
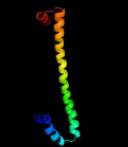











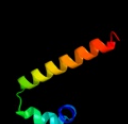

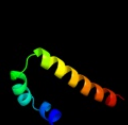



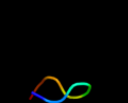


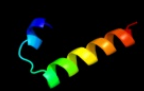
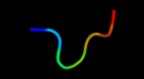

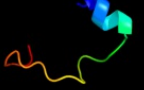







#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nr7A_	 Alignment		99.7	98	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein h-ns; PDBTitle: crystal structure of s. typhimurium h-ns 1-83
2	d1hnra_	 Alignment		99.7	100	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
3	c2levA_	 Alignment		99.4	33	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ler; PDBTitle: structure of the dna complex of the c-terminal domain of ler
4	c2jr1A_	 Alignment		98.9	18	PDB header: dna binding protein Chain: A: PDB Molecule: virulence regulator; PDBTitle: solution structure of the dna binding domain of a nucleoid-associated2 protein, h-ns, from the phytopathogen xylella fastidiosa.
5	c2l92A_	 Alignment		98.9	39	PDB header: dna binding protein Chain: A: PDB Molecule: histone family protein nucleoid-structuring protein h-ns; PDBTitle: solution structure of the c-terminal domain of h-ns like protein bv3f
6	d1lr1a_	 Alignment		98.6	98	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
7	d1ov9a_	 Alignment		98.4	58	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
8	d1ni8a_	 Alignment		98.4	100	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
9	d1y7ya1	 Alignment		50.8	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
10	d1ayja_	 Alignment		34.2	38	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Plant defensins
11	c3gbhC_	 Alignment		32.6	13	PDB header: oxidoreductase Chain: C: PDB Molecule: nad(p)h-flavin oxidoreductase; PDBTitle: crystal structure of a putative nad(p)h:fmn oxidoreductase (se1966)2 from staphylococcus epidermidis atcc 12228 at 2.00 a resolution

12	c3bpjD_	Alignment		27.1	18	PDB header: translation Chain: D: PDB Molecule: eukaryotic translation initiation factor 3 subunit j; PDBTitle: crystal structure of human translation initiation factor 3, subunit 12 alpha
13	d1bk8a_	Alignment		23.6	43	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Plant defensins
14	d1zcha1	Alignment		21.6	29	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
15	d2cyua1	Alignment		17.8	13	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
16	c2eq7C_	Alignment		17.7	13	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate dehydrogenase e2 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
17	c2eq9C_	Alignment		17.7	22	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
18	c3ivpD_	Alignment		17.5	17	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
19	c3gagB_	Alignment		17.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadh dehydrogenase, nadph nitroreductase; PDBTitle: crystal structure of a nitroreductase-like protein (smu.346) from2 streptococcus mutans at 1.70 a resolution
20	d1f5va_	Alignment		17.4	13	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
21	d1o17a1	Alignment	not modelled	16.6	25	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
22	d1w4ha1	Alignment	not modelled	16.2	13	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
23	c3d6zA_	Alignment	not modelled	16.1	16	PDB header: transcription regulator/dna Chain: A: PDB Molecule: multi drug-efflux transporter 1 regulator; PDBTitle: crystal structure of r275e mutant of bmrr bound to dna and rhodamine
24	c3dv0I_	Alignment	not modelled	15.7	13	PDB header: oxidoreductase/transferase Chain: I: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
25	c2cooA_	Alignment	not modelled	15.5	17	PDB header: transferase Chain: A: PDB Molecule: lipoamide acyltransferase component of branched- PDBTitle: solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
26	c1w3dA_	Alignment	not modelled	15.0	13	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
27	c2eq8C_	Alignment	not modelled	14.3	22	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from

						thermus thermophilus2 hb8 with psbdp
28	d1w85j_	Alignment	not modelled	14.3	13	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
29	c2jo8B_	Alignment	not modelled	14.2	23	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase 4; PDBTitle: solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
30	d1brwa1	Alignment	not modelled	13.7	13	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
31	c1w4kA_	Alignment	not modelled	11.9	17	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase e2; PDBTitle: peripheral-subunit binding domains from mesophilic, 2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
32	c1zwvA_	Alignment	not modelled	11.6	17	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase component of branched- PDBTitle: solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
33	d2h9da1	Alignment	not modelled	11.3	12	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Dimeric chorismate mutase
34	d2ewca1	Alignment	not modelled	11.2	8	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
35	d2ifaal	Alignment	not modelled	11.1	16	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
36	d1bala_	Alignment	not modelled	11.0	13	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
37	c3hdlA_	Alignment	not modelled	10.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: royal palm tree peroxidase; PDBTitle: crystal structure of highly glycosylated peroxidase from royal palm2 tree
38	d1iwga5	Alignment	not modelled	10.5	13	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
39	c1o7dB_	Alignment	not modelled	10.0	31	PDB header: hydrolase Chain: B: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
40	d2bjca1	Alignment	not modelled	9.9	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
41	d1ic8a2	Alignment	not modelled	9.7	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
42	d1k4ta3	Alignment	not modelled	9.3	12	Fold: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment Superfamily: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment Family: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
43	c2rpbA_	Alignment	not modelled	9.3	30	PDB header: membrane protein Chain: A: PDB Molecule: hypothetical membrane protein; PDBTitle: the solution structure of membrane protein
44	c1o17A_	Alignment	not modelled	9.3	25	PDB header: transferase Chain: A: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyl-transferase (trpd)
45	c2q9lA_	Alignment	not modelled	9.1	13	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of imazg from vibrio dat 722: ctgag-imazg (p43212)
46	d1iqpa1	Alignment	not modelled	8.7	20	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
47	c3bs3A_	Alignment	not modelled	8.4	16	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
48	d1chma1	Alignment	not modelled	8.3	29	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain
49	d1r8ea1	Alignment	not modelled	8.1	16	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
50	d1iwga6	Alignment	not modelled	8.1	27	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN

						and DC subdomains
51	c2o38A	Alignment	not modelled	7.9	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
52	d2o38a1	Alignment	not modelled	7.9	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
53	c3ge6B	Alignment	not modelled	7.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: nitroreductase; PDBTitle: crystal structure of a putative nitroreductase in complex with fmh2 (exig_2970) from exigobacterium sibiricum 255-15 at 1.85 a3 resolution
54	d2a6ca1	Alignment	not modelled	7.9	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
55	c2kpiA	Alignment	not modelled	7.9	5	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
56	c1g6uB	Alignment	not modelled	7.8	27	PDB header: de novo protein Chain: B: PDB Molecule: domain swapped dimer; PDBTitle: crystal structure of a domain swapped dimer
57	d1i9za	Alignment	not modelled	7.8	25	Fold: DNase I-like Superfamily: DNase I-like Family: Inositol polyphosphate 5-phosphatase (IPP5)
58	c3bemA	Alignment	not modelled	7.6	27	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nad(p)h nitroreductase ydfn; PDBTitle: crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution
59	c3gpvA	Alignment	not modelled	7.4	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
60	c3obcB	Alignment	not modelled	7.4	15	PDB header: hydrolase Chain: B: PDB Molecule: pyrophosphatase; PDBTitle: crystal structure of a pyrophosphatase (af1178) from archaeoglobus2 fulgidus at 1.80 a resolution
61	c1k5gH	Alignment	not modelled	7.4	13	PDB header: signaling protein/signaling activator Chain: H: PDB Molecule: ran-specific gtpase-activating protein; PDBTitle: crystal structure of ran-gdp-alfx-ranbp1-rangap complex
62	d1k5db	Alignment	not modelled	7.4	13	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Ran-binding domain
63	c2l5pA	Alignment	not modelled	7.1	14	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 12; PDBTitle: solution nmr structure of protein lipocalin 12 from rat epididymis
64	d2cxfA1	Alignment	not modelled	7.1	30	Fold: RUN domain-like Superfamily: RUN domain-like Family: RUN domain
65	d2ofya1	Alignment	not modelled	6.9	0	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
66	d1juba	Alignment	not modelled	6.9	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
67	d2ay0a1	Alignment	not modelled	6.8	38	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: PutA pre-N-terminal region-like
68	c3b7hA	Alignment	not modelled	6.7	7	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
69	c2jeeA	Alignment	not modelled	6.7	17	PDB header: cell cycle Chain: A: PDB Molecule: yiii; PDBTitle: xray structure of e. coli yiii
70	c2jvdA	Alignment	not modelled	6.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0291 protein ynzc; PDBTitle: solution nmr structure of the folded n-terminal fragment of2 upf0291 protein ynzc from bacillus subtilis. northeast3 structural genomics target sr384-1-46
71	c2h0uA	Alignment	not modelled	6.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph-flavin oxidoreductase; PDBTitle: crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
72	d1sxjc1	Alignment	not modelled	6.5	14	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
73	c3gp4B	Alignment	not modelled	6.5	17	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
74	c3cs5B	Alignment	not modelled	6.3	32	PDB header: photosynthesis Chain: B: PDB Molecule: phycobilisome degradation protein nbla; PDBTitle: nbla protein from synechococcus elongatus pcc 7942
75	c3ebwA	Alignment	not modelled	6.3	10	PDB header: allergen Chain: A: PDB Molecule: per a 4 allergen; PDBTitle: crystal structure of major allergens, per a 4 from2 cockroaches
76	c3otzA	Alignment	not modelled	6.1	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative translation initiation inhibitor;

76	c3y2a_	Alignment	not modelled	6.1	43	PDBTitle: crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium
77	c1yw5A_	Alignment	not modelled	6.0	19	PDB header: isomerase Chain: A: PDB Molecule: peptidyl prolyl cis/trans isomerase; PDBTitle: peptidyl-prolyl isomerase ess1 from candida albicans
78	d1r69a_	Alignment	not modelled	6.0	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
79	c2xstA_	Alignment	not modelled	6.0	9	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 15; PDBTitle: crystal structure of the human lipocalin 15
80	c1r22B_	Alignment	not modelled	5.9	27	PDB header: transcription repressor Chain: B: PDB Molecule: transcriptional repressor smtb; PDBTitle: crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
81	d1j1va_	Alignment	not modelled	5.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV
82	c3pvpA_	Alignment	not modelled	5.7	11	PDB header: dna binding protein/dna Chain: A: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
83	d1z3eb1	Alignment	not modelled	5.7	17	Fold: SAM domain-like Superfamily: C-terminal domain of RNA polymerase alpha subunit Family: C-terminal domain of RNA polymerase alpha subunit
84	c3i10B_	Alignment	not modelled	5.7	26	PDB header: hydrolase Chain: B: PDB Molecule: aminopeptidase p; xaa-pro aminopeptidase; PDBTitle: the crystal structure of the aminopeptidase p, xaa-pro aminopeptidase2 from streptococcus thermophilus
85	d1ykia1	Alignment	not modelled	5.6	17	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
86	d1lvfa_	Alignment	not modelled	5.6	18	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
87	d2i8ga1	Alignment	not modelled	5.6	45	Fold: Mog1p/PsbP-like Superfamily: Mog1p/PsbP-like Family: DIP2269-like
88	c2k2pA_	Alignment	not modelled	5.5	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1203; PDBTitle: solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
89	c2k5eA_	Alignment	not modelled	5.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
90	c3izct_	Alignment	not modelled	5.5	35	PDB header: ribosome Chain: T: PDB Molecule: 60s ribosomal protein rpl19 (l19e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
91	d2zjrv1	Alignment	not modelled	5.5	13	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
92	c3clcC_	Alignment	not modelled	5.5	0	PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
93	d1sxjb1	Alignment	not modelled	5.4	17	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
94	c3bhpA_	Alignment	not modelled	5.4	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0291 protein ynzc; PDBTitle: crystal structure of upf0291 protein ynzc from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
95	d1utxa_	Alignment	not modelled	5.4	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
96	c2k23A_	Alignment	not modelled	5.3	9	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 2; PDBTitle: solution structure analysis of the rlcn2
97	d2hsqa1	Alignment	not modelled	5.3	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
98	d1v29a_	Alignment	not modelled	5.3	16	Fold: Nitrile hydratase alpha chain Superfamily: Nitrile hydratase alpha chain Family: Nitrile hydratase alpha chain
99	d2r1j11	Alignment	not modelled	5.3	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors