







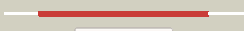















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2i6sA_	 Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
2	c2ok5A_	 Alignment		99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: complement factor b; PDBTitle: human complement factor b
3	c1rs0A_	 Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: complement factor b; PDBTitle: crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)
4	d2ok5a1	 Alignment		99.9	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
5	d1shux_	 Alignment		99.9	14	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
6	c3n2nC_	 Alignment		99.9	16	PDB header: toxin receptor Chain: C: PDB Molecule: anthrax toxin receptor 1; PDBTitle: the crystal structure of tumor endothelial marker 8 (tem8)2 extracellular domain
7	d1u0oc1	 Alignment		99.8	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
8	d1atza_	 Alignment		99.8	15	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
9	d1ijba_	 Alignment		99.8	12	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
10	c2xggB_	 Alignment		99.8	14	PDB header: hydrolase Chain: B: PDB Molecule: microneme protein 2; PDBTitle: structure of toxoplasma gondii micronemal protein 2 a_i2 domain
11	d1n3ya_	 Alignment		99.8	15	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain

12	d1q0pa_	<div><div></div><div>Alignment</div></div>		99.8	14	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
13	c3gxbB_	<div><div></div><div>Alignment</div></div>		99.8	12	PDB header: cell adhesion Chain: B: PDB Molecule: von willebrand factor; PDBTitle: crystal structure of vwf a2 domain
14	d1v7pc_	<div><div></div><div>Alignment</div></div>		99.8	15	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
15	d1ck4a_	<div><div></div><div>Alignment</div></div>		99.8	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
16	c3ibsA_	<div><div></div><div>Alignment</div></div>		99.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein batb; PDBTitle: crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron
17	d1mf7a_	<div><div></div><div>Alignment</div></div>		99.8	17	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
18	d1pt6a_	<div><div></div><div>Alignment</div></div>		99.7	14	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
19	c2b2xB_	<div><div></div><div>Alignment</div></div>		99.7	15	PDB header: immune system Chain: B: PDB Molecule: integrin alpha-1; PDBTitle: via1 rdelta i-domain complexed with a quadruple mutant of the aqc22 fab
20	c2x31F_	<div><div></div><div>Alignment</div></div>		99.7	15	PDB header: ligase Chain: F: PDB Molecule: magnesium-chelataase 60 kda subunit; PDBTitle: modelling of the complex between subunits bchi and bchd of magnesium2 chelataase based on single-particle cryo-em reconstruction at 7.5 ang
21	c2x5nA_	<div><div></div><div>Alignment</div></div>	not modelled	99.7	13	PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: crystal structure of the sprpn10 vwa domain
22	d1mjna_	<div><div></div><div>Alignment</div></div>	not modelled	99.7	14	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
23	c2iueA_	<div><div></div><div>Alignment</div></div>	not modelled	99.6	11	PDB header: membrane protein Chain: A: PDB Molecule: pactolus i-domain; PDBTitle: pactolus i-domain: functional switching of the rossmann2 fold
24	d1jeya2	<div><div></div><div>Alignment</div></div>	not modelled	99.6	12	Fold: vWA-like Superfamily: vWA-like Family: Ku70 subunit N-terminal domain
25	d1jeyb2	<div><div></div><div>Alignment</div></div>	not modelled	99.5	12	Fold: vWA-like Superfamily: vWA-like Family: Ku80 subunit N-terminal domain
26	d1tyeb2	<div><div></div><div>Alignment</div></div>	not modelled	99.4	8	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
27	c3fcuB_	<div><div></div><div>Alignment</div></div>	not modelled	99.2	10	PDB header: cell adhesion/blood clotting Chain: B: PDB Molecule: integrin beta-3; PDBTitle: structure of headpiece of integrin aiiib3 in open conformation
28	d1pd0a3	<div><div></div><div>Alignment</div></div>	not modelled	99.2	10	Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
		<div><div></div><div></div></div>				Fold: vWA-like

29	d1yvra2	Alignment	not modelled	99.1	15	Superfamily: vWA-like Family: RoRNP C-terminal domain-like
30	c3v4pB	Alignment	not modelled	99.1	13	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-7; PDBTitle: crystal structure of a4b7 headpiece complexed with fab act-1
31	c3ragA	Alignment	not modelled	99.1	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
32	c1jevB	Alignment	not modelled	99.1	12	PDB header: dna binding protein/dna Chain: B: PDB Molecule: ku80; PDBTitle: crystal structure of the ku heterodimer bound to dna
33	c1u8cB	Alignment	not modelled	99.0	9	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: a novel adaptation of the integrin psi domain revealed from its2 crystal structure
34	c2nvoA	Alignment	not modelled	98.8	15	PDB header: rna binding protein Chain: A: PDB Molecule: ro sixty-related protein, rsr; PDBTitle: crystal structure of deinococcus radiodurans ro (rsr) protein
35	c3k6sB	Alignment	not modelled	98.5	15	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-2; PDBTitle: structure of integrin alphaxbeta2 ectodomain
36	c1pd0A	Alignment	not modelled	98.0	13	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
37	c1m2vB	Alignment	not modelled	97.7	12	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
38	c3egxB	Alignment	not modelled	97.6	20	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24a; PDBTitle: crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22b and3 bound to the transport signal sequence of the snare protein4 bet1
39	d2qtv3	Alignment	not modelled	97.6	17	Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
40	c1yvrA	Alignment	not modelled	97.4	14	PDB header: rna binding protein Chain: A: PDB Molecule: 60-kda ss-a/ro ribonucleoprotein; PDBTitle: ro autoantigen
41	c1jeqA	Alignment	not modelled	97.4	13	PDB header: dna binding protein Chain: A: PDB Molecule: ku70; PDBTitle: crystal structure of the ku heterodimer
42	c3eg9A	Alignment	not modelled	97.1	13	PDB header: protein transport Chain: A: PDB Molecule: protein transport protein sec23a; PDBTitle: crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
43	c3eh2B	Alignment	not modelled	96.8	16	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24c; PDBTitle: crystal structure of the human copii-coat protein sec24c
44	c1m2oA	Alignment	not modelled	96.6	16	PDB header: protein transport/signaling protein Chain: A: PDB Molecule: protein transport protein sec23; PDBTitle: crystal structure of the sec23-sar1 complex
45	c3eg9B	Alignment	not modelled	95.0	15	PDB header: protein transport Chain: B: PDB Molecule: sec24 related gene family, member d; PDBTitle: crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
46	d1cja2	Alignment	not modelled	37.4	15	Fold: FabD/Lysophospholipase-like Superfamily: FabD/Lysophospholipase-like Family: Lysophospholipase
47	c1sy7B	Alignment	not modelled	23.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase 1; PDBTitle: crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
48	c1j9zB	Alignment	not modelled	20.2	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-cytochrome p450 reductase; PDBTitle: cypor-w677g
49	d1qvwa	Alignment	not modelled	19.7	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/PfpI
50	c1cyjB	Alignment	not modelled	17.6	15	PDB header: hydrolase Chain: B: PDB Molecule: protein (cytosolic phospholipase a2); PDBTitle: human cytosolic phospholipase a2
51	c2bpoA	Alignment	not modelled	14.6	13	PDB header: reductase Chain: A: PDB Molecule: nadh-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
52	c1tIIA	Alignment	not modelled	13.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase, brain; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
53	c3dxvA	Alignment	not modelled	10.8	14	PDB header: isomerase Chain: A: PDB Molecule: alpha-amino-epsilon-caprolactam racemase; PDBTitle: the crystal structure of alpha-amino-epsilon-caprolactam racemase from2 achromobacter obae
54	d2nx2a1	Alignment	not modelled	10.1	11	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: YpsA-like

55	d2vgna3	Alignment	not modelled	9.1	15	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
56	d1r9ja2	Alignment	not modelled	9.0	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
57	c3cneD	Alignment	not modelled	8.7	8	PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
58	c3fseB	Alignment	not modelled	8.4	17	PDB header: hydrolase Chain: B: PDB Molecule: two-domain protein containing dj-1/thij/pfpi-like and PDBTitle: crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
59	d1x6va3	Alignment	not modelled	8.4	7	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5' phosphosulfate kinase (APS kinase)
60	c1p81A	Alignment	not modelled	8.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: catalase hpii; PDBTitle: crystal structure of the d181e variant of catalase hpii2 from e. coli
61	d1tlla2	Alignment	not modelled	8.0	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
62	d1b1ca	Alignment	not modelled	7.5	22	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
63	c3l82B	Alignment	not modelled	6.8	7	PDB header: cell cycle Chain: B: PDB Molecule: f-box only protein 4; PDBTitle: x-ray crystal structure of trf1 and fbx4 complex
64	d1we3a2	Alignment	not modelled	6.7	15	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
65	d1p80a1	Alignment	not modelled	6.7	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
66	d2nlyal	Alignment	not modelled	6.5	13	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: Divergent polysaccharide deacetylase
67	c2o1sC	Alignment	not modelled	6.4	13	PDB header: transferase Chain: C: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 escherichia coli
68	d2c42a3	Alignment	not modelled	6.1	15	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
69	c3kkIA	Alignment	not modelled	5.8	22	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
70	d1bvyl	Alignment	not modelled	5.4	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
71	c1bvyl	Alignment	not modelled	5.4	14	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (cytochrome p450 bm-3); PDBTitle: complex of the heme and fnn-binding domains of the2 cytochrome p450(bm-3)
72	d1nn5a	Alignment	not modelled	5.3	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
73	d1fs0g	Alignment	not modelled	5.3	12	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
74	c3n39D	Alignment	not modelled	5.2	10	PDB header: oxidoreductase Chain: D: PDB Molecule: protein nrdf; PDBTitle: ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdf
75	d1ltza1	Alignment	not modelled	5.2	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module