Phyre^2

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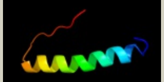
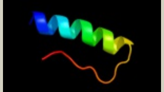
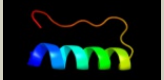
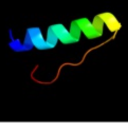
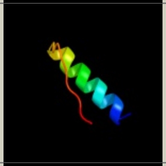
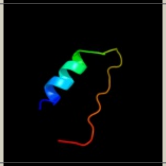
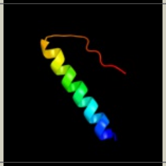
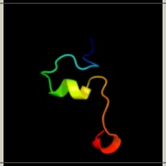
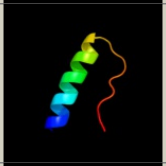
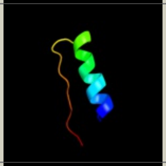
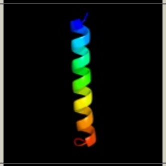
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1iuqa_	Alignment		98.4	14	**Fold:**Glycerol-3-phosphate (1)-acyltransferase **Superfamily:**Glycerol-3-phosphate (1)-acyltransferase **Family:**Glycerol-3-phosphate (1)-acyltransferase
2	c3jurA_	Alignment		38.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exo-poly-alpha-d-galacturonosidase; **PDBTitle:** the crystal structure of a hyperthermoactive exopolygalacturonase from2 thermotoga maritima
3	c2pyhB_	Alignment		23.7	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**poly(beta-d-mannuronate) c5 epimerase 4; **PDBTitle:** azotobacter vinelandii mannuronan c-5 epimerase alge4 a-module2 complexed with mannuronan trisaccharide
4	c3eqnB_	Alignment		23.4	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucan 1,3-beta-glucosidase; **PDBTitle:** crystal structure of beta-1,3-glucanase from phanerochaete2 chrysosporium (lam55a)
5	c3hkxA_	Alignment		21.5	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidase; **PDBTitle:** crystal structure analysis of an amidase from nesterenkonia sp.
6	c2vhiG_	Alignment		13.2	11	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cg3027-pa; **PDBTitle:** crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
7	d1uf5a_	Alignment		11.6	14	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
8	c3n2sD_	Alignment		11.0	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadph-dependent nitro/flavin reductase; **PDBTitle:** structure of nfra1 nitroreductase from b. subtilis
9	d1j31a_	Alignment		11.0	12	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
10	c2w1vA_	Alignment		10.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nitrilase homolog 2; **PDBTitle:** crystal structure of mouse nitrilase-2 at 1.4a resolution
11	d1emsa2	Alignment		9.9	14	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase

12	c3n05B_	Alignment		8.8	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
13	c3ilvA_	Alignment		8.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
14	c2inuC_	Alignment		8.3	7	**PDB header:**lyase **Chain:** C: **PDB Molecule:**insulin fructotransferase; **PDBTitle:** crystal structure of insulin fructotransferase in the absence of2 substrate
15	c2e2kC_	Alignment		8.2	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formamidase; **PDBTitle:** helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
16	d2cvea2	Alignment		7.2	47	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**YigZ C-terminal domain-like
17	c3dlaD_	Alignment		6.6	8	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
18	d1rmga_	Alignment		6.5	8	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
19	c1avoA_	Alignment		6.4	15	**PDB header:**proteasome activator **Chain:** A: **PDB Molecule:**11s regulator; **PDBTitle:** proteasome activator reg(alpha)
20	c1czfB_	Alignment		6.0	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polygalacturonase ii; **PDBTitle:** endo-polygalacturonase ii from aspergillus niger
21	d1czfa_	Alignment	not modelled	6.0	8	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
22	c2plqA_	Alignment	not modelled	6.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aliphatic amidase; **PDBTitle:** crystal structure of the amidase from geobacillus pallidus rapc8
23	d2hthb1	Alignment	not modelled	5.9	25	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**VPS36 N-terminal domain-like
24	c2h3nD_	Alignment	not modelled	5.7	33	**PDB header:**immune system **Chain:** D: **PDB Molecule:**ig lambda-5; **PDBTitle:** crystal structure of a surrogate light chain (lambda5 and2 vpreb) homodimer
25	d2a4aa1	Alignment	not modelled	5.7	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
26	c3hykB_	Alignment	not modelled	5.3	5	**PDB header:**transferase **Chain:** B: **PDB Molecule:**holo-[acyl-carrier-protein] synthase; **PDBTitle:** 2.31 angstrom resolution crystal structure of a holo-(acyl-carrier-2 protein) synthase from bacillus anthracis str. ames in complex with3 coa (3',5'-adp)
27	d1f89a_	Alignment	not modelled	5.2	14	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase
28	c3efdK_	Alignment	not modelled	5.2	10	**PDB header:**immune system **Chain:** K: **PDB Molecule:**kcsa; **PDBTitle:** the crystal structure of the cytoplasmic domain of kcsa