


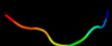

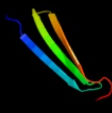





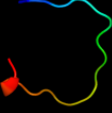



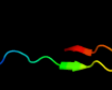

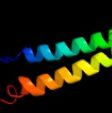






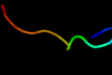

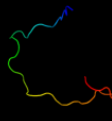

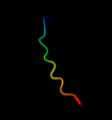

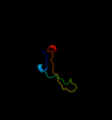


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hrva_	 Alignment		47.0	75	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
2	c1z8rA_	 Alignment		43.3	75	PDB header: hydrolase Chain: A: PDB Molecule: coxsackievirus b4 polyprotein; PDBTitle: 2a cysteine proteinase from human coxsackievirus b4 (strain2 jvb / benschooten / new york / 51)
3	d1bupa2	 Alignment		34.2	31	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
4	d1jcea2	 Alignment		23.3	28	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
5	c2he4A_	 Alignment		23.3	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: the crystal structure of the second pdz domain of human2 nherf-2 (slc9a3r2) interacting with a mode 1 pdz binding3 motif
6	c3dgsA_	 Alignment		21.5	32	PDB header: viral protein Chain: A: PDB Molecule: coat protein a; PDBTitle: changing the determinants of protein stability from2 covalent to non-covalent interactions by in-vitro3 evolution: a structural and energetic analysis
7	c3nvbA_	 Alignment		21.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
8	d2hf3a1	 Alignment		16.8	33	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
9	d1bxa_	 Alignment		16.1	22	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
10	c2v90E_	 Alignment		15.6	15	PDB header: protein-binding Chain: E: PDB Molecule: pdz domain-containing protein 3; PDBTitle: crystal structure of the 3rd pdz domain of intestine- and2 kidney-enriched pdz domain ikepp (pdzd3)
11	d1ysga1	 Alignment		14.6	22	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death

12	d1be9a_	Alignment		14.3	18	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
13	d2c4ka1	Alignment		14.3	11	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
14	c2jr3A_	Alignment		13.6	55	PDB header: antimicrobial protein Chain: A: PDB Molecule: pelovaterin; PDBTitle: antibacterial peptide from eggshell matrix: structure and2 self-assembly of beta-defensin like peptide from the3 chinese soft-shelled turtle eggshell
15	d1t95a3	Alignment		13.6	21	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: Hypothetical protein AF0491, C-terminal domain
16	d2naca2	Alignment		13.3	19	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
17	d1p9qc3	Alignment		12.9	21	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: Hypothetical protein AF0491, C-terminal domain
18	d2e8aa2	Alignment		12.9	36	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
19	c2vyaB_	Alignment		12.8	35	PDB header: hydrolase Chain: B: PDB Molecule: fatty-acid amide hydrolase 1; PDBTitle: crystal structure of fatty acid amide hydrolase conjugated2 with the drug-like inhibitor pf-750
20	c1g0dA_	Alignment		12.2	39	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: crystal structure of red sea bream transglutaminase
21	d1q59a_	Alignment	not modelled	11.4	20	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
22	d1dkua1	Alignment	not modelled	11.3	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
23	d1x6ma_	Alignment	not modelled	11.1	44	Fold: Mss4-like Superfamily: Mss4-like Family: Glutathione-dependent formaldehyde-activating enzyme, Gfa
24	c2d90A_	Alignment	not modelled	10.9	22	PDB header: protein binding Chain: A: PDB Molecule: pdz domain containing protein 1; PDBTitle: solution structure of the third pdz domain of pdz domain2 containing protein 1
25	c1dkrB_	Alignment	not modelled	10.8	13	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
26	d1pbya2	Alignment	not modelled	10.5	29	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
27	c1l9mB_	Alignment	not modelled	10.5	32	PDB header: transferase Chain: B: PDB Molecule: protein-glutamine glutamyltransferase e3; PDBTitle: three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation PDB header: transferase

28	c3g9bA	Alignment	not modelled	10.5	11	Chain: A: PDB Molecule: dolichyl-diphosphooligosaccharide-protein PDBTitle: crystal structure of reduced ost6l
29	c3pk1A	Alignment	not modelled	10.5	11	PDB header: apoptosis/apoptosis regulator Chain: A: PDB Molecule: induced myeloid leukemia cell differentiation protein mcl- PDBTitle: crystal structure of mcl-1 in complex with the baxbh3 domain
30	d3eeqa2	Alignment	not modelled	10.1	11	Fold: CbiG N-terminal domain-like Superfamily: CbiG N-terminal domain-like Family: CbiG N-terminal domain-like
31	d1g5ma	Alignment	not modelled	9.9	20	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
32	d1zy3a1	Alignment	not modelled	9.9	22	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
33	d2ponb1	Alignment	not modelled	9.9	22	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
34	c2k2wA	Alignment	not modelled	9.5	46	PDB header: cell cycle Chain: A: PDB Molecule: recombination and dna repair protein; PDBTitle: second brct domain of nbs1
35	c2dazA	Alignment	not modelled	9.5	12	PDB header: protein binding Chain: A: PDB Molecule: inad-like protein; PDBTitle: solution structure of the 7th pdz domain of inad-like2 protein
36	d1wmaa1	Alignment	not modelled	9.4	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
37	c2yv6A	Alignment	not modelled	9.4	22	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2 homologous antagonist/killer; PDBTitle: crystal structure of human bcl-2 family protein bak
38	d1o0la	Alignment	not modelled	9.1	24	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
39	d1f16a	Alignment	not modelled	9.0	13	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
40	d1q5xa	Alignment	not modelled	9.0	40	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
41	c3qbrA	Alignment	not modelled	8.8	13	PDB header: apoptosis Chain: A: PDB Molecule: sjchgc06286 protein; PDBTitle: bakbh3 in complex with sj
42	d1ln4a	Alignment	not modelled	8.8	29	Fold: IF3-like Superfamily: YhbY-like Family: YhbY-like
43	d1ul1x1	Alignment	not modelled	8.6	11	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
44	d1n7ea	Alignment	not modelled	8.5	14	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
45	c3q87A	Alignment	not modelled	8.3	67	PDB header: transferase activator/transferase Chain: A: PDB Molecule: putative uncharacterized protein ecu08_1170; PDBTitle: structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
46	d1l0wa2	Alignment	not modelled	8.1	15	Fold: DcOH-like Superfamily: GAD domain-like Family: GAD domain
47	d2i7pa2	Alignment	not modelled	8.1	8	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
48	d1k8ka1	Alignment	not modelled	8.0	33	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
49	d1q18a1	Alignment	not modelled	8.0	25	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
50	d1jmx2	Alignment	not modelled	8.0	25	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
51	d1l8wa	Alignment	not modelled	7.7	8	Fold: Variable surface antigen VlsE Superfamily: Variable surface antigen VlsE Family: Variable surface antigen VlsE
52	c1l8wA	Alignment	not modelled	7.7	8	PDB header: immune system Chain: A: PDB Molecule: vlsel1; PDBTitle: crystal structure of lyme disease variable surface antigen2 vlsE of borrelia burgdorferi
53	c2nacA	Alignment	not modelled	7.6	19	PDB header: oxidoreductase(aldehyde(d),nad+(a)) Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: high resolution structures of holo and apo formate dehydrogenase
54	d1roda	Alignment	not modelled	7.6	24	Fold: IL8-like Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines

55	d1mt5a_	Alignment	not modelled	7.4	41	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
56	c2egkC_	Alignment	not modelled	7.4	13	PDB header: protein binding Chain: C: PDB Molecule: general receptor for phosphoinositides 1- PDBTitle: crystal structure of tamalin pdz-intrinsic ligand fusion2 protein
57	d1dkgd2	Alignment	not modelled	7.3	56	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
58	d1c0aa2	Alignment	not modelled	7.3	19	Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
59	c2ph7B_	Alignment	not modelled	7.2	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein af_2093; PDBTitle: crystal structure of af2093 from archaeoglobus fulgidus
60	d1u9ya1	Alignment	not modelled	7.2	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
61	c3hfwA_	Alignment	not modelled	7.1	27	PDB header: hydrolase Chain: A: PDB Molecule: protein adp-ribosylarginine hydrolase; PDBTitle: crystal structure of human adp-ribosylhydrolase 1 (harh1)
62	d1v4va_	Alignment	not modelled	7.1	21	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
63	d1vp1a1	Alignment	not modelled	6.8	75	Fold: Lipocalins Superfamily: Lipocalins Family: Dinoflagellate luciferase repeat
64	c2xa0A_	Alignment	not modelled	6.8	19	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis regulator bcl-2; PDBTitle: crystal structure of bcl-2 in complex with a bax bh32 peptide
65	c2nrhA_	Alignment	not modelled	6.5	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: transcriptional activator, putative, baf family; PDBTitle: crystal structure of conserved putative baf family2 transcriptional activator from campylobacter jejuni
66	c2jkbB_	Alignment	not modelled	6.5	17	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 - monophosphate) (orthorhombic crystal form)
67	c3eeqB_	Alignment	not modelled	6.3	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cobalamin biosynthesis protein g PDBTitle: crystal structure of a putative cobalamin biosynthesis2 protein g homolog from sulfolobus solfataricus
68	c3c8oB_	Alignment	not modelled	6.1	47	PDB header: hydrolase regulator Chain: B: PDB Molecule: regulator of ribonuclease activity a; PDBTitle: the crystal structure of rraa from pao1
69	d1bwva2	Alignment	not modelled	6.0	22	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
70	c2o2fa_	Alignment	not modelled	6.0	20	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis regulator bcl-2; PDBTitle: solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand
71	c3lnoA_	Alignment	not modelled	6.0	33	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of domain of unknown function duf59 from2 bacillus anthracis
72	c1kv3F_	Alignment	not modelled	5.9	50	PDB header: transferase Chain: F: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: human tissue transglutaminase in gdp bound form
73	c2yuyA_	Alignment	not modelled	5.8	14	PDB header: signaling protein Chain: A: PDB Molecule: rho gtpase activating protein 21; PDBTitle: solution structure of pdz domain of rho gtpase activating2 protein 21
74	c3iraA_	Alignment	not modelled	5.5	46	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
75	c2dc0A_	Alignment	not modelled	5.4	34	PDB header: hydrolase Chain: A: PDB Molecule: probable amidase; PDBTitle: crystal structure of amidase
76	d1rxwa1	Alignment	not modelled	5.4	14	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
77	d1j9ba_	Alignment	not modelled	5.4	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: ArsC-like
78	d8ruca2	Alignment	not modelled	5.3	7	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
79	d1ee8a1	Alignment	not modelled	5.3	33	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
80	d1ujva_	Alignment	not modelled	5.3	36	Fold: PDZ domain-like Superfamily: PDZ domain-like

					Family: PDZ domain
81	d1svda2	Alignment	not modelled	5.1	13 Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
82	c2gx5B	Alignment	not modelled	5.1	5 PDB header: transcription Chain: B: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: n-terminal gaf domain of transcriptional pleiotropic repressor cody
83	d1vi4a	Alignment	not modelled	5.1	27 Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
84	d1pq1a	Alignment	not modelled	5.0	20 Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
85	d2jm6b1	Alignment	not modelled	5.0	13 Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
86	d1wjpa2	Alignment	not modelled	5.0	50 Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2