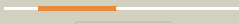
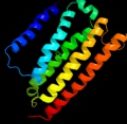
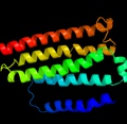
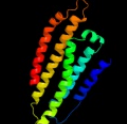
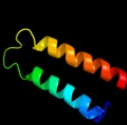
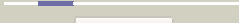
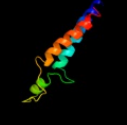


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mk7K_	 Alignment		96.9	14	PDB header: oxidoreductase Chain: K: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit n; PDBTitle: the structure of cbb3 cytochrome oxidase
2	d1ffa_	 Alignment		87.9	15	Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like
3	c1fftF_	 Alignment		87.9	15	PDB header: oxidoreductase Chain: F: PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli
4	c1m56G_	 Alignment		78.0	15	PDB header: oxidoreductase Chain: G: PDB Molecule: cytochrome c oxidase; PDBTitle: structure of cytochrome c oxidase from rhodobactor2 sphaeroides (wild type)
5	d1aria_	 Alignment		73.1	15	Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like
6	d1v54a_	 Alignment		72.7	13	Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like
7	d3dtua1	 Alignment		69.4	15	Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like
8	c3o0rB_	 Alignment		62.7	9	PDB header: immune system/oxidoreductase Chain: B: PDB Molecule: nitric oxide reductase subunit b; PDBTitle: crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
9	d1xmea1	 Alignment		40.0	19	Fold: Cytochrome c oxidase subunit I-like Superfamily: Cytochrome c oxidase subunit I-like Family: Cytochrome c oxidase subunit I-like
10	c3kp9A_	 Alignment		30.9	20	PDB header: blood coagulation, oxidoreductase Chain: A: PDB Molecule: vkorc1/thioredoxin domain protein; PDBTitle: structure of a bacterial homolog of vitamin k epoxide reductase
11	c2bbjB_	 Alignment		16.4	15	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter

12	d2p3ha1	Alignment		14.1	7	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
13	c3fh6F_	Alignment		13.3	8	PDB header: transport protein Chain: F: PDB Molecule: maltose transport system permease protein malf; PDBTitle: crystal structure of the resting state maltose transporter from e.2 coli
14	d2r2za1	Alignment		12.6	29	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
15	d2a65a1	Alignment		12.4	15	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
16	c3mepC_	Alignment		12.2	25	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein eca2234; PDBTitle: crystal structure of eca2234 protein from erwinia2 carotovora, northeast structural genomics consortium target3 ewr44
17	d3deda1	Alignment		10.9	36	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
18	d2o3ga1	Alignment		10.6	29	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
19	c3dedB_	Alignment		9.0	36	PDB header: membrane protein Chain: B: PDB Molecule: probable hemolysin; PDBTitle: c-terminal domain of probable hemolysin from chromobacterium violaceum
20	c3k11A_	Alignment		9.0	10	PDB header: hydrolase Chain: A: PDB Molecule: putative glycosyl hydrolase; PDBTitle: crystal structure of putative glycosyl hydrolase (np_813087.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution
21	c2l9uA_	Alignment	not modelled	7.8	13	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain
22	c2r6gF_	Alignment	not modelled	7.8	9	PDB header: hydrolase/transport protein Chain: F: PDB Molecule: maltose transport system permease protein malf; PDBTitle: the crystal structure of the e. coli maltose transporter
23	d2oaia1	Alignment	not modelled	7.7	36	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
24	c3pijA_	Alignment	not modelled	7.5	26	PDB header: hydrolase Chain: A: PDB Molecule: beta-fructofuranosidase; PDBTitle: beta-fructofuranosidase from bifidobacterium longum - complex with2 fructose
25	d1y4wa2	Alignment	not modelled	7.1	16	Fold: 5-bladed beta-propeller Superfamily: Arabinanase/levansucrase/invertase Family: Glycosyl hydrolases family 32 N-terminal domain
26	d2nqwa1	Alignment	not modelled	7.1	21	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
27	c3ugfB_	Alignment	not modelled	7.0	21	PDB header: transferase Chain: B: PDB Molecule: sucrose:(sucrose/fructan) 6-fructosyltransferase; PDBTitle: crystal structure of a 6-ssf/6-sft from pachysandra terminalis
28	c3lemA_	Alignment	not modelled	6.9	19	PDB header: hydrolase Chain: A: PDB Molecule: fructosyltransferase; PDBTitle: crystal structure of fructosyltransferase (d191a) from a. japonicus in2 complex with nystose

29	c1hgvA_	Alignment	not modelled	6.9	23	PDB header: virus Chain: A: PDB Molecule: ph75 inovirus major coat protein; PDBTitle: filamentous bacteriophage ph75
30	c2aezA_	Alignment	not modelled	6.8	16	PDB header: hydrolase Chain: A: PDB Molecule: fructan 1-exohydrolase iia; PDBTitle: crystal structure of fructan 1-exohydrolase iia (e201q) from cichorium2 intybus in complex with 1-kestose
31	d2pls1a1	Alignment	not modelled	6.7	29	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
32	d2rk5a1	Alignment	not modelled	6.6	29	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
33	d2r6gf2	Alignment	not modelled	6.3	8	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
34	d2gz4a1	Alignment	not modelled	6.0	8	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
35	d2d5ja1	Alignment	not modelled	5.9	20	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyl Hydrolase Family 88
36	c3lw52_	Alignment	not modelled	5.7	17	PDB header: photosynthesis Chain: 2: PDB Molecule: type ii chlorophyll a/b binding protein from photosystem i; PDB Fragment: residues 81-246; PDBTitle: improved model of plant photosystem i
37	c3llbA_	Alignment	not modelled	5.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
38	c3eh4A_	Alignment	not modelled	5.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c oxidase subunit 1; PDBTitle: structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus
39	c3pmmA_	Alignment	not modelled	5.3	16	PDB header: hydrolase Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578
40	d2o1ra1	Alignment	not modelled	5.2	14	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
41	c2km1A_	Alignment	not modelled	5.1	18	PDB header: protein binding Chain: A: PDB Molecule: protein dre2; PDBTitle: solution structure of the n-terminal domain of the yeast protein dre2
42	c2kcoA_	Alignment	not modelled	5.0	50	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s8e; PDBTitle: solution nmr structure of ribosomal protein sso0164 from2 sulfolobus solfataricus. northeast structural genomics3 consortium (nesg) target sst4.