







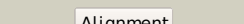

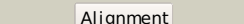

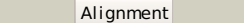

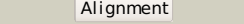

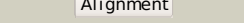

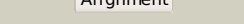

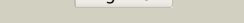
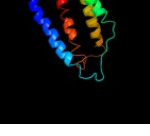
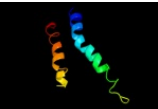
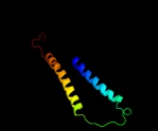
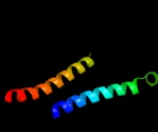

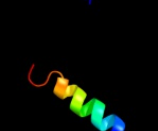
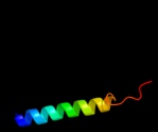
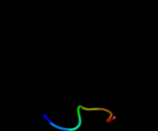
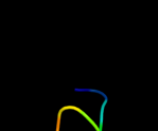
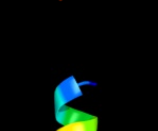


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3giaA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj0609; <b>PDBTitle:</b> crystal structure of apct transporter
2	<a href="#">c3lrcC_</a>	 Alignment		100.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> arginine/agmatine antiporter; <b>PDBTitle:</b> structure of e. coli adic (p1)
3	<a href="#">c2jlnA_</a>	 Alignment		99.9	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
4	<a href="#">c2xq2A_</a>	 Alignment		99.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> structure of the k294a mutant of vsgl
5	<a href="#">c3dh4A_</a>	 Alignment		98.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
6	<a href="#">c2w8aC_</a>	 Alignment		97.0	16	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
7	<a href="#">d2a65a1</a>	 Alignment		96.6	13	<b>Fold:</b> SNF-like <b>Superfamily:</b> SNF-like <b>Family:</b> SNF-like
8	<a href="#">c3hfxA_</a>	 Alignment		95.2	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-carnitine/gamma-butyrobetaine antiporter; <b>PDBTitle:</b> crystal structure of carnitine transporter
9	<a href="#">c2kncA_</a>	 Alignment		15.0	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
10	<a href="#">c1m57H_</a>	 Alignment		13.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant)
11	<a href="#">d1fftC_</a>	 Alignment		10.5	13	<b>Fold:</b> Cytochrome c oxidase subunit III-like <b>Superfamily:</b> Cytochrome c oxidase subunit III-like <b>Family:</b> Cytochrome c oxidase subunit III-like

12	<a href="#">d1fftb2</a>	Alignment		10.2	9	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
13	<a href="#">c1qleB_</a>	Alignment		9.9	10	<b>PDB header:</b> oxidoreductase/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide ii; <b>PDBTitle:</b> cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
14	<a href="#">d3ehbb2</a>	Alignment		9.4	20	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
15	<a href="#">c2k9yA_</a>	Alignment		9.4	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
16	<a href="#">c2k9yB_</a>	Alignment		9.4	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
17	<a href="#">c2k1aA_</a>	Alignment		9.1	26	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iiB) transmembrane segment
18	<a href="#">d1dt9a3</a>	Alignment		9.0	50	<b>Fold:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 <b>Superfamily:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 <b>Family:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1
19	<a href="#">c2l1uA_</a>	Alignment		8.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-r-sulfoxide reductase b2, mitochondrial; <b>PDBTitle:</b> structure-functional analysis of mammalian msrb2 protein
20	<a href="#">c3b71E_</a>	Alignment		8.7	44	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> t-cell surface glycoprotein cd4; <b>PDBTitle:</b> cd4 endocytosis motif bound to the focal adhesion targeting (fat)2 domain of the focal adhesion kinase
21	<a href="#">c3b71D_</a>	Alignment	not modelled	8.7	44	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> t-cell surface glycoprotein cd4; <b>PDBTitle:</b> cd4 endocytosis motif bound to the focal adhesion targeting (fat)2 domain of the focal adhesion kinase
22	<a href="#">c3rceA_</a>	Alignment	not modelled	8.5	19	<b>PDB header:</b> transferase/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> oligosaccharide transferase to n-glycosylate proteins; <b>PDBTitle:</b> bacterial oligosaccharyltransferase pglb
23	<a href="#">d3dtub2</a>	Alignment	not modelled	8.3	20	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
24	<a href="#">c3qe7A_</a>	Alignment	not modelled	8.3	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> uracil permease; <b>PDBTitle:</b> crystal structure of uracil transporter--uraa
25	<a href="#">c3e20C_</a>	Alignment	not modelled	8.0	40	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> eukaryotic peptide chain release factor subunit 1; <b>PDBTitle:</b> crystal structure of s.pombe erf1/erf3 complex
26	<a href="#">c2kfeA_</a>	Alignment	not modelled	7.9	56	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> meucin-24; <b>PDBTitle:</b> solution structure of meucin-24
27	<a href="#">d1xg8a_</a>	Alignment	not modelled	7.7	5	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> YuzD-like
28	<a href="#">d2obpa1</a>	Alignment	not modelled	7.7	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ReutB4095-like
						<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel

29	<a href="#">c2k21A_</a>	Alignment	not modelled	7.4	10	subfamily e <b>PDBTitle:</b> nmr structure of human kcnk1 in 1mpg micelles at ph 6.0 and 2 40 degree c
30	<a href="#">d1t98a2</a>	Alignment	not modelled	7.2	8	<b>Fold:</b> STAT-like <b>Superfamily:</b> MukF C-terminal domain-like <b>Family:</b> MukF C-terminal domain-like
31	<a href="#">clar1B_</a>	Alignment	not modelled	7.1	20	<b>PDB header:</b> complex (oxidoreductase/antibody) <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
32	<a href="#">d2cmyb1</a>	Alignment	not modelled	7.1	29	<b>Fold:</b> Toxic hairpin <b>Superfamily:</b> VhTI-like <b>Family:</b> VhTI-like
33	<a href="#">c2cmyB_</a>	Alignment	not modelled	7.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> veronica hederifolia trypsin inhibitor; <b>PDBTitle:</b> crystal complex between bovine trypsin and veronica2 hederifolia trypsin inhibitor
34	<a href="#">d1vc4a_</a>	Alignment	not modelled	6.9	40	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
35	<a href="#">c1uj1A_</a>	Alignment	not modelled	6.8	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h <b>PDBTitle:</b> solution structure of the herg k+ channel s5-p2 extracellular linker
36	<a href="#">d1xmec1</a>	Alignment	not modelled	6.6	23	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Bacterial ba3 type cytochrome c oxidase subunit IIa <b>Family:</b> Bacterial ba3 type cytochrome c oxidase subunit IIa
37	<a href="#">d1ic8a2</a>	Alignment	not modelled	6.2	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
38	<a href="#">c3dwuA_</a>	Alignment	not modelled	6.1	60	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor tu-b; <b>PDBTitle:</b> transition-state model conformation of the switch i region2 fitted into the cryo-em map of the eef2.80s.alf4.gdp3 complex
39	<a href="#">d1a53a_</a>	Alignment	not modelled	6.0	40	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
40	<a href="#">d1iwpa_</a>	Alignment	not modelled	6.0	44	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> Diol dehydratase, alpha subunit
41	<a href="#">d1eexa_</a>	Alignment	not modelled	6.0	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> Diol dehydratase, alpha subunit
42	<a href="#">c2cpbA_</a>	Alignment	not modelled	5.9	12	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> m13 major coat protein; <b>PDBTitle:</b> solution nmr structures of the major coat protein of2 filamentous bacteriophage m13 solubilized in3 dodecylphosphocholine micelles, 25 lowest energy structures
43	<a href="#">c1t0fC_</a>	Alignment	not modelled	5.8	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> transposon tn7 transposition protein tnsC; <b>PDBTitle:</b> crystal structure of the tnsa/tnsc(504-555) complex
44	<a href="#">c2rddB_</a>	Alignment	not modelled	5.7	10	<b>PDB header:</b> membrane protein/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> upf0092 membrane protein yajc; <b>PDBTitle:</b> x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
45	<a href="#">d1efea_</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> Insulin-like <b>Superfamily:</b> Insulin-like <b>Family:</b> Insulin-like
46	<a href="#">d2iuba2</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Magnesium transport protein CorA, transmembrane region <b>Family:</b> Magnesium transport protein CorA, transmembrane region
47	<a href="#">d1joya_</a>	Alignment	not modelled	5.5	15	<b>Fold:</b> ROP-like <b>Superfamily:</b> Homodimeric domain of signal transducing histidine kinase <b>Family:</b> Homodimeric domain of signal transducing histidine kinase
48	<a href="#">c1unhD_</a>	Alignment	not modelled	5.5	11	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> cyclin-dependent kinase 5 activator 1; <b>PDBTitle:</b> structural mechanism for the inhibition of cdk5-p25 by2 roscovitine, aloisine and indirubin.
49	<a href="#">d1lr7a1</a>	Alignment	not modelled	5.4	12	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> EGF/Laminin <b>Family:</b> Follistatin (FS) module N-terminal domain, FS-N
50	<a href="#">d1unld_</a>	Alignment	not modelled	5.4	11	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Cyclin
51	<a href="#">d2nr9a1</a>	Alignment	not modelled	5.4	9	<b>Fold:</b> Rhomboid-like <b>Superfamily:</b> Rhomboid-like <b>Family:</b> Rhomboid-like
52	<a href="#">d1eah1_</a>	Alignment	not modelled	5.3	57	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
53	<a href="#">d1pmxa_</a>	Alignment	not modelled	5.2	40	<b>Fold:</b> Insulin-like <b>Superfamily:</b> Insulin-like <b>Family:</b> Insulin-like
54	<a href="#">d1j75a_</a>	Alignment	not modelled	5.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Z-DNA binding domain
						<b>PDB header:</b> hydrolase

55	<a href="#">c2qtyB_</a>	Alignment	not modelled	5.1	23	<b>Chain:</b> B: <b>PDB Molecule:</b> poly(adp-ribose) glycohydrolase arh3; <b>PDBTitle:</b> crystal structure of mouse adp-ribosylhydrolase 3 (marh3)
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