	ACCTGATTTT
CTGGTCCTGTCAACATTGGATCCATTCTTTGTTTCCACTCCCGCTGC				ACGGGCAAAA
HMPREF1120_09134	+	920	8.85e-15	TTCTTCCAGT
CGCTCGTTTTGGATCTTGGTCTCTTTGCTCGTTGACCGTGTACCTT				GACAATAA
HMPREF1120_01817	+	934	1.35e-14	CCAGACTCAA
CTCTATCTCTGTCTCATCTTCCAACTCTTCTCCAACCAAACCTTC				ATACCAACTC

Motif CDCTTGCTBTCRATNTYGKMYTCTTTSAWCWKTTYVAAMYTSRACTTC MEME-7 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
HMPREF1120_07049		5.1e-25	326_[-7]_624
HMPREF1120_07050		5.1e-25	284_[+7]_666
HMPREF1120_07397		3.8e-17	287_[+7]_663
HMPREF1120_09019		4.5e-15	13_[+7]_937
HMPREF1120_04574		7.9e-15	878_[+7]_72
HMPREF1120_09134		8.9e-15	919_[+7]_31
HMPREF1120_01817		1.4e-14	933_[+7]_17

Motif CDCTTGCTBTCRATNTYGKMYTCTTTSAWCWKTTYVAAMYTSRACTTC MEME-7 in BLOCKS format

BL	MOTIF	width=50	seqs=7
HMPREF1120_07049	(327)	CGTTGCTCTCAATTTCCGACTGTTTGATCAGGTTTCAAACCTCGACTTC	1
HMPREF1120_07050	(285)	CGTTGCTCTCAATTTCCGACTGTTTGATCAGGTTTCAAACCTCGACTTC	1
HMPREF1120_07397	(288)	AAGTTGTTGTCAATGTTGACTTCTTTCCACTTTTGCCAGACTTCAACCTC	1
HMPREF1120_09019	(14)	AACTTGCTTGCAGATCGTCTCCTTTGAGCTGGATATGTAGATGAACTTT	1
HMPREF1120_04574	(879)	CTGGTCCTGTCAACATTGGATCCATTCTTTGTTTCCACTCCCGCTGC	1
HMPREF1120_09134	(920)	CGCTCGTTTTGGATCTTGGTCTCTTTGCTCGTTGACCGTGTACCTT	1

HMPREF1120_01817
//

(934) CTCTATCTCTCTGTCTCATCTTCATCCAACCTTTCTCCAACCAAACCTTC 1

Motif CDCTTGCTBTCRATNTYGKMYTCTTSAWCWKTTYVAAMYTSRACTTC MEME-7 position-specific scoring matrix

log-odds matrix: alength= 4 w= 50 n= 443895 bayes= 15.7964 E= 5.9e-001

24	147	-945	-945
24	-945	74	24
-945	147	15	-945
-945	-945	-85	182
-76	-85	-945	156
-945	-85	147	-76
-945	147	-945	24
-945	-945	-945	204
-945	74	15	24
-945	-945	-85	182
-945	173	-85	-945
123	-945	15	-76
182	-945	-85	-945
-945	-85	-85	156
24	15	-85	24
-945	-945	-945	204
-945	115	-945	82
-76	-945	173	-945
-76	-945	115	24
82	74	-945	-76
-945	74	-945	123
-945	15	-945	156
-945	147	15	-945
24	-945	-945	156
-945	-945	-945	204
-945	-85	-945	182
-945	74	115	-945
156	15	-945	-945
24	-945	-85	123
-945	173	-945	-76
24	-945	-85	123
-945	-85	74	82
-945	-945	115	82
-76	-85	-945	156
-945	-945	15	156
-76	15	-945	123
-945	115	-945	82
82	15	15	-945
123	-85	-85	-76
156	15	-945	-945
82	74	-85	-945
-76	74	-85	24
-945	15	-945	156
-76	115	15	-945
82	-85	15	-76
182	-945	-85	-945
-945	196	-945	-945
-945	15	-945	156
-945	-945	-85	182
-945	147	-945	24

Motif CDCTTGCTBTCRATNTYGKMYTCTTSAWCWKTTYVAAMYTSRACTTC MEME-7 position-specific probability matrix

letter-probability matrix: alength= 4 w= 50 nsites= 7 E= 5.9e-001

0.285714	0.714286	0.000000	0.000000
0.285714	0.000000	0.428571	0.285714
0.000000	0.714286	0.285714	0.000000

0.000000	0.000000	0.142857	0.857143
0.142857	0.142857	0.000000	0.714286
0.000000	0.142857	0.714286	0.142857
0.000000	0.714286	0.000000	0.285714
0.000000	0.000000	0.000000	1.000000
0.000000	0.428571	0.285714	0.285714
0.000000	0.000000	0.142857	0.857143
0.000000	0.857143	0.142857	0.000000
0.571429	0.000000	0.285714	0.142857
0.857143	0.000000	0.142857	0.000000
0.000000	0.142857	0.142857	0.714286
0.285714	0.285714	0.142857	0.285714
0.000000	0.000000	0.000000	1.000000
0.000000	0.571429	0.000000	0.428571
0.142857	0.000000	0.857143	0.000000
0.142857	0.000000	0.571429	0.285714
0.428571	0.428571	0.000000	0.142857
0.000000	0.428571	0.000000	0.571429
0.000000	0.285714	0.000000	0.714286
0.000000	0.714286	0.285714	0.000000
0.285714	0.000000	0.000000	0.714286
0.000000	0.000000	0.000000	1.000000
0.000000	0.142857	0.000000	0.857143
0.000000	0.428571	0.571429	0.000000
0.714286	0.285714	0.000000	0.000000
0.285714	0.000000	0.142857	0.571429
0.000000	0.857143	0.000000	0.142857
0.285714	0.000000	0.142857	0.571429
0.000000	0.142857	0.428571	0.428571
0.000000	0.000000	0.571429	0.428571
0.142857	0.142857	0.000000	0.714286
0.000000	0.000000	0.285714	0.714286
0.142857	0.285714	0.000000	0.571429
0.000000	0.571429	0.000000	0.428571
0.428571	0.285714	0.285714	0.000000
0.571429	0.142857	0.142857	0.142857
0.714286	0.285714	0.000000	0.000000
0.428571	0.428571	0.142857	0.000000
0.142857	0.428571	0.142857	0.285714
0.000000	0.285714	0.000000	0.714286
0.142857	0.571429	0.285714	0.000000
0.428571	0.142857	0.285714	0.142857
0.857143	0.000000	0.142857	0.000000
0.000000	1.000000	0.000000	0.000000
0.000000	0.285714	0.000000	0.714286
0.000000	0.000000	0.142857	0.857143
0.000000	0.714286	0.000000	0.285714

Motif CDCTTGCTBTCRATNTYGKMYTCTTSAWCWKTTYVAAMYTSRACTTC MEME-7 regular expression

[CA][GAT][CG]TTG[CT]T[CGT]TC[AG]AT[ACT]T[CT]G[GT][AC][TC][TC][CG][TA]TT[GC][AC][TA]C[TA][GT][GT]T[TG][TC][CT][ACG]A[AC][AC][CT][TC][CG][AG]AC[TC]T[CT]

Time 3474.58 secs.

MOTIF WGCTWCKYMKSCCASCASKTCGARRCCSKTGCCTGAAMT MEME-8 width = 41 sites = 3 llr = 141 E-value = 2.1e+005

Motif WGCTWCKYMKSCCACRASKTCGARRCCSKTGCCTGAAMT MEME-8 Description

Simplified pos.-specific probability matrix A 3:::7:::3:::a:7a:::a33:::aa7: C ::a::a:77:7aa:a::3::a:::aa3:::a:a:::3: G :a:::3::33:::3:73::a:77::77:a:a:::a::: T 7::a3:73:7:::7a:::3a:::aa:::a

bits 2.0 *** * **** * **** ** ***** * 1.8 *** * **** * **** ** ***** * 1.6 *** * **** * **** ** ***** * 1.4 *** * **** * **** ** ***** * 1.2 ***** **** * **** ** ***** * 1.0 ***** 0.8 ***** 0.6 ***** 0.4 ***** 0.2 ***** 0.0

Multilevel consensus sequence TGCTACTCCTCCCACAAGTTCGAGGCCGGTGCCTTGAAT A T GTAGG G CG AA CT C

Motif WGCTWCKYMKSCCACRASKTCGARRCCSKTGCCTGAAMT MEME-8 sites sorted by position p-value

Table with 5 columns: Sequence name, Strand, Start, P-value, Site. Rows include HMPREF1120_07049, HMPREF1120_07050, and HMPREF1120_06238.

Motif WGCTWCKYMKSCCACRASKTCGARRCCSKTGCCTGAAMT MEME-8 block diagrams

Table with 4 columns: SEQUENCE NAME, POSITION, P-VALUE, MOTIF DIAGRAM. Rows show motif diagrams for HMPREF1120_07049, HMPREF1120_07050, and HMPREF1120_06238.

Motif WGCTWCKYMKSCCACRASKTCGARRCCSKTGCCTGAAMT MEME-8 in BLOCKS format

BL MOTIF WGCTWCKYMKSCCACRASKTCGARRCCSKTGCCTGAAMT width=41 seqs=3 HMPREF1120_07049 (567) TGCTACTCCTCCCACAAGTTCGAGGCCGGTGCCTTGAAT 1 HMPREF1120_07050 (54) TGCTACTCCTCCCACAAGTTCGAGGCCGGTGCCTTGAAT 1 HMPREF1120_06238 (427) AGCTTCGTAGGCCACGACGTCGAAACCCTTGCCTTGAAT 1 //

Motif WGCTWCKYMKSCCACRASKTCGARRCCSKTGCCTGAAMT MEME-8 position-specific scoring matrix

log-odds matrix: alength= 4 w= 41 n= 448098 bayes= 15.9661 E= 2.1e+005 46 -823 -823 145 -823 -823 195 -823 -823 195 -823 -823 -823 -823 204 145 -823 -823 46 -823 195 -823 -823

```

-823 -823 37 145
-823 137 -823 46
46 137 -823 -823
-823 -823 37 145
-823 137 37 -823
-823 195 -823 -823
-823 195 -823 -823
204 -823 -823 -823
-823 195 -823 -823
145 -823 37 -823
204 -823 -823 -823
-823 37 137 -823
-823 -823 37 145
-823 -823 -823 204
-823 195 -823 -823
-823 -823 195 -823
204 -823 -823 -823
46 -823 137 -823
46 -823 137 -823
-823 195 -823 -823
-823 195 -823 -823
-823 37 137 -823
-823 -823 137 46
-823 -823 -823 204
-823 -823 195 -823
-823 195 -823 -823
-823 -823 195 -823
-823 195 -823 -823
-823 -823 -823 204
-823 -823 -823 204
-823 -823 195 -823
204 -823 -823 -823
204 -823 -823 -823
145 37 -823 -823
-823 -823 -823 204

```


Motif WGCTWCKYMKSCACRASKTCGARRCCSKTGCGCTTGAAMT MEME-8 position-specific probability matrix

letter-probability matrix: alength= 4 w= 41 nsites= 3 E= 2.1e+005

```

0.333333 0.000000 0.000000 0.666667
0.000000 0.000000 1.000000 0.000000
0.000000 1.000000 0.000000 0.000000
0.000000 0.000000 0.000000 1.000000
0.666667 0.000000 0.000000 0.333333
0.000000 1.000000 0.000000 0.000000
0.000000 0.000000 0.333333 0.666667
0.000000 0.666667 0.000000 0.333333
0.333333 0.666667 0.000000 0.000000
0.000000 0.000000 0.333333 0.666667
0.000000 0.666667 0.333333 0.000000
0.000000 1.000000 0.000000 0.000000
0.000000 1.000000 0.000000 0.000000
1.000000 0.000000 0.000000 0.000000
0.000000 1.000000 0.000000 0.000000
0.666667 0.000000 0.333333 0.000000
1.000000 0.000000 0.000000 0.000000
0.000000 0.333333 0.666667 0.000000
0.000000 0.000000 0.333333 0.666667
0.000000 0.000000 0.000000 1.000000
0.000000 1.000000 0.000000 0.000000
0.000000 0.000000 1.000000 0.000000
1.000000 0.000000 0.000000 0.000000
0.333333 0.000000 0.666667 0.000000
0.333333 0.000000 0.666667 0.000000
0.000000 1.000000 0.000000 0.000000
0.000000 1.000000 0.000000 0.000000
0.000000 0.333333 0.666667 0.000000

```

```

0.000000 0.000000 0.666667 0.333333
0.000000 0.000000 0.000000 1.000000
0.000000 0.000000 1.000000 0.000000
0.000000 1.000000 0.000000 0.000000
0.000000 0.000000 1.000000 0.000000
0.000000 1.000000 0.000000 0.000000
0.000000 0.000000 0.000000 1.000000
0.000000 0.000000 0.000000 1.000000
0.000000 0.000000 1.000000 0.000000
1.000000 0.000000 0.000000 0.000000
1.000000 0.000000 0.000000 0.000000
0.666667 0.333333 0.000000 0.000000
0.000000 0.000000 0.000000 1.000000

```

Motif WGCTWCKYMKSCACRASKTCGARRCCSKTGCCTTGAAMT MEME-8 regular expression

[TA]GCT[AT]C[TG][CT][CA][TG][CG]CCAC[AG]A[GC][TG]TCGA[GA][GA]CC[GC][GT]TGCCTTGAA[AC]T

Time 3961.07 secs.

MOTIF GTACAATGTWSTACAWYGTW MEME-9 width = 20 sites = 8 llr = 158 E-value = 2.5e+002

Motif GTACAATGTWSTACAWYGTW MEME-9 Description

```

Simplified      A  ::a:aa:::6:19:851::6
pos.-specific  C  :::a::1:::5:19:14:1:
probability     G  9:::~:~:a::5::13:183:
matrix          T  1a:::~:9:a4:9:::44364

```

```

bits 2.0 ***** **
      1.8 ***** **
      1.6 ***** **
      1.4 ***** **
Relative Entropy (28.5 bits) 1.2 ***** **
                               1.0 ***** **
                               0.8 ***** **
                               0.6 ***** **
                               0.4 ***** **
                               0.2 ***** **
                               0.0 -----

```

```

Multilevel      GTACAATGTACTACAACGTA
consensus       TG  GTTTGT
sequence

```

Motif GTACAATGTWSTACAWYGTW MEME-9 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
HMPREF1120_00038	+	317	1.44e-12	ACTAGATACT GTACAATGTACTACAATGTA CTAGTCATCG
HMPREF1120_00264	+	118	1.78e-11	CGGCTCAGTT GTACAATGTTGTACATCGTA GAGCAGGAGC
HMPREF1120_05730	+	923	1.21e-10	GTGCTCCACC GTACAATGTTGTACAATGGT ATCCCCAAC
HMPREF1120_06864	+	604	4.94e-10	GCGGTAGTAT GTACAATGTTGTACAACGTG GGTGGCAGTC
HMPREF1120_08770	+	870	5.77e-10	TACAATGGTT GTACAATGTAGTACAAGCT GAGAGATCCG
HMPREF1120_03399	-	799	3.26e-09	TCATCTCCGG GTACAACGTACAACGTTGTA TACAACGTGC

```
HMPREF1120_02776      -   776  3.42e-09 CCCTGGCACT GTACAATGTACTCGGTCGTA GTAAGATAAG
HMPREF1120_07908      -   761  3.91e-09 TTCAACGGCT TTACAATGTACTACACATTA TGCACACTCG
```

 Motif GTACAATGTWSTACAWYGTW MEME-9 block diagrams

```
-----  

SEQUENCE NAME          POSITION P-VALUE  MOTIF DIAGRAM  

-----  

HMPREF1120_00038      1.4e-12  316_[+9]_664  

HMPREF1120_00264      1.8e-11  117_[+9]_863  

HMPREF1120_05730      1.2e-10  922_[+9]_58  

HMPREF1120_06864      4.9e-10  603_[+9]_377  

HMPREF1120_08770      5.8e-10  869_[+9]_111  

HMPREF1120_03399      3.3e-09  798_-9]_182  

HMPREF1120_02776      3.4e-09  775_-9]_205  

HMPREF1120_07908      3.9e-09  760_-9]_220  

-----
```

 Motif GTACAATGTWSTACAWYGTW MEME-9 in BLOCKS format

```
-----  

BL  MOTIF GTACAATGTWSTACAWYGTW width=20 seqs=8  

HMPREF1120_00038      ( 317) GTACAATGTACTACAATGTA 1  

HMPREF1120_00264      ( 118) GTACAATGTTGTACATCGTA 1  

HMPREF1120_05730      ( 923) GTACAATGTTGTACAATGGT 1  

HMPREF1120_06864      ( 604) GTACAATGTTGTACAACGT 1  

HMPREF1120_08770      ( 870) GTACAATGTAGTACAAGGCT 1  

HMPREF1120_03399      ( 799) GTACAACGTACAACGTTGTA 1  

HMPREF1120_02776      ( 776) GTACAATGTACTCGGTCGTA 1  

HMPREF1120_07908      ( 761) TTACAATGTACTACACATTA 1  

//
```

 Motif GTACAATGTWSTACAWYGTW MEME-9 position-specific scoring matrix

```
-----  

log-odds matrix: alength= 4 w= 20 n= 457905 bayes= 16.5416 E= 2.5e+002  

-965 -965 176 -96  

-965 -965 -965 204  

204 -965 -965 -965  

-965 196 -965 -965  

204 -965 -965 -965  

204 -965 -965 -965  

-965 -104 -965 185  

-965 -965 196 -965  

-965 -965 -965 204  

136 -965 -965 63  

-965 96 96 -965  

-96 -965 -965 185  

185 -104 -965 -965  

-965 176 -104 -965  

163 -965 -4 -965  

104 -104 -965 63  

-96 54 -104 63  

-965 -965 154 4  

-965 -104 -4 136  

136 -965 -965 63  

-----
```

 Motif GTACAATGTWSTACAWYGTW MEME-9 position-specific probability matrix

```
-----  

letter-probability matrix: alength= 4 w= 20 nsites= 8 E= 2.5e+002  

0.000000 0.000000 0.875000 0.125000  

0.000000 0.000000 0.000000 1.000000  

1.000000 0.000000 0.000000 0.000000  

0.000000 1.000000 0.000000 0.000000  

-----
```



```

1.000000 0.000000 0.000000 0.000000
1.000000 0.000000 0.000000 0.000000
0.000000 0.125000 0.000000 0.875000
0.000000 0.000000 1.000000 0.000000
0.000000 0.000000 0.000000 1.000000
0.625000 0.000000 0.000000 0.375000
0.000000 0.500000 0.500000 0.000000
0.125000 0.000000 0.000000 0.875000
0.875000 0.125000 0.000000 0.000000
0.000000 0.875000 0.125000 0.000000
0.750000 0.000000 0.250000 0.000000
0.500000 0.125000 0.000000 0.375000
0.125000 0.375000 0.125000 0.375000
0.000000 0.000000 0.750000 0.250000
0.000000 0.125000 0.250000 0.625000
0.625000 0.000000 0.000000 0.375000

```

Motif GTACAATGTWSTACAWYGTW MEME-9 regular expression

GTACAATGT[AT][CG]TAC[AG][AT][CT][GT][TG][AT]

Time 4445.84 secs.

MOTIF GTKATGGTCWTGGYCSADMAAGCGCCDGTGBTDCBYGCY MEME-10 width = 39 sites = 5 llr = 175 E-value = 7.8e+003

Motif GTKATGGTCWTGGYCSADMAAGCGCCDGTGBTDCBYGCY MEME-10 Description

```

Simplified      A  :::8::22:6:2:::84688:::4:::22:::2::
pos.-specific  C  :2:2:::2a:::684::4:::8:aa:2::4::646:a4
probability     G  a:6::a8:::8a::6:2:2:82a::482a4:424:8::
matrix          T  :84:a::6:4a::42:24::22:::2:8:284224::6

```

```

bits  2.0 *  **  * * *          ***  *  *
      1.8 *  **  * * *          ***  *  *
      1.6 *  **  * * *          ***  *  *
      1.4 *  **  * * *          ***  *  *

```

```

Relative Entropy (50.5 bits)
1.2 ** **** * *** * *  **** * * **
1.0 ***** ***** ***** ** * ****
0.8 ***** ***** ***** ** * ****
0.6 ***** ***** ***** ** * * ****
0.4 ***** ***** *****
0.2 ***** ***** *****
0.0 -----

```

```

Multilevel consensus sequence
      GTGATGGTCATGGCCGAAAAAGCGCCAGTGCTGCCCGCT
      CTC AA T A TTCTTCGTTG GCG GATGGTA C
      C G T T ATT

```

Motif GTKATGGTCWTGGYCSADMAAGCGCCDGTGBTDCBYGCY MEME-10 sites sorted by position p-value

Sequence name	Strand	Start	P-value	Site
HMPREF1120_07049 TTGGGTGTCT	-	281	9.74e-21	TTCCGACGAG GTTATGGTCATGGTCGATCAAGCGCCAGTGCTGCGCGCT

```

HMPREF1120_07050      +   342  9.74e-21  TTCCGACGAG  GTTATGGTCATGGTCGATCAAGCGCCAGTGCTGCGCGCT
TTGGGTGTCT
HMPREF1120_02021      +   453  2.85e-16  GTCGTCAATG  GTGATGGACTTGGCCCAAAGAGCGCCTCTGGTAGCTGCT
CGAGACTCGG
HMPREF1120_09162      +   264  3.40e-15  TTTGCGCTCT  GCGATGGTCATAGCTGTGAATTCGCCGGTGGTTCTTACC
GGGACCAGCC
HMPREF1120_04805      +   356  4.93e-15  ACCGTATAAA  GTGCTGACCTTGGCCAAAAAGGGCCGGGGTATTTCCGC
AAAGGATGGA

```

Motif GTKATGGTCWTGGYCSADMAAGCGCCDGTGBTDGBYGCY MEME-10 block diagrams

SEQUENCE NAME	POSITION	P-VALUE	MOTIF DIAGRAM
HMPREF1120_07049		9.7e-21	280_[-10]_681
HMPREF1120_07050		9.7e-21	341_[+10]_620
HMPREF1120_02021		2.8e-16	452_[+10]_509
HMPREF1120_09162		3.4e-15	263_[+10]_698
HMPREF1120_04805		4.9e-15	355_[+10]_606

Motif GTKATGGTCWTGGYCSADMAAGCGCCDGTGBTDGBYGCY MEME-10 in BLOCKS format

```

BL  MOTIF GTKATGGTCWTGGYCSADMAAGCGCCDGTGBTDGBYGCY width=39 seqs=5
HMPREF1120_07049      ( 281) GTTATGGTCATGGTCGATCAAGCGCCAGTGCTGCGCGCT 1
HMPREF1120_07050      ( 342) GTTATGGTCATGGTCGATCAAGCGCCAGTGCTGCGCGCT 1
HMPREF1120_02021      ( 453) GTGATGGACTTGGCCCAAAGAGCGCCTCTGGTAGCTGCT 1
HMPREF1120_09162      ( 264) GCGATGGTCATAGCTGTGAATTCGCCGGTGGTTCTTACC 1
HMPREF1120_04805      ( 356) GTGCTGACCTTGGCCAAAAAGGGCCGGGGTATTTCCGC 1
//

```

Motif GTKATGGTCWTGGYCSADMAAGCGCCDGTGBTDGBYGCY MEME-10 position-specific scoring matrix

```

log-odds matrix: alength= 4 w= 39 n= 449032 bayes= 15.8889 E= 7.8e+003
-897 -897 196 -897
-897 -36 -897 172
-897 -897 122 72
172 -36 -897 -897
-897 -897 -897 204
-897 -897 196 -897
-28 -897 163 -897
-28 -36 -897 130
-897 196 -897 -897
130 -897 -897 72
-897 -897 -897 204
-28 -897 163 -897
-897 -897 196 -897
-897 122 -897 72
-897 163 -897 -28
-897 64 122 -897
172 -897 -897 -28
72 -897 -36 72
130 64 -897 -897
172 -897 -36 -897
172 -897 -897 -28
-897 -897 163 -28
-897 163 -36 -897
-897 -897 196 -897
-897 196 -897 -897
-897 196 -897 -897
72 -897 64 -28
-897 -36 163 -897
-897 -897 -36 172
-897 -897 196 -897

```

```

-897    64    64    -28
-28   -897   -897   172
-28   -897    64    72
-897   122   -36   -28
-897    64    64   -28
-897   122   -897    72
-28   -897   163  -897
-897   196   -897  -897
-897    64   -897   130

```

Motif GTKATGGTCWTGGYCSADMAAGCGCCDGTGBTDGBYGCY MEME-10 position-specific probability matrix

letter-probability matrix: alength= 4 w= 39 nsites= 5 E= 7.8e+003

```

0.000000 0.000000 1.000000 0.000000
0.000000 0.200000 0.000000 0.800000
0.000000 0.000000 0.600000 0.400000
0.800000 0.200000 0.000000 0.000000
0.000000 0.000000 0.000000 1.000000
0.000000 0.000000 1.000000 0.000000
0.200000 0.000000 0.800000 0.000000
0.200000 0.200000 0.000000 0.600000
0.000000 1.000000 0.000000 0.000000
0.600000 0.000000 0.000000 0.400000
0.000000 0.000000 0.000000 1.000000
0.200000 0.000000 0.800000 0.000000
0.000000 0.000000 1.000000 0.000000
0.000000 0.600000 0.000000 0.400000
0.000000 0.800000 0.000000 0.200000
0.000000 0.400000 0.600000 0.000000
0.800000 0.000000 0.000000 0.200000
0.400000 0.000000 0.200000 0.400000
0.600000 0.400000 0.000000 0.000000
0.800000 0.000000 0.200000 0.000000
0.800000 0.000000 0.000000 0.200000
0.000000 0.000000 0.800000 0.200000
0.000000 0.800000 0.200000 0.000000
0.000000 0.000000 1.000000 0.000000
0.000000 1.000000 0.000000 0.000000
0.000000 1.000000 0.000000 0.000000
0.400000 0.000000 0.400000 0.200000
0.000000 0.200000 0.800000 0.000000
0.000000 0.000000 0.200000 0.800000
0.000000 0.000000 1.000000 0.000000
0.000000 0.400000 0.400000 0.200000
0.200000 0.000000 0.000000 0.800000
0.200000 0.000000 0.400000 0.400000
0.000000 0.600000 0.200000 0.200000
0.000000 0.400000 0.400000 0.200000
0.000000 0.600000 0.000000 0.400000
0.200000 0.000000 0.800000 0.000000
0.000000 1.000000 0.000000 0.000000
0.000000 0.400000 0.000000 0.600000

```

Motif GTKATGGTCWTGGYCSADMAAGCGCCDGTGBTDGBYGCY MEME-10 regular expression

```

G[TC][GT][AC]TG[GA][TAC]C[AT]T[GA]G[CT][CT][GC][AT][ATG][AC][AG][AT][GT][CG]GCC[AGT][GC][TG]G[CGT][TA][GTA]
[CGT][CGT][CT][GA]C[TC]

```

Time 4928.92 secs.

SUMMARY OF MOTIFS

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

SEQUENCE NAME	COMBINED P-VALUE	MOTIF DIAGRAM
HMPREF1120_00418	2.28e-02	272_[-4(1.81e-05)]_152_\
		[-5(2.14e-05)]_321_[-1(3.49e-06)]_186
HMPREF1120_02408	3.17e-01	346_[-8(5.64e-05)]_74_\
		[-7(5.08e-05)]_489
HMPREF1120_01131	1.79e-02	606_[+9(1.06e-05)]_3_[-2(1.32e-05)]_\
		350
HMPREF1120_08232	4.43e-01	940_[-5(6.14e-05)]_20
HMPREF1120_01106	1.70e-03	87_[+3(2.38e-05)]_170_\
		[+5(2.21e-08)]_143_[-3(6.86e-05)]_25_[-10(6.75e-05)]_225_[+1(6.99e-06)]_\
		220
HMPREF1120_00342	5.97e-01	32_[+1(6.99e-06)]_95_[+1(6.99e-06)]_\
		855
HMPREF1120_05503	2.07e-02	29_[+8(8.01e-05)]_247_\
		[+2(4.12e-05)]_69_[-7(2.16e-05)]_110_[+2(1.13e-06)]_132_[-7(5.40e-06)]_103_\
		[+2(3.57e-06)]_106
HMPREF1120_06548	7.02e-01	566_[+6(7.41e-05)]_26_\
		[+3(1.18e-05)]_337
HMPREF1120_06442	4.47e-01	177_[-7(4.92e-05)]_559_\
		[+2(2.50e-05)]_59_[-8(9.84e-05)]_93
HMPREF1120_03392	2.25e-01	289_[+6(6.07e-05)]_7_[-6(5.33e-05)]_\
		221_[-3(4.91e-05)]_20_[-10(3.49e-05)]_143_[-3(5.82e-05)]_139
HMPREF1120_00104	7.63e-02	447_[-8(1.10e-05)]_457_\
		[+3(1.60e-05)]_34
HMPREF1120_06522	2.22e-01	739_[-7(5.08e-05)]_98_\
		[+8(2.92e-05)]_72
HMPREF1120_02117	2.14e-08	55_[-5(2.20e-05)]_53_[+8(9.84e-05)]_\
		20_[-3(8.71e-05)]_286_[+4(8.61e-05)]_122_[-1(4.28e-05)]_193_[-5(4.25e-11)]_\
		45_[+3(2.31e-08)]_34
HMPREF1120_00243	2.00e-01	444_[-3(1.02e-06)]_380_\
		[-6(9.77e-05)]_105
HMPREF1120_07631	4.49e-01	954_[-2(1.44e-05)]_25
HMPREF1120_04377	7.98e-03	50_[-7(1.99e-05)]_85_[-3(1.54e-06)]_\
		535_[-2(7.70e-06)]_48_[-2(5.76e-05)]_122_[-3(4.91e-05)]_26
HMPREF1120_07528	1.58e-03	108_[+5(7.27e-06)]_337_\
		[-1(3.49e-06)]_89_[+5(2.38e-05)]_31_[-1(5.35e-05)]_[-1(6.99e-06)]_46_\
		[+3(1.45e-05)]_15_[-1(9.56e-05)]_184_[-8(7.78e-05)]_12
HMPREF1120_00627	4.08e-04	77_[-5(2.38e-05)]_530_\
		[-5(5.56e-05)]_262_[+1(6.99e-06)]_17_[-3(1.17e-06)]_4
HMPREF1120_06863	3.33e-01	124_[-2(2.80e-05)]_106_\
		[-8(3.30e-05)]_115_[+6(8.39e-05)]_443_[-4(6.87e-05)]_80
HMPREF1120_08881	2.52e-01	214_[-8(8.56e-05)]_465_\
		[+7(1.57e-05)]_230
HMPREF1120_04665	1.83e-01	649_[-7(2.87e-05)]_99_\
		[-2(3.85e-05)]_73_[+7(4.09e-06)]_58
HMPREF1120_08459	6.37e-01	832_[+10(7.24e-05)]_129
HMPREF1120_03061	4.68e-03	105_[-7(9.57e-05)]_219_\
		[+9(2.42e-05)]_206_[-1(2.84e-05)]_8_[+3(2.59e-07)]_362
HMPREF1120_07509	5.35e-01	157_[-7(2.83e-05)]_392_\
		[-2(5.22e-05)]_380
HMPREF1120_06129	5.09e-04	4_[-4(4.92e-09)]_14_[+1(6.05e-05)]_\
		751_[-7(7.38e-05)]_88_[-1(3.49e-06)]_55
HMPREF1120_05730	3.35e-04	40_[-2(5.58e-05)]_14_[+2(1.32e-05)]_\
		530_[+5(4.91e-05)]_256_[+9(1.21e-10)]_58
HMPREF1120_01971	9.44e-01	695_[-1(9.56e-05)]_296
HMPREF1120_05552	3.02e-01	221_[-7(1.51e-05)]_729
HMPREF1120_02631	2.08e-03	85_[-7(8.21e-06)]_123_\
		[-1(3.49e-06)]_56_[-3(3.78e-05)]_426_[-10(7.78e-05)]_79_[-8(7.50e-06)]_71
HMPREF1120_06634	9.84e-01	1000

HMPREF1120_03639 7.00e-01 718 [-8(5.93e-05)]_241
 HMPREF1120_05086 4.92e-01 372 [-8(8.56e-05)]_408_\n
 [+9(3.05e-05)]_4_[+1(6.38e-05)]_146
 HMPREF1120_03771 2.76e-02 61 [-2(1.38e-05)]_117_\n
 [+6(9.63e-05)]_265_[+4(1.65e-05)]_113_[+1(6.05e-05)]_45_[+2(2.07e-05)]_209_\n
 [-1(1.77e-05)]_60
 HMPREF1120_01653 2.07e-01 305 [-9(7.86e-05)]_265_\n
 [+5(8.22e-05)]_147_[+1(2.14e-05)]_49_[-1(1.05e-05)]_44_[-1(4.61e-05)]_103
 HMPREF1120_02703 2.42e-03 62 [+2(4.57e-05)]_84_\n
 [-10(7.04e-05)]_155_[-2(5.76e-05)]_121_[-2(5.22e-05)]_110_[+5(1.42e-05)]_4_\n
 [+1(3.21e-05)]_120_[+3(1.76e-06)]_172
 HMPREF1120_03835 2.87e-04 44 [+1(6.99e-06)]_236_\n
 [-3(6.32e-05)]_23_[+4(2.15e-07)]_249_[-1(9.56e-05)]_44_[+3(7.61e-06)]_162_\n
 [+3(9.42e-05)]_52_[+7(1.73e-05)]_39
 HMPREF1120_02790 5.29e-01 162 [-3(3.15e-05)]_817
 HMPREF1120_01095 1.47e-03 256 [+3(9.42e-05)]_31_\n
 [+8(9.89e-06)]_88_[+4(3.17e-06)]_230_[-9(4.76e-07)]_122_[+7(9.72e-05)]_121
 HMPREF1120_03541 8.41e-02 99 [+9(2.64e-05)]_463_\n
 [-3(1.06e-05)]_304_[-1(2.14e-05)]_29_[-3(2.61e-05)]_34
 HMPREF1120_02172 1.35e-02 56 [-6(6.07e-05)]_20_[+9(4.48e-06)]_\n
 445_[+3(2.38e-05)]_388
 HMPREF1120_00689 8.85e-03 259 [-4(1.30e-05)]_123_\n
 [+1(8.86e-05)]_283_[+1(6.99e-06)]_25_[-3(3.45e-05)]_251
 HMPREF1120_03048 5.23e-03 280 [-8(6.42e-07)]_100_\n
 [+6(2.59e-05)]_336_[+9(4.19e-06)]_173
 HMPREF1120_03880 6.05e-01 2 [+6(7.95e-06)]_144_[-6(3.89e-05)]_\n
 754
 HMPREF1120_06931 8.83e-01 435 [-10(9.63e-05)]_526
 HMPREF1120_08377 1.21e-03 432 [+6(4.13e-05)]_183_\n
 [+2(8.15e-11)]_171_[-2(8.48e-05)]_122
 HMPREF1120_00312 4.30e-02 367 [-10(1.79e-05)]_268_\n
 [-6(7.62e-05)]_276
 HMPREF1120_04902 7.01e-01 929 [-3(5.41e-06)]_50
 HMPREF1120_06823 1.24e-01 74 [-10(2.58e-05)]_369_\n
 [+1(1.05e-05)]_471_[-3(9.42e-05)]_17
 HMPREF1120_06746 1.34e-01 24 [-10(1.68e-05)]_259_\n
 [-8(2.01e-05)]_105_[-1(7.44e-05)]_523
 HMPREF1120_02714 5.91e-01 87 [+5(5.42e-05)]_38_[+5(3.81e-05)]_\n
 459_[+3(2.87e-05)]_315
 HMPREF1120_08389 1.38e-01 151 [+3(4.50e-05)]_326_\n
 [+6(6.63e-06)]_312_[-2(7.96e-05)]_119
 HMPREF1120_02139 9.02e-03 203 [+3(4.50e-05)]_248_\n
 [-6(3.83e-05)]_67_[-8(5.22e-05)]_234_[-3(1.31e-05)]_115
 HMPREF1120_05939 4.90e-02 310 [+2(2.54e-06)]_303_\n
 [-2(8.57e-08)]_98_[+2(4.89e-05)]_226
 HMPREF1120_07217 3.80e-01 908 [-3(6.32e-05)]_71
 HMPREF1120_07962 2.14e-02 59 [-5(3.62e-05)]_57_[-6(2.97e-05)]_\n
 490_[-1(3.49e-06)]_240_[-3(4.91e-05)]_34
 HMPREF1120_01351 6.80e-02 25 [-6(1.18e-05)]_4_[+4(6.73e-05)]_\n
 93_[-7(5.58e-05)]_758
 HMPREF1120_01636 9.62e-02 52 [+9(2.35e-05)]_584_\n
 [+2(5.74e-06)]_259_[-6(6.34e-05)]_14
 HMPREF1120_05323 5.68e-01 1000
 HMPREF1120_04126 4.34e-03 339 [-3(2.38e-05)]_86_\n
 [+5(2.51e-05)]_71_[+1(6.73e-05)]_282_[-7(6.60e-07)]_[-8(4.25e-05)]_61
 HMPREF1120_07074 9.29e-02 211 [+3(4.89e-07)]_399_\n
 [-3(9.42e-05)]_348
 HMPREF1120_05589 9.67e-01 1000
 HMPREF1120_08630 1.08e-02 732 [+4(4.12e-08)]_248
 HMPREF1120_04575 8.64e-01 379 [-3(3.15e-05)]_600
 HMPREF1120_06595 1.31e-01 243 [+6(1.64e-05)]_360_\n
 [+3(4.50e-05)]_104_[+6(9.24e-05)]_172
 HMPREF1120_04938 7.04e-04 64 [+1(3.91e-05)]_54_[+5(6.05e-06)]_\n
 275_[+3(3.45e-05)]_324_[-7(3.72e-06)]_163
 HMPREF1120_05123 1.57e-03 148 [+3(1.02e-06)]_250_\n
 [-6(8.39e-05)]_311_[-2(2.41e-08)]_199
 HMPREF1120_06825 2.54e-01 666 [+5(4.32e-05)]_177_\n
 [-4(2.86e-05)]_97
 HMPREF1120_04438 3.89e-01 572 [+1(4.28e-05)]_419

HMPREF1120_03953 3.84e-01 256_[+3(1.77e-05)]_723
 HMPREF1120_02531 1.16e-04 347_-4(6.73e-05)]_319_\n
 [+4(8.12e-11)]_64_-9(7.02e-06)]_210
 HMPREF1120_05950 1.08e-03 119_[+7(6.52e-05)]_99_\n
 [+3(8.05e-05)]_52_-9(5.25e-05)]_30_[+1(8.86e-05)]_64_[+10(3.31e-05)]_46_\n
 [-8(9.51e-05)]_136_-8(3.14e-05)]_26_-6(5.01e-06)]_110_-1(3.49e-06)]_38
 HMPREF1120_01967 1.51e-02 351_[+3(1.45e-05)]_15_\n
 [+3(8.71e-05)]_543_[+1(3.49e-06)]_9_-2(1.11e-05)]_10
 HMPREF1120_05644 3.04e-03 82_-2(3.59e-05)]_36_\n
 [+10(6.20e-05)]_136_[+4(3.89e-05)]_47_-6(6.81e-05)]_67_-2(1.63e-05)]_36_\n
 [-9(3.05e-05)]_341_[+1(6.99e-06)]_75
 HMPREF1120_01546 2.58e-01 217_[+6(8.05e-05)]_133_\n
 [-2(6.56e-05)]_120_-4(6.32e-05)]_236_-2(9.04e-05)]_22_[+1(6.38e-05)]_151
 HMPREF1120_00797 4.77e-01 386_-1(8.86e-05)]_95_\n
 [+2(9.33e-05)]_323_-3(1.96e-05)]_145
 HMPREF1120_08663 1.60e-02 197_[+2(3.32e-08)]_221_\n
 [-1(7.79e-05)]_94_[+3(1.60e-05)]_437
 HMPREF1120_05462 8.82e-01 1000
 HMPREF1120_07533 6.87e-03 118_-2(4.20e-07)]_228_\n
 [-7(2.31e-05)]_33_-2(9.62e-05)]_134_[+3(9.49e-06)]_68_[+1(4.28e-05)]_297
 HMPREF1120_03675 8.86e-01 1000
 HMPREF1120_06581 8.26e-01 458_-3(1.45e-05)]_521
 HMPREF1120_02779 1.53e-01 54_-1(4.98e-05)]_109_\n
 [+9(5.11e-05)]_158_-1(2.47e-05)]_641
 HMPREF1120_04883 2.87e-03 68_[+9(9.39e-06)]_67_-5(1.07e-05)]_\n
 138_[+10(5.38e-05)]_254_[+6(2.97e-05)]_285_[+4(1.99e-06)]_19
 HMPREF1120_04910 1.46e-01 133_-10(2.53e-05)]_49_\n
 [-8(7.55e-05)]_49_-8(1.38e-05)]_143_-3(4.13e-05)]_484
 HMPREF1120_07397 2.37e-08 171_[+1(8.86e-05)]_107_\n
 [+7(3.85e-17)]_663
 HMPREF1120_02089 4.79e-01 509_-6(6.52e-05)]_164_\n
 [-5(6.29e-05)]_237
 HMPREF1120_07479 8.85e-03 399_-8(8.27e-05)]_67_\n
 [+4(8.97e-05)]_41_-9(3.45e-08)]_15_[+3(2.16e-05)]_241_[+3(6.86e-05)]_114
 HMPREF1120_02715 1.52e-01 397_-5(7.27e-06)]_196_\n
 [-6(7.30e-05)]_81_-1(4.98e-05)]_227
 HMPREF1120_04920 1.98e-02 289_-8(3.07e-05)]_550_\n
 [-4(8.05e-07)]_26_[+1(9.56e-05)]_65
 HMPREF1120_08523 9.38e-02 93_[+3(1.31e-05)]_336_\n
 [+3(9.49e-06)]_352_[+5(1.47e-06)]_137
 HMPREF1120_05339 3.54e-01 662_-4(8.44e-05)]_172_\n
 [+9(1.21e-05)]_126
 HMPREF1120_06790 6.01e-01 561_-3(1.96e-05)]_418
 HMPREF1120_06758 2.33e-01 27_[+3(1.45e-05)]_569_\n
 [-1(9.56e-05)]_65_[+3(9.49e-06)]_288
 HMPREF1120_07664 9.38e-05 67_-9(6.43e-05)]_9_-6(9.63e-05)]_\n
 178_-1(4.28e-05)]_118_-5(4.01e-09)]_92_-5(5.70e-05)]_261_-3(9.42e-05)]_\n
 33_[+1(3.49e-06)]_53
 HMPREF1120_03399 1.20e-07 604_-6(7.95e-06)]_144_\n
 [-9(3.26e-09)]_22_[+3(5.69e-07)]_20_-5(1.34e-05)]_45_-1(4.28e-05)]_\n
 [-1(9.56e-05)]_16
 HMPREF1120_02769 2.77e-02 15_[+8(9.51e-05)]_488_\n
 [+3(6.32e-05)]_120_[+4(5.39e-05)]_88_-2(4.12e-05)]_117_-7(1.46e-05)]_19
 HMPREF1120_03104 2.69e-01 14_-5(2.79e-05)]_668_\n
 [+7(3.87e-05)]_228
 HMPREF1120_05710 9.01e-03 76_-1(6.05e-05)]_15_[+3(8.71e-05)]_\n
 66_-1(3.49e-06)]_308_[+4(8.79e-05)]_7_[+9(4.48e-06)]_2_-2(4.41e-05)]_426
 HMPREF1120_02138 1.61e-01 121_-3(3.78e-05)]_347_\n
 [+5(6.61e-05)]_374_[+8(7.83e-05)]_56
 HMPREF1120_05753 6.82e-01 508_-3(7.44e-05)]_471
 HMPREF1120_07854 4.21e-01 855_[+9(7.86e-05)]_125
 HMPREF1120_04684 2.56e-01 50_[+1(4.61e-05)]_154_\n
 [-2(6.35e-05)]_766
 HMPREF1120_00585 3.35e-02 368_[+1(2.14e-05)]_32_\n
 [+6(2.13e-05)]_253_-2(3.99e-05)]_267
 HMPREF1120_06490 1.08e-08 425_-6(1.93e-15)]_187_\n
 [-1(3.49e-06)]_171_-10(8.26e-05)]_119
 HMPREF1120_02566 5.69e-02 139_-4(6.45e-05)]_242_\n
 [-3(3.35e-06)]_31_-1(3.54e-05)]_367_-3(4.91e-05)]_150

HMPREF1120_07951 5.21e-05 210_[+3(1.06e-05)]_17_\n
 [+7(8.47e-05)]_50_[+2(3.35e-05)]_88_[+3(7.61e-06)]_214_-8(8.21e-05)]_73_\n
 [-2(2.99e-08)]_9_-1(6.99e-06)]_155

HMPREF1120_05725 9.45e-01 811_-7(5.32e-05)]_139

HMPREF1120_07128 3.10e-01 445_-3(1.45e-05)]_133_\n
 [-2(9.93e-05)]_102_-1(9.56e-05)]_269

HMPREF1120_02118 1.88e-01 158_-4(5.02e-05)]_109_\n
 [+1(6.99e-06)]_292_-10(8.51e-06)]_373

HMPREF1120_05801 1.48e-04 20_-7(4.06e-05)]_48_[+1(3.54e-05)]_\n
 136_[+1(6.99e-06)]_54_[+5(6.29e-05)]_125_-8(8.05e-05)]_154_-8(2.99e-05)]_\n
 200_-4(3.24e-08)]_53

HMPREF1120_06188 1.68e-01 496_[+3(9.42e-05)]_154_\n
 [-10(3.62e-05)]_174_[+1(6.99e-06)]_107

HMPREF1120_03768 2.16e-01 284_-6(8.28e-05)]_383_\n
 [+3(6.61e-07)]_1_[+3(1.96e-05)]_4_[+3(6.07e-06)]_215

HMPREF1120_00286 7.21e-01 324_[+8(9.66e-05)]_635

HMPREF1120_02424 1.83e-05 98_[+9(1.03e-06)]_172_\n
 [-8(1.13e-06)]_113_[+5(5.56e-05)]_82_-4(2.84e-07)]_[+8(7.86e-05)]_31_\n
 [-1(8.86e-05)]_333

HMPREF1120_00652 2.22e-04 104_[+4(4.76e-07)]_90_\n
 [-1(2.84e-05)]_187_[+5(6.45e-05)]_79_-1(3.49e-06)]_98_[+2(8.48e-05)]_140_\n
 [-6(3.60e-06)]_153

HMPREF1120_08713 8.39e-01 858_-8(7.25e-05)]_101

HMPREF1120_07632 2.96e-03 487_[+2(4.89e-05)]_283_\n
 [+3(2.85e-08)]_14_-2(4.20e-07)]_153

HMPREF1120_00149 6.31e-01 483_-1(4.98e-05)]_508

HMPREF1120_02287 6.01e-01 299_-1(3.54e-05)]_219_\n
 [-6(5.09e-05)]_423

HMPREF1120_04393 1.02e-01 276_[+2(8.48e-05)]_467_\n
 [+1(8.86e-05)]_55_[+3(1.45e-05)]_151

HMPREF1120_06862 5.88e-01 353_[+2(2.07e-05)]_348_\n
 [+4(6.87e-05)]_258

HMPREF1120_06895 4.67e-01 1000

HMPREF1120_01920 1.95e-01 267_-7(2.64e-05)]_320_\n
 [-2(4.72e-05)]_342

HMPREF1120_06329 2.83e-03 24_[+2(2.32e-05)]_88_[+4(1.06e-05)]_\n
 54_[+6(2.40e-05)]_42_[+6(2.79e-05)]_463_-2(6.35e-05)]_70_-10(4.56e-05)]_\n
 58

HMPREF1120_05252 6.01e-01 439_-5(6.77e-05)]_521

HMPREF1120_02898 1.20e-01 693_[+7(7.05e-05)]_23_\n
 [+7(1.91e-06)]_16_-9(5.82e-05)]_148

HMPREF1120_00045 1.73e-01 75_[+2(5.58e-05)]_90_[+3(8.71e-05)]_\n
 25_-10(8.38e-05)]_316_[+1(6.38e-05)]_395_-1(9.56e-05)]

HMPREF1120_05635 4.32e-01 247_-9(9.69e-05)]_132_\n
 [-1(3.91e-05)]_231_[+6(8.75e-05)]_311

HMPREF1120_03442 1.13e-01 75_-7(6.60e-07)]_317_\n
 [+9(4.71e-05)]_538

HMPREF1120_01547 1.96e-01 8_[+5(7.11e-05)]_519_[+3(1.31e-05)]_\n
 308_-1(6.38e-05)]_22_[+2(9.04e-05)]_52

HMPREF1120_07039 1.81e-01 158_-9(6.28e-05)]_131_\n
 [-5(6.14e-05)]_179_-7(1.51e-05)]_422

HMPREF1120_02634 1.14e-02 18_[+1(3.49e-06)]_123_\n
 [+7(8.21e-06)]_306_[+3(3.78e-06)]_4_-5(7.29e-05)]_429

HMPREF1120_03876 5.85e-01 73_[+9(6.43e-05)]_409_\n
 [+5(3.02e-05)]_458

HMPREF1120_02275 5.85e-02 237_-3(2.87e-05)]_579_\n
 [+3(7.61e-06)]_121_-3(3.58e-07)]

HMPREF1120_03066 3.51e-01 172_-4(8.79e-05)]_21_\n
 [+3(2.16e-05)]_6_[+3(5.82e-05)]_739

HMPREF1120_02373 2.75e-01 131_-1(8.86e-05)]_423_\n
 [+10(5.15e-05)]_341_-3(8.51e-06)]_36

HMPREF1120_06864 6.07e-05 39_[+5(4.11e-05)]_309_\n
 [-9(1.03e-06)]_81_[+2(2.24e-05)]_57_[+2(4.89e-05)]_15_[+9(4.94e-10)]_377

HMPREF1120_02274 4.05e-03 344_[+3(3.58e-07)]_116_\n
 [-3(7.61e-06)]_498

HMPREF1120_08525 3.31e-02 587_[+10(4.63e-05)]_119_\n
 [-8(6.61e-06)]_159_[+2(3.35e-05)]_34

HMPREF1120_07050 1.77e-80 53_[+8(2.34e-25)]_53_-5(6.15e-15)]_\n
 25_[+6(1.40e-24)]_22_[+7(5.12e-25)]_7_[+10(9.74e-21)]_3_[+3(5.35e-05)]_63_\n

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[-3(7.61e-06)]_202_[-4(5.14e-05)]_141_[+9(2.35e-05)]_129
HMPREF1120_05273      1.39e-01  356_[-8(1.86e-05)]_92_\
[-10(4.92e-05)]_137_[+1(7.79e-05)]_326
HMPREF1120_07048      1.19e-01  96_[+9(7.86e-05)]_655_\
[+1(1.77e-05)]_220
HMPREF1120_04516      2.06e-01  203_[-7(4.26e-05)]_333_\
[-9(6.89e-05)]_179_[+1(2.47e-05)]_206
HMPREF1120_07996      1.55e-03  122_[+7(1.59e-05)]_336_\
[+1(3.49e-06)]_232_[-2(7.80e-08)]_127_[-1(1.05e-05)]_94
HMPREF1120_03503      7.59e-02  84_[-10(1.13e-05)]_351_\
[+3(4.81e-06)]_505
HMPREF1120_02653      4.01e-01  402_[-4(6.32e-05)]_32_\
[-1(1.77e-05)]_537
HMPREF1120_01129      8.76e-01  809_[+2(8.76e-05)]_170
HMPREF1120_01052      3.48e-01  669_[-3(2.38e-05)]_216_\
[-2(6.56e-05)]_73
HMPREF1120_01536      8.09e-01  51_[+10(8.51e-05)]_755_\
[-3(7.44e-05)]_134
HMPREF1120_06676      7.22e-02  79_[-6(1.00e-05)]_339_\
[+5(1.87e-05)]_209_[+5(4.22e-05)]_243
HMPREF1120_08308      4.57e-02  166_[+10(1.57e-05)]_3_\
[+5(3.62e-05)]_183_[-1(6.99e-06)]_560
HMPREF1120_04375      9.14e-01  1000
HMPREF1120_09262      9.32e-03  89_[+7(6.94e-05)]_126_\
[+5(7.29e-05)]_191_[+1(1.05e-05)]_34_[-2(4.87e-07)]_98_[-1(3.54e-05)]_56_\
[+1(6.99e-06)]_268
HMPREF1120_00244      2.09e-01  26_[+6(9.77e-05)]_380_\
[+3(1.02e-06)]_523
HMPREF1120_06537      5.90e-02  216_[-8(2.67e-05)]_160_\
[+4(5.02e-05)]_48_[+8(6.97e-05)]_285_[-3(7.61e-06)]_157_[-1(5.35e-05)]_2
HMPREF1120_00235      2.55e-02  171_[+6(1.00e-05)]_356_\
[-4(1.12e-05)]_108_[-3(5.35e-05)]_110_[+8(2.62e-05)]_123
HMPREF1120_01435      2.03e-01  178_[-3(1.06e-05)]_801
HMPREF1120_01637      1.31e-01  68_[-4(9.74e-05)]_246_\
[-3(9.42e-05)]_117_[-3(7.44e-05)]_3_[-3(4.91e-05)]_134_[+9(3.31e-06)]_69_\
[+3(8.71e-05)]_2_[-5(9.05e-05)]_197
HMPREF1120_07508      5.61e-01  361_[+3(3.45e-05)]_200_\
[-3(8.71e-05)]_397
HMPREF1120_04934      1.10e-05  40_[+2(3.71e-13)]_ [+2(3.71e-13)]_\
[+2(3.71e-13)]_32_[+2(3.71e-13)]_ [+2(3.71e-13)]_ [+2(3.71e-13)]_\
[+2(3.71e-13)]_309_[-2(4.27e-05)]_150_[-1(2.47e-05)]_91_[-2(4.53e-07)]_107_\
[-2(2.80e-05)]_52
HMPREF1120_02072      3.92e-02  168_[-5(8.20e-06)]_294_\
[+3(3.78e-06)]_45_[+6(3.89e-05)]_382
HMPREF1120_02791      8.76e-03  29_[+9(2.17e-05)]_176_\
[-10(9.94e-05)]_90_[+8(7.52e-05)]_139_[+9(6.28e-05)]_271_[+10(8.36e-06)]_\
55_[+3(1.31e-05)]_60
HMPREF1120_04834      3.46e-01  128_[+5(6.14e-05)]_152_\
[+3(7.61e-06)]_659
HMPREF1120_01817      1.57e-09  25_[-6(4.52e-05)]_127_\
[+1(1.05e-05)]_8_[+3(1.60e-05)]_43_[+5(2.14e-05)]_610_[+7(1.35e-14)]_17
HMPREF1120_03202      1.48e-02  80_[+3(2.29e-06)]_197_\
[-6(3.61e-05)]_154_[+7(1.27e-05)]_27_[-5(1.92e-05)]_92_[-3(3.78e-05)]_268
HMPREF1120_07674      7.63e-02  439_[-2(3.85e-05)]_69_\
[-5(5.16e-05)]_105_[+3(4.81e-06)]_116_[-8(4.47e-05)]_148
HMPREF1120_07633      1.55e-03  92_[+2(4.20e-07)]_14_[-3(2.85e-08)]_\
283_[-2(4.89e-05)]_548
HMPREF1120_01995      5.35e-02  88_[-2(5.58e-05)]_132_\
[+3(9.42e-05)]_68_[-2(1.11e-05)]_137_[+5(4.91e-05)]_413_[+10(5.00e-05)]_20
HMPREF1120_00159      3.48e-01  395_[+1(7.44e-05)]_463_\
[+2(2.60e-05)]_112
HMPREF1120_08773      6.17e-01  638_[+1(1.77e-05)]_353
HMPREF1120_04488      5.98e-01  117_[+2(4.72e-05)]_862
HMPREF1120_03846      1.15e-07  339_[+5(1.89e-13)]_334_\
[+4(7.62e-05)]_67_[-9(4.45e-05)]_73_[-1(1.77e-05)]_98
HMPREF1120_00041      3.79e-03  203_[-8(8.75e-05)]_278_\
[+1(6.99e-06)]_40_[+5(6.77e-05)]_141_[-10(2.92e-05)]_152_[+3(1.35e-06)]_36
HMPREF1120_05330      6.24e-01  449_[-2(3.35e-05)]_530
HMPREF1120_07767      7.29e-01  110_[+8(4.58e-05)]_849

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HMPREF1120_01851 1.16e-01 425_[+8(6.61e-06)]_398_\n
 [+2(5.46e-06)]_115
 HMPREF1120_06902 2.85e-04 550_[+5(3.16e-10)]_47_\n
 [-8(5.64e-05)]_87_[+7(5.24e-05)]_185
 HMPREF1120_09146 5.11e-01 258_[+10(9.05e-05)]_346_\n
 [-7(1.68e-05)]_307
 HMPREF1120_03095 1.76e-01 257_-1(6.99e-06)]_734
 HMPREF1120_07560 2.52e-11 40_-5(1.07e-11)]_212_\n
 [+1(1.77e-05)]_207_-3(1.56e-07)]_294_-4(5.88e-08)]_2_[+9(2.87e-05)]_135
 HMPREF1120_00546 2.44e-01 205_-8(5.64e-05)]_17_\n
 [-3(6.32e-05)]_249_[+8(9.84e-05)]_58_-3(1.06e-05)]_317_[+9(8.85e-05)]_10
 HMPREF1120_04401 3.22e-01 18_[+9(2.64e-05)]_191_\n
 [+9(3.53e-05)]_315_-4(2.46e-05)]_416
 HMPREF1120_03941 1.43e-05 76_-1(6.99e-06)]_6_-1(1.05e-05)]_\n
 206_-2(6.51e-07)]_379_-8(7.03e-05)]_12_[+2(2.52e-10)]_15_[+2(9.29e-06)]_\n
 33_-1(3.21e-05)]_34_-3(5.41e-06)]_87
 HMPREF1120_05534 1.33e-01 355_-8(4.01e-06)]_531_\n
 [+10(7.56e-05)]_34
 HMPREF1120_01968 1.18e-01 806_-10(7.67e-05)]_35_\n
 [+1(3.54e-05)]_60_[+2(1.11e-05)]_9_-1(3.49e-06)]_12
 HMPREF1120_05435 7.72e-03 172_-9(1.91e-05)]_592_\n
 [+5(8.05e-09)]_176
 HMPREF1120_02359 3.22e-01 254_-1(3.49e-06)]_737
 HMPREF1120_04788 5.46e-01 316_-1(7.09e-05)]_527_\n
 [-9(2.17e-05)]_128
 HMPREF1120_05477 3.21e-01 531_[+3(8.71e-05)]_131_\n
 [-6(6.25e-05)]_154_-8(2.14e-05)]_72
 HMPREF1120_06974 1.15e-03 560_[+5(6.45e-05)]_68_\n
 [-4(1.49e-09)]_254_[+9(4.45e-05)]_38
 HMPREF1120_04831 2.75e-01 7_[+3(5.41e-06)]_972
 HMPREF1120_02501 7.19e-02 88_[+9(4.20e-05)]_107_\n
 [+4(1.06e-05)]_305_[+4(3.17e-07)]_137_-9(4.71e-05)]_283
 HMPREF1120_04925 3.45e-01 16_-10(8.51e-05)]_693_\n
 [+9(8.52e-05)]_156_[+8(8.65e-05)]_35
 HMPREF1120_02021 3.88e-09 75_-9(3.14e-05)]_357_\n
 [+10(2.85e-16)]_331_-1(3.49e-06)]_169
 HMPREF1120_06363 8.49e-03 18_[+3(1.77e-05)]_24_\n
 [+10(5.00e-05)]_225_[+7(4.54e-05)]_105_-7(6.23e-05)]_126_[+3(8.84e-07)]_\n
 147_-1(3.21e-05)]_165
 HMPREF1120_07673 1.23e-01 32_-10(9.48e-05)]_8_-5(2.58e-05)]_\n
 476_-5(8.84e-05)]_223_[+9(1.81e-05)]_122
 HMPREF1120_07049 4.88e-79 172_[+3(7.61e-06)]_63_\n
 [-3(5.35e-05)]_3_-10(9.74e-21)]_7_-7(5.12e-25)]_22_-6(1.40e-24)]_25_\n
 [+5(6.15e-15)]_53_-8(2.34e-25)]_209_-3(4.27e-06)]_163
 HMPREF1120_07792 8.36e-02 380_-3(2.61e-06)]_470_\n
 [+7(1.11e-05)]_24_[+5(6.94e-05)]_15
 HMPREF1120_03151 1.47e-02 204_-2(1.14e-08)]_775
 HMPREF1120_08650 2.52e-02 61_-7(8.35e-05)]_457_\n
 [+3(7.44e-05)]_140_[+1(3.49e-06)]_186_-3(4.91e-05)]_55
 HMPREF1120_06770 2.50e-05 15_-5(8.91e-11)]_59_[+1(8.86e-05)]_\n
 24_[+10(5.46e-05)]_71_[+7(7.50e-05)]_353_-4(5.91e-05)]_259_-5(8.84e-05)]_\n
 21
 HMPREF1120_07390 3.48e-01 364_[+5(1.27e-05)]_596
 HMPREF1120_05935 2.61e-02 41_[+10(9.05e-05)]_41_\n
 [+3(2.96e-06)]_79_-8(2.08e-05)]_111_[+4(8.44e-05)]_493_[+3(5.35e-05)]_93
 HMPREF1120_01293 3.60e-01 65_-8(4.89e-05)]_215_\n
 [+7(2.83e-05)]_146_[+8(7.25e-05)]_212_[+7(7.38e-05)]_180
 HMPREF1120_07658 2.01e-04 82_[+3(4.27e-06)]_25_[+7(4.12e-05)]_\n
 605_[+2(1.65e-09)]_196
 HMPREF1120_06441 1.08e-15 192_-6(1.31e-15)]_162_\n
 [-5(1.21e-11)]_206_-8(7.83e-05)]_60_-2(7.34e-06)]_186_[+3(4.27e-06)]_21
 HMPREF1120_00898 2.10e-01 161_-7(5.76e-05)]_232_\n
 [-1(2.14e-05)]_11_[+2(3.12e-05)]_65_[+2(1.84e-05)]_319_-1(2.47e-05)]_102
 HMPREF1120_08578 1.37e-01 510_[+8(8.27e-05)]_107_\n
 [-9(3.64e-05)]_177_[+6(4.32e-05)]_95
 HMPREF1120_06580 2.26e-01 148_-10(5.07e-05)]_10_\n
 [-2(5.95e-05)]_565_[+3(1.45e-05)]_196
 HMPREF1120_07908 2.77e-05 11_[+7(2.47e-05)]_140_\n
 [+3(1.77e-05)]_92_[+9(4.58e-05)]_300_-1(2.14e-05)]_117_-9(3.91e-09)]_220

HMPREF1120_07157 1.27e-01 487_[-8(3.66e-05)]_21_\n
 [-3(5.82e-05)]_317_[-1(4.28e-05)]_104
 HMPREF1120_06748 3.59e-03 244_[-8(1.88e-05)]_415_\n
 [-2(1.45e-09)]_279
 HMPREF1120_01579 9.93e-02 261_[+8(6.39e-05)]_53_\n
 [-7(8.87e-05)]_346_[-1(3.49e-06)]_240
 HMPREF1120_07981 7.12e-01 455_[-3(7.44e-05)]_524
 HMPREF1120_04574 9.47e-09 180_[-3(2.87e-05)]_298_\n
 [+3(2.38e-05)]_210_[+1(3.91e-05)]_96_[+9(5.97e-05)]_23_[+7(7.94e-15)]_72
 HMPREF1120_03688 1.87e-01 621_[-7(8.35e-05)]_39_\n
 [-3(1.60e-05)]_146_[+10(1.30e-05)]_84
 HMPREF1120_03067 8.84e-01 1000
 HMPREF1120_08344 4.27e-04 39_[+1(7.44e-05)]_156_\n
 [-5(6.94e-05)]_32_[-6(4.13e-05)]_217_[-3(2.38e-05)]_152_[+2(5.74e-06)]_41_\n
 [+3(6.61e-07)]_201
 HMPREF1120_04843 9.77e-02 368_[-1(9.56e-05)]_483_\n
 [-1(3.91e-05)]_32_[-5(1.63e-06)]_59
 HMPREF1120_06583 1.08e-01 322_[+8(2.57e-05)]_435_\n
 [+7(1.82e-05)]_108_[-3(2.87e-05)]_23
 HMPREF1120_01375 1.71e-01 28_[-3(6.86e-05)]_56_[-7(8.22e-05)]_\n
 184_[-1(3.49e-06)]_652
 HMPREF1120_08154 2.19e-02 183_[-3(3.15e-05)]_267_\n
 [-3(4.81e-06)]_20_[+1(3.49e-06)]_255_[-10(6.65e-05)]_185
 HMPREF1120_02698 1.06e-02 56_[-7(3.23e-05)]_22_[+9(6.12e-05)]_\n
 130_[+4(1.76e-05)]_72_[+3(3.78e-05)]_234_[-1(6.99e-06)]_253_[+9(6.89e-05)]_\n
 93
 HMPREF1120_08138 2.24e-01 157_[-1(9.56e-05)]_243_\n
 [+5(5.70e-05)]_150_[-2(7.00e-05)]_6_[-1(3.49e-06)]_313_[-1(4.98e-05)]_43
 HMPREF1120_08448 4.60e-03 55_[+2(4.43e-06)]_121_\n
 [+7(1.95e-05)]_253_[+4(1.56e-05)]_337_[-1(2.84e-05)]_25_[+3(8.71e-05)]_13_\n
 [+2(3.12e-05)]_54
 HMPREF1120_08742 1.48e-01 6_[+1(1.77e-05)]_635_[-3(2.16e-05)]_\n
 227_[-2(8.48e-05)]_81
 HMPREF1120_00007 1.74e-01 366_[+9(5.53e-05)]_243_\n
 [-4(4.88e-06)]_98_[+7(3.62e-05)]_203
 HMPREF1120_02578 6.68e-02 430_[-1(3.21e-05)]_225_\n
 [+3(2.87e-05)]_40_[+6(4.52e-05)]_188_[-1(6.99e-06)]_28
 HMPREF1120_02127 8.15e-04 571_[-5(8.05e-09)]_200_\n
 [-1(2.14e-05)]_18_[+9(2.56e-05)]_142
 HMPREF1120_06618 7.34e-01 1000
 HMPREF1120_02904 6.16e-05 47_[-7(3.80e-05)]_164_\n
 [-2(6.35e-05)]_49_[-2(5.40e-05)]_168_[+4(1.12e-09)]_16_[+2(9.33e-05)]_129_\n
 [+2(6.78e-05)]_67_[-3(9.42e-05)]_131_[-3(9.49e-06)]_33
 HMPREF1120_00716 4.46e-03 160_[+2(1.21e-05)]_280_\n
 [-4(4.76e-07)]_79_[-2(6.56e-05)]_28_[+5(9.49e-05)]_207_[-3(2.38e-05)]_123
 HMPREF1120_06341 6.51e-02 248_[-4(5.91e-05)]_124_\n
 [-5(1.17e-05)]_43_[+7(4.54e-05)]_475
 HMPREF1120_04563 1.45e-05 32_[+3(4.89e-07)]_9_[+3(2.38e-05)]_\n
 152_[-2(3.98e-06)]_33_[+2(5.95e-05)]_16_[+2(6.46e-08)]_33_[+4(4.08e-06)]_\n
 88_[+3(8.05e-05)]_491
 HMPREF1120_06646 8.44e-01 852_[+2(9.62e-05)]_127
 HMPREF1120_02776 1.43e-13 387_[+4(1.20e-10)]_323_\n
 [+1(3.49e-06)]_36_[-9(3.42e-09)]_79_[-1(6.99e-06)]_10_[+2(6.99e-07)]_55_\n
 [+3(7.63e-08)]_10
 HMPREF1120_06679 2.37e-01 208_[+1(6.99e-06)]_100_\n
 [+7(9.29e-05)]_156_[-3(5.35e-05)]_456
 HMPREF1120_05155 3.64e-01 422_[-7(1.25e-05)]_387_\n
 [-7(5.32e-05)]_91
 HMPREF1120_01512 4.08e-01 623_[+2(8.48e-05)]_214
 HMPREF1120_01172 5.09e-02 99_[-7(9.01e-05)]_66_[+5(1.11e-06)]_\n
 280_[-8(3.85e-05)]_424
 HMPREF1120_09135 5.17e-01 707_[+7(7.16e-05)]_243
 HMPREF1120_08781 1.30e-02 47_[+2(5.22e-05)]_260_\n
 [+7(4.40e-05)]_194_[+5(2.95e-07)]_329_[-3(2.61e-05)]_38
 HMPREF1120_01519 1.23e-02 71_[-1(4.61e-05)]_253_\n
 [+5(2.72e-05)]_[-8(7.33e-05)]_474_[+4(6.57e-06)]_92
 HMPREF1120_00622 2.19e-01 8_[+5(8.84e-05)]_375_[+5(5.56e-05)]_\n
 71_[+2(3.99e-05)]_180_[+5(5.56e-05)]_150_[-4(2.11e-05)]_55
 HMPREF1120_03297 2.09e-02 96_[+7(4.84e-05)]_379_\n

[-4(6.75e-06)]_270_[-10(4.14e-05)]_20_[+1(1.77e-05)]_117
 HMPREF1120_08211 5.99e-02 309_[+3(1.02e-06)]_350_\n
 [+10(9.48e-05)]_281
 HMPREF1120_05905 8.51e-03 153_[+3(3.78e-05)]_133_\n
 [+7(1.79e-05)]_165_[+1(8.86e-05)]_191_[+9(1.91e-05)]_163_[+6(8.49e-06)]_45
 HMPREF1120_03649 1.40e-03 [+10(2.31e-05)]_119_[-1(3.49e-06)]_\n
 105_[-1(3.49e-06)]_88_[+3(3.78e-05)]_334_[-3(1.76e-06)]_177_[+6(7.72e-05)]_\n
 28
 HMPREF1120_00621 8.72e-02 219_[+1(6.38e-05)]_201_\n
 [+8(1.36e-05)]_60_[+5(9.71e-05)]_138_[-8(8.56e-05)]_251
 HMPREF1120_01082 1.21e-01 410_[+6(2.21e-06)]_144_\n
 [+3(1.96e-05)]_375
 HMPREF1120_08679 4.78e-02 331_[+3(5.41e-06)]_558_\n
 [+4(1.71e-05)]_70
 HMPREF1120_06393 2.72e-03 225_[+3(2.96e-06)]_9_[-1(3.91e-05)]_\n
 88_[-3(9.42e-05)]_290_[-2(1.47e-07)]_248_[+3(2.38e-05)]_47
 HMPREF1120_03733 9.47e-01 1000
 HMPREF1120_00978 5.65e-02 199_[+4(9.35e-05)]_89_\n
 [+9(7.69e-05)]_207_[-7(2.35e-05)]_16_[-5(8.84e-05)]_230_[-5(4.01e-05)]_4_\n
 [+7(9.29e-05)]_35
 HMPREF1120_00006 5.54e-02 44_[-5(4.32e-05)]_35_[+8(5.54e-05)]_\n
 469_[-7(3.62e-05)]_98_[+4(4.88e-06)]_203
 HMPREF1120_06138 1.14e-02 [+2(3.72e-05)]_111_[-7(2.47e-05)]_\n
 103_[-3(1.06e-05)]_368_[+1(3.91e-05)]_14_[-5(4.91e-05)]_263
 HMPREF1120_04842 6.22e-01 529_[-8(2.67e-05)]_430
 HMPREF1120_02509 1.37e-11 635_[+3(4.50e-05)]_29_\n
 [-6(1.48e-20)]_42_[-3(4.81e-06)]_202
 HMPREF1120_08480 3.00e-02 107_[-8(7.19e-05)]_21_\n
 [-2(3.33e-07)]_27_[+8(7.08e-05)]_429_[+3(5.82e-05)]_292
 HMPREF1120_00717 2.58e-02 372_[+3(2.01e-06)]_158_\n
 [-10(3.03e-05)]_183_[-1(2.47e-05)]_141_[+10(6.65e-05)]_38
 HMPREF1120_07062 1.57e-04 176_[-9(1.70e-06)]_220_\n
 [+3(5.35e-05)]_37_[+10(3.81e-05)]_229_[+3(6.32e-08)]_4_[+7(8.51e-06)]_56_\n
 [-9(4.20e-05)]_107
 HMPREF1120_08684 2.80e-01 231_[-1(2.14e-05)]_760
 HMPREF1120_05439 1.17e-02 66_[+5(2.72e-05)]_519_\n
 [+5(7.04e-09)]_335
 HMPREF1120_07638 4.07e-01 330_[-7(7.50e-05)]_137_\n
 [-9(2.56e-05)]_463
 HMPREF1120_00405 9.60e-02 239_[+9(2.78e-06)]_180_\n
 [+3(3.45e-05)]_540
 HMPREF1120_08447 1.32e-03 395_[-7(1.27e-05)]_3_[+6(6.16e-05)]_\n
 63_[-3(5.35e-05)]_19_[-2(3.59e-05)]_25_[-1(3.54e-05)]_20_[-1(3.49e-06)]_\n
 160_[-1(3.49e-06)]_120_[-1(3.49e-06)]_17
 HMPREF1120_01764 4.73e-02 21_[+2(5.40e-05)]_49_[+7(2.83e-05)]_\n
 169_[+3(1.45e-05)]_569_[+6(1.26e-05)]_50
 HMPREF1120_04550 1.05e-05 162_[+6(3.50e-05)]_11_\n
 [+10(7.77e-06)]_25_[+9(2.89e-06)]_7_[-3(9.49e-06)]_7_[+1(3.54e-05)]_64_\n
 [+2(4.57e-05)]_328_[-10(8.77e-05)]_51_[+6(1.02e-05)]_96
 HMPREF1120_02510 4.82e-13 175_[-9(9.69e-05)]_111_\n
 [+10(7.24e-05)]_118_[-2(5.05e-05)]_178_[-3(3.78e-06)]_189_[+3(4.81e-06)]_\n
 42_[+6(1.48e-20)]_15
 HMPREF1120_04120 1.71e-01 445_[-3(5.82e-05)]_128_\n
 [-4(5.91e-05)]_333_[+8(2.85e-05)]_12
 HMPREF1120_03732 9.41e-01 1000
 HMPREF1120_02286 5.95e-02 158_[+1(2.47e-05)]_123_\n
 [-10(4.68e-06)]_174_[+4(4.21e-05)]_254_[+1(6.99e-06)]_15_[-1(3.49e-06)]_\n
 190
 HMPREF1120_03724 2.77e-01 1_[-7(9.30e-06)]_872_[-8(9.66e-05)]_\n
 36
 HMPREF1120_06645 2.10e-03 14_[-10(3.20e-05)]_196_\n
 [+10(2.98e-05)]_76_[+2(7.10e-08)]_75_[-2(9.41e-08)]_342_[-1(3.49e-06)]_83_\n
 [-5(9.27e-05)]_45
 HMPREF1120_04812 8.57e-02 100_[+3(9.42e-05)]_628_\n
 [-4(5.02e-05)]_98_[+7(2.60e-05)]_83
 HMPREF1120_05987 6.61e-01 664_[-3(1.18e-05)]_17_\n
 [-3(4.13e-05)]_277
 HMPREF1120_07793 1.14e-04 301_[-3(5.41e-06)]_58_\n
 [-2(1.08e-09)]_14_[+5(4.11e-05)]_545

HMPREF1120_00375 3.27e-02 270_[+5(1.68e-05)]_9_[+1(4.28e-05)]_\n255_[+5(3.81e-05)]_62_[+3(8.05e-05)]_50_[-6(2.33e-05)]_151_[-1(6.99e-06)]_\n34

HMPREF1120_01149 2.75e-01 115_[+2(3.85e-05)]_341_\n[+5(2.58e-05)]_135_[+2(4.89e-05)]_327

HMPREF1120_02526 4.74e-01 224_[-9(7.22e-05)]_453_\n[-10(3.31e-05)]_101_[+9(3.43e-05)]_143

HMPREF1120_02305 2.89e-04 15_[+2(9.93e-05)]_13_[+2(5.74e-06)]_\n131_[-4(7.10e-06)]_3_[+9(9.01e-06)]_171_[+1(3.49e-06)]_456_[-1(6.99e-06)]_\n68_[+3(2.61e-05)]_22

HMPREF1120_06671 1.45e-04 173_[-7(4.01e-06)]_122_\n[-2(1.56e-06)]_63_[+10(7.90e-05)]_69_[-2(1.06e-06)]_80_[+1(1.05e-05)]_141_\n[+2(9.93e-05)]_67_[+7(7.27e-05)]_74

HMPREF1120_05694 1.93e-01 99_[-6(9.37e-05)]_270_\n[+3(5.82e-05)]_69_[-8(2.26e-05)]_450

HMPREF1120_09019 2.51e-09 13_[+7(4.52e-15)]_54_[-7(9.87e-05)]_\n494_[+7(9.01e-05)]_69_[+1(3.49e-06)]_211

HMPREF1120_06616 6.07e-01 13_[+6(5.48e-05)]_937

HMPREF1120_05142 4.27e-03 360_[-1(6.99e-06)]_94_\n[-8(1.18e-05)]_54_[+3(5.69e-07)]_317_[-4(9.95e-05)]_84

HMPREF1120_07623 1.08e-01 502_[+1(3.49e-06)]_489

HMPREF1120_09134 3.50e-12 72_[+10(3.55e-05)]_157_\n[+1(3.49e-06)]_120_[+1(3.49e-06)]_193_[-6(7.94e-05)]_7_[+3(1.56e-07)]_242_\n[+7(8.85e-15)]_31

HMPREF1120_05354 3.63e-05 316_[-3(2.87e-05)]_50_\n[+3(1.86e-07)]_146_[+3(1.18e-05)]_4_[-1(6.99e-06)]_93_[-3(2.29e-06)]_31_\n[-1(7.09e-05)]_68_[-8(6.85e-05)]_23_[-1(6.99e-06)]_14_[-2(1.89e-07)]_3_\n[-2(5.24e-07)]_58

HMPREF1120_01508 1.60e-01 313_[-2(5.40e-05)]_90_\n[-4(4.10e-05)]_149_[-10(3.37e-05)]_118_[+3(9.42e-05)]_229

HMPREF1120_00838 3.09e-01 578_[+7(9.72e-05)]_11_\n[+4(8.10e-05)]_240_[-2(3.47e-05)]_80

HMPREF1120_07321 6.37e-02 663_[+3(1.06e-05)]_316

HMPREF1120_02454 1.94e-05 11_[-1(3.54e-05)]_155_\n[-1(1.05e-05)]_262_[+2(8.22e-05)]_99_[-3(1.96e-05)]_197_[+9(2.27e-08)]_71_\n[+6(3.35e-05)]_75

HMPREF1120_06644 3.18e-02 253_[+3(3.45e-05)]_46_\n[+5(6.14e-05)]_85_[+10(8.77e-05)]_181_[+5(9.27e-05)]_83_[+1(3.49e-06)]_203

HMPREF1120_08477 2.53e-01 96_[+2(6.78e-05)]_734_\n[-7(1.32e-05)]_99

HMPREF1120_05234 2.35e-01 75_[-3(4.91e-05)]_137_\n[+1(6.99e-06)]_285_[-9(4.97e-05)]_56_[+1(7.79e-05)]_388

HMPREF1120_03386 2.29e-02 16_[-3(2.61e-05)]_412_\n[-3(8.84e-07)]_192_[+1(2.47e-05)]_256_[-2(3.99e-05)]_52

HMPREF1120_05842 1.92e-01 288_[-3(1.76e-06)]_691

HMPREF1120_00264 1.93e-04 117_[+9(1.78e-11)]_341_\n[-1(6.05e-05)]_266_[-1(3.49e-06)]_238

HMPREF1120_06777 2.84e-03 399_[-2(1.77e-05)]_34_\n[+1(3.49e-06)]_93_[+1(6.99e-06)]_326_[+2(5.05e-05)]_6_[+3(5.41e-06)]_61

HMPREF1120_04224 7.75e-03 162_[+3(6.32e-05)]_33_\n[+8(5.80e-06)]_43_[-8(6.94e-06)]_14_[-8(2.43e-05)]_382_[+2(8.22e-05)]_63_\n[-1(3.49e-06)]_129

HMPREF1120_01423 1.71e-01 280_[+8(5.11e-05)]_124_\n[+9(5.67e-05)]_282_[+2(8.48e-05)]_14_[+4(2.61e-05)]_198

HMPREF1120_06279 1.44e-02 166_[-5(1.31e-05)]_442_\n[-3(1.17e-06)]_331

HMPREF1120_05665 5.35e-02 21_[-3(6.32e-05)]_362_\n[-2(5.22e-05)]_199_[+8(3.87e-06)]_95_[+4(8.44e-05)]_132_[-3(1.77e-05)]_67

HMPREF1120_08115 4.56e-01 195_[-1(1.05e-05)]_654_\n[-1(6.73e-05)]_133

HMPREF1120_05585 1.42e-02 21_[-5(4.28e-06)]_177_\n[+8(2.71e-06)]_326_[-2(4.41e-05)]_374

HMPREF1120_02014 8.28e-01 1000

HMPREF1120_03609 1.29e-01 116_[+2(1.21e-05)]_35_\n[-5(6.45e-05)]_7_[+7(9.87e-05)]_318_[-3(5.35e-05)]_392

HMPREF1120_00924 3.19e-02 41_[-7(4.40e-05)]_473_\n[+2(1.60e-07)]_238_[+3(1.77e-05)]_156

HMPREF1120_01403 6.85e-02 6_[-2(7.47e-05)]_146_[+1(6.99e-06)]_\n40_[-2(1.63e-05)]_318_[-1(3.49e-06)]_430

HMPREF1120_01833 4.23e-04 364_[+7(5.58e-05)]_200_\n
 [+2(3.85e-05)]_88_[+2(1.91e-05)]_6_[+2(1.04e-10)]_229
 HMPREF1120_07608 2.84e-03 415_[+6(6.81e-05)]_35_\n
 [+1(1.77e-05)]_97_-2(3.59e-05)]_16_-2(7.10e-08)]_66_[+2(6.66e-06)]_145_\n
 [-2(6.56e-05)]_83
 HMPREF1120_01522 9.39e-03 609_-10(2.12e-05)]_162_\n
 [+4(2.66e-08)]_68_-5(5.99e-05)]_62
 HMPREF1120_06047 4.44e-03 424_[+3(1.60e-05)]_273_\n
 [+4(5.63e-08)]_174_[+6(6.43e-05)]_3_[+2(9.04e-05)]_14
 HMPREF1120_01923 5.37e-02 74_[+1(1.77e-05)]_693_\n
 [-3(1.60e-05)]_57_[+2(2.90e-05)]_125
 HMPREF1120_05100 4.42e-01 134_-3(2.61e-05)]_404_\n
 [+5(8.22e-05)]_401
 HMPREF1120_09238 5.69e-02 315_[+7(2.24e-05)]_427_\n
 [-1(6.99e-06)]_148_-1(3.21e-05)]_42
 HMPREF1120_00374 2.83e-01 40_-7(3.39e-05)]_58_\n
 [-10(9.33e-05)]_56_-3(8.51e-06)]_92_-3(6.32e-05)]_623
 HMPREF1120_06528 4.14e-02 543_-1(1.05e-05)]_367_\n
 [+3(6.61e-07)]_60
 HMPREF1120_07676 5.47e-02 514_-3(3.78e-05)]_101_\n
 [-2(7.71e-05)]_195_-1(2.47e-05)]_110_[+1(1.77e-05)]_3_[+1(3.49e-06)]_8
 HMPREF1120_00038 2.15e-14 11_[+1(3.49e-06)]_67_-1(6.99e-06)]_28_\n
 [-2(7.71e-05)]_46_[+9(8.68e-05)]_105_[+9(1.44e-12)]_89_-5(1.97e-10)]_121_\n
 [-9(7.69e-05)]_336_[+2(2.99e-08)]_37
 HMPREF1120_01099 6.79e-03 446_-1(3.49e-06)]_224_\n
 [-5(6.77e-05)]_226_-4(2.42e-06)]_35
 HMPREF1120_05642 3.09e-02 50_-10(8.51e-05)]_194_\n
 [-9(8.85e-05)]_154_-2(7.70e-06)]_136_-9(9.53e-05)]_219_[+5(1.68e-05)]_83_\n
 [+3(9.42e-05)]_3
 HMPREF1120_06290 5.77e-02 84_-6(9.24e-05)]_96_-1(2.47e-05)]_117_\n
 [-1(6.99e-06)]_19_-2(6.15e-05)]_595
 HMPREF1120_09136 4.27e-01 42_[+6(8.51e-05)]_908
 HMPREF1120_03296 1.45e-01 334_[+3(6.86e-05)]_479_\n
 [+4(8.72e-07)]_146
 HMPREF1120_03603 5.30e-04 301_[+5(3.20e-06)]_407_\n
 [+2(7.80e-08)]_24_-1(6.99e-06)]_89_[+1(3.54e-05)]_100
 HMPREF1120_07937 2.28e-01 463_-3(2.61e-05)]_207_\n
 [+9(1.54e-05)]_289
 HMPREF1120_04140 3.00e-03 166_-8(1.27e-05)]_24_\n
 [+3(8.51e-06)]_110_[+1(4.28e-05)]_52_[+2(6.56e-05)]_150_-3(5.35e-05)]_48_\n
 [-3(6.86e-05)]_113_[+10(2.82e-05)]_61_-4(7.31e-05)]_83
 HMPREF1120_05088 2.47e-01 379_[+10(8.02e-05)]_388_\n
 [-2(5.95e-05)]_173
 HMPREF1120_01710 3.57e-01 927_[+4(7.10e-06)]_53
 HMPREF1120_03451 1.21e-01 192_-1(3.49e-06)]_268_\n
 [-7(3.50e-05)]_440_[+9(3.64e-05)]_21
 HMPREF1120_01909 5.44e-01 873_[+3(1.31e-05)]_106
 HMPREF1120_03636 2.63e-01 46_-7(4.33e-05)]_52_-7(6.49e-06)]_157_\n
 [-7(3.07e-05)]_595
 HMPREF1120_01980 5.73e-01 266_-2(1.38e-05)]_135_\n
 [-2(9.93e-05)]_557
 HMPREF1120_03973 3.29e-01 802_-9(9.80e-06)]_178
 HMPREF1120_01020 1.99e-01 101_[+1(6.99e-06)]_75_\n
 [-8(1.72e-05)]_530_-1(6.99e-06)]_235
 HMPREF1120_07372 1.43e-02 1_-8(4.89e-05)]_245_[+7(8.98e-06)]_106_\n
 [-2(1.16e-05)]_163_[+1(2.47e-05)]_260_[+2(4.41e-05)]_83
 HMPREF1120_00101 1.55e-01 317_[+8(2.00e-05)]_86_\n
 [-8(7.75e-05)]_95_[+6(1.30e-05)]_370
 HMPREF1120_07003 1.52e-01 46_[+3(8.05e-05)]_390_\n
 [+3(1.02e-06)]_236_[+5(6.94e-05)]_246
 HMPREF1120_08674 3.17e-01 673_[+8(3.87e-06)]_286
 HMPREF1120_04734 2.71e-02 762_[+10(9.49e-07)]_40_\n
 [+4(4.43e-05)]_113_[+1(3.49e-06)]_17
 HMPREF1120_00197 7.28e-01 1000
 HMPREF1120_01451 6.60e-01 264_[+8(3.56e-05)]_274_\n
 [-3(5.35e-05)]_400
 HMPREF1120_01182 1.18e-02 123_-7(2.35e-05)]_18_\n
 [-7(9.29e-05)]_170_-10(9.33e-05)]_213_[+4(2.05e-05)]_25_-1(3.49e-06)]_283

HMPREF1120_03772 1.06e-02 152_[-7(4.69e-05)]_50_
 [-10(2.01e-05)]_50_[+3(7.44e-05)]_10_[+1(1.05e-05)]_271_[+3(1.06e-05)]_327
 HMPREF1120_04068 1.49e-01 115_[+7(1.65e-05)]_286_
 [-8(4.89e-05)]_508
 HMPREF1120_01282 2.03e-01 130_[+7(8.60e-05)]_178_
 [-3(9.42e-05)]_15_[-3(8.71e-05)]_256_[+1(5.35e-05)]_50_[+7(2.13e-05)]_220
 HMPREF1120_05091 7.23e-01 1000
 HMPREF1120_05843 1.78e-03 88_[+7(5.24e-05)]_195_
 [+8(4.14e-05)]_78_[-5(1.96e-08)]_508
 HMPREF1120_05820 8.40e-01 1000
 HMPREF1120_03646 3.36e-01 557_[+1(3.54e-05)]_400_
 [+4(1.26e-05)]_14
 HMPREF1120_04805 9.95e-07 206_[-5(8.84e-05)]_109_
 [+10(4.93e-15)]_606
 HMPREF1120_01777 5.97e-03 77_[+5(1.92e-05)]_48_
 [+10(7.35e-05)]_26_[+7(2.56e-05)]_151_[-1(7.79e-05)]_132_[+1(2.84e-05)]_
 272_[-9(1.54e-05)]_62_[+2(1.63e-05)]_44
 HMPREF1120_06780 3.39e-01 302_[+5(3.81e-05)]_302_
 [+4(5.52e-05)]_336
 HMPREF1120_07526 2.19e-01 46_[-7(2.20e-05)]_495_
 [+1(8.86e-05)]_6_[-4(6.32e-05)]_374
 HMPREF1120_00198 2.92e-01 266_[+10(9.19e-05)]_64_
 [-1(3.49e-06)]_166_[+5(9.71e-05)]_416
 HMPREF1120_05027 3.15e-01 814_[-1(2.47e-05)]_177
 HMPREF1120_04430 3.09e-01 419_[-3(1.06e-05)]_171_
 [+2(6.15e-05)]_368
 HMPREF1120_07017 4.89e-03 116_[-10(8.51e-05)]_205_
 [+4(5.38e-06)]_32_[+4(1.92e-06)]_80_[+4(1.04e-08)]_250_[-2(2.50e-05)]_197
 HMPREF1120_09162 4.83e-09 263_[+10(3.40e-15)]_195_
 [+3(1.96e-05)]_294_[-8(1.64e-05)]_64_[-1(4.98e-05)]_74
 HMPREF1120_08770 2.35e-03 413_[-7(3.50e-05)]_406_
 [+9(5.77e-10)]_111
 HMPREF1120_06046 6.37e-01 611_[+1(2.47e-05)]_146_
 [+6(8.99e-05)]_184
 HMPREF1120_05715 1.38e-03 24_[+5(6.27e-08)]_278_
 [+6(1.69e-05)]_109_[+8(2.36e-05)]_22_[-7(6.42e-05)]_386
 HMPREF1120_01343 4.36e-01 836_[-4(3.12e-05)]_144
 HMPREF1120_01315 4.25e-02 53_[-6(8.05e-05)]_232_
 [-5(9.79e-06)]_179_[+8(1.61e-05)]_27_[+3(3.45e-05)]_119_[-5(1.59e-05)]_126_
 [+5(7.65e-05)]_32
 HMPREF1120_03196 2.29e-01 634_[-7(2.09e-05)]_61_
 [-3(6.86e-05)]_165_[+7(5.32e-05)]_19
 HMPREF1120_03454 2.11e-02 170_[+1(4.98e-05)]_49_
 [-3(2.38e-05)]_67_[-2(8.76e-05)]_447_[-4(6.41e-06)]_[-2(2.50e-05)]_175
 HMPREF1120_00902 1.98e-01 13_[-9(1.36e-05)]_281_
 [+1(6.99e-06)]_677
 HMPREF1120_02198 9.20e-01 886_[+4(3.03e-05)]_94
 HMPREF1120_05841 2.80e-03 84_[-8(5.93e-05)]_360_
 [-1(6.99e-06)]_5_[-3(5.35e-05)]_40_[+4(6.10e-06)]_133_[+2(3.01e-05)]_24_
 [-6(8.51e-05)]_162_[+2(3.59e-05)]_9
 HMPREF1120_07391 1.99e-02 307_[-7(1.65e-05)]_76_
 [+8(2.48e-05)]_65_[+9(1.19e-06)]_441
 HMPREF1120_00954 1.22e-01 238_[-5(2.32e-05)]_268_
 [+1(2.47e-05)]_69_[+1(8.86e-05)]_313_[-5(6.05e-06)]_14
 HMPREF1120_08769 2.29e-01 871_[+10(2.01e-05)]_14_
 [+6(5.02e-05)]_26
 HMPREF1120_07879 7.41e-03 462_[-1(6.38e-05)]_282_
 [-1(3.49e-06)]_9_[+3(4.91e-05)]_1_[+3(1.45e-05)]_186
 HMPREF1120_05009 8.09e-01 282_[+1(9.56e-05)]_709
 HMPREF1120_03199 5.40e-01 493_[-10(2.48e-05)]_252_
 [+7(8.74e-05)]_166
 HMPREF1120_00196 3.42e-02 156_[+8(4.58e-05)]_61_
 [-3(1.76e-06)]_34_[+7(6.63e-05)]_637
 HMPREF1120_06146 1.21e-01 128_[+3(2.16e-05)]_372_
 [+2(8.22e-05)]_175_[-6(3.20e-05)]_233
 HMPREF1120_02306 6.47e-01 254_[-6(3.01e-05)]_696
 HMPREF1120_01981 5.42e-01 357_[+2(9.93e-05)]_135_
 [+2(1.38e-05)]_466
 HMPREF1120_04784 5.03e-01 378_[-1(6.05e-05)]_463_

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[-3(1.06e-05)]_87_[+3(4.13e-05)]_21
HMPREF1120_05366      9.33e-01  414_[+9(9.02e-05)]_566
HMPREF1120_06238      8.94e-13  160_[+10(6.75e-05)]_227_\
[+8(4.08e-20)]_168_-1(6.05e-05)]_83_-3(4.13e-05)]_252
HMPREF1120_02122      3.15e-01  405_-1(3.49e-06)]_258_\
[-4(6.04e-05)]_121_-1(3.49e-06)]_156_[+4(3.59e-05)]_2
HMPREF1120_06617      1.26e-01  62_[+3(1.31e-05)]_117_\
[-7(1.46e-05)]_71_-7(8.22e-05)]_266_[+1(1.77e-05)]_354
HMPREF1120_06465      7.41e-03  461_[+1(3.49e-06)]_387_\
[+3(3.35e-06)]_32_-6(8.28e-05)]_40
HMPREF1120_07460      1.71e-01  132_[+6(1.75e-05)]_490_\
[+10(5.00e-05)]_289
HMPREF1120_03504      8.47e-02  287_-8(6.85e-05)]_189_\
[-6(6.90e-05)]_24_-4(2.46e-05)]_251_[+3(4.50e-05)]_117
HMPREF1120_06251      6.64e-01  112_-8(6.39e-05)]_1_[+6(8.16e-05)]_\
796
HMPREF1120_06104      1.77e-01  91_[+3(8.71e-05)]_164_\
[+5(1.01e-05)]_684
HMPREF1120_05260      3.58e-02  278_-1(8.86e-05)]_323_\
[+5(1.98e-05)]_29_-3(2.96e-06)]_27_[+7(2.27e-05)]_3_[+3(1.31e-05)]_199
HMPREF1120_02938      2.20e-02  124_[+7(2.20e-05)]_127_\
[-9(1.45e-05)]_158_[+1(3.49e-06)]_55_-1(3.91e-05)]_448
HMPREF1120_06484      2.05e-02  359_[+1(3.49e-06)]_26_\
[+9(4.83e-05)]_586
HMPREF1120_06164      3.80e-01  70_[+4(4.32e-05)]_414_\
[+1(6.05e-05)]_169_[+6(5.33e-05)]_268
HMPREF1120_06689      2.84e-01  1_-8(6.85e-05)]_430_\
[-10(3.78e-06)]_489
HMPREF1120_01406      2.74e-01  283_-3(3.78e-05)]_85_\
[+3(3.45e-05)]_361_[+2(2.90e-05)]_38_[+7(8.35e-05)]_120
HMPREF1120_00109      8.89e-02  146_[+7(3.50e-05)]_146_\
[-5(9.49e-05)]_452_-5(9.61e-07)]_126
HMPREF1120_05453      1.04e-01  51_[+4(3.99e-05)]_222_\
[+2(3.02e-06)]_260_-9(8.66e-06)]_406
HMPREF1120_04014      1.79e-02  134_[+8(2.91e-06)]_109_\
[-10(9.05e-05)]_147_-7(8.22e-05)]_207_-9(6.43e-05)]_40_-5(7.47e-05)]_\
173
HMPREF1120_06399      7.25e-01  458_-9(1.00e-05)]_522
HMPREF1120_00404      8.83e-02  288_-3(3.45e-05)]_180_\
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HMPREF1120_06148      7.27e-03  325_[+9(2.56e-05)]_196_\
[-4(2.46e-05)]_301_-4(6.49e-09)]_118
HMPREF1120_02792      1.51e-01  86_-1(2.47e-05)]_251_\
[+1(3.49e-06)]_645
HMPREF1120_08633      9.74e-02  9_-3(2.87e-05)]_368_-2(8.48e-05)]_\
69_-5(1.72e-05)]_390_-4(8.44e-05)]_62
HMPREF1120_02853      8.81e-01  58_[+3(8.71e-05)]_921
HMPREF1120_01156      5.19e-04  100_[+1(8.86e-05)]_109_\
[+1(4.61e-05)]_104_[+1(3.91e-05)]_130_-5(6.05e-06)]_236_[+2(1.73e-08)]_\
[-3(8.71e-05)]_92_-8(6.47e-05)]_79
HMPREF1120_01982      6.21e-02  441_[+3(6.32e-05)]_127_\
[-1(6.99e-06)]_296_-2(6.56e-05)]_85
HMPREF1120_07880      1.11e-03  116_-8(5.32e-06)]_214_\
[+1(7.44e-05)]_42_-2(1.99e-05)]_155_-7(7.97e-05)]_82_-3(1.18e-05)]_1_\
[-3(1.10e-07)]_227
HMPREF1120_06804      7.29e-02  92_-6(4.52e-05)]_63_[+1(3.54e-05)]_\
240_-8(9.22e-05)]_302_[+1(6.99e-06)]_59_-10(4.14e-05)]_96
HMPREF1120_02225      2.58e-02  8_-3(2.16e-05)]_235_-1(4.98e-05)]_\
321_-3(4.13e-05)]_88_[+3(1.35e-06)]_36_-7(1.65e-05)]_190
HMPREF1120_01029      9.17e-02  14_-2(9.62e-05)]_39_[+7(6.42e-05)]_\
8_-6(2.51e-05)]_291_[+7(4.40e-05)]_91_-9(3.43e-05)]_366
HMPREF1120_03745      1.39e-01  141_-8(8.15e-05)]_263_\
[+9(6.43e-05)]_165_-8(8.10e-05)]_129_[+3(2.87e-05)]_7_[+3(6.32e-05)]_7_\
[-1(4.98e-05)]_135
HMPREF1120_03411      2.61e-02  145_[+8(2.21e-05)]_81_\
[+1(3.54e-05)]_53_-9(6.58e-05)]_170_[+2(9.33e-05)]_371_[+1(7.79e-05)]_80
HMPREF1120_05790      1.31e-03  207_[+1(3.49e-06)]_219_\
[+3(6.86e-05)]_122_[+5(4.15e-06)]_108_-5(8.03e-05)]_109_[+3(8.51e-06)]_53_\
[-5(4.55e-05)]_11

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HMPREF1120_07971 3.04e-02 289_[+2(3.59e-05)]_100_\n
 [+1(8.86e-05)]_114_[-7(1.51e-05)]_393_[+3(3.78e-06)]_3
 HMPREF1120_02802 3.12e-01 118_[+5(1.82e-05)]_297_\n
 [+8(2.32e-05)]_504
 HMPREF1120_01015 6.94e-02 71_[-7(1.51e-05)]_264_\n
 [+1(9.56e-05)]_248_[+10(3.87e-05)]_51_[-1(5.35e-05)]_259
 HMPREF1120_07241 5.80e-02 98_[+9(8.03e-05)]_165_\n
 [+3(7.61e-06)]_358_[+1(3.49e-06)]_192_[-3(1.96e-05)]_1_[+3(2.87e-05)]_94
 HMPREF1120_01137 6.47e-01 685_[+6(6.43e-05)]_61_\n
 [-7(5.94e-05)]_154
 HMPREF1120_01523 1.22e-02 182_[+6(3.48e-06)]_329_\n
 [-10(4.63e-05)]_204_[+1(2.47e-05)]_148_[+3(9.49e-06)]_18
 HMPREF1120_03195 4.07e-01 147_[+2(6.78e-05)]_82_\n
 [+3(8.51e-06)]_729
 HMPREF1120_08439 2.92e-01 141_[+5(5.84e-05)]_74_\n
 [+1(3.91e-05)]_395_[-2(6.78e-05)]_320
 HMPREF1120_04980 1.15e-01 7_[-9(8.52e-05)]_270_[+1(2.84e-05)]_\n
 500_[+6(8.99e-05)]_55_[+4(6.32e-05)]_69
 HMPREF1120_08783 1.78e-02 39_[-1(3.49e-06)]_128_\n
 [+9(9.01e-06)]_221_[-3(2.87e-05)]_334_[-3(1.18e-05)]_36_[-1(3.54e-05)]_76_\n
 [-2(6.78e-05)]_29_[+1(2.47e-05)]_27
 HMPREF1120_07216 4.87e-01 837_[+7(7.50e-05)]_113
 HMPREF1120_03803 5.44e-08 339_[-6(1.62e-05)]_16_\n
 [+3(1.68e-11)]_36_[-10(7.90e-05)]_339_[-3(8.05e-05)]_37_[+1(3.49e-06)]_47_\n
 [-9(9.05e-07)]_26
 HMPREF1120_04197 2.57e-01 394_[+9(3.23e-05)]_359_\n
 [+6(3.72e-06)]_177
 HMPREF1120_07677 3.57e-01 82_[-3(1.77e-05)]_771_\n
 [-6(6.34e-05)]_76
 HMPREF1120_06028 1.99e-02 922_[-3(3.51e-08)]_57
 HMPREF1120_06922 6.91e-02 333_[-5(5.70e-05)]_138_\n
 [+4(8.44e-05)]_150_[+9(1.73e-05)]_88_[+4(3.40e-05)]_66_[+3(3.45e-05)]_104
 HMPREF1120_06027 5.19e-03 233_[+1(1.77e-05)]_221_\n
 [-7(1.17e-05)]_14_[+3(3.51e-08)]_452
 HMPREF1120_04736 1.81e-01 181_[+9(9.53e-05)]_265_\n
 [-7(4.77e-05)]_362_[+2(4.20e-06)]_101
 HMPREF1120_08058 9.80e-01 1000
 HMPREF1120_03622 9.05e-02 179_[-3(4.27e-06)]_61_\n
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 HMPREF1120_00523 1.28e-02 146_[+9(7.06e-05)]_137_\n
 [+1(6.99e-06)]_174_[+3(2.61e-06)]_185_[+3(2.59e-07)]_134_[-1(6.38e-05)]_\n
 144
 HMPREF1120_06308 9.57e-03 452_[+2(6.46e-08)]_392_\n
 [+5(4.86e-06)]_95
 HMPREF1120_04947 8.76e-06 219_[-4(1.76e-05)]_259_\n
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 HMPREF1120_01818 2.92e-01 187_[-3(6.86e-05)]_20_\n
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 HMPREF1120_01896 9.87e-02 214_[-9(4.33e-05)]_6_[-7(5.00e-05)]_\n
 41_[+4(6.45e-05)]_100_[+3(8.05e-05)]_190_[+3(2.61e-05)]_138_[+1(6.05e-05)]_\n
 170
 HMPREF1120_03417 2.23e-02 62_[-3(2.38e-05)]_766_\n
 [+1(3.49e-06)]_142
 HMPREF1120_07182 2.47e-03 429_[-6(8.16e-05)]_73_\n
 [-1(6.99e-06)]_98_[-2(1.55e-08)]_320
 HMPREF1120_08026 7.34e-01 493_[+3(6.86e-05)]_486
 HMPREF1120_04558 5.19e-02 312_[+1(6.05e-05)]_31_\n
 [+4(1.34e-05)]_58_[-10(9.94e-05)]_82_[-1(8.86e-05)]_7_[+2(9.04e-05)]_3_\n
 [+7(5.50e-05)]_97_[-4(9.74e-05)]_242
 HMPREF1120_04424 2.82e-01 51_[+1(7.79e-05)]_631_\n
 [+3(1.60e-05)]_288
 HMPREF1120_00714 6.05e-01 315_[-7(5.32e-05)]_635
 HMPREF1120_06026 3.45e-01 697_[-5(9.05e-05)]_263
 HMPREF1120_05486 2.09e-01 332_[+1(1.05e-05)]_57_\n
 [+1(6.99e-06)]_547_[+3(1.45e-05)]_25
 HMPREF1120_02756 5.31e-02 522_[+1(3.49e-06)]_20_\n
 [-2(9.93e-05)]_62_[-4(6.18e-05)]_171_[+2(2.50e-05)]_154
 HMPREF1120_02623 1.09e-04 188_[+3(1.96e-05)]_1_[-1(7.44e-05)]_\n
 176_[+3(4.13e-05)]_11_[-3(6.80e-06)]_34_[-5(2.57e-09)]_83_[-3(2.61e-06)]_\n


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58_[+3(8.84e-07)]_89_[+3(3.15e-05)]_95_[+3(1.35e-06)]_8_[+7(3.34e-05)]_11
HMPREF1120_08078      2.76e-01  64_[+3(6.80e-06)]_12_[+7(9.15e-05)]_
349_[-7(9.57e-05)]_300_[-7(3.87e-05)]_35_[-10(5.62e-05)]_30
HMPREF1120_04804      2.39e-01  124_[-10(4.07e-05)]_472_
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HMPREF1120_06752      4.77e-01  68_[-9(4.83e-05)]_148_
[-6(2.13e-05)]_118_[+3(9.42e-05)]_145_[+3(5.35e-05)]_409
HMPREF1120_04359      4.03e-02  258_[-3(1.06e-05)]_124_
[+1(1.05e-05)]_58_[-2(4.57e-05)]_68_[+2(5.95e-05)]_420
HMPREF1120_05433      3.11e-01  316_[-10(4.85e-05)]_363_
[+2(9.93e-05)]_157_[-6(3.89e-05)]_54
HMPREF1120_02391      1.99e-01  396_[-7(3.87e-05)]_107_
[-1(3.49e-06)]_438
HMPREF1120_08476      2.64e-02  21_[+10(1.26e-05)]_170_
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[-3(3.15e-05)]_1
HMPREF1120_05622      2.39e-03  71_[-2(2.60e-05)]_31_[+1(3.49e-06)]_
311_[+5(4.11e-05)]_116_[-3(1.17e-06)]_333_[-2(6.78e-05)]_26
HMPREF1120_01983      3.43e-02  147_[-6(4.26e-05)]_103_
[+7(3.39e-06)]_100_[-10(9.63e-05)]_361_[+4(9.35e-05)]_130
HMPREF1120_05846      9.97e-01  1000
HMPREF1120_05848      8.12e-01  645_[-1(8.86e-05)]_155_
[-1(3.21e-05)]_182
HMPREF1120_03154      1.53e-01  609_[-8(4.25e-05)]_203_
[-7(6.03e-06)]_97
HMPREF1120_00901      4.27e-01  185_[-7(2.56e-05)]_64_
[-8(7.78e-05)]_660
HMPREF1120_03453      3.55e-01  7_[+5(9.95e-05)]_219_[+8(4.36e-05)]_
693
HMPREF1120_06719      9.03e-01  1000
HMPREF1120_01453      2.57e-01  105_[+8(6.55e-05)]_561_
[-1(2.47e-05)]_255_[+1(8.86e-05)]_20
HMPREF1120_01601      1.86e-01  56_[+2(4.12e-05)]_536_
[+1(3.49e-06)]_378
HMPREF1120_07322      2.65e-02  288_[-2(3.60e-07)]_159_
[+1(8.86e-05)]_15_[+1(8.86e-05)]_461_[+3(1.18e-05)]_17

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Stopped because requested number of motifs (10) found.
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