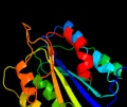


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nvoA_	 Alignment		99.7	14	PDB header: rna binding protein Chain: A; PDB Molecule: ro sixty-related protein, rsr; PDBTitle: crystal structure of deinococcus radiodurans ro (rsr) protein
2	c3ibsA_	 Alignment		99.7	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: conserved hypothetical protein batb; PDBTitle: crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron
3	c2x5nA_	 Alignment		99.6	11	PDB header: nuclear protein Chain: A; PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: crystal structure of the sprpn10 vwa domain
4	c2i6sA_	 Alignment		99.6	18	PDB header: hydrolase Chain: A; PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
5	c1rs0A_	 Alignment		99.6	19	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)
6	c2x31F_	 Alignment		99.6	19	PDB header: ligase Chain: F; PDB Molecule: magnesium-chelatase 60 kda subunit; PDBTitle: modelling of the complex between subunits bchi and bchd of magnesium2 chelatase based on single-particle cryo-em reconstruction at 7.5 ang
7	c2ok5A_	 Alignment		99.6	19	PDB header: hydrolase Chain: A; PDB Molecule: complement factor b; PDBTitle: human complement factor b
8	d1jeyb2	 Alignment		99.5	22	Fold: vWA-like Superfamily: vWA-like Family: Ku80 subunit N-terminal domain
9	d2ok5a1	 Alignment		99.5	19	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
10	d1yvra2	 Alignment		99.5	20	Fold: vWA-like Superfamily: vWA-like Family: RoRNP C-terminal domain-like
11	c1yvra_	 Alignment		99.5	15	PDB header: rna binding protein Chain: A; PDB Molecule: 60-kda ss-a/ro ribonucleoprotein; PDBTitle: ro autoantigen

12	dljeya2	Alignment		99.5	21	Fold: vWA-like Superfamily: vWA-like Family: Ku70 subunit N-terminal domain
13	dlshux	Alignment		99.4	18	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
14	c2b2xB	Alignment		99.3	15	PDB header: immune system Chain: B: PDB Molecule: integrin alpha-1; PDBTitle: vla1 rdeltah i-domain complexed with a quadruple mutant of the aqc22 fab
15	c2iueA	Alignment		99.3	21	PDB header: membrane protein Chain: A: PDB Molecule: pactolus i-domain; PDBTitle: pactolus i-domain: functional switching of the rossmann2 fold
16	c2xggB	Alignment		99.3	19	PDB header: hydrolase Chain: B: PDB Molecule: microneme protein 2; PDBTitle: structure of toxoplasma gondii micronemal protein 2 a_i2 domain
17	dlpd0a3	Alignment		99.3	22	Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
18	c3n2nC	Alignment		99.3	18	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
19	dlu0oc1	Alignment		99.2	15	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
20	dljiba	Alignment		99.2	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
21	dlatza	Alignment	not modelled	99.1	16	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
22	c3gxbB	Alignment	not modelled	99.1	13	PDB header: cell adhesion Chain: B: PDB Molecule: von willebrand factor; PDBTitle: crystal structure of vwf a2 domain
23	cljeyB	Alignment	not modelled	99.1	17	PDB header: dna binding protein/dna Chain: B: PDB Molecule: ku80; PDBTitle: crystal structure of the ku heterodimer bound to dna
24	dlv7pc	Alignment	not modelled	99.1	18	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
25	dln3ya	Alignment	not modelled	99.1	14	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
26	dlck4a	Alignment	not modelled	99.1	17	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
27	dlq0pa	Alignment	not modelled	99.1	21	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
28	dlpt6a	Alignment	not modelled	98.9	16	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
29	dlmf7a	Alignment	not modelled	98.9	13	Fold: vWA-like Superfamily: vWA-like

					Family: Integrin A (or I) domain
30	d1tyeb2	Alignment	not modelled	98.9	21 Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
31	d1mjna	Alignment	not modelled	98.6	19 Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
32	c3fcuB	Alignment	not modelled	98.6	21 PDB header: cell adhesion/blood clotting Chain: B: PDB Molecule: integrin beta-3; PDBTitle: structure of headpiece of integrin aiibb3 in open conformation
33	c3ragA	Alignment	not modelled	98.5	17 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
34	c1u8cB	Alignment	not modelled	98.4	22 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
35	c1jeqA	Alignment	not modelled	98.2	18 PDB header: dna binding protein Chain: A: PDB Molecule: ku70; PDBTitle: crystal structure of the ku heterodimer
36	c1pd0A	Alignment	not modelled	98.0	23 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	c3k6sB	Alignment	not modelled	97.8	19 PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-2; PDBTitle: structure of integrin alphaxbeta2 ectodomain
38	c1m2vB	Alignment	not modelled	97.6	26 PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
39	c3eh2B	Alignment	not modelled	97.6	17 PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24c; PDBTitle: crystal structure of the human copii-coat protein sec24c
40	c3egxB	Alignment	not modelled	97.5	18 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
41	c3eg9A	Alignment	not modelled	97.5	19 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
42	d2qtvA3	Alignment	not modelled	97.4	19 Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
43	c3eg9B	Alignment	not modelled	97.3	16 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
44	c1m2oA	Alignment	not modelled	97.0	18 PDB header: protein transport/signaling protein Chain: A: PDB Molecule: protein transport protein sec23; PDBTitle: crystal structure of the sec23-sar1 complex
45	c3eyaE	Alignment	not modelled	84.0	13 PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase [cytochrome]; PDBTitle: structural basis for membrane binding and catalytic2 activation of the peripheral membrane enzyme pyruvate3 oxidase from escherichia coli
46	d2djia3	Alignment	not modelled	77.6	14 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
47	d1jsca3	Alignment	not modelled	73.7	18 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
48	c1jsca	Alignment	not modelled	67.6	18 PDB header: lyase Chain: A: PDB Molecule: acetohydroxy-acid synthase; PDBTitle: crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
49	d1twda	Alignment	not modelled	64.0	19 Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like
50	d2ji7a3	Alignment	not modelled	63.6	18 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
51	d2piaa2	Alignment	not modelled	61.7	13 Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
52	d1li4a2	Alignment	not modelled	56.9	21 Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
53	d1t9ba3	Alignment	not modelled	54.3	18 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
54	d1dkua2	Alignment	not modelled	54.1	18 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
					Fold: Thiamin diphosphate-binding fold (THDP-binding)

55	dlozha3	Alignment	not modelled	51.7	17	Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
56	c3iwpK	Alignment	not modelled	51.1	16	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein cutc
57	dlybha3	Alignment	not modelled	49.9	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
58	d1wd5a	Alignment	not modelled	46.4	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
59	c2bdqA	Alignment	not modelled	46.2	17	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
60	dly0ba1	Alignment	not modelled	44.7	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
61	c3d64A	Alignment	not modelled	44.3	19	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
62	c3oneA	Alignment	not modelled	42.3	17	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
63	c2yzkC	Alignment	not modelled	40.2	17	PDB header: transferase Chain: C: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
64	d2ez9a3	Alignment	not modelled	39.6	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
65	c2vf7B	Alignment	not modelled	38.6	20	PDB header: dna-binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
66	c2wnsB	Alignment	not modelled	37.1	19	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: human orotate phosphoribosyltransferase (oprtae) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
67	d2aeaa1	Alignment	not modelled	37.1	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
68	c2djiA	Alignment	not modelled	36.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
69	c1d4fD	Alignment	not modelled	36.7	17	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
70	c3m3hA	Alignment	not modelled	34.9	19	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
71	d2r8oa2	Alignment	not modelled	34.2	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
72	c3pihA	Alignment	not modelled	33.7	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
73	c2jlaD	Alignment	not modelled	32.2	12	PDB header: transferase Chain: D: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase - semet3 protein
74	d1l1qa	Alignment	not modelled	31.3	13	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
75	c2pgnA	Alignment	not modelled	31.3	13	PDB header: hydrolase Chain: A: PDB Molecule: cyclohexane-1,2-dione hydrolase (cdh); PDBTitle: the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
76	c2ji6B	Alignment	not modelled	30.4	20	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: x-ray structure of oxalyl-coa decarboxylase in complex with2 3-deaza-thdp and oxalyl-coa
77	c1sy7B	Alignment	not modelled	29.4	14	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.
78	c1upaC	Alignment	not modelled	29.2	13	PDB header: synthase Chain: C: PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
79	c3n58D	Alignment	not modelled	28.9	19	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and

						adenosine, orthorhombic3 form
80	c3gvpB_	Alignment	not modelled	28.6	17	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
81	c1ozhD_	Alignment	not modelled	28.4	17	PDB header: lyase Chain: D: PDB Molecule: acetolactate synthase, catabolic; PDBTitle: the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusual3 intermediate.
82	d1pvda3	Alignment	not modelled	26.7	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
83	c1j9zB_	Alignment	not modelled	26.0	12	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-cytochrome p450 reductase; PDBTitle: cypor-w677g
84	c1t9dB_	Alignment	not modelled	25.9	18	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase, mitochondrial; PDBTitle: crystal structure of yeast acetoxyhydroxyacid synthase in2 complex with a sulfonylurea herbicide, metsulfuron methyl
85	c2hgsA_	Alignment	not modelled	25.4	13	PDB header: amine/carboxylate ligase Chain: A: PDB Molecule: protein (glutathione synthetase); PDBTitle: human glutathione synthetase
86	d1q6za3	Alignment	not modelled	25.2	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
87	c3gbCA_	Alignment	not modelled	24.6	10	PDB header: hydrolase Chain: A: PDB Molecule: pyrazinamidase/nicotinamidase pnca; PDBTitle: determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide
88	c1y1A_	Alignment	not modelled	24.5	14	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetoxyhydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
89	d1chda_	Alignment	not modelled	24.4	8	Fold: Methylesterase CheB, C-terminal domain Superfamily: Methylesterase CheB, C-terminal domain Family: Methylesterase CheB, C-terminal domain
90	d1v8ba2	Alignment	not modelled	23.6	15	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
91	c3efhB_	Alignment	not modelled	23.2	19	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
92	d1itza1	Alignment	not modelled	22.7	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
93	c2panF_	Alignment	not modelled	22.4	15	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
94	c4a2iV_	Alignment	not modelled	22.2	12	PDB header: ribosome/hydrolase Chain: V: PDB Molecule: putative ribosome biogenesis gtpase rsga; PDBTitle: cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
95	c2bpoA_	Alignment	not modelled	21.7	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.
96	c2c4kD_	Alignment	not modelled	21.4	11	PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase- PDBTitle: crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
97	c1cqxB_	Alignment	not modelled	21.3	11	PDB header: lipid binding protein Chain: B: PDB Molecule: flavoheмоprotein; PDBTitle: crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
98	c3sftA_	Alignment	not modelled	21.2	11	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
99	c2x7jA_	Alignment	not modelled	21.2	16	PDB header: transferase Chain: A: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
100	c3cueM_	Alignment	not modelled	21.2	6	PDB header: protein transport Chain: M: PDB Molecule: transport protein particle 23 kda subunit; PDBTitle: crystal structure of a trapp subassembly activating the rab2 ypt1p
101	c2dy0A_	Alignment	not modelled	20.8	20	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli
102	d1gpua1	Alignment	not modelled	20.3	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
103	c1t4IA_	Alignment	not modelled	20.1	14	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.