Phyre^2

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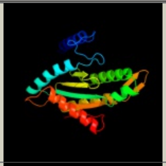
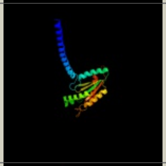
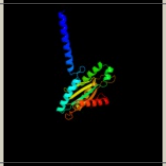
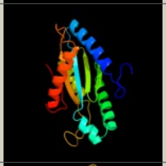
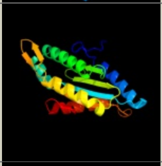
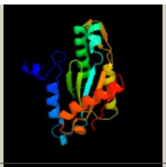
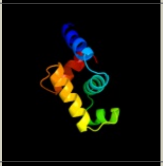
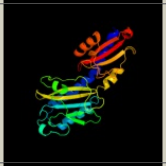
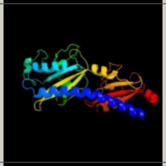
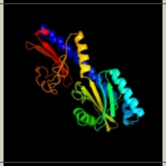
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w25B_	Alignment		100.0	34	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
2	c3ezuA_	Alignment		100.0	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef domain protein; **PDBTitle:** crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
3	c3breA_	Alignment		100.0	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
4	c3i5aA_	Alignment		100.0	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
5	c3i5cA_	Alignment		100.0	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fusion of general control protein gcn4 and wspr response **PDBTitle:** crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa
6	c3i5bA_	Alignment		100.0	34	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
7	c3ignA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase; **PDBTitle:** crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a
8	c3hvaA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
9	c3qyyB_	Alignment		100.0	31	**PDB header:**signaling protein/inhibitor **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp
10	c3iclA_	Alignment		100.0	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**eal/ggdef domain protein; **PDBTitle:** x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c
11	d1w25a3	Alignment		100.0	38	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain

12	c3mtkA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase/phosphodiesterase; **PDBTitle:** x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
13	c3pjwA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
14	c3hvwA_	Alignment		100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diguanylate-cyclase (dgc); **PDBTitle:** crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
15	c3gfzB_	Alignment		99.8	10	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
16	c3p7nB_	Alignment		99.0	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
17	c3liaA_	Alignment		98.0	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**hypothetical sensory transduction histidine kinase; **PDBTitle:** crystal structure of the extracellular domain of the putative2 histidine kinase mmhk1s-z2
18	c3libA_	Alignment		98.0	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**hypothetical sensory transduction histidine kinase; **PDBTitle:** crystal structure of the extracellular domain of the putative2 histidine kinase mmhk1s-z3
19	c2p7jA_	Alignment		97.6	14	**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
20	c3licA_	Alignment		97.6	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the extracellular domain of the putative2 histidine kinase sohk1s-z6
21	c3c8cB_	Alignment	not modelled	97.3	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of mcp_n and cache domains of methyl-2 accepting chemotaxis protein from vibrio cholerae
22	c2qv6D_	Alignment	not modelled	97.3	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii; **PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
23	c3fosA_	Alignment	not modelled	97.3	16	**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
24	c3e4pB_	Alignment	not modelled	97.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**c4-dicarboxylate transport sensor protein dctb; **PDBTitle:** crystal structure of malonate occupied dctb
25	c3lifA_	Alignment	not modelled	97.0	12	**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
26	c1cjkA_	Alignment	not modelled	96.9	8	**PDB header:**lyase/lyase/signaling protein **Chain:** A: **PDB Molecule:**adenylate cyclase, type v; **PDBTitle:** complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
27	d1azsa_	Alignment	not modelled	96.7	8	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
28	c2w01C_	Alignment	not modelled	96.2	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**adenylate cyclase;

						PDBTitle: crystal structure of the guanylyl cyclase cya2
29	c3by9A_	Alignment	not modelled	95.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the v. cholerae histidine kinase dctb2 sensor domain
30	d1wc1a_	Alignment	not modelled	95.9	14	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
31	c3mr7B_	Alignment	not modelled	95.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenylate/guanylate cyclase/hydrolase, alpha/beta fold **PDBTitle:** crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
32	c1wc6B_	Alignment	not modelled	95.7	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
33	d1fx2a_	Alignment	not modelled	95.4	14	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
34	c3uvjC_	Alignment	not modelled	94.8	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**guanylate cyclase soluble subunit alpha-3; **PDBTitle:** crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
35	d2p7ja2	Alignment	not modelled	94.1	15	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**YkuI C-terminal domain-like
36	c1yk9A_	Alignment	not modelled	93.5	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
37	c1y10C_	Alignment	not modelled	93.5	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
38	c1ybuA_	Alignment	not modelled	92.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipj; **PDBTitle:** mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
39	c3r5gB_	Alignment	not modelled	92.9	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cyab; **PDBTitle:** crystal structure of the adenylyl cyclase cyab from p. aeruginosa
40	d1fx4a_	Alignment	not modelled	92.5	27	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
41	c2aq4A_	Alignment	not modelled	88.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp.
42	c3et6A_	Alignment	not modelled	86.9	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**soluble guanylyl cyclase beta; **PDBTitle:** the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
43	c3onqB_	Alignment	not modelled	86.5	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**regulator of polyketide synthase expression; **PDBTitle:** crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
44	c1k1qA_	Alignment	not modelled	80.3	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dbh protein; **PDBTitle:** crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
45	c3mr2A_	Alignment	not modelled	79.7	31	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
46	d2basa2	Alignment	not modelled	79.5	14	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**YkuI C-terminal domain-like
47	c1s97D_	Alignment	not modelled	78.6	25	**PDB header:**transferase/dna **Chain:** D: **PDB Molecule:**dna polymerase iv; **PDBTitle:** dpo4 with gt mismatch
48	c3gqcB_	Alignment	not modelled	76.8	20	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
49	c2wz1B_	Alignment	not modelled	76.8	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**guanylate cyclase soluble subunit beta-1; **PDBTitle:** structure of the catalytic domain of human soluble2 guanylate cyclase 1 beta 3.
50	d1jx4a2	Alignment	not modelled	74.5	21	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
51	c2r8kB_	Alignment	not modelled	74.0	30	**PDB header:**replication, transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase eta; **PDBTitle:** structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna
52	d1im4a_	Alignment	not modelled	71.5	25	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
53	d1azsb_	Alignment	not modelled	70.0	13	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain

54	d1k1sa2	Alignment	not modelled	66.7	25	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
55	c2oh2B_	Alignment	not modelled	66.6	23	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
56	c1jihA_	Alignment	not modelled	65.9	30	**PDB header:**translation **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** yeast dna polymerase eta
57	d1jiha2	Alignment	not modelled	59.0	30	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
58	d1gx1a_	Alignment	not modelled	56.9	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
59	c2fllA_	Alignment	not modelled	55.5	31	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** ternary complex of human dna polymerase iota with dna and dttp
60	d1t0aa_	Alignment	not modelled	50.7	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
61	c3f0gA_	Alignment	not modelled	48.8	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
62	c1t3nB_	Alignment	not modelled	48.8	21	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**polymerase (dna directed) iota; **PDBTitle:** structure of the catalytic core of dna polymerase iota in2 complex with dna and dttp
63	d1w55a2	Alignment	not modelled	47.8	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
64	c3oheA_	Alignment	not modelled	47.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
65	d1iv3a_	Alignment	not modelled	43.7	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
66	c2pmpA_	Alignment	not modelled	43.3	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
67	c3l7xA_	Alignment	not modelled	37.0	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative hit-like protein involved in cell-cycle **PDBTitle:** the crystal structure of smu.412c from streptococcus mutans ua159
68	c3p0tB_	Alignment	not modelled	34.6	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
69	c3i24B_	Alignment	not modelled	34.1	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family hydrolase; **PDBTitle:** crystal structure of a hit family hydrolase protein from2 vibrio fischeri. northeast structural genomics consortium3 target id vfr176
70	c1t94B_	Alignment	not modelled	33.0	21	**PDB header:**replication **Chain:** B: **PDB Molecule:**polymerase (dna directed) kappa; **PDBTitle:** crystal structure of the catalytic core of human dna2 polymerase kappa
71	d2o5aa1	Alignment	not modelled	28.7	21	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
72	d1y23a_	Alignment	not modelled	28.2	12	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
73	d1yhta1	Alignment	not modelled	25.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
74	c1xaxA_	Alignment	not modelled	23.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004; **PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
75	c2ylaA_	Alignment	not modelled	23.5	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
76	c2yl8A_	Alignment	not modelled	23.4	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
77	c3imiB_	Alignment	not modelled	23.0	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
78	c1qgeE_	Alignment	not modelled	22.4	23	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
						Fold:TIM beta/alpha-barrel

79	d1vr6a1	Alignment	not modelled	22.0	18	**Superfamily:**Aldolase **Family:**Class I DAHP synthetase
80	c3rpmA_	Alignment	not modelled	21.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetyl-hexosaminidase; **PDBTitle:** crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
81	d1vh8a_	Alignment	not modelled	21.0	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
82	c3b6nA_	Alignment	not modelled	20.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate **PDBTitle:** crystal structure of 2c-methyl-d-erythritol 2,4-2 cyclodiphosphate synthase pv003920 from plasmodium vivax
83	d2axta1	Alignment	not modelled	18.3	16	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
84	c3nrdB_	Alignment	not modelled	17.9	17	**PDB header:**nucleotide binding protein **Chain:** B: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
85	d1fi4a1	Alignment	not modelled	17.3	26	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
86	c3fgeA_	Alignment	not modelled	17.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative flavin reductase with split barrel domain; **PDBTitle:** crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution
87	d1l9bm_	Alignment	not modelled	16.9	23	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
88	c2yf0A_	Alignment	not modelled	16.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**myotubularin-related protein 6; **PDBTitle:** human myotubularin related protein 6 (mtmr6)
89	d1t94a2	Alignment	not modelled	16.5	30	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
90	d1eysl_	Alignment	not modelled	16.4	26	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
91	d2i5nl1	Alignment	not modelled	16.3	32	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
92	d2axtd1	Alignment	not modelled	15.7	16	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
93	d2j8cl1	Alignment	not modelled	15.3	26	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
94	d2i5nm1	Alignment	not modelled	15.2	26	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
95	d1oz9a_	Alignment	not modelled	15.1	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
96	d1zsqa2	Alignment	not modelled	13.8	10	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Myotubularin-like phosphatases
97	d1eysm_	Alignment	not modelled	13.8	26	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
98	d2j8cm1	Alignment	not modelled	13.7	23	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
99	c1m04A_	Alignment	not modelled	13.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)