

Input Parameters Results Raw Output Probability Plot Query_Template MSA Query_MSA



Vis Hits Aln | Select All Forward Forward_Query_A3M Model_using_selection Download_HHR Color_Seqs Wrap_Seqs

Number of Hits: 250

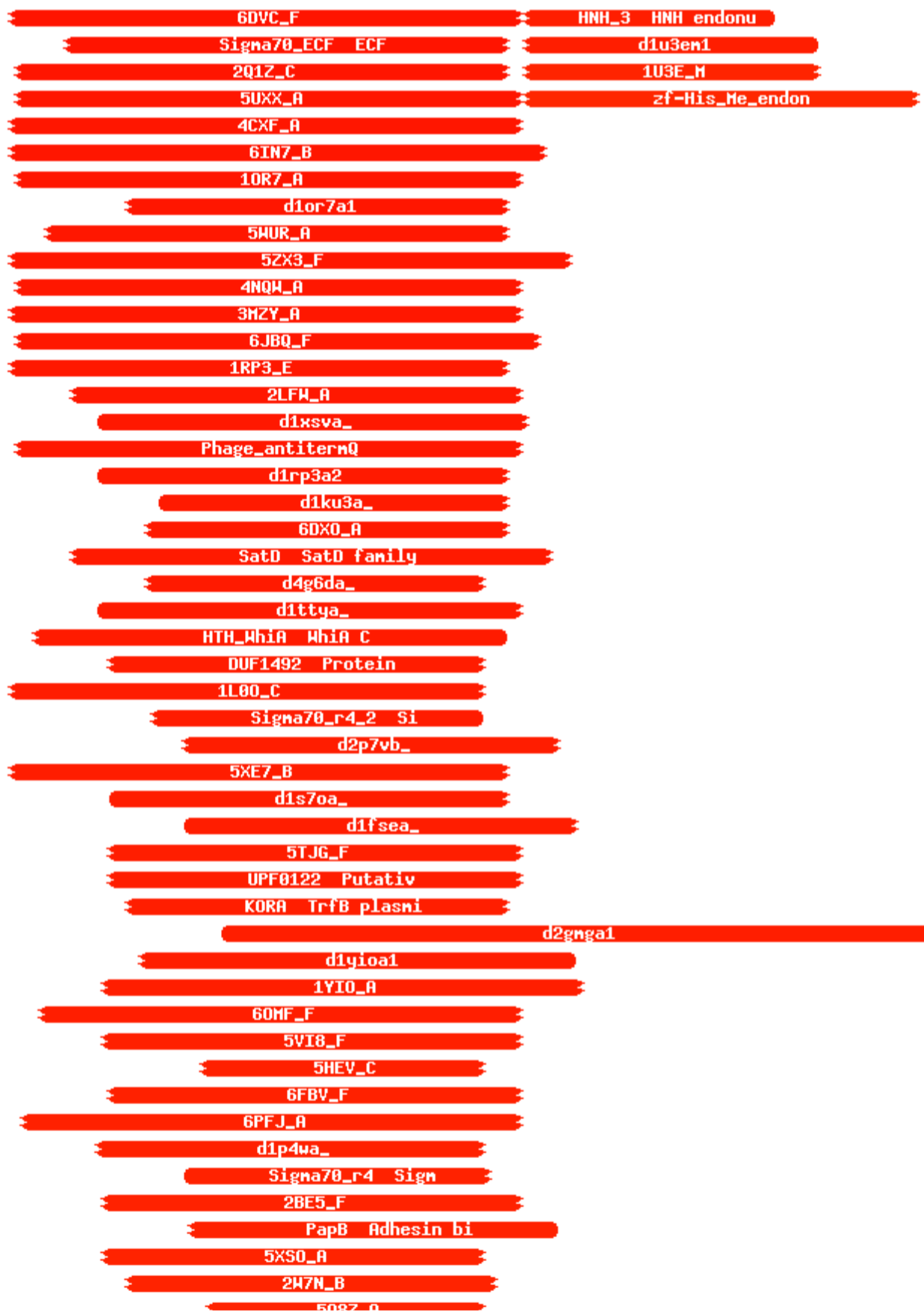
Detected sequence features: ■ Coiled coil segment(s)

Visualization

Resubmit Section

7

89



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Got it!

4GVP_A
 3T8Y_C
 HTH_Tnp_4 Helix-
 4HYE_B
 DUF134 Protein
 4LJZ_L
 HTH_40 Helix-tur
 208X_B
 DUF3489 Protein
 d1rr7a_
 6JHE_A
 3VFZ_A
 cd06170
 3C3W_B
 d1a04a1
 HTH_7 Helix-tur
 d1jhga_
 HTH_psq helix-t
 3CNO_X
 5F64_D
 6PST_L
 digdta1
 GerE Bacterial
 GcrA GcrA cell
 d3c57a_
 DUF2481 Protein
 HTH_49 Cry35Ab
 6ONU_D
 d2jpca_
 Terminase_5 Put
 d1tc3c_
 3P7N_B
 6FI7_A
 HTH_10 HTH DNA
 cd10988
 d1l3la1
 4QIC_A
 Phage_terminase
 6KJU_B
 6ID0_B
 d2ao9a1
 HTH_Tnp_Tc3_1 Tc
 DUF2089 Protein
 d2rnja_
 2H27_A
 d1zs4a1
 2L0K_A
 HTH_Tnp_IS630 T
 DUF746 Domain o
 HTH_38 Helix-tur
 Put_DNA-bind_N
 3T72_o
 HTH_29 Winged he
 d2o3fa1
 6ENI_A
 DUF603 Protein
 d2g7ga1
 HTH_23 Homeodona
 PAX Paired box
 d1k78a1
 d1vz0a1
 SoPB_HTH Centron
 d1zk8a1
 5FGM_A
 DUF1804 Protein
 d1r71a_
 Trp_repressor T
 d3ulqb_
 HTH_Tnp_ISL3 Hel
 HTH_Tnp_1_2 Hel
 1TTY_A
 d2hyja1
 d4onyg_
 HTH_6 Helix-tur
 d2gena1
 Phage_terminase

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Got it!

HTH_Mga_H prote
 d2fq4a1
 3KOR_D
 3NOR_A
 d2id3a1
 cd00131
 2LVS_A
 d2d6ya1
 1GDT_A
 d2g7la1
 pX02-72 Uncl
 d2fbqa1
 Mor Mor transcr
 CENP-B_N CENP-B
 RepB RepB plasm
 HTH_24 Winged he
 d3gw2a_
 d2coba1
 4G94_A
 cd10995
 d2gfna1
 d2hkua1
 1TLH_B
 1JHG_A
 1KU3_A
 d1sgna1
 HTH_22 HTH domai
 d3rqia_
 d2o7ta1
 DUF2774 Protein
 HTH_8 Bacterial
 d2fd5a1
 DUF1133 Protein
 4G97_A
 d2jj7a1
 1S70_B
 HTH_28 Helix-tur
 d2np5a1
 Phage_NinH Phag
 cd10994
 1RR7_A
 KorB KorB de
 d2xpa1
 d2g3ba1
 d1z0xa1
 d1u78a2
 d1rita_
 BrkDBD Brinker
 1XSV_B
 d2lkpa_
 Crp Bacterial
 6PAX_A
 DUF1153 Protein
 d2yvea1
 d2p5va1
 3IMF_A
 1PDM_C
 d4ggga_
 d2cfxa1
 d4jyka1
 Sigma54_OBD Sig
 d3iwza2
 HTH_50 Helix-tur
 4L5J_A
 d2lcva_
 HTH_Tnp_1 Trans
 HTH_5 Bacterial
 d1j9ia_
 RMP-RK RMP-RK c
 d1qbja_
 d1vi0a1
 d2id6a1
 5DCL_A
 4G6D_A
 B-block_TFIIIC
 10000

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Got it!

- 3MKZ_N
- 2LVS_A
- ArsR ArsR transc
- DUF658 Protein
- d1ui5a1
- 2R0Q_D
- HTH_11 HTH doma
- cd00492
- 3MKM_P
- d2hzta1
- 3PVV_B
- d1i1ga1
- 1Q1H_A
- DUF2582 Winged h
- DUF2802 Protein
- d2iu5a1
- 1XMR_D
- d1ub9a_
- 3RQI_A
- d2np3a1
- cd10996

Hitlist

Show Entries

Search:

Nr	Hit	Name	Probability	E-value	SS	Cols	Target Length
<input type="checkbox"/> 1	6DVC_F	DNA-directed RNA polymerase/ECF RNA polymerase; Mycobacterium tuberculosis, RNA polymerase, ECF; 3.3A {Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)}; Related PDB entries: 6DVD_F 6DVE_F 6TYF_F 6TYG_F 6DV9_F 6TYE_F 6DVB_F ; Related PDB entries: 6DV9_F 6DVB_F 6DVD_F 6DVE_F 6TYE_F 6TYF_F 6TYG_F	98.31	0.000025	10.6	82	177
<input type="checkbox"/> 2	PF07638.11	; Sigma70_ECF ; ECF sigma factor	98.29	0.000017	9.2	70	183
<input type="checkbox"/> 3	2Q1Z_C	Sigma24, RpoE, Transcriptional activator chrR; ECF sigma factor, anti-sigma factor; 2.4A {Rhodobacter sphaeroides}; Related PDB entries: 2Z2S_A 2Z2S_C 2Z2S_E 2Z2S_G 2Q1Z_A ; Related PDB entries: 2Q1Z_A 2Z2S_G 2Z2S_E 2Z2S_A 2Z2S_C	98.19	0.000034	9.1	79	184
<input type="checkbox"/> 4	5UXX_A	BaquA.17208.a, BaquA.17842.a; SSGCID, Bartonella quintana, sigma factor; HET: MSE, SO4; 2.45A {Bartonella quintana}; Related PDB entries: 5UXX_C	98.14	0.000024	7.2	81	164
<input type="checkbox"/> 5	4CXF_A	RNA POLYMERASE SIGMA FACTOR CNRH; TRANSCRIPTION, ECF-TYPE SIGMA, ANTISIGMA; HET: SO4; 1.75A {CUPRIAVIDUS METALLIDURANS CH34}	98.13	0.000006	9.2	82	191
<input type="checkbox"/> 6	6IN7_B	Sigma factor AlgU negative regulatory; Sigma factor, TRANSCRIPTION; 1.96A {Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)}	98.13	0.000095	10.2	86	193
<input type="checkbox"/> 7	1OR7_A	RNA polymerase sigma-E factor, Sigma-E; regulation, DNA-BINDING, TRANSMEMBRANE, TRANSCRIPTION; 2.0A {Escherichia coli} SCOP: l.1.1.1, a.4.13.2, a.177.1.1; Related PDB entries: 1OR7_B; Related PDB entries: 1OR7_B	98.11	0.000073	9.4	81	194
<input type="checkbox"/> 8	d1or7a1	a.4.13.2 (A:120-187) SigmaE factor (RpoE) {Escherichia coli [TaxId: 562]}	98.09	0.000098	8.3	61	68
<input type="checkbox"/> 9	5WUR_A	ECF RNA polymerase sigma factor; Sigma-anti-sigma complex, sigma binding motif 2 CA {Bacillus subtilis subsp. subtilis str. 168}	98.04	0.00011	9.2	74	187

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Nr	Hit	Name	Probability	E-value	SS	Cols	Target Length
<input type="checkbox"/> 10	5ZX3_F	DNA-directed RNA polymerase subunit alpha; Mycobacterium tuberculosis, RNA polymerase, holoenzyme; 2.751A {Mycobacterium tuberculosis H37Rv}; Related PDB entries: 6JCY_F 6KOO_F 6JCX_F 6KOO_F 6KON_F 6KOP_F 5ZX2_F; Related PDB entries: 6JCY_F 6JCX_F 6KON_F 6KOO_F 6KOP_F 6KOO_F 5ZX2_F	97.98	0.00013	8.8	90	218
<input type="checkbox"/> 11	4NQW_A	ECF RNA polymerase sigma factor; sigma factor, transcription initiation, DNA; HET: CD; 2.4A {Mycobacterium tuberculosis}	97.96	0.00012	8.3	81	204
<input type="checkbox"/> 12	3MZY_A	RNA polymerase sigma-H factor; PSI, MCSG, Structural Genomics, Midwest; 2.5A {Fusobacterium nucleatum subsp. nucleatum}	97.96	0.00027	9.7	81	164
<input type="checkbox"/> 13	6JBQ_F	DNA-directed RNA polymerase subunit alpha; RNA polymerase, Extra-Cytoplasmic Function sigma; 4.02A {Escherichia coli (strain K12)}	97.96	0.00018	9.2	84	219
<input type="checkbox"/> 14	1RP3_E	RNA polymerase sigma factor FliA; TRANSCRIPTION, SIGMA FACTOR; 2.3A {Aquifex aeolicus} SCOP: a.4.13.1, a.4.13.2, a.177.1.1; Related PDB entries: 1RP3_G 1RP3_A 1RP3_C 1SC5_A	97.9	0.00025	9.3	80	239
<input type="checkbox"/> 15	2LFW_A	PhyR sigma-like domain, NepR anti; signal transduction, response regulator, sigma; NMR {Sphingomonas sp. Fr1}	97.86	0.00029	8.4	72	157
<input type="checkbox"/> 16	d1xsva	a.4.13.3 (A:) Hypothetical protein SAV1236 {Staphylococcus aureus, strain Mu50 / ATCC 700699 [TaxId: 1280]}	97.85	0.00067	9.8	69	106
<input type="checkbox"/> 17	PF06530.12	; Phage_antitermQ ; Phage antitermination protein Q	97.85	0.00079	10.3	81	118
<input type="checkbox"/> 18	d1rp3a2	a.4.13.2 (A:164-234) Sigma factor sigma-28 (FliA) {Aquifex aeolicus [TaxId: 63363]}	97.84	0.00074	9.1	66	71
<input type="checkbox"/> 19	d1ku3a	a.4.13.2 (A:) Sigma70 (SigA, RpoD) {Thermus aquaticus [TaxId: 271]}	97.82	0.00028	6.6	56	61
<input type="checkbox"/> 20	6DXO_A	Putative RNA polymerase ECF-subfamily sigma; BldN, RsbN, Sigma, anti-sigma, ECF; 1.8A {Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)}	97.81	0.00023	7.2	58	151
<input type="checkbox"/> 21	PF16264.5	; SatD ; SatD family (SatD)	97.77	0.00059	9.3	77	211
<input type="checkbox"/> 22	d4g6da	a.4.13.2 (A:) automated matches {Staphylococcus aureus [TaxId: 93061]}	97.76	0.00043	6.9	54	62
<input type="checkbox"/> 23	d1ttya	a.4.13.2 (A:) Sigma70 (SigA, RpoD) {Thermotoga maritima [TaxId: 2336]}	97.69	0.00097	8.2	67	87
<input type="checkbox"/> 24	PF02650.14	; HTH_WhiA ; WhiA C-terminal HTH domain	97.65	0.00051	6.4	74	84
<input type="checkbox"/> 25	PF07374.11	; DUF1492 ; Protein of unknown function (DUF1492)	97.61	0.0013	8	60	100

Displaying 1 to 25 of 250 hits

Alignments

[Template alignment](#) | [Template 3D Structure](#) | [PDBe](#)

1. [6DVC_F](#) DNA-directed RNA polymerase/ECF RNA polymerase; Mycobacterium tuberculosis, RNA polymerase, ECF; 3.3A {Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)}; Related PDB entries: 6DVD_F 6DVE_F 6TYF_F 6TYG_F 6DV9_F 6TYE_F 6DVB_F ; Related PDB entries: 6DV9_F 6DVB_F 6DVD_F 6DVE_F 6TYE_F 6TYF_F 6TYG_F

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Got it!


```
.....+.....+..+..| ++.....+.....|+|..|||+..|+|. .+|++..+..+..+
T Consensus 111 ~~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l 184 (187)
T 5WUR_A 111 VADGVLPEDAVSLLELSNTIQKILK-LPKYRTVIVLKYIDELSLIETGEILNIPVGTVKTRIHGREALRKQL 184 (187)
T ss_dssp -----CHHHHHHHHHTS-CHHHHHHCCCCCCCCCHHHHHHHTSCHHHHHHHHHHHHHHHH
T ss_pred hhCCCCCHHHHHHHHHHHHHHHhC-CHHHHHHHHHhCCCCHHHHHHhCCCHHHHHHHHHHHHHH
```

[Template alignment](#) | [Template 3D Structure](#) | [PDBe](#)

5ZX3_F DNA-directed RNA polymerase subunit alpha; Mycobacterium tuberculosis, RNA polymerase, holoenzyme; 2.751A {Mycobacterium

- 10. **tuberculosis H37Rv}; Related PDB entries: 6JCY_F 6KOQ_F 6JCX_F 6KOO_F 6KON_F 6KOP_F 5ZX2_F; Related PDB entries: 6JCY_F 6JCX_F 6KON_F 6KOO_F 6KOP_F 6KOQ_F 5ZX2_F**

Probability: 97.98%, E-value: 0.00013, Score: 57.5, Aligned cols: 90, Identities: 13%, Similarity: -0.032,

```
Q ss_pred cccccccccccccchHHHHHHhhcchHHHHhCCcHHHHHHHHHHCCCCCHHHHHHHCCCHHHHHHHHHHHHHHHH
Q Q_Heath_gp71 7 ELEDDEPDTKGWQPDLLLVPALLAGSPTTMADLCPADRAWAVAGLMRAGHTAERIRDRMGCSLRTVRMVSAAATTAMML 86 (188)
Q Consensus 7 ~~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l 86 (188)
.....+.....+..+..| ++.....+.....|+|..|||+..|+|. .+|++..+..+..+
T Consensus 118 ~~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l 196 (218)
T 5ZX3_F 118 SNAEHSSTGLRSAEVEALEALPDETEIKALQAL-PEEFMAVYVADVEGFPYKEIAEIMDTPIGTVMSRLHRGRRQLRGL 196 (218)
T ss_dssp HHHHTSSSCCCHHHHHHHTSCSSHHHHHHS-CHHHHHHCCCCCCCCCHHHHHHHTTCCCHHHHHHHHHHHHHHHH
T ss_pred cccccCCCCcHHHHHHhCCHHHHHHHhC-CHHHHHHHHHhCCCCHHHHHHhCCCHHHHHHHHHHHHHH
```

```
Q ss_pred HHHHHHHHH
Q Q_Heath_gp71 87 LQEETEHFQDE 97 (188)
Q Consensus 87 ~~~~~f~~~~ 97 (188)
+.....+
T Consensus 197 l~~~~~ 207 (218)
T 5ZX3_F 197 LADVARDRGFA 207 (218)
T ss_dssp CCCSCC-----
T ss_pred HHHHHHHhCH
```

[Template alignment](#) | [Template 3D Structure](#) | [PDBe](#)

- 11. **4NQW_A ECF RNA polymerase sigma factor; sigma factor, transcription initiation, DNA; HET: CD; 2.4A {Mycobacterium tuberculosis}**

Probability: 97.96%, E-value: 0.00012, Score: 57.18, Aligned cols: 81, Identities: 12%, Similarity: 0.036,

```
Q ss_pred cccccccccccccchHHHHHHhhcchHHHHhCCcHHHHHHHHHHCCCCCHHHHHHHCCCHHHHHHHHHHHHHHHH
Q Q_Heath_gp71 8 ELEDDEPDTKGWQPDLLLVPALLAGSPTTMADLCPADRAWAVAGLMRAGHTAERIRDRMGCSLRTVRMVSAAATTAMML 87 (188)
Q Consensus 8 ~~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l 87 (188)
.+.....+.....+..+..| ++.....+.....|+|..|||+..|+|. .+|+++..+++..+|...+
T Consensus 123 ~~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l 201 (204)
T 4NQW_A 123 GAANVDPASDVADLAIGDERRRVTECLKAL-TDTRQCIELAYGGGLTVYEVSRRLAANLSTIKSRMRDALRS LRNCL 201 (204)
T ss_dssp -----CHHHHHHHHHHHHHS-CHHHHHHCCCCCTCCCHHHHHHTTCCCHHHHHHHHHHHHHHHH
T ss_pred cccccCCCCcHHHHHHhhHHHHHHHHHHhC-CHHHHHHHHHhCCCCHHHHHHhCCCHHHHHHHHHHHHHH
```

```
Q ss_pred HH
Q Q_Heath_gp71 88 QE 89 (188)
Q Consensus 88 ~ 89 (188)
..
T Consensus 202 ~ 203 (204)
T 4NQW_A 202 DV 203 (204)
T ss_dssp C-
T ss_pred cc
```

[Template alignment](#) | [Template 3D Structure](#) | [PDBe](#)

- 12. **3MZY_A RNA polymerase sigma-H factor; PSI, MCSG, Structural Genomics, Midwest; 2.5A {Fusobacterium nucleatum subsp. nucleatum}**

Probability: 97.96%, E-value: 0.00027, Score: 52.39, Aligned cols: 81, Identities: 9%, Similarity: 0.006,

```
Q ss_pred cccccccccccccchHHHHHHhhcchH--HH-HhCCcHHHHHHHHHHCCCCCHHHHHHHCCCHHHHHHHHHHHHHH
Q Q_Heath_gp71 7 ELEDDEPDTKGWQPDLLLVPALLAGSPT--TM-ADLCPADRAWAVAGLMRAGHTAERIRDRMGCSLRTVRMVSAAATT 82 (188)
Q Consensus 7 ~~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l 82 (188)
.....+.....+..+..| ++.....+.....|+|..|||+..|+|. .+|++..+..+..+
T Consensus 74 ~~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l~~~~l 151 (164)
T 3MZY_A 74 DEGHINNYKSSSENP EAYLKEEIEEFKFKSENNF--SKFEKVELTYLIRGYSYREIATILSKNLKSIDNTIQIRKK 151 (164)
T ss_dssp -----CHHHHHHHHHHHHHHHS--CHHHHHHHHTTCCCHHHHHHTTCCCHHHHHHHHHHHHHH
T ss_pred CCCCCccccCCCCchHHhhCCHHHHHHHHHhC-CHHHHHHHHHhCCCCHHHHHHhCCCHHHHHHHHHHHH
```

```
Q ss_pred HHHHHH
Q Q_Heath_gp71 83 AMMLLQE 89 (188)
Q Consensus 83 l~~~~~ 89 (188)
+.....+
```


[Template alignment](#) | [Template 3D Structure](#) | [PDB](#) | [NCBI](#)

22. **d4g6da** a.4.13.2 (A): **automated matches {Staphylococcus aureus [TaxId: 93061]}**
Probability: 97.76%, E-value: 0.00043, Score: 43.29, Aligned cols: 54, Identities: 13%, Similarity: 0.091,

Q ss_pred		HhccHHHHHCcCHHHHHHHHHCC----CCHHHHHHHCCCHHHHHHHHHHHHHHHHH	
Q Q_Heath_gp71	29	LAGSPPTMADLCPADRAWAVAGLMRAG---HTAERIRDRMGCSLRTVRMVSAAWATTA	83 (188)
Q Consensus	29	~~~~~ ~L~::~:~ ~G~----~s~veIA~lgiS~rtV~::~:~ ~a~::~:~	83 (188)
		.+.+.+.+.+. +.+.+.+.+. ++.+. +.+ +.+ + .+.+.+.+.+	
T Consensus	2	~~~~~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~	59 (62)
T d4g6da_	2	KEQLEDVLDL-TDREENVRLRFGLDGRTRTLLEEVGKVFVTRERIRQIEAKALRKL	59 (62)
T ss_dssp		HHHHHHHHHTS-CCHHHHHHHHHHTTTTSCCHHHHHHHHTSCHHHHHHHHHHHHHHHHH	
T ss_pred		hHHHHHHHhC-CCHHHHHHHHHCCCCCccCHHHHHHHCCCHHHHHHHHHHHHHHHHh	

[Template alignment](#) | [Template 3D Structure](#) | [PDB](#) | [NCBI](#)

23. **d1titya** a.4.13.2 (A): **Sigma70 (SigA, RpoD) {Thermotoga maritima [TaxId: 2336]}**
Probability: 97.69%, E-value: 0.00097, Score: 45.86, Aligned cols: 67, Identities: 10%, Similarity: 0.033,

Q ss_pred		ChHHHHHHHcchHHHHHCcCHHHHHHHHHHH----CCCCHHHHHHHCCCHHHHHHHHHHHHHHHHHHH	
Q Q_Heath_gp71	21	DLLLVPALLAGSPPTMADLCPADRAWAVAGLMR-----AGHTAERIRDRMGCSLRTVRMVSAAWATTA	89 (188)
Q Consensus	21	~~~~~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~	89 (188)
	+.+.+.+. ++.+.+.+.+. . .+.+. .+.+. .+.+. .+.+.	
T Consensus	1	~~~~~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~	72 (87)
T d1titya_	1	KEAMRLMREELKVLKTL--SPREAVLRLMYGLLKGPKTLEEVGQYFVTRERIRQIEVKALRKLKLRHPSRS	72 (87)
T ss_dssp		CTCCCCCSHHHHHTTS--CHHHHHHHHHHTTTTSSCCHHHHHHHHTCCHHHHHHHHHHHHHBTBSS	
T ss_pred		ChHHHHHHHHHHHHHHhC--CHHHHHHHHHhCCCCCccCHHHHHHHCCCHHHHHHHHHHHHHhchhhh	

[Template alignment](#) | [CDD](#)

24. **PF02650.14**; **HTH_WhiA**; **WhiA C-terminal HTH domain**
Probability: 97.65%, E-value: 0.00051, Score: 46.83, Aligned cols: 74, Identities: 5%, Similarity: -0.008,

Q ss_pred		CCCCCCCCcCHHHHHHHhchHH--HhCCcCHHHHHHHHHHC-CCCHHHHHHHCCCHHHHHHHHHHHHHHHHH	
Q Q_Heath_gp71	11	DEPDTKGWQPDLLLVPALLAGSPPT--MADLCPADRAWAVAGLMRA-GHTAERIRDRMGCSLRTVRMVSAAWATTA	87 (188)
Q Consensus	11	~~~~~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~	87 (188)
		+.....+.+.+.+. .+.+.+.+. .+.+.+.+. .+.+.+.+. .+.+.+.+. .+.+.+.+.	
T Consensus	8	d~~~~~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~	84 (84)
T PF02650.14	8	EAANINKTVSASVKTQDIRYIQDITVGLQLT-PDNLKAVAELELKYQDASLKEGLERLNPRVG--KSGVNHRLEKIGRIA	84 (84)
T ss_pred		HhchhHHHHHHHHHHHHHHhChhC-CCHHHHHHHHHCCCCCHHHHHHHCCCHHHHHHHHHHHHHhC	

[Template alignment](#) | [CDD](#)

25. **PF07374.11**; **DUF1492**; **Protein of unknown function (DUF1492)**
Probability: 97.61%, E-value: 0.0013, Score: 45.7, Aligned cols: 60, Identities: 13%, Similarity: -0.048,

Q ss_pred		HHHHHHHcchHHHHHCc-CHHHHHHHHHHHCCCCCHHHHHHHHHCCCHHHHHHHHHHHHHHHHH	
Q Q_Heath_gp71	23	LLVPAALLAGSPPTMADLCP-ADRAWAVAGLMRAGHTAERIRDRMGCSLRTVRMVSAAWATTA	83 (188)
Q Consensus	23	~~~~~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~	83 (188)
	+.+.+.+. +.+.+.+.+. ++.+. .+. .+. .+. .+.	
T Consensus	39	~~~~~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~	99 (100)
T PF07374.11	39	AEAIKQKLEFRRIANI-EDIDARSLQMVYIQDGIWQICDKLGISRATYYVKLRQAEKYL	99 (100)
T ss_pred		HHHHHHHHHHHHHHCC-CCHHHHHHHHHhCCCCCHHHHHHHCCCHHHHHHHHHHHHHhh	

[Template alignment](#) | [Template 3D Structure](#) | [PDB](#)

26. **1L00_C** **Anti-sigma F factor/sigma factor complex; Bergerat fold, helix-turn-helix, PROTEIN BINDING; HET: ADP; 2.9A {Geobacillus stearothermophilus} SCOP: a.4.13.2**

Probability: 97.6%, E-value: 0.00054, Score: 54.61, Aligned cols: 76, Identities: 9%, Similarity: -0.101,

Q ss_pred		ccccccccccccCHHHHHHHhchHHHHHCcCHHHHHHHHHHHCCCCCHHHHHHHCCCHHHHHHHHHHHHH	
Q Q_Heath_gp71	7	ELEDEPDTKGWQPDLLLVPALLAGSPPTMADLCPADRAWAVAGLMRAGHTAERIRDRMGCSLRTVRMVSAAWATTA	83 (188)
Q Consensus	7	~~~~~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~	83 (188)
		..+.+.+.+.+.+.+.+.+. ++.+.+.+.+. .+. .+. .+. .+. .+.	
T Consensus	167	~~~~~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~ ~L~::~:~	242 (243)
T 1L00_C	167	NDGDPITLLDQIADADEASWFDKIALKKAIEEL-DEERELIIVYLRYYKDQTSQEVASRLGISQVQMSRLEKKILQHI	242 (243)
T ss_dssp		-----	
T ss_pred		CCCCcehhhhCccCcCHHHHHHHHHHHhC-CCHHHHHHHHHCCCCCHHHHHHHCCCHHHHHHHHHHHhC	

[Template alignment](#) | [CDD](#)

27. **PF08281.12**; **Sigma70_r4_2**; **Sigma-70, region 4**
Probability: 97.57%, E-value: 0.00023, Score: 33.07, Aligned cols: 50, Identities: 42%, Similarity: 0.137,

T 5TJG_F 269 AAQSLLESELEKALSKL--SEREA VLKLRKGLIDGREHTLEEVGAYFVGVTREIRIQIENKALRKLYHESR 338 (347)
T ss_dssp HHHHHHHHHHHHHHTTS--CHHHHHHHHHHTTTTTSSCCCHHHHHHHHTCCHHHHHHHHHHHHHHHHHHHHHHHH
T ss_pred HHHHHHHHHHHHHHcC--CHHHHHHHHHCCCCCCcCCHHHHHHHCCCCHHHHHHHHHHHHHHcchhh

[Template alignment](#) | [CDD](#)

33. PF13392.6 ; HNH_3 ; HNH endonuclease
Probability: 97.42%, E-value: 0.000037, Score: 46.42, Aligned cols: 39, Identities: 8%, Similarity: 0.022,

Q ss_pred		HHHHHHHHHHchHHHHHhCCccccHhhhHhccchHHHh	
Q Q_Heath_gp71	90	ETEHFQDEYRMQASEIARLRELATSEATAKRYQDQLANVL	130 (188)
Q Consensus	90	~~~~f~~~~~V~h~g~~~~~L~nt~en~	130 (188)
		..+. + .+..+.. . . ++. +++ + . ++ +.	
T Consensus	7	V~~~~g~~~~~V~h~g~~~~~NL~nt~n~	45 (45)
T PF13392.6	7	VFLME-G-LDISGKIVDHDICDRQNNRRDLRLVTPLENAY	45 (45)
T ss_pred		HHHhC-C-CCCCcEEECccccCCCCCHHHEEECHHHHcC	

[Template alignment](#) | [CDD](#)

34. PF04297.14 ; UPF0122 ; Putative helix-turn-helix protein, YlxM / p13 like
Probability: 97.42%, E-value: 0.0049, Score: 42.54, Aligned cols: 66, Identities: 9%, Similarity: -0.173,

Q ss_pred		HHHHHHHhchHHHHHCCcHHHHHHHHHHCCCCHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHH	
Q Q_Heath_gp71	23	LLVPALLAGSPTMADLCPADRAWAVAGLMRAGHTAERIIRDRMGCSLRTVRMVSAAWAATTAMMLLQE	89 (188)
Q Consensus	23	~~~~~i~L~L~~~~~i~L~n~G~s~veIA~l~g~i~S~r~t~V~L~a~L~	89 (188)
	+.+.+.+.+. ++.....+.+.+. ++.+. .+. .+. ++++.+.+.+.+.+.+.+.+.+	
T Consensus	2	~~~~~i~L~L~~~~~i~L~n~G~s~veIA~l~g~i~S~r~t~V~L~a~L~	67 (96)
T PF04297.14	2	NKRWYLIALYDIYQGLL-TTKQCEYFNLYHFKDLSEFSEIAELKEISKSAISDCLNKVCDQLLKYEQA	67 (96)
T ss_pred		chHHHHHHHHHHhC-C-CHHHHHHHHHCCCCHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHH	

[Template alignment](#) | [CDD](#)

35. PF16509.5 ; KORA ; TrfB plasmid transcriptional repressor
Probability: 97.41%, E-value: 0.0044, Score: 42.01, Aligned cols: 61, Identities: 7%, Similarity: -0.096,

Q ss_pred		HHHHhchHHHHhCCcHHHHHHHHHHCCCCHHHHHHHCCCHHHHHHHHHHHHHHHHHHH	
Q Q_Heath_gp71	26	PALLAGSPTMADLCPADRAWAVAGLMRAGHTAERIIRDRMGCSLRTVRMVSAAWAATTAMMLL	87 (188)
Q Consensus	26	~~~~~i~L~L~~~~~i~L~n~G~s~veIA~l~g~i~S~r~t~V~L~a~L~	87 (188)
		.+.+.+.+.+. ++.....+.+.+. ++.+. +.+. +.+. ++++.+.+.+.+.+.+.+.+.+	
T Consensus	3	~~~~~i~L~L~~~~~i~L~n~G~s~veIA~l~g~i~S~r~t~V~L~a~L~	63 (87)
T PF16509.5	3	QEEWDRILPAMETF-ADITTQIAYLVLVKDEKQSDVATNLARSKQNVGNVAVKRVDLYTELE	63 (87)
T ss_pred		HHHHHHHHHHhC-C-CHHHHHHHHHCCCCHHHHHHHCCCHHHHHHHHHHHHHHHHHHH	

[Template alignment](#) | [Template 3D Structure](#) | [PDB](#) | [NCBI](#)

36. d1u3em1 d.4.1.3 (M:1-105) Intron-encoded homing endonuclease I-HmuI {Bacteriophage SPO1 [TaxId: 10685]}
Probability: 97.41%, E-value: 0.00006, Score: 54.01, Aligned cols: 47, Identities: 19%, Similarity: 0.225,

Q ss_pred		HHHHHHHHHHchHHHHHhCCccccHhhhHhccchHHHhccCC	
Q Q_Heath_gp71	90	ETEHFQDEYRMQASEIARLRELATSEATAKRYQDQLANVLDLSYLTGE	137 (188)
Q Consensus	90	~~~~f~~~~~V~h~g~~~~~L~nt~en~~~~~~G~	137 (188)
		..++ .+.+. + ++.+. ++ +. . ++ .+.+.+. +	
T Consensus	59	V~~~~f~g~n~~~~~~V~h~d~~~~~d~n~L~nt~n~n~n~n~n~n~g~	105 (105)
T d1u3em1	59	VATHFCGYE-EGLVVDHKDGNKDNNLSTNLRVWTQKINVENQMSRGT	105 (105)
T ss_dssp		HHHHHCTTCC-TTCEEEETTCTTCCCGGEEEECHHHHHHHHHHHTC	
T ss_pred		HHHHhCCCC-CCcEECCCCCCCCCHHHEEECHHHHHHHHHhCC	

[Template alignment](#) | [Template 3D Structure](#) | [PDB](#) | [NCBI](#)

37. d2gmga1 a.4.5.82 (A:10-105) Hypothetical protein PF0610 {Pyrococcus furiosus [TaxId: 2261]}
Probability: 97.39%, E-value: 0.00076, Score: 47.79, Aligned cols: 91, Identities: 9%, Similarity: 0.054,

Q ss_pred		cHHHHHHHHHHCCCCHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHHHHHHhchHHHHHhCCccccHhhh	
Q Q_Heath_gp71	41	PADRAWAVAGLMRAGHTAERIIRDRMGCSLRTVRMVSAAWAATTAMMLLQEETEHFQDEYRMQASEIARLRELATSEATAK	120 (188)
Q Consensus	41	~~~~~i~L~n~G~s~veIA~l~g~i~S~r~t~V~L~a~L~f~~~~~V~h~g~~~~~L~nt~n~n~n~L	120 (188)
		++.+.+.+.+.+.+.+. . . +.+. +.+. +.+. .+. +.+. +.+. +.+. +.+. +.+. +.+. +.+. +.+. +.+.	
T Consensus	1	~~~~~i~L~n~G~s~veIA~l~g~i~S~r~t~V~L~a~L~f~~~~~V~h~g~~~~~L~nt~n~n~n~L	74 (96)
T d2gmga1	1	ATRREKIIELLEGDYSPELARILDMRGKSKKVILEDLKVISKIAKR-----EGMVLLIKPAQCRKCGFVFKAEINI-	74 (96)
T ss_dssp		HHHHHHHHHTTSCBCTTHHHSSCCSSCHHHHHHHHHHHHHHHHHHTT-----TTEEECCCBTTTCCBCCSSC-	
T ss_pred		CcHHHHHHHHHHCCCCHHHHHHHCCCCCCHHHHHHHHHHHHHHHHH-----cCCeeceeeCccccCeeccccc-	

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Got it!