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Description	P77306
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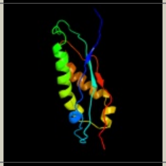
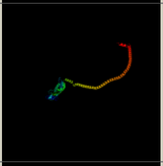
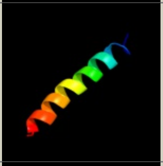
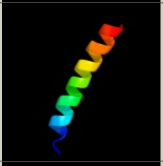
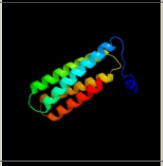
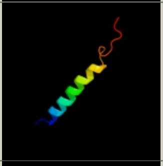
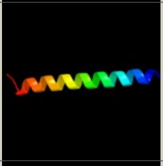
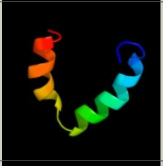
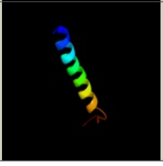
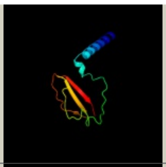
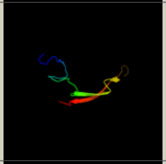
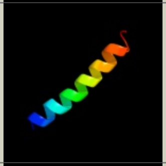
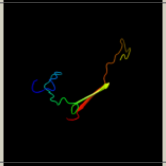
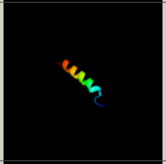
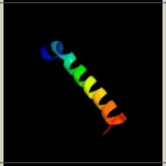
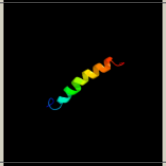
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wina_	Alignment		99.8	16	**Fold:**EF-Ts domain-like **Superfamily:**Band 7/SPFH domain **Family:**Band 7/SPFH domain
2	c3bk6C_	Alignment		99.8	21	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ph stomatin; **PDBTitle:** crystal structure of a core domain of stomatin from2 pyrococcus horikoshii
3	c2rpbA_	Alignment		99.7	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical membrane protein; **PDBTitle:** the solution structure of membrane protein
4	c2zv4O_	Alignment		99.3	10	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
5	d2axtj1	Alignment		78.4	24	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein J, PsbJ **Family:**PsbJ-like
6	c2kncA_	Alignment		74.5	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
7	c1y4cA_	Alignment		72.0	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
8	c2k1aA_	Alignment		70.6	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
9	c2jwaA_	Alignment		54.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
10	c3peuB_	Alignment		39.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoporin gle1; **PDBTitle:** s. cerevisiae dbp5 l327v c-terminal domain bound to gle1 h337r and ip6
11	c3mk7F_	Alignment		32.4	6	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase

12	c1xmeB_	Alignment		32.1	5	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** structure of recombinant cytochrome ba3 oxidase from thermus2 thermophilus
13	c3dktD_	Alignment		31.1	16	**PDB header:**structural protein/virus like particle **Chain:** D: **PDB Molecule:**maritimacin; **PDBTitle:** crystal structure of thermotoga maritima encapsulin
14	c3hd7A_	Alignment		30.3	20	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
15	c2e0zA_	Alignment		25.4	24	**PDB header:**virus like particle **Chain:** A: **PDB Molecule:**virus-like particle; **PDBTitle:** crystal structure of virus-like particle from pyrococcus2 furiosus
16	d2axth1	Alignment		21.3	23	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II 10 kDa phosphoprotein PsbH **Family:**PsbH-like
17	c3hfxA_	Alignment		18.4	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter; **PDBTitle:** crystal structure of carnitine transporter
18	c2w8aC_	Alignment		17.5	23	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
19	c1cn3F_	Alignment		17.4	33	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fragment of coat protein vp2; **PDBTitle:** interaction of polyomavirus internal protein vp2 with major2 capsid protein vp1 and implications for participation of3 vp2 in viral entry
20	c2kncB_	Alignment		15.9	12	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
21	c3kdpG_	Alignment	not modelled	13.8	22	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
22	c3kdpH_	Alignment	not modelled	13.8	22	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
23	c3o2qB_	Alignment	not modelled	11.7	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
24	c1h4uA_	Alignment	not modelled	10.9	10	**PDB header:**extracellular matrix protein **Chain:** A: **PDB Molecule:**nidogen-1; **PDBTitle:** domain g2 of mouse nidogen-1
25	c3fdfA_	Alignment	not modelled	10.8	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fr253; **PDBTitle:** crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
26	c3o2sB_	Alignment	not modelled	9.9	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72 complex
27	c1zzaA_	Alignment	not modelled	9.6	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**stannin; **PDBTitle:** solution nmr structure of the membrane protein stannin
28	c3mk7B_	Alignment	not modelled	9.3	6	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit

28	c3mk7B_		Alignment	not modelled	9.5	6	o; **PDBTitle:** the structure of cbb3 cytochrome oxidase
29	d2ix0a3		Alignment	not modelled	8.7	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
30	c1iijA_		Alignment	not modelled	8.2	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**erbb-2 receptor protein-tyrosine kinase; **PDBTitle:** solution structure of the neu/erbb-2 membrane spanning2 segment
31	c2jo1A_		Alignment	not modelled	8.0	12	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
32	c1fftG_		Alignment	not modelled	7.7	15	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
33	c2l2tA_		Alignment	not modelled	7.6	4	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
34	d2o4ta1		Alignment	not modelled	7.5	11	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like
35	d2pila_		Alignment	not modelled	7.2	18	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
36	d1oqwa_		Alignment	not modelled	7.2	27	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
37	c3fcmA_		Alignment	not modelled	7.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a nudix hydrolase from clostridium2 perfringens
38	c3ipdB_		Alignment	not modelled	7.0	26	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
39	c3sokB_		Alignment	not modelled	7.0	23	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
40	c2jp3A_		Alignment	not modelled	6.8	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
41	c3a0bL_		Alignment	not modelled	6.8	5	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
42	d1jb0i_		Alignment	not modelled	6.7	22	**Fold:**Single transmembrane helix **Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI **Family:**Subunit VIII of photosystem I reaction centre, PsaI
43	d2r6gf1		Alignment	not modelled	6.7	13	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
44	c2j7aC_		Alignment	not modelled	6.6	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**cytochrome c quinol dehydrogenase nrfh; **PDBTitle:** crystal structure of cytochrome c nitrite reductase nrfha2 complex from desulfovibrio vulgaris
45	c1s5ll_		Alignment	not modelled	6.5	5	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
46	c3a0hl_		Alignment	not modelled	6.5	5	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
47	c3a0hL_		Alignment	not modelled	6.5	5	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
48	c1s5lL_		Alignment	not modelled	6.5	5	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
49	c3kziL_		Alignment	not modelled	6.5	5	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
50	c2axtL_		Alignment	not modelled	6.5	5	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
51	c2axtl_		Alignment	not modelled	6.5	5	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
52	c3arcL_		Alignment	not modelled	6.5	5	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
53	c3bz2L_		Alignment	not modelled	6.5	5	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
54	c3prrL_		Alignment	not modelled	6.5	5	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second

						monomer of psii3 dimer
55	c3a0bl_	Alignment	not modelled	6.5	5	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
56	c3prqL_	Alignment	not modelled	6.5	5	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
57	d2axtl1	Alignment	not modelled	6.5	5	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
58	c3bz1L_	Alignment	not modelled	6.5	5	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
59	d1fftb2	Alignment	not modelled	6.5	6	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
60	c2zxeG_	Alignment	not modelled	6.2	35	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
61	c1p58F_	Alignment	not modelled	5.8	21	**PDB header:**virus **Chain:** F: **PDB Molecule:**envelope protein m; **PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
62	d1id3b_	Alignment	not modelled	5.7	15	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
63	c2btwA_	Alignment	not modelled	5.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alr0975 protein; **PDBTitle:** crystal structure of alr0975
64	c3arcl_	Alignment	not modelled	5.7	5	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
65	c2l16A_	Alignment	not modelled	5.7	30	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**sec-independent protein translocase protein tatad; **PDBTitle:** solution structure of bacillus subtilits tatad protein in dpc micelles
66	c1yewI_	Alignment	not modelled	5.6	10	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
67	c3rgbA_	Alignment	not modelled	5.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
68	d1uxca_	Alignment	not modelled	5.6	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
69	d1j0ha1	Alignment	not modelled	5.6	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
70	d2cnza1	Alignment	not modelled	5.5	15	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
71	c2ks1B_	Alignment	not modelled	5.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
72	d1jvaa3	Alignment	not modelled	5.4	21	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
73	d2bu3a1	Alignment	not modelled	5.4	17	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Phytochelatin synthase
74	d3dtub2	Alignment	not modelled	5.3	3	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
75	c2wtoB_	Alignment	not modelled	5.3	9	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**orf131 protein; **PDBTitle:** crystal structure of apo-form czce from c. metallidurans ch34
76	c3cf6E_	Alignment	not modelled	5.3	17	**PDB header:**signaling protein/gtp-binding protein **Chain:** E: **PDB Molecule:**rap guanine nucleotide exchange factor (gef) 4; **PDBTitle:** structure of epac2 in complex with cyclic-amp and rap
77	c3sbtB_	Alignment	not modelled	5.3	20	**PDB header:**splicing **Chain:** B: **PDB Molecule:**a1 cistron-splicing factor aar2; **PDBTitle:** crystal structure of a aar2-prp8 complex
78	d2ix0a1	Alignment	not modelled	5.2	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
79	c3f6aA_	Alignment	not modelled	5.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a hydrolase, nudix family from2 clostridium perfringens
						Fold: ImmE5-like

80	d2fhza1	Alignment	not modelled	5.1	33	**Superfamily:**ImmE5-like **Family:**ImmE5-like
81	c2kluA_	Alignment	not modelled	5.0	15	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
82	c1bhbA_	Alignment	not modelled	5.0	12	**PDB header:**photoreceptor **Chain:** A: **PDB Molecule:**bacteriorhodopsin; **PDBTitle:** three-dimensional structure of (1-71) bacterioopsin2 solubilized in methanol-chloroform and sds micelles3 determined by 15n-1h heteronuclear nmr spectroscopy
83	d3ehbb2	Alignment	not modelled	5.0	8	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region