Phyre2

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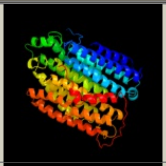
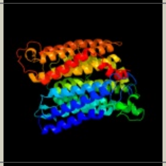
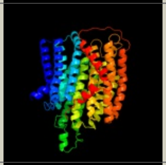
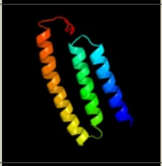
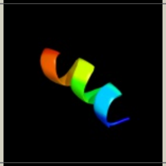
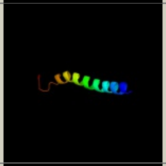
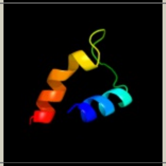
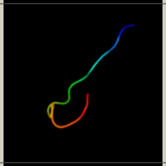
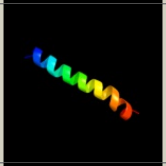
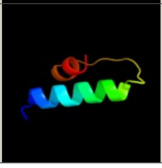
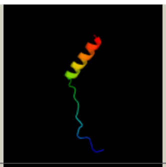
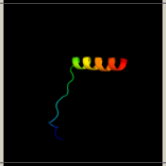
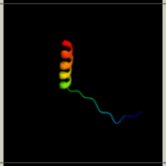
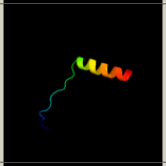
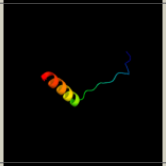
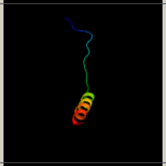
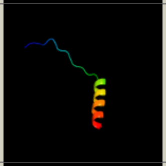
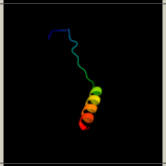
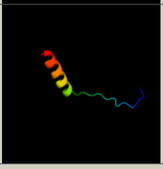
Description	P77437
Date	Thu Jan 5 12:29:18 GMT 2012
Unique Job ID	df3a97ad84902093

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rkoL_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**nadh-quinone oxidoreductase subunit l; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
2	c3rkoM_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**nadh-quinone oxidoreductase subunit m; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
3	c3rkoN_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**nadh-quinone oxidoreductase subunit n; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
4	c3rkoK_	Alignment		40.9	17	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**nadh-quinone oxidoreductase subunit k; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
5	c2l3iA_	Alignment		34.4	58	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**aoxki4a, antimicrobial peptide in spider venom; **PDBTitle:** oxki4a, spider derived antimicrobial peptide
6	d1o8bb1	Alignment		22.7	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
7	c2kncA_	Alignment		20.6	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
8	d1a6qa1	Alignment		20.2	20	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
9	d1s1qa_	Alignment		15.5	31	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
10	d2gf4a1	Alignment		12.6	10	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Vng1086c-like **Family:**Vng1086c-like
11	c3u7jA_	Alignment		12.4	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis

12	c3arcl_	Alignment		12.3	13	**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
13	c3bz1L_	Alignment		11.8	13	**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
14	d2axtl1	Alignment		11.8	13	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
15	c3a0hL_	Alignment		11.8	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
16	c3arcL_	Alignment		11.8	13	**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
17	c2axtl_	Alignment		11.8	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
18	c2axtL_	Alignment		11.8	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
19	c1s5ll_	Alignment		11.8	13	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
20	c1s5lL_	Alignment		11.8	13	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
21	c3prqL_	Alignment	not modelled	11.8	13	**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
22	c3kziL_	Alignment	not modelled	11.8	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
23	c3prrL_	Alignment	not modelled	11.8	13	**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
24	c3a0bl_	Alignment	not modelled	11.8	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
25	c3bz2L_	Alignment	not modelled	11.8	13	**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
26	c3a0bL_	Alignment	not modelled	11.8	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
27	c3a0hl_	Alignment	not modelled	11.8	13	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
28	d1xmec1	Alignment	not modelled	11.4	15	**Fold:**Single transmembrane helix **Superfamily:**Bacterial ba3 type cytochrome c oxidase subunit IIa **Family:**Bacterial ba3 type cytochrome c oxidase subunit IIa

29	c3na2C_	Alignment	not modelled	10.7	58	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from mine drainage2 metagenome leptospirillum rubarum
30	c3c25A_	Alignment	not modelled	10.6	67	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**noti restriction endonuclease; **PDBTitle:** crystal structure of noti restriction endonuclease bound to cognate2 dna
31	d1n9wa2	Alignment	not modelled	10.0	63	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
32	c1n9wA_	Alignment	not modelled	9.9	63	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase 2; **PDBTitle:** crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
33	c3rkoF_	Alignment	not modelled	9.8	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nadh-quinone oxidoreductase subunit j; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
34	c3bjuB_	Alignment	not modelled	9.3	38	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
35	d1j4na_	Alignment	not modelled	8.9	9	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
36	c1b8aB_	Alignment	not modelled	8.6	63	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
37	d3d37a2	Alignment	not modelled	8.3	57	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
38	d1bcce2	Alignment	not modelled	8.3	5	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
39	c1wydB_	Alignment	not modelled	8.3	63	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
40	c1x55A_	Alignment	not modelled	8.1	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase; **PDBTitle:** crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
41	c2k1aA_	Alignment	not modelled	8.1	16	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
42	c1e22A_	Alignment	not modelled	8.1	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
43	c2xgtB_	Alignment	not modelled	8.0	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic; **PDBTitle:** asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
44	c3r24A_	Alignment	not modelled	7.9	33	**PDB header:**transferase, viral protein **Chain:** A: **PDB Molecule:**2'-o-methyl transferase; **PDBTitle:** crystal structure of nsp10/nsp16 complex of sars coronavirus" if2 possible
45	c2ks1B_	Alignment	not modelled	7.8	18	**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
46	c3mesB_	Alignment	not modelled	7.7	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline kinase; **PDBTitle:** crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
47	c1asyA_	Alignment	not modelled	7.6	38	**PDB header:**complex (aminoacyl-trna synthase/trna) **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
48	c2kwtA_	Alignment	not modelled	7.5	29	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protease ns2-3; **PDBTitle:** solution structure of ns2 [27-59]
49	c1ceuA_	Alignment	not modelled	7.4	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hiv-1 regulatory protein n-terminal **PDBTitle:** nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
50	c2p04B_	Alignment	not modelled	7.3	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**signal transduction histidine kinase; **PDBTitle:** 2.1 ang structure of the dimerized pas domain of signal transduction2 histidine kinase from nostoc punctiforme pcc 73102 with homology to3 the h-noxa/h-noba domain of the soluble guanylyl cyclase
51	d1unca_	Alignment	not modelled	7.2	21	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
52	c2re3A_	Alignment	not modelled	7.2	45	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
						Fold:VHP, Villin headpiece domain

53	d1yu8x1	Alignment	not modelled	7.1	22	**Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
54	d1ppje2	Alignment	not modelled	7.0	5	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
55	c3e9hB_	Alignment	not modelled	7.0	50	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
56	c1efwA_	Alignment	not modelled	7.0	38	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli
57	d1r6ra_	Alignment	not modelled	7.0	19	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
58	c1r6rA_	Alignment	not modelled	7.0	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** solution structure of dengue virus capsid protein reveals a2 new fold
59	c3m4qA_	Alignment	not modelled	6.9	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
60	d1unda_	Alignment	not modelled	6.9	22	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
61	c2ejbA_	Alignment	not modelled	6.5	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
62	c2voyK_	Alignment	not modelled	6.5	23	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
63	d2axti1	Alignment	not modelled	6.4	13	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
64	d1jhda1	Alignment	not modelled	6.2	11	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
65	d1oqwa_	Alignment	not modelled	6.2	20	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
66	d2f05a1	Alignment	not modelled	6.2	30	**Fold:**PAH2 domain **Superfamily:**PAH2 domain **Family:**PAH2 domain
67	d1ca1a2	Alignment	not modelled	6.2	11	**Fold:**Lipase/lipooxygenase domain (PLAT/LH2 domain) **Superfamily:**Lipase/lipooxygenase domain (PLAT/LH2 domain) **Family:**Alpha-toxin, C-terminal domain
68	c3kv0A_	Alignment	not modelled	6.2	57	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**het-c2; **PDBTitle:** crystal structure of het-c2: a fungal glycolipid transfer protein2 (gltp)
69	d1swxa_	Alignment	not modelled	6.1	30	**Fold:**Glycolipid transfer protein, GLTP **Superfamily:**Glycolipid transfer protein, GLTP **Family:**Glycolipid transfer protein, GLTP
70	d1l0wa3	Alignment	not modelled	6.1	38	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
71	c3rpfC_	Alignment	not modelled	5.9	33	**PDB header:**transferase **Chain:** C: **PDB Molecule:**molybdopterin converting factor, subunit 1 (moad); **PDBTitle:** protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
72	c2pjmA_	Alignment	not modelled	5.9	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
73	d1c0aa3	Alignment	not modelled	5.9	38	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
74	c1eqrC_	Alignment	not modelled	5.8	38	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
75	c3jzdA_	Alignment	not modelled	5.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of putative alcohol dehedrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
76	d1qzpa_	Alignment	not modelled	5.7	7	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
77	d1eova2	Alignment	not modelled	5.7	38	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
78	c2jwaA_	Alignment	not modelled	5.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
						Fold: Class II aaRS and biotin synthetases

79	d1b8aa2	Alignment	not modelled	5.7	63	**Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
80	d1x6va1	Alignment	not modelled	5.7	33	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
81	d1zvpa1	Alignment	not modelled	5.6	22	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
82	c3i7fA_	Alignment	not modelled	5.6	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
83	c3bwrC_	Alignment	not modelled	5.6	38	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**capsid protein vp1; **PDBTitle:** sv40 vp1 pentamer in complex with gm1 oligosaccharide
84	c2k6nA_	Alignment	not modelled	5.6	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**supervillin; **PDBTitle:** solution structure of human supervillin headpiece, minimized2 average
85	d1uzxa_	Alignment	not modelled	5.6	27	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
86	c2l3xA_	Alignment	not modelled	5.6	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ablim2 protein; **PDBTitle:** villin head piece domain of human ablim2
87	c2i3fA_	Alignment	not modelled	5.6	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glycolipid transfer-like protein; **PDBTitle:** crystal structure of a glycolipid transfer-like protein2 from galdieria sulphuraria
88	d1yu5x1	Alignment	not modelled	5.5	22	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
89	c2uwjG_	Alignment	not modelled	5.5	42	**PDB header:**chaperone **Chain:** G: **PDB Molecule:**type iii export protein pscg; **PDBTitle:** structure of the heterotrimeric complex which regulates2 type iii secretion needle formation
90	c3pisA_	Alignment	not modelled	5.4	38	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**kazal-type serine protease inhibitor spi-1; **PDBTitle:** crystal structure of carcinoscorpius rotundicauda serine protease2 inhibitor domain 1
91	d1sva1_	Alignment	not modelled	5.4	38	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group I dsDNA viruses **Family:**Papovaviridae-like VP
92	d1ujsa_	Alignment	not modelled	5.4	11	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
93	c1v55B_	Alignment	not modelled	5.3	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** bovine heart cytochrome c oxidase at the fully reduced state
94	d1sbza_	Alignment	not modelled	5.3	30	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
95	c3mk7F_	Alignment	not modelled	5.1	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
96	c3sokB_	Alignment	not modelled	5.1	24	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
97	d2axte1	Alignment	not modelled	5.1	26	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome b559 subunits **Family:**Cytochrome b559 subunits
98	c1h2sB_	Alignment	not modelled	5.0	27	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**sensory rhodopsin ii transducer; **PDBTitle:** molecular basis of transmenbrane signalling by sensory2 rhodopsin ii-transducer complex