Phyre^2

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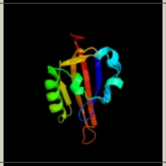
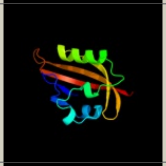
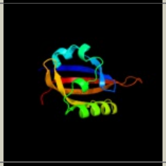
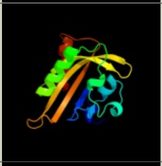
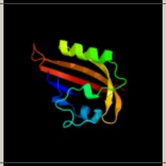
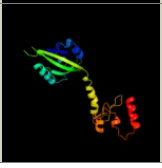
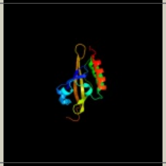
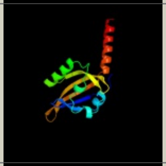
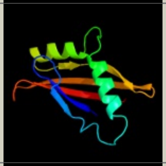
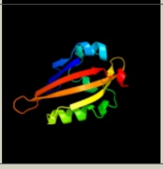
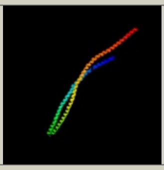
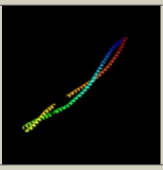
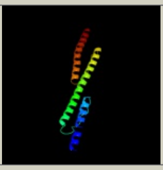
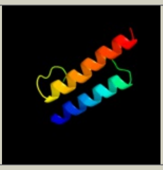
Description	P50466
Date	Thu Jan 5 12:04:47 GMT 2012
Unique Job ID	dcf4218dc4c88ada

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wkqA_	Alignment		99.9	20	**PDB header:**transferase, cell adhesion **Chain:** A: **PDB Molecule:**nph1-1, ras-related c3 botulinum toxin substrate **PDBTitle:** structure of a photoactivatable rac1 containing the lov22 c450a mutant
2	d1p97a_	Alignment		99.8	19	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Hypoxia-inducible factor Hif2a, C-terminal domain
3	c3rtyA_	Alignment		99.8	6	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** structure of an enclosed dimer formed by the drosophila period protein
4	d1jnua_	Alignment		99.8	19	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
5	c2z6dB_	Alignment		99.8	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phototropin-2; **PDBTitle:** crystal structure of lov1 domain of phototropin2 from2 arabidopsis thaliana
6	d1bywa_	Alignment		99.7	18	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
7	c3f1oB_	Alignment		99.7	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**aryl hydrocarbon receptor nuclear translocator; **PDBTitle:** crystal structure of the high affinity heterodimer of hif22 alpha and arnt c-terminal pas domains, with an internally-3 bound artificial ligand
8	c2v1bA_	Alignment		99.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nph1-1; **PDBTitle:** n- and c-terminal helices of oat lov2 (404-546) are2 involved in light-induced signal transduction (room3 temperature (293k) light structure of lov2 (404-546))
9	c2kdkA_	Alignment		99.7	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**aryl hydrocarbon receptor nuclear translocator-like protein **PDBTitle:** structure of human circadian clock protein bmal2 c-terminal pas domain
10	d1n9la_	Alignment		99.7	22	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Flavin-binding PAS domain
11	c3ewkA_	Alignment		99.7	30	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos

12	c2vlgD_	Alignment		99.7	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sporulation kinase a; **PDBTitle:** kina pas-a domain, homodimer
13	c3gdiB_	Alignment		99.7	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**period circadian protein homolog 2; **PDBTitle:** mammalian clock protein mper2 - crystal struture of a pas2 domain fragment
14	c2pr6A_	Alignment		99.7	22	**PDB header:**flavoprotein, signaling protein **Chain:** A: **PDB Molecule:**blue-light photoreceptor; **PDBTitle:** structural basis for light-dependent signaling in the dimeric lov2 photosensor ytva (light structure)
15	c2l4rA_	Alignment		99.7	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily h member 2; **PDBTitle:** nmr solution structure of the n-terminal pas domain of herg
16	d1oj5a_	Alignment		99.7	12	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PAS domain of steroid receptor coactivator 1A, NCo-A1
17	c3mjqB_	Alignment		99.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the pas domain of q24qt8_deshy protein from2 desulfitobacterium hafniense. northeast structural genomics3 consortium target dhr85c.
18	c3lyxA_	Alignment		99.6	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sensory box/ggdef domain protein; **PDBTitle:** crystal structure of the pas domain of the protein cps_12912 from colwellia psychrerythraea. northeast structural3 genomics consortium target id csr222b
19	c2gj3A_	Alignment		99.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nitrogen fixation regulatory protein; **PDBTitle:** crystal structure of the fad-containing pas domain of the2 protein nifl from azotobacter vinelandii.
20	c3h9wA_	Alignment		99.6	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**diguanylate cyclase with pas/pac sensor; **PDBTitle:** crystal structure of the n-terminal domain of diguanylate cyclase with2 pas/pac sensor (maqu_2914) from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr66c
21	c3oloB_	Alignment	not modelled	99.6	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**two-component sensor histidine kinase; **PDBTitle:** crystal structure of a pas domain from two-component sensor histidine2 kinase
22	c2pdtD_	Alignment	not modelled	99.6	19	**PDB header:**circadian clock protein **Chain:** D: **PDB Molecule:**vivid pas protein vvd; **PDBTitle:** 2.3 angstrom structure of phosphodiesterase treated vivid
23	c3mqoB_	Alignment	not modelled	99.6	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** the crystal structure of the pas domain in complex with isopropanol of2 a transcriptional regulator in the luxr family from burkholderia3 thailandensis to 1.7a
24	c3b33A_	Alignment	not modelled	99.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the pas domain of nitrogen regulation protein2 nr(ii) from vibrio parahaemolyticus
25	d1xj3a1	Alignment	not modelled	99.6	16	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
26	c1v9yA_	Alignment	not modelled	99.6	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**heme pas sensor protein; **PDBTitle:** crystal structure of the heme pas sensor domain of ec dos (ferric2 form)
27	d1v9ya_	Alignment	not modelled	99.6	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
28	c3caxA_	Alignment	not modelled	99.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf0695; **PDBTitle:** crystal structure of uncharacterized protein pf0695

29	c3gecA_	Alignment	not modelled	99.6	11	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** crystal structure of a tandem pas domain fragment of2 drosophila period
30	c1wa9A_	Alignment	not modelled	99.6	9	**PDB header:**circadian rhythm **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** crystal structure of the pas repeat region of the2 drosophila clock protein period
31	c3mfxA_	Alignment	not modelled	99.6	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sensory box/ggdef family protein; **PDBTitle:** crystal structure of the sensory box domain of the sensory-2 box/ggdef protein so_1695 from shewanella oneidensis,3 northeast structural genomics consortium target sor288b
32	d1ew0a_	Alignment	not modelled	99.5	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
33	d1y28a_	Alignment	not modelled	99.5	14	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
34	c3fg8B_	Alignment	not modelled	99.5	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rha05790; **PDBTitle:** crystal structure of pas domain of rha05790
35	c3luqC_	Alignment	not modelled	99.5	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of a pas domain from a sensory box2 histidine kinase regulator from geobacter sulfurreducens to3 2.5a
36	c3p7nB_	Alignment	not modelled	99.5	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
37	c2r78D_	Alignment	not modelled	99.5	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of a domain of the sensory box sensor2 histidine kinase/response regulator from geobacter3 sulfurreducens
38	c3bwlA_	Alignment	not modelled	99.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
39	c3mr0B_	Alignment	not modelled	99.5	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**sensory box histidine kinase/response regulator; **PDBTitle:** crystal structure of sensory box histidine kinase/response regulator2 from burkholderia thailandensis e264
40	c3fc7B_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**htr-like protein; **PDBTitle:** the crystal structure of a domain of htr-like protein from haloarcula2 marismortui atcc 43049
41	d1ll8a_	Alignment	not modelled	99.4	18	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**N-terminal PAS domain of Pas kinase
42	c3a0vA_	Alignment	not modelled	99.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)
43	c3eehA_	Alignment	not modelled	99.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative light and redox sensing histidine kinase; **PDBTitle:** the crystal structure of the domain of the putative light and redox2 sensing histidine kinase from haloarcula marismortui
44	c1qu7A_	Alignment		99.4	51	**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
45	c3njaC_	Alignment	not modelled	99.4	10	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**probable ggdef family protein; **PDBTitle:** the crystal structure of the pas domain of a ggdef family protein from2 chromobacterium violaceum atcc 12472.
46	d1nwza_	Alignment	not modelled	99.3	9	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
47	d1otda_	Alignment	not modelled	99.3	10	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
48	c3mxqC_	Alignment	not modelled	99.3	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
49	d1mzua_	Alignment	not modelled	99.3	11	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
50	c3icyB_	Alignment	not modelled	99.3	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of sensory box histidine2 kinase/response regulator domain from chlorobium tepidum3 tls
51	d1xfna1	Alignment	not modelled	99.2	9	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
52	c2oolA_	Alignment	not modelled	99.2	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbphp3 from r. palustris
						PDB header:signaling protein

53	c3k3dA_	Alignment	not modelled	99.2	18	**Chain:** A: **PDB Molecule:**protein rv1364c/mt1410; **PDBTitle:** the n-terminal pas domain crystal structure of rv1364c from2 mycobacterium tuberculosis at 2.3 angstrom
54	c2o9bA_	Alignment	not modelled	99.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
55	c3a0rA_	Alignment	not modelled	99.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
56	c2qkpD_	Alignment	not modelled	99.1	11	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans
57	c2jheB_	Alignment	not modelled	99.0	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription regulator tyrr; **PDBTitle:** n-terminal domain of tyrr transcription factor (residues 1 -2 190)
58	c3kx0X_	Alignment	not modelled	99.0	19	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**uncharacterized protein rv1364c/mt1410; **PDBTitle:** crystal structure of the pas domain of rv1364c
59	c2w0nA_	Alignment	not modelled	98.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein dcus; **PDBTitle:** plasticity of pas domain and potential role for signal2 transduction in the histidine-kinase dcus
60	c2veaA_	Alignment	not modelled	98.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phytochrome-like protein cph1; **PDBTitle:** the complete sensory module of the cyanobacterial2 phytochrome cph1 in the pr-state.
61	c2ch7A_	Alignment		98.9	22	**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
62	c3cloC_	Alignment	not modelled	98.7	10	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
63	c3g67A_	Alignment	not modelled	98.3	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of a soluble chemoreceptor from thermotoga2 maritima
64	c3c2wB_	Alignment	not modelled	97.8	14	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of the photosensory core domain of p.2 aeruginosa bacteriophytochrome pabphp in the pfr state
65	c3lnrA_	Alignment		97.4	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**aerotaxis transducer aer2; **PDBTitle:** crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
66	d2oola2	Alignment	not modelled	97.2	7	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**BphP N-terminal domain-like
67	d2o9ca2	Alignment	not modelled	96.6	13	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**BphP N-terminal domain-like
68	d3c2wa3	Alignment	not modelled	95.9	16	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**BphP N-terminal domain-like
69	d2veaa3	Alignment	not modelled	95.6	12	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**BphP N-terminal domain-like
70	d2asxa1	Alignment		95.2	29	**Fold:**HAMP domain-like **Superfamily:**HAMP domain-like **Family:**HAMP domain
71	c2rm8A_	Alignment	not modelled	93.8	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sensory rhodopsin ii transducer; **PDBTitle:** the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis
72	c3zrwB_	Alignment	not modelled	92.2	19	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**af1503 protein, osmolarity sensor protein envz; **PDBTitle:** the structure of the dimeric hamp-dhp fusion a291v mutant
73	c2wpqA_	Alignment	not modelled	89.2	6	**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)
74	d1p0za_	Alignment	not modelled	88.9	19	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
75	c1ei3E_	Alignment	not modelled	88.7	9	**PDB header:** **PDB COMPND:**

76	c3ghgK_	Alignment	not modelled	78.7	14	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
77	c1deqO_	Alignment	not modelled	78.1	15	**PDB header:** **PDB COMPND:**
78	c3fosA_	Alignment	not modelled	77.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of two-component sensor histidine kinase domain from2 bacillus subtilis subsp. subtilis str. 168
79	c1sfcJ_	Alignment	not modelled	75.1	3	**PDB header:**transport protein **Chain:** J: **PDB Molecule:**protein (syntaxin 1a); **PDBTitle:** neuronal synaptic fusion complex
80	c1ei3C_	Alignment	not modelled	74.7	7	**PDB header:** **PDB COMPND:**
81	c3b5nF_	Alignment	not modelled	74.1	13	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**protein sso1; **PDBTitle:** structure of the yeast plasma membrane snare complex
82	c3ojaB_	Alignment	not modelled	73.6	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
83	c2qhkA_	Alignment	not modelled	70.0	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of methyl-accepting chemotaxis protein from vibrio2 parahaemolyticus rimd 2210633
84	c1m1jA_	Alignment	not modelled	64.2	10	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**fibrinogen alpha subunit; **PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands
85	d1joya_	Alignment	not modelled	63.8	15	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
86	c3ipdB_	Alignment	not modelled	63.7	3	**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
87	c2npsB_	Alignment	not modelled	62.4	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**syntaxin 13; **PDBTitle:** crystal structure of the early endosomal snare complex
88	d3by8a1	Alignment	not modelled	61.9	23	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
89	c1deqF_	Alignment	not modelled	58.0	7	**PDB header:** **PDB COMPND:**
90	c1n7sB_	Alignment	not modelled	57.5	3	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**syntaxin 1a; **PDBTitle:** high resolution structure of a truncated neuronal snare2 complex
91	c3ka5A_	Alignment	not modelled	56.5	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**ribosome-associated protein y (psrp-1); **PDBTitle:** crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
92	d2p7ja2	Alignment	not modelled	48.5	10	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Ykul C-terminal domain-like
93	c1kmiZ_	Alignment	not modelled	48.2	13	**PDB header:**signaling protein **Chain:** Z: **PDB Molecule:**chemotaxis protein chez; **PDBTitle:** crystal structure of an e.coli chemotaxis protein, chez
94	d2c2aa1	Alignment	not modelled	46.9	14	**Fold:**ROP-like **Superfamily:**Homodimeric domain of signal transducing histidine kinase **Family:**Homodimeric domain of signal transducing histidine kinase
95	c2qltA_	Alignment	not modelled	43.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(dl)-glycerol-3-phosphatase 1; **PDBTitle:** crystal structure of an isoform of dl-glycerol-3-phosphatase, rhr2p,2 from saccharomyces cerevisiae
96	c3k2tA_	Alignment	not modelled	42.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2511 protein; **PDBTitle:** crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
97	c3lifA_	Alignment	not modelled	40.5	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative diguanylate cyclase (ggdef) with pas/pac domain; **PDBTitle:** crystal structure of the extracellular domain of the putative2 histidine kinase rphk1s-z16
98	c3c25A_	Alignment	not modelled	34.2	17	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**noti restriction endonuclease; **PDBTitle:** crystal structure of noti restriction endonuclease bound to cognate2 dna
99	c2d4yA_	Alignment	not modelled	31.9	8	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**flagellar hook-associated protein 1; **PDBTitle:** crystal structure of a 49k fragment of hap1 (flgk)
100	c1s94A_	Alignment	not modelled	30.0	6	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**s-syntaxin; **PDBTitle:** crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
101	d1s94a_	Alignment	not modelled	30.0	6	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins

102	c2d3eD_	 Alignment	not modelled	25.5	8	**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
103	c2p7jA_	 Alignment	not modelled	25.0	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative sensory box/ggdef family protein; **PDBTitle:** crystal structure of the domain of putative sensory box/ggdef family2 protein from vibrio parahaemolyticus
104	c3u59C_	 Alignment	not modelled	21.8	14	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
105	c2pkeA_	 Alignment	not modelled	21.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid delahogenase-like family hydrolase; **PDBTitle:** crystal structure of haloacid delahogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution
106	c2xhaB_	 Alignment	not modelled	21.4	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)