


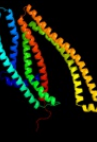

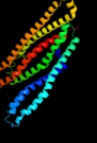

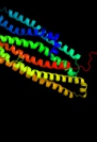
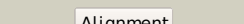
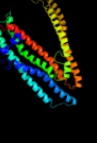
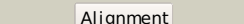

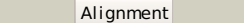
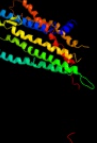
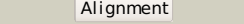

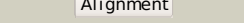
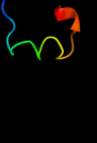
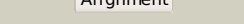

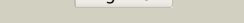



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3b60a2	 Alignment		99.9	11	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
2	c2yl4A_	 Alignment		99.9	11	PDB header: membrane protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 10, PDBTitle: structure of the human mitochondrial abc transporter, abcb10
3	d2hyda2	 Alignment		99.9	10	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
4	c2hydB_	 Alignment		99.9	10	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
5	c3g5uB_	 Alignment		99.9	8	PDB header: membrane protein Chain: B: PDB Molecule: multidrug resistance protein 1a; PDBTitle: structure of p-glycoprotein reveals a molecular basis for 2 poly-specific drug binding
6	c3b5wE_	 Alignment		99.8	13	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
7	d1pf4a2	 Alignment		99.6	13	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
8	c3b5xB_	 Alignment		99.6	11	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
9	d1ou5a1	 Alignment		63.8	42	Fold: Poly A polymerase C-terminal region-like Superfamily: Poly A polymerase C-terminal region-like Family: Poly A polymerase C-terminal region-like
10	d1miwa1	 Alignment		21.2	33	Fold: Poly A polymerase C-terminal region-like Superfamily: Poly A polymerase C-terminal region-like Family: Poly A polymerase C-terminal region-like
11	d1n2aa1	 Alignment		19.4	9	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain

12	c3gehA_	Alignment		18.3	12	PDB header: hydrolase Chain: A: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
13	d1aw9a1	Alignment		18.2	11	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
14	d2gsqa1	Alignment		17.1	11	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
15	c1m0uB_	Alignment		17.1	12	PDB header: transferase Chain: B: PDB Molecule: gst2 gene product; PDBTitle: crystal structure of the drosophila glutathione s-2 transferase-2 in complex with glutathione
16	c3a0hk_	Alignment		16.0	50	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of i-substituted photosystem ii complex
17	d2gsta1	Alignment		15.5	14	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
18	d1hiob_	Alignment		14.3	11	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
19	c1vheA_	Alignment		13.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aminopeptidase/glucanase homolog; PDBTitle: crystal structure of a aminopeptidase/glucanase homolog
20	c2uz8A_	Alignment		12.8	7	PDB header: rna-binding protein Chain: A: PDB Molecule: eukaryotic translation elongation factor 1 PDBTitle: the crystal structure of p18, human translation elongation2 factor 1 epsilon 1
21	d1p3mh_	Alignment	not modelled	12.8	11	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
22	c1aw9A_	Alignment	not modelled	12.2	7	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase iii; PDBTitle: structure of glutathione s-transferase iii in apo form
23	d1tw9a1	Alignment	not modelled	12.2	9	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
24	d1iwpA_	Alignment	not modelled	11.7	26	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Diol dehydratase, alpha subunit
25	c2hsmA_	Alignment	not modelled	10.8	8	PDB header: ligase/rna binding protein Chain: A: PDB Molecule: glutamyl-trna synthetase, cytoplasmic; PDBTitle: structural basis of yeast aminoacyl-trna synthetase complex2 formation revealed by crystal structures of two binary sub-3 complexes
26	c1z23A_	Alignment	not modelled	10.5	26	PDB header: cell adhesion Chain: A: PDB Molecule: crk-associated substrate; PDBTitle: the serine-rich domain from crk-associated substrate2 (p130cas)
27	c2l81A_	Alignment	not modelled	10.1	21	PDB header: cell adhesion Chain: A: PDB Molecule: enhancer of filamentation 1; PDBTitle: solution nmr structure of the serine-rich domain of hef1 (enhancer of2 filamentation 1) from homo sapiens, northeast structural genomics3 consortium target hr5554a
28	c3a0bK_	Alignment	not modelled	10.1	50	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of br-substituted photosystem ii complex

29	c3a0bk_	Alignment	not modelled	10.1	50	PDB header: electron transport Chain: K: PDB Molecule: photosystem ii reaction center protein k; PDBTitle: crystal structure of br-substituted photosystem ii complex
30	d1eexa_	Alignment	not modelled	9.7	19	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Diol dehydratase, alpha subunit
31	d1b4pa1	Alignment	not modelled	9.7	12	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
32	d1wspa1	Alignment	not modelled	8.6	36	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: DIX domain
33	d1id3d_	Alignment	not modelled	8.5	11	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
34	c2qx2A_	Alignment	not modelled	7.4	3	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sex pheromone staph-cam373; PDBTitle: structure of the c-terminal domain of sex pheromone staph-cam3732 precursor from staphylococcus aureus
35	c1byeA_	Alignment	not modelled	7.0	7	PDB header: transferase Chain: A: PDB Molecule: protein (glutathione s-transferase); PDBTitle: glutathione s-transferase i from mais in complex with2 atrazine glutathione conjugate
36	c2yruA_	Alignment	not modelled	6.6	19	PDB header: apoptosis Chain: A: PDB Molecule: steroid receptor rna activator 1; PDBTitle: solution structure of mouse steroid receptor rna activator2 1 (sra1) protein
37	d1pd3a_	Alignment	not modelled	6.4	18	Fold: ROP-like Superfamily: Nonstructural protein ns2, Nep, M1-binding domain Family: Nonstructural protein ns2, Nep, M1-binding domain
38	d1tzyb_	Alignment	not modelled	6.1	11	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
39	c3lszA_	Alignment	not modelled	5.7	10	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of glutathione s-transferase from2 rhodobacter sphaeroides
40	d1b8xa1	Alignment	not modelled	5.4	13	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
41	d1tu7a1	Alignment	not modelled	5.4	9	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
42	c2akfB_	Alignment	not modelled	5.3	18	PDB header: protein binding Chain: B: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1
43	c2akfA_	Alignment	not modelled	5.3	18	PDB header: protein binding Chain: A: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1
44	c2akfC_	Alignment	not modelled	5.3	18	PDB header: protein binding Chain: C: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1
45	d2axtk1	Alignment	not modelled	5.3	50	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein K, PsbK Family: PsbK-like
46	c2fq8A_	Alignment	not modelled	5.2	36	PDB header: unknown function Chain: A: PDB Molecule: 2f; PDBTitle: nmr structure of 2f associated with lipid disc
47	c2fq5A_	Alignment	not modelled	5.2	36	PDB header: unknown function Chain: A: PDB Molecule: peptide 2f; PDBTitle: nmr structure of 2f associated with lipid disc
48	c1zvaA_	Alignment	not modelled	5.2	14	PDB header: viral protein Chain: A: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of sars virus membrane fusion
49	c1ou5A_	Alignment	not modelled	5.1	54	PDB header: translation, transferase Chain: A: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of human cca-adding enzyme
50	d1gnwa1	Alignment	not modelled	5.0	16	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain