Function	Protein Name	Source	Accession Number	Location
Transcriptional Control Proteins	BirA	*Escherichia coli*	73188	20
	LacI	*Escherichia coli*	2506562	4
	CytR	*Escherichia coli*	72535	10
	PurR	*Escherichia coli*	72538	2
	RbtR	*Klebsiella aerogenes*	132163	4
	DeoR	*Escherichia coli*	73076	22
	AsnC	*Escherichia coli*	73064	23
	TrpR	*Escherichia coli*	73074	66
	CAP	*Escherichia coli*	1789756	168
	AraC	*Escherichia coli*	1786251	195
	AraC	*Erwinia carotovora*	78255	200
	Fnr	*Escherichia coli*	73019	195
	Ada	*Escherichia coli*	66479	100
	DicA	*Escherichia coli*	73095	21
	DicC	*Escherichia coli*	72932	11
	Fis	*Escherichia coli*	145973	72
	LysR	*Escherichia coli*	73060	19
	MetR	*Escherichia coli*	96181	17
	IlvY	*Escherichia coli*	73068	16
	AmpR	*Enterobacter cloacae*	78250	21
	TrpI	*Pseudomonas aeruginosa*	77686	21
	NodD	*Rhizobium meliloti*	73063	24
	NodD2	*Rhizobium meliloti*	78005	21
	XylS	*Pseudomonas putida*	77772	228
	NifA	*Klebsiella pneumoniae*	73053	494
	NifA	*Rhizobium meliloti*	128225	511
	NtrC	*Klebsiella pneumoniae*	128601	443
	NtrC	*Rhizobium meliloti*	77994	450
	MerR	*Bacillus* sp.	127011	3
	MerR	*Staphylococcus aureus*	127015	3
	MerR	Tn21	150778	8
	NahR	pNAH7	94931	21
	TrfB	RK2	125522	35
	TetR	Tn10	73100	25
	TetR	pSC101	150946	25
	TnpR	Tn21	72976	162
	TnpR	Tn501	94819	162
	TnpR	γδ (Tn1000)	125945	159

Replication Proteins	InvP	Phage PI C	76812	159
	Hin	*Salmonella sp.*	72977	160
	InsA	IS1	76271	64
	Nu1	Phage λ	215105	3
	B	Phage Mu	76119	19
Phage Transcritional Control Proteins	Cro	Phage λ	73101	14
	cI	Phage λ	215147	32
	cII	Phage λ	73106	24
	c1	Phage 434	224174	16
	Cro	Phage 434	73091	17
	C2	Phage P22	73090	19
	c1	Phage P22	73105	24
	Cro	Phage P22	73102	11
	CI	Phage ø80	540747	17
	gene 30	Phage ø80	540743	21
	ORF C	Phage 16-3	225830	24
	Repressor	Phage ø105	75994	19
	C	Phage P2	133374	18
	Cox	Phage P2	137589	12
	APL	Phage 186	137450	15
	Ner	Phage Mu	2144762	24
	C	Phage Mu	76121	98
	Ner	Phage D108	70840	26
RNA Polymmerase Sigma Factors	RpoD	*Escherichia coli*	1072030	561
	RpoH	*Escherichia coli*	1789871	251
	RpoD	*Bacillus subtilis*	2634967	330
	SpoIIAC	*Bacillus subtilis*	1304000	219
	SigB	*Bacillus subtilis*	133469	222
	SpoIIG	*Bacillus subtilis*	224259	204
	NtrA	*Klebsiella pneumoniae*	78979	365
	NtrA	*Rhizobium meliloti*	95222	393
	NtrA	*Azotobacter vinelandii*	77882	390
Replication or Chromosome Partition	Initiation Prot	R6K	418716	57
	ParB	Phage P1	73187	166
	D	pMini-F	78383	161
	SopB	Phage F	421170	177
	Prd	*Drosophila melanogaster*	85138	241
	Eve	*Drosophila melanogaster*	157387	98
	En	*Drosophila melanogaster*	123358	482
	Zen1	*Drosophila melanogaster*	280613	118

	PHO2	*Saccharomyces cerevisiae*	82888	105
	Oct-1	*Homo Sapiens*	539651	430
	Unc-86	*Caenorhabditis elegans*	84475	391
	Rat Pit-1	*Rattus norvegicus*	285136	268

HTH Motif	GYM Scores	Alternate Id	# motifs Detected
SGEQLGETLGMSRAAINKHI	33	BVECBF	1
TLYDVAEYAGVSYQTVSRVV	78	P03023	1
TMKDVALKAKVSTATVSRAI	62	RPECCT	1
TIKDVAKRANVSTTTVSHVI	77	RPECDU	2
TIYDLAELSGVSASAVSAII	76	P07760	1
HLKDAAALLGVSEMTIRRDI	83	RPECDO	1
AYAELAKQFGVSPGTIHVRV	64	QQECE1	1
SQRELKNELGAGIATITRGS	44	RPECW	1
TRQEIGQIVGCSRETVGRII	53	AAC76382	1
DIASVAQHVCLSPSRLSHLF	58	AAC73175	1
RIDEVARHVCLSPSRLAHLF	69	A25027	1
TRGDIGNYLGLTVETISRLI	60	RGECF	1
TLEALADQVAMSPFHLHRLF	67	XYECO2	1
TQRSLAKALKISHVSVSQWF	78	BVECDA	1
SKTKLAQAAGIRLASLYSWF	60	CEECDC	1
NQTRAALMMGINRGTLRKKI	84	AAA98812	1
SLTEAAHLLHTSQPTVSREI	82	RGECK	1
SLAAAAATLHQTQSALSHQF	66	A36066	1
HFGRSARAMHVSPSTLSRQI	59	RGECIY	1
SFTHAAIELNVTHSAISQHV	68	A25686	1
SISLAAEELHVTHGAVSRQV	56	A30769	1
KLTAAARRINLSQPAMSAAI	76	ZZZRDM	1
KLTAAARRVKLSQPAMSAAI	76	B25788	1
SLERLAELAMMSPRSLYNLF	59	A24987	1
VQAKAARLLGMTPRQVAYRI	59	RGKBAP	1
NQAKAARILEKTPRQVGYAI	53	P03028	2
HKQEAARLLGWGRNTLTRKI	82	P03029	2
NQIKAADLLGLNRNTLRKKI	92	A26934	2
RIGELADKCGVNKETIRYYF	85	P22853	1
KISELAKACDVNKETVRYYF	73	P22874	1
TIGVFAKAAGVNVETIRFYC	77	AAA19678	2
RVSITAENLGLTQPAVSNAI	75	A32837	1
PQATFATSLGLTRGAVSQAV	53	P03052	1
TTRKLAQKLGVEQPTLYWHV	87	RPECTN	1
TTRRLAERLGVQQPALYWHF	92	AAA25677	1
QKTKLAREFGISRETLYQYI	90	RPEC21	1
PKAQLAREFNISRETLYQYI	86	S09632	1
[illegible]	20	[illegible]	1

PRKQVAIIYDVAVSTLYKKF	74	S07175	1
PRQQLAIIFGIGVSTLYRYF	94	JWEBT	1
GCRATARIMGVGLNTIFRHI	70	IEECB9	1
NKKQLADIFGASIRTIQNWQ	59	AAA96533	1
TFKQIALESGLSTGTISSFI	66	ZBBPU2	2
GQTKTAKDLGVYQSAINKAI	70	RCBPL	1
SQESVADKMGMGQSGVGALF	57	AAA96581	1
GTEKTAEAVGVDKSQISRWK	75	QCBP2L	1
NQAELAQKVGTTQQSIEQLF	69	1011238A	1
TQTELATKAGVKQQSIQLIF	74	RCBP4	1
RQAALGKMVGVSNVAISQWF	71	RPBP22	1
GQRKVADALGINESQISRWK	96	Z1BPC2	1
TQRAVAKALGISDAAVSQWK	93	RGBP22	1
KQRDLAEALSTSPQTVNNWI	92	S04828	1
SQKVLAEKVGVTPQAINMLK	92	S04829	1
TQAELARRVGQSQQAINNLF	99	1314257A	1
TQVQLAEKANLSRSYLADIF	72	RPBPF5	2
SRQQLADLTGVPYGTLSYYF	78	P04132	1
PYQEFAKLIGKSTGAVRRMI	55	P07695	1
TLQQFAELEGVSERTAYRWT	77	P21681	1
SLSALSRQFGYAPTTLANAI	38	DNBPNU	1
NMEELRRQYRLSQPQIYQII	55	ZCBPU2	1
SLAELGRSNHLSSSTLKNAI	34	DNBPD8	2
TLEEVGKQFDVTRERIRQIF	62	AAB60181	2
TLQELADRYGVSAERVRQLF	80	AAC76486	2
TLEEVGKVFGVTRERIRQIF	72	CAB14463	2
TQSEVAERLGISQVQVSRLF	88	BAA12655	2
SQKETGDILGISQMHVSRLQ	55	P06574	2
TQKDVADMMGISQSYISRLF	85	1012299A	**1**
VLADIAQAVEMHESTISRVT	67	A24115	2
NLRTVADAIKMHESTVSRVT	72	A33966	2
VLHDIAEAVGMHESTISRVT	82	S00720	2
RAEDLAALAKITPSLAYRQI	54	IDECRK	1
SQKDIAAKEGLSQAKVTRAI	61	BVECPB	1
GRTEKARIWEVTDRTVRTWI	52	A24716	1
NISALADAENISRKIITRCI	40	S28096	1
TREELAQRTNLTEARIQVWF	73	A26062	1
RRCELAAQLNLPESTIKVWF	86	AAA28522	1
RRQQLSSELGLNEAQIKIWF	67	P02836	1
RRIFIAQRLSLGERQVKIWF	81	A43697	1

ERKKISDLIGMPEKNVRIWF	50	A25872	1
EITMIADQLNMEKEVIRVWF	67	A47001	2
RIASIADRLDLKKNVVRVWF	64	A30042	1
EIMRMAEELNLEKEVVRVWF	72	S22705	1