Phyre^{2}

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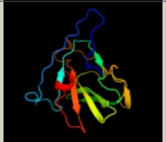
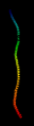
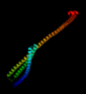
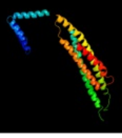
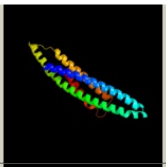
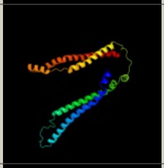
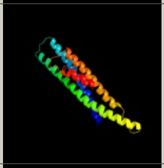
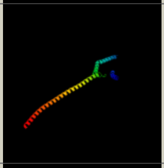
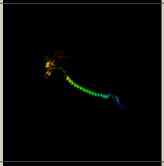
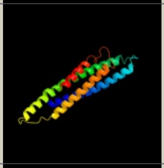
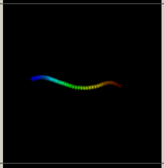
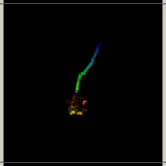
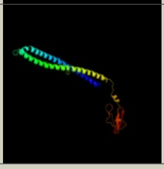
Detailed template information

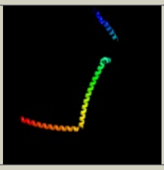
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gu1A_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
2	c2hsiB_	Alignment		100.0	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative peptidase m23; **PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
3	d1qwya_	Alignment		100.0	27	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Peptidoglycan hydrolase LytM
4	c3nyyA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycyl-glycine endopeptidase lytm; **PDBTitle:** crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
5	c2b44A_	Alignment		99.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm; **PDBTitle:** truncated s. aureus lytm, p 32 2 1 crystal form
6	c3it5B_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protease lasa; **PDBTitle:** crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
7	c3csqC_	Alignment		99.8	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
8	c1c1gA_	Alignment		98.1	14	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**tropomyosin; **PDBTitle:** crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
9	c1ciiA_	Alignment		97.6	11	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
10	c3na7A_	Alignment		97.6	12	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
11	c1yvlB_	Alignment		97.5	11	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** structure of unphosphorylated stat1

12	c1bg1A_	Alignment		97.5	13	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (transcription factor stat3b); **PDBTitle:** transcription factor stat3b/dna complex
13	c2oevA_	Alignment		97.5	8	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** crystal structure of alix/aip1
14	c1bf5A_	Alignment		97.4	8	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
15	c3ojaB_	Alignment		97.3	11	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
16	c1deqF_	Alignment		97.2	11	**PDB header:** **PDB COMPND:**
17	c3cwgA_	Alignment		97.2	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** unphosphorylated mouse stat3 core fragment
18	c2efrB_	Alignment		97.0	13	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 alpha chain; **PDBTitle:** crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
19	c3ghgK_	Alignment		97.0	12	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
20	c1jchC_	Alignment		96.9	7	**PDB header:**ribosome inhibitor, hydrolase **Chain:** C: **PDB Molecule:**colicin e3; **PDBTitle:** crystal structure of colicin e3 in complex with its immunity protein
21	c1deqO_	Alignment	not modelled	96.9	11	**PDB header:** **PDB COMPND:**
22	c2oexB_	Alignment	not modelled	96.8	8	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** structure of alix/aip1 v domain
23	c2d3eD_	Alignment	not modelled	96.5	11	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 **PDBTitle:** crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
24	c1ei3E_	Alignment	not modelled	96.5	10	**PDB header:** **PDB COMPND:**
25	d2f3ga_	Alignment	not modelled	96.4	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
26	d1glaf_	Alignment	not modelled	96.4	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
27	c2v71A_	Alignment	not modelled	96.2	10	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** coiled-coil region of nudel
28	d2gpra_	Alignment	not modelled	96.0	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
						PDB header:contractile protein

29	c2fxmB_	Alignment	not modelled	96.0	12	**Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
30	c3u59C_	Alignment	not modelled	95.9	9	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
31	d1gpra_	Alignment	not modelled	95.9	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
32	c3ol1A_	Alignment	not modelled	95.9	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** crystal structure of vimentin (fragment 144-251) from homo sapiens,2 northeast structural genomics consortium target hr4796b
33	c3o0zD_	Alignment	not modelled	95.8	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**rho-associated protein kinase 1; **PDBTitle:** crystal structure of a coiled-coil domain from human rock i
34	c2aukA_	Alignment	not modelled	95.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
35	c1ei3C_	Alignment	not modelled	95.6	12	**PDB header:** **PDB COMPND:**
36	c3l9oA_	Alignment	not modelled	95.5	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
37	c3r6nA_	Alignment	not modelled	95.5	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**desmoplakin; **PDBTitle:** crystal structure of a rigid four spectrin repeat fragment of the2 human desmoplakin plakin domain
38	c2gl2B_	Alignment	not modelled	95.3	10	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**adhesion a; **PDBTitle:** crystal structure of the tetra muntant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
39	c3hnwB_	Alignment	not modelled	95.2	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
40	c2i1jA_	Alignment	not modelled	95.1	8	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**moesin; **PDBTitle:** moesin from spodoptera frugiperda at 2.1 angstroms resolution
41	c3ojaA_	Alignment	not modelled	94.8	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
42	c2y3aB_	Alignment	not modelled	94.6	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit beta; **PDBTitle:** crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
43	c1q90A_	Alignment	not modelled	94.2	21	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**apocytochrome f; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
44	c1e2vB_	Alignment	not modelled	94.2	21	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
45	c3dtpA_	Alignment	not modelled	94.0	10	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
46	c2kccA_	Alignment	not modelled	93.9	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
47	c1f5nA_	Alignment	not modelled	93.9	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**interferon-induced guanylate-binding protein 1; **PDBTitle:** human guanylate binding protein-1 in complex with the gtp2 analogue, gmppnp.
48	c1g8xB_	Alignment	not modelled	93.7	7	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**myosin ii heavy chain fused to alpha-actinin 3; **PDBTitle:** structure of a genetically engineered molecular motor
49	c3g67A_	Alignment	not modelled	93.4	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of a soluble chemoreceptor from thermotoga2 maritima
50	c1ctmA_	Alignment	not modelled	93.3	17	**PDB header:**electron transport(cytochrome) **Chain:** A: **PDB Molecule:**cytochrome f; **PDBTitle:** crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
51	d1dcza_	Alignment	not modelled	93.2	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
52	c1sjjB_	Alignment	not modelled	92.7	8	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**actinin; **PDBTitle:** cryo-em structure of chicken gizzard smooth muscle alpha-2 actinin
53	c2b9cA_	Alignment	not modelled	92.7	11	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**striated-muscle alpha tropomyosin; **PDBTitle:** structure of tropomyosin's mid-region: bending and binding2 sites for actin
						Fold: Barrel-sandwich hybrid

54	d1ci3m2	Alignment	not modelled	91.9	22	**Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
55	c2jxmB_	Alignment	not modelled	91.8	23	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
56	c2ch7A_	Alignment	not modelled	91.6	9	**PDB header:**chemotaxis **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
57	c2b8gA_	Alignment	not modelled	91.6	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**biotin/lipoyl attachment protein; **PDBTitle:** solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
58	d1e2wa2	Alignment	not modelled	91.4	29	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
59	d1brwa3	Alignment	not modelled	91.4	27	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
60	d1bdoa_	Alignment	not modelled	91.0	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
61	c4a55B_	Alignment	not modelled	90.9	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
62	c3tnfB_	Alignment	not modelled	90.8	9	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**lida; **PDBTitle:** lida from legionella in complex with active rab8a
63	c2ejgD_	Alignment	not modelled	90.7	28	**PDB header:**ligase **Chain:** D: **PDB Molecule:**149aa long hypothetical methylmalonyl-coa decarboxylase **PDBTitle:** crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
64	c3ipkA_	Alignment	not modelled	90.1	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**agi/ii; **PDBTitle:** crystal structure of a3vp1 of agi/ii of streptococcus mutans
65	c2wpqA_	Alignment	not modelled	89.7	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**trimeric autotransporter adhesin fragment; **PDBTitle:** salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion)
66	d2tpta3	Alignment	not modelled	89.7	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
67	c1l8dB_	Alignment	not modelled	89.3	16	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
68	c2dn8A_	Alignment	not modelled	89.1	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
69	c2xgjA_	Alignment	not modelled	89.0	8	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
70	d1ghja_	Alignment	not modelled	88.5	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
71	c2j0fC_	Alignment	not modelled	88.4	37	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
72	c1y4cA_	Alignment	not modelled	88.2	14	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
73	c3u1aC_	Alignment	not modelled	88.0	16	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**smooth muscle tropomyosin alpha; **PDBTitle:** n-terminal 81-aa fragment of smooth muscle tropomyosin alpha
74	c1otpA_	Alignment	not modelled	88.0	25	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
75	c3a7pB_	Alignment	not modelled	88.0	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
76	c1tu2B_	Alignment	not modelled	87.9	20	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**apocytochrome f; **PDBTitle:** the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
77	c3hizB_	Alignment	not modelled	87.7	11	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
78	c3h5qA_	Alignment	not modelled	87.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside

						phosphorylase2 from staphylococcus aureus
79	c2v66C_	Alignment	not modelled	86.5	17	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** crystal structure of the coiled-coil domain of ndel1 (a.a.2 58 to 169)c
80	c3n6rK_	Alignment	not modelled	86.0	14	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
81	d1o78a_	Alignment	not modelled	85.9	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
82	c2v1yB_	Alignment	not modelled	85.1	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha; **PDBTitle:** structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
83	c2nrjA_	Alignment	not modelled	84.7	13	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hbl b protein; **PDBTitle:** crystal structure of hemolysin binding component from2 bacillus cereus
84	c1t5eB_	Alignment	not modelled	84.5	35	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
85	c2e75C_	Alignment	not modelled	84.5	18	**PDB header:**photosynthesis **Chain:** C: **PDB Molecule:**apocytochrome f; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
86	c2zv4O_	Alignment	not modelled	84.4	10	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
87	d1iyua_	Alignment	not modelled	84.0	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
88	c3lnnB_	Alignment	not modelled	83.8	28	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**membrane fusion protein (mfp) heavy metal cation efflux **PDBTitle:** crystal structure of zneb from cupriavidus metallidurans
89	c2dq3A_	Alignment	not modelled	83.7	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
90	c1deqD_	Alignment	not modelled	83.7	1	**PDB header:** **PDB COMPND:**
91	d1vf7a_	Alignment	not modelled	83.2	32	**Fold:**HlyD-like secretion proteins **Superfamily:**HlyD-like secretion proteins **Family:**HlyD-like secretion proteins
92	d1laba_	Alignment	not modelled	83.1	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
93	c2f1mA_	Alignment	not modelled	82.8	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
94	d1qjoa_	Alignment	not modelled	82.6	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
95	c1brwB_	Alignment	not modelled	82.5	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
96	c2qf7A_	Alignment	not modelled	82.4	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
97	c1qu7A_	Alignment	not modelled	82.1	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein i; **PDBTitle:** four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
98	c2dsjA_	Alignment	not modelled	81.6	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
99	c2no2A_	Alignment	not modelled	81.6	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**huntingtin-interacting protein 1; **PDBTitle:** crystal structure of the dllrkn-containing coiled-coil2 domain of huntingtin-interacting protein 1
100	d1k8ma_	Alignment	not modelled	81.3	9	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
101	c3qh9A_	Alignment	not modelled	81.3	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**liprin-beta-2; **PDBTitle:** human liprin-beta2 coiled-coil
102	c2k33A_	Alignment	not modelled	81.2	26	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**acra; **PDBTitle:** solution structure of an n-glycosylated protein using in2 vitro glycosylation
103	d1gjxa_	Alignment	not modelled	81.2	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
						PDB header:ligase

104	c2ejmA_	Alignment	not modelled	81.0	13	**Chain:** A: **PDB Molecule:**methylcrotonoyl-coa carboxylase subunit alpha; **PDBTitle:** solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
105	c3fppB_	Alignment	not modelled	80.8	22	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**macrolide-specific efflux protein maca; **PDBTitle:** crystal structure of e.coli maca
106	c2aujD_	Alignment	not modelled	80.8	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
107	c1gk4A_	Alignment	not modelled	80.7	9	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
108	c1n73C_	Alignment	not modelled	80.6	10	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrin gamma chain; **PDBTitle:** fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide
109	c1quuA_	Alignment	not modelled	79.0	9	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**human skeletal muscle alpha-actinin 2; **PDBTitle:** crystal structure of two central spectrin-like repeats from2 alpha-actinin
110	c1hciB_	Alignment	not modelled	78.9	9	**PDB header:**triple-helix coiled coil **Chain:** B: **PDB Molecule:**alpha-actinin 2; **PDBTitle:** crystal structure of the rod domain of alpha-actinin
111	c3fmcC_	Alignment	not modelled	78.6	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative succinylglutamate desuccinylase / aspartoacylase; **PDBTitle:** crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
112	c2q8iB_	Alignment	not modelled	78.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
113	c2qj8B_	Alignment	not modelled	78.1	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
114	d1y8ob1	Alignment	not modelled	77.6	16	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
115	c2q6oB_	Alignment	not modelled	77.2	25	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** sall-y70t with sam and cl
116	c2l5tA_	Alignment	not modelled	75.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
117	c2dneA_	Alignment	not modelled	74.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
118	c2jeeA_	Alignment	not modelled	74.4	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
119	c1i84V_	Alignment		74.0	9	**PDB header:**contractile protein **Chain:** V: **PDB Molecule:**smooth muscle myosin heavy chain; **PDBTitle:** cryo-em structure of the heavy meromyosin subfragment of2 chicken gizzard smooth muscle myosin with regulatory light3 chain in the dephosphorylated state. only c alphas4 provided for regulatory light chain. only backbone atoms5 provided for s2 fragment.
120	d2pnrc1	Alignment	not modelled	73.3	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains