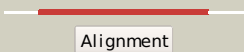

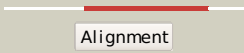




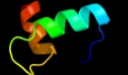


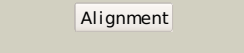

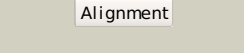

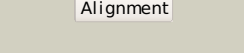



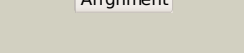

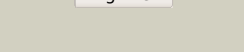
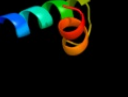






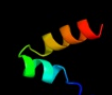





























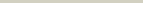


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fmtF_	 Alignment		100.0	100	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna
2	dlj3ea_	 Alignment		100.0	98	Fold: Replication modulator SeqA, C-terminal DNA-binding domain Superfamily: Replication modulator SeqA, C-terminal DNA-binding domain Family: Replication modulator SeqA, C-terminal DNA-binding domain
3	dlxra1	 Alignment		99.7	94	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like
4	clxrD_	 Alignment		99.7	94	PDB header: replication inhibitor Chain: D: PDB Molecule: seqa protein; PDBTitle: crystal structure of a dna-binding protein
5	d3djba1	 Alignment		52.4	13	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
6	c2oq2B_	 Alignment		32.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
7	d2qgsa1	 Alignment		28.5	13	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
8	c2hncC_	 Alignment		26.3	17	PDB header: transferase Chain: C: PDB Molecule: sam-dependent o-methyltransferase; PDBTitle: crystal structure of sam-dependent o-methyltransferase from2 pathogenic bacterium leptospira interrogans
9	c2o0cB_	 Alignment		22.4	23	PDB header: signaling protein Chain: B: PDB Molecule: alr2278 protein; PDBTitle: crystal structure of the h-nox domain from nostoc sp. pcc 71202 complexed to no
10	d2byfa1	 Alignment		21.8	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
11	c2kiIA_	 Alignment		21.6	15	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state

12	c2ragB_	Alignment		21.1	15	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidase; PDBTitle: crystal structure of aminohydrolase from caulobacter crescentus
13	d1qbjc_	Alignment		21.0	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
14	d2gxba1	Alignment		20.4	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
15	d1u55a_	Alignment		20.2	27	Fold: Ligand-binding domain in the NO signalling and Golgi transport Superfamily: Ligand-binding domain in the NO signalling and Golgi transport Family: H-NOX domain
16	c2i5gB_	Alignment		18.7	20	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase; PDBTitle: crystal strcuture of amidohydrolase from pseudomonas2 aeruginosa
17	d1p9oa_	Alignment		18.1	13	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
18	d1qgpa_	Alignment		17.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
19	c2i9bA_	Alignment		16.1	18	PDB header: transcription Chain: A: PDB Molecule: mrna 3'-end-processing protein rna15; PDBTitle: heterodimer between rna14p monkeytail domain and rna15p hinge domain2 of the yeast cf ia complex
20	c1bm4A_	Alignment		15.9	40	PDB header: viral protein Chain: A: PDB Molecule: protein (moloney murine leukemia virus capsid); PDBTitle: momlv capsid protein major homology region peptide analog
21	d1wxaa1	Alignment	not modelled	15.3	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
22	d1hlva2	Alignment	not modelled	14.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
23	c3kc2A_	Alignment	not modelled	14.1	21	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
24	c2k7qA_	Alignment	not modelled	13.6	50	PDB header: structural protein Chain: A: PDB Molecule: filamin-a; PDBTitle: filamin a ig-like domains 18-19
25	c3fdgA_	Alignment	not modelled	13.3	14	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidase ac. metallo peptidase. merops family m19; PDBTitle: the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19
26	d2ev0a2	Alignment	not modelled	13.2	20	Fold: Iron-dependent repressor protein, dimerization domain Superfamily: Iron-dependent repressor protein, dimerization domain Family: Iron-dependent repressor protein, dimerization domain
27	d2isya2	Alignment	not modelled	12.7	19	Fold: Iron-dependent repressor protein, dimerization domain Superfamily: Iron-dependent repressor protein, dimerization domain Family: Iron-dependent repressor protein, dimerization domain
28	d1uura2	Alignment	not modelled	12.5	50	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: STAT DNA-binding domain

29	c2hjmB	 Alignment	not modelled	12.5	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein pf1176; PDBTitle: crystal structure of a singleton protein pf1176 from p. furiosus
30	d1ltua	 Alignment	not modelled	12.3	0	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Renal dipeptidase
31	d2c5lc1	 Alignment	not modelled	11.4	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
32	c3itcA	 Alignment	not modelled	11.3	3	PDB header: hydrolase Chain: A: PDB Molecule: renal dipeptidase; PDBTitle: crystal structure of sco3058 with bound citrate and glycerol
33	c3ec8A	 Alignment	not modelled	11.1	17	PDB header: cell adhesion Chain: A: PDB Molecule: putative uncharacterized protein flj10324; PDBTitle: the crystal structure of the ra domain of flj10324 (radil)
34	c3jszA	 Alignment	not modelled	10.9	33	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: legionella pneumophila glucosyltransferase Igt1 n293a with udp-glc
35	d1mp1a	 Alignment	not modelled	10.9	12	Fold: PWI domain Superfamily: PWI domain Family: PWI domain
36	c1fe6D	 Alignment	not modelled	10.6	50	PDB header: protein binding Chain: D: PDB Molecule: tetrabrachion; PDBTitle: crystal structure of a naturally occurring parallel right-2 handed coiled-coil tetramer
37	c2x48B	 Alignment	not modelled	10.6	22	PDB header: viral protein Chain: B: PDB Molecule: cag38821; PDBTitle: orf 55 from sulfolobus islandicus rudivirus 1
38	c2jpfA	 Alignment	not modelled	9.9	18	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical protein; PDBTitle: bpp3783_115-220
39	d2pq7a1	 Alignment	not modelled	9.7	13	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
40	d2dmca1	 Alignment	not modelled	9.4	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
41	c1ksrA	 Alignment	not modelled	9.2	31	PDB header: actin binding protein Chain: A: PDB Molecule: gelation factor; PDBTitle: the repeating segments of the f-actin cross-linking2 gelation factor (abp-120) have an immunoglobulin fold, nmr, 3 20 structures
42	d1pzxa	 Alignment	not modelled	9.0	10	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DegV-like
43	c3lu2B	 Alignment	not modelled	8.9	11	PDB header: hydrolase Chain: B: PDB Molecule: lmo2462 protein; PDBTitle: structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
44	d3dtoa1	 Alignment	not modelled	8.4	11	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
45	d1ho8a	 Alignment	not modelled	8.2	11	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Regulatory subunit H of the V-type ATPase
46	c1mv4B	 Alignment	not modelled	8.1	55	PDB header: de novo protein Chain: B: PDB Molecule: tropomyosin 1 alpha chain; PDBTitle: tm9a251-284: a peptide model of the c-terminus of a rat2 striated alpha tropomyosin
47	d2hh8a1	 Alignment	not modelled	8.0	28	Fold: YdfO-like Superfamily: YdfO-like Family: YdfO-like
48	c1icfB	 Alignment	not modelled	7.8	30	PDB header: hydrolase Chain: B: PDB Molecule: protein (cathepsin I: light chain); PDBTitle: crystal structure of mhc class ii associated p41 ii fragment in2 complex with cathepsin I
49	c3b40A	 Alignment	not modelled	7.7	10	PDB header: hydrolase Chain: A: PDB Molecule: probable dipeptidase; PDBTitle: crystal structure of the probable dipeptidase pvdm from2 pseudomonas aeruginosa
50	d2di9a1	 Alignment	not modelled	7.5	40	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
51	c1v0dA	 Alignment	not modelled	7.1	31	PDB header: hydrolase Chain: A: PDB Molecule: dna fragmentation factor 40 kda subunit; PDBTitle: crystal structure of caspase-activated dnase (cad)
52	d1v0da	 Alignment	not modelled	7.1	31	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: Caspase-activated DNase, CAD (DffB, DFF40)
53	d1nj1a2	 Alignment	not modelled	7.0	27	Fold: IF3-like Superfamily: C-terminal domain of ProRS Family: C-terminal domain of ProRS
54	c2e9jA	 Alignment	not modelled	6.8	23	PDB header: structural protein Chain: A: PDB Molecule: filamin-b; PDBTitle: solution structure of the 14th filamin domain from human2 filamin-b
55	c2v9pH	 Alignment	not modelled	6.7	15	PDB header: hydrolase Chain: H: PDB Molecule: replication protein e1; PDBTitle: crystal structure of papillomavirus e1 hexameric

						helicase2 dna-free form
56	c2dchX	Alignment	not modelled	6.7	36	PDB header: hydrolase Chain: X: PDB Molecule: putative homing endonuclease; PDBTitle: crystal structure of archaeal intron-encoded homing endonuclease i-2 tsp061i
57	d1dpua	Alignment	not modelled	6.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of RPA32
58	c1dpuA	Alignment	not modelled	6.6	13	PDB header: dna binding protein Chain: A: PDB Molecule: replication protein a (rpa32) c-terminal domain; PDBTitle: solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
59	c2qupA	Alignment	not modelled	6.6	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh1478 protein; PDBTitle: crystal structure of uncharacterized protein bh1478 from bacillus2 halodurans
60	c2j3sB	Alignment	not modelled	6.6	36	PDB header: structural protein Chain: B: PDB Molecule: filamin-a; PDBTitle: crystal structure of the human filamin a ig domains 19 to2 21
61	c1dzlA	Alignment	not modelled	6.5	15	PDB header: virus Chain: A: PDB Molecule: late major capsid protein l1; PDBTitle: l1 protein of human papillomavirus 16
62	d1dzla	Alignment	not modelled	6.5	15	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group I dsDNA viruses Family: Papovaviridae-like VP
63	c3n92A	Alignment	not modelled	6.5	22	PDB header: transferase Chain: A: PDB Molecule: alpha-amylase, gh57 family; PDBTitle: crystal structure of tk1436, a gh57 branching enzyme from2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose
64	c2egrA	Alignment	not modelled	6.2	8	PDB header: transcription Chain: A: PDB Molecule: nuclear receptor corepressor 1; PDBTitle: solution structure of the first sant domain from human2 nuclear receptor corepressor 1
65	d1jb0d	Alignment	not modelled	6.2	31	Fold: Photosystem I subunit Psd Superfamily: Photosystem I subunit Psd Family: Photosystem I subunit Psd
66	c2eayB	Alignment	not modelled	6.1	22	PDB header: ligase Chain: B: PDB Molecule: biotin [acetyl-coa-carboxylase] ligase; PDBTitle: crystal structure of biotin protein ligase from aquifex2 aeolicus
67	c2htuA	Alignment	not modelled	6.1	35	PDB header: hydrolase Chain: A: PDB Molecule: neuraminidase; PDBTitle: n8 neuraminiase in complex with peramivir
68	d1cuka1	Alignment	not modelled	6.1	7	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
69	d2hq7a1	Alignment	not modelled	5.8	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
70	c3h87D	Alignment	not modelled	5.7	23	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
71	c2gxaA	Alignment	not modelled	5.7	15	PDB header: replication/dna Chain: A: PDB Molecule: replication protein e1; PDBTitle: crystal structure of papillomavirus e1 hexameric helicase2 with ssdna and mgadp
72	c3salB	Alignment	not modelled	5.6	29	PDB header: hydrolase Chain: B: PDB Molecule: neuraminidase; PDBTitle: crystal structure of influenza a virus neuraminidase n5
73	c2bkxB	Alignment	not modelled	5.5	29	PDB header: hydrolase Chain: B: PDB Molecule: glucosamine-6-phosphate deaminase; PDBTitle: structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily
74	d2cpwa1	Alignment	not modelled	5.4	29	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
75	d1hc7a3	Alignment	not modelled	5.4	50	Fold: IF3-like Superfamily: C-terminal domain of ProRS Family: C-terminal domain of ProRS
76	c3r3hA	Alignment	not modelled	5.3	31	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase, sam-dependent; PDBTitle: crystal structure of o-methyltransferase from legionella pneumophila
77	c2vgqA	Alignment	not modelled	5.3	20	PDB header: immune system/transport Chain: A: PDB Molecule: maltose-binding periplasmic protein, PDBTitle: crystal structure of human ips-1 card
78	d1f5ta2	Alignment	not modelled	5.2	11	Fold: Iron-dependent repressor protein, dimerization domain Superfamily: Iron-dependent repressor protein, dimerization domain Family: Iron-dependent repressor protein, dimerization domain
79	c1lnsA	Alignment	not modelled	5.1	13	PDB header: hydrolase Chain: A: PDB Molecule: x-prolyl dipeptidyl aminopeptidase; PDBTitle: crystal structure analysis of the x-prolyl dipeptidyl2 aminopeptidase from lactococcus lactis
80	d1zpsa1	Alignment	not modelled	5.1	21	Fold: Hisl-like Superfamily: Hisl-like Family: Hisl-like
81	c1z23A	Alignment	not modelled	5.1	14	PDB header: cell adhesion Chain: A: PDB Molecule: crk-associated substrate; PDBTitle: the serine-rich domain from crk-associated substrate2

						(p130cas)
82	d2vl8a1	 Alignment	not modelled	5.1	100	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleoti de-diphospho-sugar transferases Family: Glycosylating toxin catalytic domain-like
83	d2a9ua1	Alignment	not modelled	5.0	19	Fold: alpha-alpha superhelix Superfamily: USP8 N-terminal domain-like Family: USP8 N-terminal domain-like