








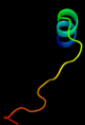

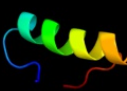
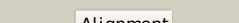




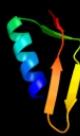




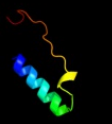


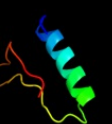
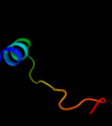

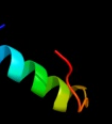
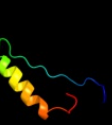



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2jnaa1	 Alignment		100.0	32	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
2	d2noca1	 Alignment		99.9	22	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
3	c3b9nB_	 Alignment		32.1	8	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
4	c2y1bA_	 Alignment		22.5	13	PDB header: membrane protein Chain: A: PDB Molecule: putative outer membrane protein, signal; PDBTitle: crystal structure of the e. coli outer membrane lipoprotein2 rcsf
5	c1hl8B_	 Alignment		20.7	21	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of thermotoga maritima alpha-fucosidase
6	d1luca_	 Alignment		20.3	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
7	c3sdoB_	 Alignment		19.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase; PDBTitle: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
8	c1oy8A_	 Alignment		18.7	10	PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
9	c3qkbB_	 Alignment		16.0	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
10	c3eypB_	 Alignment		15.9	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
11	c3mo4B_	 Alignment		15.3	13	PDB header: hydrolase Chain: B: PDB Molecule: alpha-1,3/4-fucosidase; PDBTitle: the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697

12	d2fiqa1	Alignment		13.0	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like
13	d1lucb_	Alignment		11.1	25	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
14	d1hl9a2	Alignment		10.6	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Putative alpha-L-fucosidase, catalytic domain
15	c1kqfB_	Alignment		9.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
16	c2wvsD_	Alignment		9.6	13	PDB header: hydrolase Chain: D: PDB Molecule: alpha-l-fucosidase; PDBTitle: crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
17	d1xn9a_	Alignment		9.3	14	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: Ribosomal protein S24e
18	c1z69D_	Alignment		9.2	13	PDB header: oxidoreductase Chain: D: PDB Molecule: coenzyme f420-dependent n(5),n(10)- PDBTitle: crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
19	d3etja1	Alignment		8.9	12	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
20	c3k07A_	Alignment		8.1	9	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
21	c1tv1A_	Alignment	not modelled	8.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
22	d1tv1a_	Alignment	not modelled	8.1	15	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
23	c3ir9A_	Alignment	not modelled	7.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: c-terminal domain of peptide chain release factor from2 methanosarcina mazel.
24	c2k38A_	Alignment	not modelled	7.0	25	PDB header: antimicrobial protein Chain: A: PDB Molecule: cupiennin-1a; PDBTitle: cupiennin 1a, nmr, minimized average structure
25	c2jz7A_	Alignment	not modelled	6.4	17	PDB header: selenium-binding protein Chain: A: PDB Molecule: selenium binding protein; PDBTitle: solution nmr structure of selenium-binding protein from2 methanococcus vannielii
26	c1f02T_	Alignment	not modelled	6.3	7	PDB header: cell adhesion Chain: T: PDB Molecule: translocated intimin receptor; PDBTitle: crystal structure of c-terminal 282-residue fragment of2 intimin in complex with translocated intimin receptor3 (tir) intimin-binding domain
27	d1f07a_	Alignment	not modelled	6.3	20	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
28	c3gzaB_	Alignment	not modelled	6.3	17	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

29	d1wu7a1	Alignment	not modelled	6.2	22	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
30	c2i7gA	Alignment	not modelled	6.2	0	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
31	c2k4qA	Alignment	not modelled	6.2	19	PDB header: viral protein Chain: A: PDB Molecule: major tail protein v; PDBTitle: the solution structure of gpv, the major tail protein from2 bacteriophage lambda
32	c3dfeA	Alignment	not modelled	5.8	23	PDB header: signaling protein Chain: A: PDB Molecule: putative pii-like signaling protein; PDBTitle: crystal structure of a putative pii-like signaling protein2 (yp_323533.1) from anabaena variabilis atcc 29413 at 2.35 a3 resolution
33	d1ywx1	Alignment	not modelled	5.8	18	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: Ribosomal protein S24e
34	d1kjq1	Alignment	not modelled	5.4	17	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
35	c2wgkA	Alignment	not modelled	5.3	9	PDB header: oxidoreductase Chain: A: PDB Molecule: 3,6-diketocamphane 1,6 monooxygenase; PDBTitle: type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida
36	d1nqka	Alignment	not modelled	5.2	13	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases