

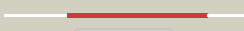
















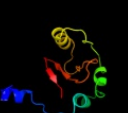


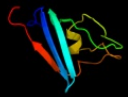


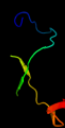



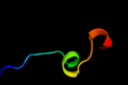



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2evra2	 Alignment		98.6	22	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NlpC/P60
2	c2xivA_	 Alignment		98.6	24	PDB header: structural protein Chain: A: PDB Molecule: hypothetical invasion protein; PDBTitle: structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
3	c3gt2A_	 Alignment		98.5	19	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
4	c3pbiA_	 Alignment		98.3	25	PDB header: hydrolase Chain: A: PDB Molecule: invasion protein; PDBTitle: structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
5	c2fg0B_	 Alignment		98.3	24	PDB header: hydrolase Chain: B: PDB Molecule: cog0791: cell wall-associated hydrolases (invasion- PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
6	c2k1gA_	 Alignment		98.3	15	PDB header: lipoprotein Chain: A: PDB Molecule: lipoprotein spr; PDBTitle: solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
7	c3i86A_	 Alignment		98.1	31	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
8	c3npfB_	 Alignment		97.8	18	PDB header: hydrolase Chain: B: PDB Molecule: putative dipeptidyl-peptidase vi; PDBTitle: crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
9	c3h41A_	 Alignment		96.4	26	PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60 family protein; PDBTitle: crystal structure of a nlp/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
10	c3m1uB_	 Alignment		95.6	14	PDB header: hydrolase Chain: B: PDB Molecule: putative gamma-d-glutamyl-l-diamino acid endopeptidase; PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dvu_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
11	c2kytA_	 Alignment		94.8	20	PDB header: hydrolase Chain: A: PDB Molecule: group xvi phospholipase a2; PDBTitle: solution struture of the h-rev107 n-terminal domain

12	c3kw0D_	Alignment		92.1	22	PDB header: hydrolase Chain: D: PDB Molecule: cysteine peptidase; PDBTitle: crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
13	d2if6a1	Alignment		87.9	28	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Yiix-like
14	c2p1gA_	Alignment		82.4	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative xylanase; PDBTitle: crystal structure of a putative xylanase from bacteroides fragilis
15	d2isba1	Alignment		58.4	34	Fold: The "swivelling" beta/beta/alpha domain Superfamily: FumA C-terminal domain-like Family: FumA C-terminal domain-like
16	c3kopB_	Alignment		46.0	34	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
17	dlzcea1	Alignment		34.0	21	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
18	d1t61c1	Alignment		33.3	29	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Noncollagenous (NC1) domain of collagen IV
19	d2iw0a1	Alignment		29.4	26	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
20	d1t61a1	Alignment		29.1	21	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Noncollagenous (NC1) domain of collagen IV
21	d1o9ya_	Alignment	not modelled	26.0	12	Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA)
22	c2kncB_	Alignment	not modelled	24.8	24	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIb-beta3 transmembrane-cytoplasmic2 heterocomplex
23	d1ofla_	Alignment	not modelled	24.4	15	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Chondroitinase B
24	d1swxa_	Alignment	not modelled	23.4	13	Fold: Glycolipid transfer protein, GLTP Superfamily: Glycolipid transfer protein, GLTP Family: Glycolipid transfer protein, GLTP
25	c2iw0A_	Alignment	not modelled	22.7	26	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
26	d1li1c1	Alignment	not modelled	22.5	21	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Noncollagenous (NC1) domain of collagen IV
27	c2wbqA_	Alignment	not modelled	22.0	40	PDB header: oxidoreductase Chain: A: PDB Molecule: l-arginine beta-hydroxylase; PDBTitle: crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
28	d2ixma1	Alignment	not modelled	21.5	25	Fold: PTPA-like Superfamily: PTPA-like Family: PTPA-like
						Fold: Rhabdovirus nucleoprotein-like

29	d2gica1	Alignment	not modelled	20.1	38	Superfamily: Rhabdovirus nucleoprotein-like Family: Rhabdovirus nucleocapsid protein
30	d1c0aa2	Alignment	not modelled	19.7	57	Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
31	c3emrA	Alignment	not modelled	19.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ectd; PDBTitle: crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
32	c2g62A	Alignment	not modelled	18.9	25	PDB header: hydrolase activator Chain: A: PDB Molecule: protein phosphatase 2a, regulatory subunit b' (pr 53); PDBTitle: crystal structure of human ptpa
33	d1o6aa	Alignment	not modelled	18.8	12	Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA)
34	d1ds1a	Alignment	not modelled	17.7	33	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Clavamate synthase
35	c3gipB	Alignment	not modelled	16.3	21	PDB header: hydrolase Chain: B: PDB Molecule: n-acyl-d-glutamate deacylase; PDBTitle: crystal structure of n-acyl-d-glutamate deacylase from2 bordetella bronchiseptica complexed with zinc, acetate and3 formate ions.
36	c1dbgA	Alignment	not modelled	15.4	15	PDB header: lyase Chain: A: PDB Molecule: chondroitinase b; PDBTitle: crystal structure of chondroitinase b
37	d2ar1a1	Alignment	not modelled	15.2	13	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
38	d1l0wa2	Alignment	not modelled	15.2	36	Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
39	c1dfwA	Alignment	not modelled	15.1	100	PDB header: immune system Chain: A: PDB Molecule: lung surfactant protein b; PDBTitle: conformational mapping of the n-terminal segment of2 surfactant protein b in lipid using 13c-enhanced fourier3 transform infrared spectroscopy (ftir)
40	d1hq0a	Alignment	not modelled	14.8	19	Fold: CNF1/YfiH-like putative cysteine hydrolases Superfamily: CNF1/YfiH-like putative cysteine hydrolases Family: Type 1 cytotoxic necrotizing factor, catalytic domain
41	d2gta1	Alignment	not modelled	14.6	56	Fold: Rhabdovirus nucleoprotein-like Superfamily: Rhabdovirus nucleoprotein-like Family: Rhabdovirus nucleocapsid protein
42	d1vk3a3	Alignment	not modelled	14.3	30	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
43	c2ysxA	Alignment	not modelled	13.5	9	PDB header: signaling protein Chain: A: PDB Molecule: signaling inositol polyphosphate phosphatase PDBTitle: solution structure of the human ship sh2 domain
44	d1leha2	Alignment	not modelled	13.4	25	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
45	d2adza1	Alignment	not modelled	13.3	20	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
46	c2fvmA	Alignment	not modelled	13.2	14	PDB header: hydrolase Chain: A: PDB Molecule: dihydropyrimidinase; PDBTitle: crystal structure of dihydropyrimidinase from saccharomyces kluyveri2 in complex with the reaction product n-carbamyl-beta-alanine
47	c1rjqA	Alignment	not modelled	13.0	21	PDB header: hydrolase Chain: A: PDB Molecule: d-aminoacylase; PDBTitle: the crystal structure of the d-aminoacylase mutant d366a
48	c2rdsA	Alignment	not modelled	13.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- PDBTitle: crystal structure of pth with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
49	c3nnlB	Alignment	not modelled	13.0	40	PDB header: biosynthetic protein Chain: B: PDB Molecule: cura; PDBTitle: halogenase domain from cura module (crystal form iii)
50	c2og5A	Alignment	not modelled	13.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of asparagine oxygenase (asno)
51	d2ixna1	Alignment	not modelled	12.9	16	Fold: PTPA-like Superfamily: PTPA-like Family: PTPA-like
52	d1hcza1	Alignment	not modelled	12.4	64	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
53	d1pvda1	Alignment	not modelled	12.4	30	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
54	c1t60W	Alignment	not modelled	12.3	25	PDB header: structural protein Chain: W: PDB Molecule: type iv collagen; PDBTitle: crystal structure of type iv collagen nc1 domain from2 bovine lens capsule
						Fold: PurM C-terminal domain-like

55	d2z1ea2	Alignment	not modelled	12.2	38	Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
56	c3lv4B_	Alignment	not modelled	12.0	26	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase yxia; PDBTitle: crystal structure of the glycoside hydrolase, family 43 yxia2 protein from bacillus licheniformis. northeast structural3 genomics consortium target bir14.
57	dljz8a3	Alignment	not modelled	11.9	27	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
58	c3mt1B_	Alignment	not modelled	11.8	14	PDB header: lyase Chain: B: PDB Molecule: putative carboxynorspermidine decarboxylase protein; PDBTitle: crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
59	d2a1xa1	Alignment	not modelled	11.8	36	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: PhyH-like
60	c1t60R_	Alignment	not modelled	11.4	25	PDB header: structural protein Chain: R: PDB Molecule: type iv collagen; PDBTitle: crystal structure of type iv collagen nc1 domain from2 bovine lens capsule
61	d1fi4a2	Alignment	not modelled	11.2	15	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate 5-di-phosphate decarboxylase
62	c1lehB_	Alignment	not modelled	11.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: leucine dehydrogenase; PDBTitle: leucine dehydrogenase from bacillus sphaericus
63	d1iufa1	Alignment	not modelled	10.9	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
64	d1zpdal	Alignment	not modelled	10.6	30	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
65	c1fi4A_	Alignment	not modelled	10.5	15	PDB header: lyase Chain: A: PDB Molecule: mevalonate 5-di-phosphate decarboxylase; PDBTitle: the x-ray crystal structure of mevalonate 5-di-phosphate decarboxylase2 at 2.3 angstrom resolution.
66	d1ovma1	Alignment	not modelled	10.5	30	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
67	d2zoda2	Alignment	not modelled	10.3	25	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
68	d2qbsa1	Alignment	not modelled	10.2	12	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
69	d1clda2	Alignment	not modelled	9.8	29	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
70	c2kafA_	Alignment	not modelled	9.8	28	PDB header: viral protein, rna binding protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: solution structure of the sars-unique domain-c from the2 nonstructural protein 3 (nsp3) of the severe acute3 respiratory syndrome coronavirus
71	d1o5ua_	Alignment	not modelled	9.8	33	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
72	c2opwA_	Alignment	not modelled	9.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: phyhd1 protein; PDBTitle: crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
73	d2j0pa1	Alignment	not modelled	9.5	38	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: HemS/ChuS-like
74	d2coha2	Alignment	not modelled	9.2	12	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
75	c3hqjA_	Alignment	not modelled	9.2	40	PDB header: transferase Chain: A: PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: structure-function analysis of mycobacterium tuberculosis2 acyl carrier protein synthase (acps).
76	d1gxha_	Alignment	not modelled	9.1	36	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
77	d1k3xa2	Alignment	not modelled	8.9	18	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
78	c2y9xG_	Alignment	not modelled	8.9	44	PDB header: oxidoreductase Chain: G: PDB Molecule: lectin-like fold protein; PDBTitle: crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone
79	c3k2za_	Alignment	not modelled	8.8	14	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
80	d2es7a1	Alignment	not modelled	8.7	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: HyaE-like

81	c3f0nB_	Alignment	not modelled	8.7	20	PDB header: lyase Chain: B: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: mus musculus mevalonate pyrophosphate decarboxylase
82	c2uz8A_	Alignment	not modelled	8.6	18	PDB header: rna-binding protein Chain: A: PDB Molecule: eukaryotic translation elongation factor 1 PDBTitle: the crystal structure of p18, human translation elongation2 factor 1 epsilon 1
83	c3mazA_	Alignment	not modelled	8.5	14	PDB header: signaling protein Chain: A: PDB Molecule: signal-transducing adaptor protein 1; PDBTitle: crystal structure of the human brdg1/stap-1 sh2 domain in complex with2 the ntl ptyr136 peptide
84	d2io8a2	Alignment	not modelled	8.2	19	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: CHAP domain
85	c1zzpA_	Alignment	not modelled	8.2	18	PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase abl1; PDBTitle: solution structure of the f-actin binding domain of bcr-2 abl/c-abl
86	d1avia_	Alignment	not modelled	8.1	27	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
87	c2hnfA_	Alignment	not modelled	8.1	24	PDB header: viral protein Chain: A: PDB Molecule: repressor protein ci101-229dm-k192a; PDBTitle: structure of a hyper-cleavable monomeric fragment of phage2 lambda repressor containing the cleavage site region
88	d2ixoa1	Alignment	not modelled	8.0	6	Fold: PTPA-like Superfamily: PTPA-like Family: PTPA-like
89	d2vlqa1	Alignment	not modelled	7.6	36	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
90	c2no8A_	Alignment	not modelled	7.6	36	PDB header: immune system Chain: A: PDB Molecule: colicin-e2 immunity protein; PDBTitle: nmr structure analysis of the colicin immunity protein im2
91	c2jx0A_	Alignment	not modelled	7.5	24	PDB header: cell adhesion, signaling protein Chain: A: PDB Molecule: arf gtpase-activating protein git1; PDBTitle: the paxillin-binding domain (pbd) of g protein coupled2 receptor (gpcr)-kinase (grk) interacting protein 1 (git1)
92	d1c3ga1	Alignment	not modelled	7.5	13	Fold: HSP40/DnaJ peptide-binding domain Superfamily: HSP40/DnaJ peptide-binding domain Family: HSP40/DnaJ peptide-binding domain
93	d2pyta1	Alignment	not modelled	7.5	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: EutQ-like
94	d3c9ua2	Alignment	not modelled	7.4	50	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
95	c3qrxB_	Alignment	not modelled	7.3	67	PDB header: metal binding protein/toxin Chain: B: PDB Molecule: melittin; PDBTitle: chlamydomonas reinhardtii centrin bound to melittin
96	d1uv4a1	Alignment	not modelled	7.3	23	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: alpha-L-arabinanase-like
97	d2c9wa2	Alignment	not modelled	7.1	11	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
98	d1jr7a_	Alignment	not modelled	7.1	13	Fold: Double-stranded beta-helix Superfamily: Clavaminic synthase-like Family: Gab protein (hypothetical protein YgaT)
99	c2jemB_	Alignment	not modelled	7.0	26	PDB header: hydrolase Chain: B: PDB Molecule: endo-beta-1,4-glucanase; PDBTitle: native family 12 xyloglucanase from bacillus licheniformis