



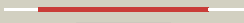



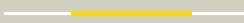





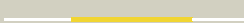







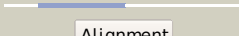
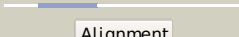

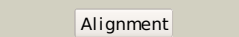
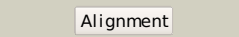
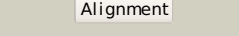


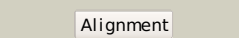





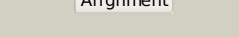
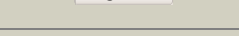










#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b4ub_	 Alignment		100.0	26	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
2	d2pw6a1	 Alignment		100.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
3	c3bd0D_	 Alignment		99.9	14	PDB header: peptide binding protein Chain: D: PDB Molecule: protein memo1; PDBTitle: crystal structure of memo, form ii
4	d1ja1a2	 Alignment		89.0	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
5	d1b1ca_	 Alignment		78.4	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
6	c2gfgC_	 Alignment		77.8	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: upf0204 protein ph0006; PDBTitle: structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
7	c2ixaA_	 Alignment		75.0	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetyl galactosaminidase; PDBTitle: a-zyyme, n-acetyl galactosaminidase
8	c2hnbA_	 Alignment		72.0	13	PDB header: electron transport Chain: A: PDB Molecule: protein mioc; PDBTitle: solution structure of a bacterial holo-flavodoxin
9	d1bvyl_	 Alignment		70.1	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
10	c1bvylF_	 Alignment		70.1	11	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (cytochrome p450 bm-3); PDBTitle: complex of the heme and fmh-binding domains of the2 cytochrome p450(bm-3)
11	c3hr4C_	 Alignment		64.5	16	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex

12	d1auga_	Alignment		64.4	15	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
13	c3a52A_	Alignment		59.0	16	PDB header: hydrolase Chain: A: PDB Molecule: cold-active alkaline phosphatase; PDBTitle: crystal structure of cold-active alkaline phosphatase from <i>Psychrophile shewanella</i> sp.
14	d1tlla2	Alignment		57.2	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
15	d2gfqa1	Alignment		56.2	18	Fold: Phosphorylase/hydrolase-like Superfamily: AF0625-like Family: AF0625-like
16	c1j9zB_	Alignment		55.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g
17	d1yqa1	Alignment		52.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: AF0625-like Family: AF0625-like
18	c1vmeB_	Alignment		51.0	12	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from <i>thermotoga maritima</i> at 2.180 Å resolution
19	d1ykga1	Alignment		51.0	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
20	c3db2C_	Alignment		50.7	12	PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from <i>desulfotobacterium hafniense</i> dcb-2 at 1.70 Å resolution
21	c3giuA_	Alignment	not modelled	48.3	11	PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: 1.25 angstrom crystal structure of pyrrolidone-carboxylate peptidase2 (pcp) from <i>staphylococcus aureus</i>
22	c3e2dB_	Alignment	not modelled	47.1	19	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: the 1.4 Å crystal structure of the large and cold-active2 <i>vibrio</i> sp. alkaline phosphatase
23	c1h6dL_	Alignment	not modelled	46.9	12	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from <i>zymomonas mobilis</i> complexed with glycerol
24	c1ofgF_	Alignment	not modelled	46.9	12	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
25	d1y6va1	Alignment	not modelled	46.2	14	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
26	c3m8yC_	Alignment	not modelled	45.0	21	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from <i>bacillus cereus</i> after glucose-1,6-bisphosphate2 activation
27	d2i09a1	Alignment	not modelled	45.0	26	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
28	d1nqka_	Alignment	not modelled	44.7	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
29	d1iu8a_	Alignment	not modelled	44.2	12	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)

					Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
30	c3q3qA_	Alignment	not modelled	43.4	16 PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: crystal structure of spap: an novel alkaline phosphatase from2 bacterium spingomonas sp. strain bsar-1
31	c2w0yB_	Alignment	not modelled	40.4	16 PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
32	c2iucB_	Alignment	not modelled	39.8	16 PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structure of alkaline phosphatase from the antarctic2 bacterium tab5
33	c2x98A_	Alignment	not modelled	39.5	16 PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
34	c3q2kB_	Alignment	not modelled	39.3	17 PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlbA dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaca
35	c3p9xB_	Alignment	not modelled	37.6	12 PDB header: transferase Chain: B: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
36	c2i09A_	Alignment	not modelled	36.7	24 PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
37	d1a2za_	Alignment	not modelled	36.6	14 Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
38	d1jkxa_	Alignment	not modelled	34.1	16 Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
39	d1q74a_	Alignment	not modelled	33.8	19 Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
40	d1npya1	Alignment	not modelled	33.2	25 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
41	c2jkzB_	Alignment	not modelled	32.7	26 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)
42	c1ew2A_	Alignment	not modelled	31.3	17 PDB header: hydrolase Chain: A: PDB Molecule: phosphatase; PDBTitle: crystal structure of a human phosphatase
43	d1zeda1	Alignment	not modelled	31.3	17 Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
44	c3gfgB_	Alignment	not modelled	31.3	15 PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
45	d1nvt1	Alignment	not modelled	30.8	18 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
46	c2kz3A_	Alignment	not modelled	30.7	23 PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein rad51l3; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
47	c3krsB_	Alignment	not modelled	29.9	18 PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution
48	c3f6sl_	Alignment	not modelled	28.9	11 PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
49	d1lauka_	Alignment	not modelled	28.4	19 Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
50	d8ruca1	Alignment	not modelled	28.3	21 Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
51	c1hl8B_	Alignment	not modelled	28.1	25 PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of thermotoga maritima alpha-fucosidase
52	c1q7tA_	Alignment	not modelled	27.7	19 PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein rv1170; PDBTitle: rv1170 (mshb) from mycobacterium tuberculosis
53	d1fmta2	Alignment	not modelled	27.6	10 Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
54	c3dcjA_	Alignment	not modelled	27.5	21 PDB header: transferase Chain: A: PDB Molecule: probable 5'-phosphoribosylglycinamide (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative

55	c3btuD_	 Alignment	not modelled	27.2	14	PDB header: transcription Chain: D: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
56	d1hl9a2	 Alignment	not modelled	26.7	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Putative alpha-L-fucosidase, catalytic domain
57	c3rfoA_	 Alignment	not modelled	26.7	22	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: crystal structure of methionyl-trna formyltransferase from bacillus2 anthracis
58	c2pjuD_	 Alignment	not modelled	26.6	14	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon2 regulatory protein prpr
59	d2nu7a1	 Alignment	not modelled	26.1	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
60	c3e9mC_	 Alignment	not modelled	26.0	11	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
61	d1iofa_	 Alignment	not modelled	25.8	8	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
62	c3kcgA_	 Alignment	not modelled	25.5	16	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
63	c1oidA_	 Alignment	not modelled	25.4	20	PDB header: hydrolase Chain: A: PDB Molecule: protein usha; PDBTitle: 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
64	c2zktB_	 Alignment	not modelled	25.3	20	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
65	c1npyA_	 Alignment	not modelled	25.1	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical shikimate 5-dehydrogenase-like PDBTitle: structure of shikimate 5-dehydrogenase-like protein hi0607
66	d1p77a1	 Alignment	not modelled	25.0	42	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
67	c2p2sA_	 Alignment	not modelled	24.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
68	d1k7ha_	 Alignment	not modelled	23.5	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
69	d1ryda1	 Alignment	not modelled	23.2	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
70	c3ezyB_	 Alignment	not modelled	23.1	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
71	c3fhIC_	 Alignment	not modelled	23.1	15	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
72	c1fmtA_	 Alignment	not modelled	22.8	10	PDB header: formyltransferase Chain: A: PDB Molecule: methionyl-trna fmet formyltransferase; PDBTitle: methionyl-trnafmet formyltransferase from escherichia coli
73	c3fd8A_	 Alignment	not modelled	22.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
74	c1evjC_	 Alignment	not modelled	22.1	13	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
75	c2w8dB_	 Alignment	not modelled	21.7	10	PDB header: transferase Chain: B: PDB Molecule: processed glycerol phosphate lipoteichoic acid synthase 2; PDBTitle: distinct and essential morphogenic functions for wall-and2 lipo-teichoic acids in bacillus subtilis
76	c3lb5B_	 Alignment	not modelled	21.1	12	PDB header: cell cycle Chain: B: PDB Molecule: hit-like protein involved in cell-cycle regulation; PDBTitle: crystal structure of hit-like protein involved in cell-cycle2 regulation from bartonella henselae with unknown ligand
77	c2ywrA_	 Alignment	not modelled	21.0	21	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of gar transformylase from aquifex2 aeolicus
78	d1o98a2	 Alignment	not modelled	21.0	15	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate

					mutase, catalytic domain
79	c1qapA	Alignment	not modelled	20.6	13 PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
80	d2pjua1	Alignment	not modelled	20.5	14 Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
81	c3kuxA	Alignment	not modelled	20.5	21 PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis
82	c3q0iA	Alignment	not modelled	20.5	14 PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: methionyl-trna formyltransferase from vibrio cholerae
83	d2a8ea1	Alignment	not modelled	20.1	18 Fold: YktB/PF0168-like Superfamily: YktB/PF0168-like Family: YktB-like
84	c3pn9C	Alignment	not modelled	20.1	11 PDB header: hydrolase Chain: C: PDB Molecule: proline dipeptidase; PDBTitle: crystal structure of a proline dipeptidase from streptococcus2 pneumoniae tigr4
85	c2q4eB	Alignment	not modelled	19.9	12 PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase at4g09670; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
86	d1qd1a2	Alignment	not modelled	19.8	18 Fold: Ferredoxin-like Superfamily: Formiminotransferase domain of formiminotransferase-cyclodeaminase. Family: Formiminotransferase domain of formiminotransferase-cyclodeaminase.
87	d1aw1a	Alignment	not modelled	19.7	15 Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
88	c1s3iA	Alignment	not modelled	19.4	13 PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: 10-formyltetrahydrofolate dehydrogenase; PDBTitle: crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
89	c3gzaB	Alignment	not modelled	19.0	14 PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
90	d1f4pa	Alignment	not modelled	18.8	20 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
91	d1vi2a1	Alignment	not modelled	18.5	29 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
92	c2eq5D	Alignment	not modelled	18.0	25 PDB header: isomerase Chain: D: PDB Molecule: 228aa long hypothetical hydantoin racemase; PDBTitle: crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
93	c3tqrA	Alignment	not modelled	17.8	14 PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
94	c3nrbD	Alignment	not modelled	17.7	12 PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
95	c1qd1A	Alignment	not modelled	17.5	16 PDB header: transferase Chain: A: PDB Molecule: formiminotransferase-cyclodeaminase; PDBTitle: the crystal structure of the formiminotransferase domain of2 formiminotransferase-cyclodeaminase.
96	d1o5xa	Alignment	not modelled	17.5	14 Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
97	d1usha2	Alignment	not modelled	17.4	20 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
98	c3gnaA	Alignment	not modelled	17.2	17 PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderia pseudomallei
99	c1zh8B	Alignment	not modelled	17.1	14 PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution