

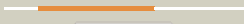





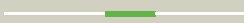



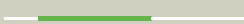




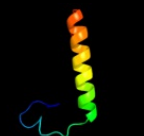

























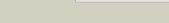
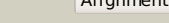



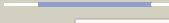
















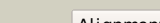










#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ca8B_	 Alignment		100.0	100	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydcf; PDBTitle: crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
2	c2q8nB_	 Alignment		86.7	13	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
3	c3k13A_	 Alignment		58.6	9	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydrofolate-homocysteine methyltransferase; PDBTitle: structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
4	d1i5ea_	 Alignment		56.2	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
5	c3dmpD_	 Alignment		54.5	12	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
6	c1zzgB_	 Alignment		53.8	14	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
7	d1iata_	 Alignment		51.7	17	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
8	c2h9aB_	 Alignment		50.9	9	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron- PDBTitle: corrinoid iron-sulfur protein
9	d2bs2a1	 Alignment		49.8	28	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
10	d1z0sa1	 Alignment		48.4	16	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
11	c1z0zC_	 Alignment		47.3	16	PDB header: transferase Chain: C: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad

12	c3afoB_	 Alignment		44.7	20	PDB header: transferase Chain: B: PDB Molecule: nadh kinase pos5; PDBTitle: crystal structure of yeast nadh kinase complexed with nadh
13	c2ehjA_	 Alignment		40.5	19	PDB header: transferase Chain: A: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of uracil phosphoribosyl transferase
14	d2fug61	 Alignment		38.7	26	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nqo6-like
15	c3fi9B_	 Alignment		38.1	12	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from porphyromonas2 gingivalis
16	d1bd3a_	 Alignment		37.9	10	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
17	d1o5oa_	 Alignment		37.9	11	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
18	d1hm5a_	 Alignment		36.3	15	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
19	d1a3xa3	 Alignment		34.9	9	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
20	c2e55D_	 Alignment		34.3	7	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of aq2163 protein from aquifex aeolicus
21	c3ljka_	 Alignment	not modelled	31.9	11	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: glucose-6-phosphate isomerase from francisella tularensis.
22	d1u0ta_	 Alignment	not modelled	30.9	19	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
23	d1v9sa1	 Alignment	not modelled	30.9	13	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
24	c2wu8A_	 Alignment	not modelled	29.1	16	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
25	d1ozha1	 Alignment	not modelled	28.7	24	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
26	c1w59B_	 Alignment	not modelled	28.5	24	PDB header: cell division Chain: B: PDB Molecule: cell division protein ftsz homolog 1; PDBTitle: ftsz dimer, empty (m. jannaschii)
27	d1t9ka_	 Alignment	not modelled	28.3	17	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
28	d1u0fa_	 Alignment	not modelled	27.9	15	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
29	c3hl5F_	 Alignment	not modelled	25.7	16	PDB header: hydrolase Chain: E: PDB Molecule: queuosine biosynthesis protein quec;

29	c3vrlE_	Alignment	not modelled	23.7	10	PDBTitle: crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
30	d1xtta1	Alignment	not modelled	24.9	8	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
31	d1c7qa_	Alignment	not modelled	24.2	13	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
32	d2nvma1	Alignment	not modelled	21.5	24	Fold: Xisl-like Superfamily: Xisl-like Family: Xisl-like
33	c2kngA_	Alignment	not modelled	20.8	50	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: solution structure of c-domain of lsr2
34	d1saza2	Alignment	not modelled	20.6	25	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
35	c2cunA_	Alignment	not modelled	20.3	14	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii o3
36	d2nlva1	Alignment	not modelled	19.8	24	Fold: Xisl-like Superfamily: Xisl-like Family: Xisl-like
37	c3ibpA_	Alignment	not modelled	19.5	23	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein mukb; PDBTitle: the crystal structure of the dimerization domain of escherichia coli2 structural maintenance of chromosomes protein mukb
38	c2k23A_	Alignment	not modelled	19.3	14	PDB header: transport protein Chain: A: PDB Molecule: lipocalin 2; PDBTitle: solution structure analysis of the rlcn2
39	c2an1D_	Alignment	not modelled	19.1	24	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
40	d2nwva1	Alignment	not modelled	18.7	12	Fold: Xisl-like Superfamily: Xisl-like Family: Xisl-like
41	d1e0ta3	Alignment	not modelled	18.5	11	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
42	c3d7qB_	Alignment	not modelled	18.3	24	PDB header: unknown function Chain: B: PDB Molecule: xisi protein-like; PDBTitle: crystal structure of a xisi-like protein (npun_ar114) from nostoc2 punctiforme pcc 73102 at 2.30 a resolution
43	c3pfnB_	Alignment	not modelled	17.8	21	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
44	d1gzda_	Alignment	not modelled	17.4	12	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
45	c3ujhB_	Alignment	not modelled	16.8	13	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
46	c2r47C_	Alignment	not modelled	16.8	22	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein mth_862; PDBTitle: crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermotrophicus
47	d1zuoa1	Alignment	not modelled	16.6	8	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
48	c1zuoaA_	Alignment	not modelled	16.6	8	PDB header: ligase Chain: A: PDB Molecule: hypothetical protein loc92912; PDBTitle: structure of human ubiquitin-conjugating enzyme (ubci)2 involved in embryo attachment and implantation
49	c2vavA_	Alignment	not modelled	16.3	22	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz pseudomonas aeruginosa gdp
50	d1saza1	Alignment	not modelled	15.4	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
51	c2h9aA_	Alignment	not modelled	14.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoid/iron- PDBTitle: corrinoid iron-sulfur protein
52	c1w5fA_	Alignment	not modelled	14.1	23	PDB header: cell division Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz, t7 mutated, domain swapped (t. maritima)
53	d2c5sa1	Alignment	not modelled	13.9	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
54	c3pr3B_	Alignment	not modelled	13.8	12	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
55	c1yt5A_	Alignment	not modelled	13.6	25	PDB header: transferase Chain: A: PDB Molecule: inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of nad kinase from thermotoga maritima

56	c3hjbA	 Alignment	not modelled	13.6	11	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
57	c3nyeA	 Alignment	not modelled	13.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
58	d1vmia	 Alignment	not modelled	13.5	15	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
59	c1vmiA	 Alignment	not modelled	13.5	15	PDB header: transferase Chain: A: PDB Molecule: putative phosphate acetyltransferase; PDBTitle: crystal structure of putative phosphate acetyltransferase2 (np_416953.1) from escherichia coli k12 at 2.32 a resolution
60	d2ji7a1	 Alignment	not modelled	13.4	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
61	d1rcua	 Alignment	not modelled	12.7	16	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
62	c1rcuB	 Alignment	not modelled	12.7	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein vt76; PDBTitle: x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
63	c3c00B	 Alignment	not modelled	12.6	31	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: escu; PDBTitle: crystal structural of the mutated g247t escu/spas c-terminal domain
64	d1b8ta2	 Alignment	not modelled	12.5	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
65	c2vt1B	 Alignment	not modelled	12.4	21	PDB header: membrane protein Chain: B: PDB Molecule: surface presentation of antigens protein spas; PDBTitle: crystal structure of the cytoplasmic domain of spa40, the2 specificity switch for the shigella flexneri type iii3 secretion system
66	d2e2ca	 Alignment	not modelled	12.3	16	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
67	d1b8ta4	 Alignment	not modelled	12.1	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
68	d1xq9a	 Alignment	not modelled	12.0	10	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
69	c2zf8A	 Alignment	not modelled	11.9	24	PDB header: structural protein Chain: A: PDB Molecule: component of sodium-driven polar flagellar motor; PDBTitle: crystal structure of moty
70	c3rofA	 Alignment	not modelled	11.9	17	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine-phosphatase ptpa; PDBTitle: crystal structure of the s. aureus protein tyrosine phosphatase ptpa
71	c2fr1A	 Alignment	not modelled	11.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: erythromycin synthase, eryai; PDBTitle: the first ketoreductase of the erythromycin synthase2 (crystal form 2)
72	d1j7ja	 Alignment	not modelled	11.6	11	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
73	d1gpma1	 Alignment	not modelled	11.1	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
74	c2cx5B	 Alignment	not modelled	11.0	15	PDB header: translation Chain: B: PDB Molecule: a putative trans-editing enzyme; PDBTitle: crystal structure of a putative trans-editing enzyme for2 prolyl trna synthetase
75	c2y9mA	 Alignment	not modelled	10.7	10	PDB header: ligase/transport protein Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2-21 kda; PDBTitle: pex4p-pex22p structure
76	c2dplA	 Alignment	not modelled	10.7	16	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from pyrococcus horikoshii ot3
77	c2yzkC	 Alignment	not modelled	10.6	26	PDB header: transferase Chain: C: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
78	c2ywtA	 Alignment	not modelled	9.7	14	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
79	c3dezA	 Alignment	not modelled	9.7	13	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
80	d2fiqa1	 Alignment	not modelled	9.6	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like

81	d1qb7a_	Alignment	not modelled	9.6	11	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
82	d1gph11	Alignment	not modelled	9.6	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
83	c2j5tF_	Alignment	not modelled	9.6	14	PDB header: transferase Chain: F: PDB Molecule: glutamate 5-kinase; PDBTitle: glutamate 5-kinase from escherichia coli complexed with2 glutamate
84	d1vg0a1	Alignment	not modelled	9.4	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
85	d2nvuc1	Alignment	not modelled	9.3	13	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
86	d2vapa1	Alignment	not modelled	9.3	24	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
87	c3t7yB_	Alignment	not modelled	9.3	24	PDB header: protein transport Chain: B: PDB Molecule: yop proteins translocation protein u; PDBTitle: structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
88	c3c01H_	Alignment	not modelled	9.3	21	PDB header: membrane protein, protein transport Chain: H: PDB Molecule: surface presentation of antigens protein spas; PDBTitle: crystal structural of native spas c-terminal domain
89	d2djia1	Alignment	not modelled	9.1	30	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
90	d1wyub1	Alignment	not modelled	9.0	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Glycine dehydrogenase subunits (GDC-P)
91	c1vbka_	Alignment	not modelled	9.0	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
92	d1g9sa_	Alignment	not modelled	8.9	11	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
93	c3dm5A_	Alignment	not modelled	8.8	10	PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
94	c2p1zA_	Alignment	not modelled	8.7	18	PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase; PDBTitle: crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
95	d2af4c1	Alignment	not modelled	8.7	17	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
96	c2dhgA_	Alignment	not modelled	8.7	16	PDB header: rna binding protein Chain: A: PDB Molecule: trna selenocysteine associated protein (secp43); PDBTitle: solution structure of the c-terminal rna recognition motif2 in trna selenocysteine associated protein
97	c3t5sA_	Alignment	not modelled	8.5	14	PDB header: immune system Chain: A: PDB Molecule: macrophage migration inhibitory factor; PDBTitle: structure of macrophage migration inhibitory factor from giardia2 lamblia
98	c3bs8A_	Alignment	not modelled	8.5	11	PDB header: isomerase Chain: A: PDB Molecule: glutamate-1-semialdehyde 2,1-aminomutase; PDBTitle: crystal structure of glutamate 1-semialdehyde aminotransferase2 complexed with pyridoxamine-5'-phosphate from bacillus subtilis
99	d1pb1a_	Alignment	not modelled	8.5	13	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases