Phyre^2

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Description	P04637
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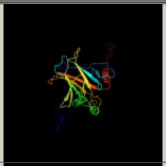
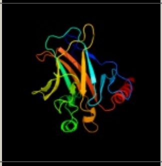
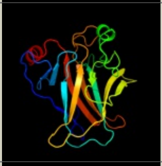
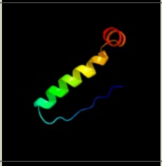
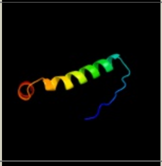
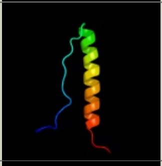
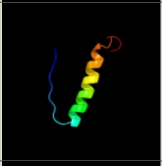
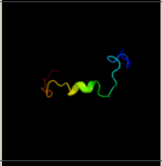
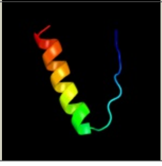
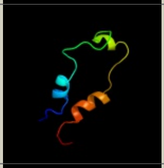
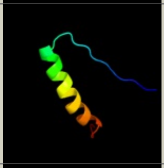
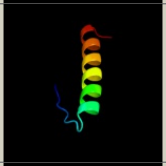
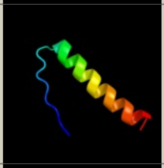
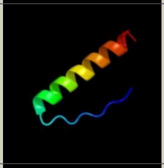
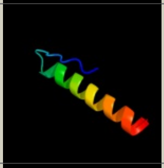
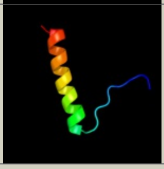
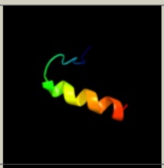
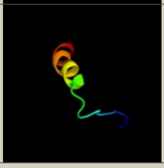
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rmnA_	Alignment		100.0	50	**PDB header:**cell cycle, antitumor protein **Chain:** A: **PDB Molecule:**tumor protein 63; **PDBTitle:** the solution structure of the p63 dna-binding domain
2	c2j1xA_	Alignment		100.0	97	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** human p53 core domain mutant m133l-v203a-y220c-n239y-n268d
3	d2ac0a1	Alignment		100.0	100	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
4	c2xipA_	Alignment		100.0	56	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**tumour protein p73; **PDBTitle:** crystal structure of the dna binding domain of human tp732 refined at 1.8 a resolution
5	d1hu8a_	Alignment		100.0	89	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
6	c4a9zD_	Alignment		99.2	35	**PDB header:**transcription **Chain:** D: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of human p63 tetramerization domain
7	c3zy1A_	Alignment		99.1	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of the human p63 tetramerization domain
8	d3saka_	Alignment		99.0	100	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
9	c2wttL_	Alignment		99.0	38	**PDB header:**transcription **Chain:** L: **PDB Molecule:**tumor protein p73; **PDBTitle:** structure of the human p73 tetramerization domain (crystal2 form ii)
10	c2k8fB_	Alignment		98.8	100	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structural basis for the regulation of p53 function by p300
11	c2wqjM_	Alignment		98.4	48	**PDB header:**transcription **Chain:** M: **PDB Molecule:**tumor protein p73; **PDBTitle:** crystal structure of a truncated variant of the human p732 tetramerization domain

12	d1t4wa_	Alignment		98.3	17	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
13	c2l14B_	Alignment		98.3	100	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structure of cbp nuclear coactivator binding domain in complex with2 p53 tad
14	d1hs5a_	Alignment		98.2	94	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
15	d1aiea_	Alignment		98.1	100	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
16	c2j10A_	Alignment		98.0	94	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
17	c2j10D_	Alignment		98.0	94	**PDB header:**transcription **Chain:** D: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
18	c2j10B_	Alignment		98.0	94	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
19	c2j11D_	Alignment		98.0	90	**PDB header:**transcription **Chain:** D: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant y327s t329g q331g
20	d1a1ua_	Alignment		97.9	90	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
21	c3zy0C_	Alignment	not modelled	96.9	43	**PDB header:**transcription **Chain:** C: **PDB Molecule:**tumor protein p63; **PDBTitle:** crystal structure of a truncated variant of the human p632 tetramerization domain lacking the c-terminal helix
22	c1q2iA_	Alignment	not modelled	93.9	100	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**pnc27; **PDBTitle:** nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
23	c1dt7Y_	Alignment		87.1	100	**PDB header:**signaling protein **Chain:** Y: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** solution structure of the c-terminal negative regulatory2 domain of p53 in a complex with ca2+-bound s100b(bb)
24	c1dt7X_	Alignment		87.1	100	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** solution structure of the c-terminal negative regulatory2 domain of p53 in a complex with ca2+-bound s100b(bb)
25	c3dacB_	Alignment	not modelled	65.2	100	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structure of the human mdmx protein bound to the p53 tumor2 suppressor transactivation domain
26	c3dacP_	Alignment	not modelled	59.1	100	**PDB header:**cell cycle **Chain:** P: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structure of the human mdmx protein bound to the p53 tumor2 suppressor transactivation domain

27	c2b3gB_	Alignment	not modelled	32.2	100	**PDB header:**replication **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53n (fragment 33-60) bound to rpa70n
28	d1iknc_	Alignment	not modelled	29.1	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
29	c3gycB_	Alignment	not modelled	27.2	43	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glycoside hydrolase; **PDBTitle:** crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
30	c3cguB_	Alignment	not modelled	22.5	44	**PDB header:**hormone/signaling protein **Chain:** B: **PDB Molecule:**protein giant-lens; **PDBTitle:** crystal structure of unliganded argos
31	c1w21D_	Alignment	not modelled	21.2	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**neuraminidase; **PDBTitle:** structure of neuraminidase from english duck subtype n62 complexed with 30 mm sialic acid (nana, neu5ac), crystal3 soaked for 43 hours at 291 k.
32	c2xdvA_	Alignment	not modelled	21.1	40	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
33	c1svcP_	Alignment	not modelled	20.1	18	**PDB header:**transcription/dna **Chain:** P: **PDB Molecule:**protein (nuclear factor kappa-b (nf-kb)); **PDBTitle:** nfkb p50 homodimer bound to dna
34	d1a6ca2	Alignment	not modelled	18.0	16	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
35	c4diqA_	Alignment	not modelled	17.5	47	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase no66; **PDBTitle:** crystal structure of human no66
36	c1nfkA_	Alignment	not modelled	14.6	18	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (nuclear factor kappa-b (nf-kb)); **PDBTitle:** structure of the nuclear factor kappa-b (nf-kb) p502 homodimer
37	c2pi2A_	Alignment	not modelled	14.0	11	**PDB header:**replication, dna binding protein **Chain:** A: **PDB Molecule:**replication protein a 32 kda subunit; **PDBTitle:** full-length replication protein a subunits rpa14 and rpa32
38	d1e42a2	Alignment	not modelled	13.7	32	**Fold:**Subdomain of clathrin and coatomer appendage domain **Superfamily:**Subdomain of clathrin and coatomer appendage domain **Family:**Clathrin adaptor appendage, alpha and beta chain-specific domain
39	c3kf6A_	Alignment	not modelled	13.7	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
40	d1imhc1	Alignment	not modelled	13.3	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
41	d2pi2a1	Alignment	not modelled	13.3	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
42	d1e7ua3	Alignment	not modelled	12.9	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
43	d1vrba1	Alignment	not modelled	12.9	20	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
44	d1e8ya3	Alignment	not modelled	12.2	36	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
45	d1g4us2	Alignment	not modelled	11.9	19	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
46	d1i96v_	Alignment	not modelled	10.3	24	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain
47	c1imhD_	Alignment	not modelled	10.2	21	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**nuclear factor of activated t cells 5; **PDBTitle:** tonebp/dna complex
48	c1nmbN_	Alignment	not modelled	9.8	26	**PDB header:**complex (hydrolase/immunoglobulin) **Chain:** N: **PDB Molecule:**n9 neuraminidase; **PDBTitle:** the structure of a complex between the nc10 antibody and influenza2 virus neuraminidase and comparison with the overlapping binding site3 of the nc41 antibody
49	d1ef1c_	Alignment	not modelled	9.5	25	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Moesin tail domain **Family:**Moesin tail domain
50	d1f8ea_	Alignment	not modelled	9.3	26	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
51	c2dfwA_	Alignment	not modelled	9.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
52	d1regx_	Alignment	not modelled	8.6	26	**Fold:**Ferredoxin-like **Superfamily:**Translational regulator protein regA **Family:**Translational regulator protein regA

53	d2je8a3	Alignment	not modelled	8.2	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
54	c1zldA_	Alignment	not modelled	8.2	62	**PDB header:**toxin **Chain:** A: **PDB Molecule:**ptr necrosis toxin; **PDBTitle:** crystal structure of a rgd-containing host-selective toxin:2 pyrenophora tritici-repentis ptr toxa
55	c3ih9A_	Alignment	not modelled	8.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure analysis of mglu in its tris form
56	c3czdA_	Alignment	not modelled	8.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaminase kidney isoform; **PDBTitle:** crystal structure of human glutaminase in complex with l-glutamate
57	c1t0pB_	Alignment	not modelled	8.0	23	**PDB header:**immune system **Chain:** B: **PDB Molecule:**intercellular adhesion molecule-3; **PDBTitle:** structural basis of icam recognition by integrin alpahlbeta2 revealed2 in the complex structure of binding domains of icam-3 and alphalbeta23 at 1.65 a
58	d2o8ia1	Alignment	not modelled	7.9	13	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
59	c2pbyB_	Alignment	not modelled	7.7	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaminase; **PDBTitle:** probable glutaminase from geobacillus kaustophilus hta426
60	c2q37A_	Alignment	not modelled	7.6	30	**PDB header:**plant protein, lyase **Chain:** A: **PDB Molecule:**ohcu decarboxylase; **PDBTitle:** crystal structure of ohcu decarboxylase in the presence of2 (s)-allantoin
61	d2q37a1	Alignment	not modelled	7.6	30	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
62	d1ko7a2	Alignment	not modelled	7.5	19	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**HPr kinase HprK C-terminal domain
63	d1fx0b1	Alignment	not modelled	7.5	33	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
64	d2aepa1	Alignment	not modelled	7.5	18	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
65	c3ss4C_	Alignment	not modelled	7.4	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glutaminase c; **PDBTitle:** crystal structure of mouse glutaminase c, phosphate-bound form
66	c2jwyA_	Alignment	not modelled	7.0	15	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yaji; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein yaji from2 escherichia coli. northeast structural genomics target er540
67	c3uo9B_	Alignment	not modelled	6.9	29	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**glutaminase kidney isoform, mitochondrial; **PDBTitle:** crystal structure of human gac in complex with glutamate and bptes
68	d1ydua1	Alignment	not modelled	6.9	18	**Fold:**At5g01610-like **Superfamily:**At5g01610-like **Family:**At5g01610-like
69	c3lsoA_	Alignment	not modelled	6.9	40	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative membrane anchored protein; **PDBTitle:** crystal structure of putative membrane anchored protein from2 corynebacterium diphtheriae
70	c2o011_	Alignment	not modelled	6.8	33	**PDB header:**photosynthesis **Chain:** 1: **PDB Molecule:**at3g54890; **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
71	c3h6qA_	Alignment	not modelled	6.8	33	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**macrocypin 1a; **PDBTitle:** macrocypin, a beta-trefoil cysteine protease inhibitor
72	d1yh5a1	Alignment	not modelled	6.8	24	**Fold:**YggU-like **Superfamily:**YggU-like **Family:**YggU-like
73	d1u60a_	Alignment	not modelled	6.7	26	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Glutaminase
74	d1mi2a_	Alignment	not modelled	6.6	30	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
75	d2p8ta1	Alignment	not modelled	6.6	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PH0730 N-terminal domain-like
76	d1w5sa1	Alignment	not modelled	6.6	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
77	d1nsca_	Alignment	not modelled	6.4	23	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
78	c3ns5B_	Alignment	not modelled	6.3	12	**PDB header:**translation **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit b;

						PDBTitle: crystal structure of the rna recognition motif of yeast eif3b residues2 76-161
79	c2o012_	Alignment	not modelled	6.3	33	**PDB header:**photosynthesis **Chain:** 2: **PDB Molecule:**type ii chlorophyll a/b binding protein from **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
80	c2nyuA_	Alignment	not modelled	6.3	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative ribosomal rna methyltransferase 2; **PDBTitle:** crystal structure of human ftsj homolog 2 (e.coli) protein2 in complex with s-adenosylmethionine
81	c1wveB_	Alignment	not modelled	6.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-cresol dehydrogenase [hydroxylating] **PDBTitle:** p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit
82	d2g9hd1	Alignment	not modelled	6.1	47	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
83	c1zggA_	Alignment	not modelled	6.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative low molecular weight protein-tyrosine- **PDBTitle:** solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
84	d1lyva_	Alignment	not modelled	6.0	29	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
85	d1zxqa2	Alignment	not modelled	5.9	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
86	d1rwta_	Alignment	not modelled	5.9	33	**Fold:**Chlorophyll a-b binding protein **Superfamily:**Chlorophyll a-b binding protein **Family:**Chlorophyll a-b binding protein
87	c3tiaC_	Alignment	not modelled	5.9	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** C: **PDB Molecule:**neuraminidase; **PDBTitle:** crystal structure of 1957 pandemic h2n2 neuraminidase complexed with2 laninamivir
88	d1ixta_	Alignment	not modelled	5.9	80	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Conotoxin
89	c1ixtA_	Alignment	not modelled	5.9	80	**PDB header:**toxin **Chain:** A: **PDB Molecule:**spasmodic protein tx9a-like protein; **PDBTitle:** structure of a novel p-superfamily spasmodic conotoxin2 reveals an inhibitory cystine knot motif
90	c3kbyB_	Alignment	not modelled	5.8	28	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of hypothetical protein from staphylococcus aureus
91	d1ivga_	Alignment	not modelled	5.8	18	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
92	c2wxoA_	Alignment	not modelled	5.8	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** the crystal structure of the murine class ia pi 3-kinase2 p110delta in complex with as5.
93	c3rh0A_	Alignment	not modelled	5.7	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
94	c2hu4D_	Alignment	not modelled	5.7	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**neuraminidase; **PDBTitle:** n1 neuraminidase in complex with oseltamivir 2
95	d1p8aa_	Alignment	not modelled	5.7	18	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
96	c3pm9A_	Alignment	not modelled	5.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution
97	d1inva_	Alignment	not modelled	5.7	22	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
98	d1skye1	Alignment	not modelled	5.6	33	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
99	c2rd0A_	Alignment	not modelled	5.6	13	**PDB header:**transferase/oncoprotein **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** structure of a human p110alpha/p85alpha complex