Phyre^2

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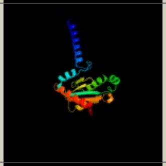
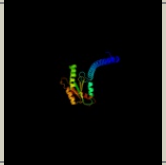
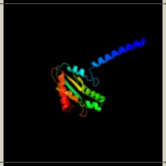
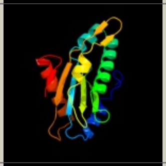
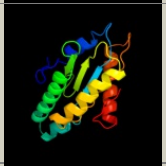
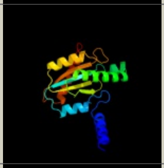
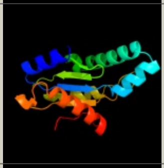
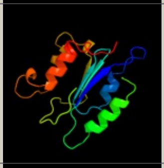
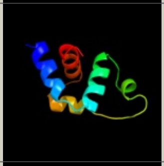
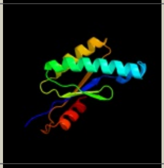
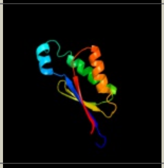
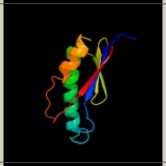
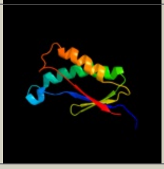
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w25B_	Alignment		100.0	32	**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	24	**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	26	**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	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
5	c3qyyB_	Alignment		100.0	27	**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
6	c3i5cA_	Alignment		100.0	30	**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
7	c3i5bA_	Alignment		100.0	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
8	c3hvaA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
9	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
10	c3ignA_	Alignment		100.0	30	**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
11	d1w25a3	Alignment		100.0	38	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain

12	c3mtkA_	Alignment		100.0	24	**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	24	**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	13	**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	13	**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		98.9	8	**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	c2qv6D_	Alignment		97.7	22	**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
18	d1fx2a_	Alignment		94.7	16	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
19	c1wc6B_	Alignment		93.6	14	**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
20	c3mr7B_	Alignment		92.7	9	**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
21	c1cjkA_	Alignment	not modelled	91.6	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
22	c2w01C_	Alignment	not modelled	91.4	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the guanylyl cyclase cya2
23	d1wc1a_	Alignment	not modelled	91.0	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
24	c1s97D_	Alignment	not modelled	90.2	15	**PDB header:**transferase/dna **Chain:** D: **PDB Molecule:**dna polymerase iv; **PDBTitle:** dpo4 with gt mismatch
25	c2aq4A_	Alignment	not modelled	89.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp.
26	c1ybuA_	Alignment	not modelled	88.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipj; **PDBTitle:** mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
27	d1azsa_	Alignment	not modelled	88.2	8	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
28	d1fx4a_	Alignment	not modelled	88.0	14	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
						PDB header:lyase

29	c3uvjC_	Alignment	not modelled	87.8	13	**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.
30	c3gqcB_	Alignment	not modelled	87.7	19	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
31	c1k1qA_	Alignment	not modelled	84.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dbh protein; **PDBTitle:** crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
32	d1k1sa2	Alignment	not modelled	83.9	15	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
33	c2r8kB_	Alignment	not modelled	80.0	24	**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
34	c3onqB_	Alignment	not modelled	79.7	4	**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
35	d1jx4a2	Alignment	not modelled	78.6	13	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
36	d1im4a_	Alignment	not modelled	76.2	14	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
37	c1jihA_	Alignment	not modelled	74.9	24	**PDB header:**translation **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** yeast dna polymerase eta
38	c3et6A_	Alignment	not modelled	72.6	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**soluble guanylyl cyclase beta; **PDBTitle:** the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
39	c1yk9A_	Alignment	not modelled	72.3	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
40	d1jiha2	Alignment	not modelled	65.7	23	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
41	c1t3nB_	Alignment	not modelled	65.3	34	**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
42	c2fllA_	Alignment	not modelled	63.1	31	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** ternary complex of human dna polymerase iota with dna and dttp
43	c1t94B_	Alignment	not modelled	62.2	24	**PDB header:**replication **Chain:** B: **PDB Molecule:**polymerase (dna directed) kappa; **PDBTitle:** crystal structure of the catalytic core of human dna2 polymerase kappa
44	c2oh2B_	Alignment	not modelled	62.0	21	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
45	c3mr2A_	Alignment	not modelled	60.4	23	**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	c1y10C_	Alignment	not modelled	56.1	9	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
47	c2wz1B_	Alignment	not modelled	44.7	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.
48	d1t94a2	Alignment	not modelled	30.8	23	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
49	c1vloA_	Alignment	not modelled	29.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of aminomethyltransferase (t protein;2 tetrahydrofolate-dependent) of glycine cleavage system (np417381)3 from escherichia coli k12 at 1.70 a resolution
50	d1yhta1	Alignment	not modelled	28.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
51	c3hf3A_	Alignment	not modelled	27.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
52	c3mpbA_	Alignment	not modelled	23.7	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
53	c2h90A_	Alignment	not modelled	21.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
54	d1ps9a1	Alignment	not modelled	19.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases

55	c1rgsA_	Alignment	not modelled	19.7	24	**PDB header:**kinase **Chain:** A: **PDB Molecule:**camp dependent protein kinase; **PDBTitle:** regulatory subunit of camp dependent protein kinase
56	c2byvE_	Alignment	not modelled	18.9	15	**PDB header:**regulation **Chain:** E: **PDB Molecule:**rap guanine nucleotide exchange factor 4; **PDBTitle:** structure of the camp responsive exchange factor epac2 in2 its auto-inhibited state
57	d1mo1a_	Alignment	not modelled	18.8	32	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
58	d1ptfa_	Alignment	not modelled	17.3	14	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
59	c1n13J_	Alignment	not modelled	17.0	17	**PDB header:**lyase **Chain:** J: **PDB Molecule:**pyruvoyl-dependent arginine decarboxylase alpha **PDBTitle:** the crystal structure of pyruvoyl-dependent arginine2 decarboxylase from methanococcus jannashii
60	c3in6A_	Alignment	not modelled	16.8	42	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**fmn-binding protein; **PDBTitle:** crystal structure of a fmn-binding protein (swol_0183) from2 syntrophomonas wolfei subsp. wolfei at 2.12 a resolution
61	d1cm3a_	Alignment	not modelled	16.5	12	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
62	d1zeta2	Alignment	not modelled	16.4	41	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
63	d3c9fa2	Alignment	not modelled	15.8	24	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
64	c3ihsB_	Alignment	not modelled	15.6	28	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphocarrier protein hpr; **PDBTitle:** crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
65	c1o7fA_	Alignment	not modelled	15.1	14	**PDB header:**regulation **Chain:** A: **PDB Molecule:**camp-dependent rap1 guanine-nucleotide exchange **PDBTitle:** crystal structure of the regulatory domain of epac2
66	d1zvvj1	Alignment	not modelled	13.6	32	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
67	c3le1B_	Alignment	not modelled	12.5	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, hpr-related proteins; **PDBTitle:** crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis
68	c3k30B_	Alignment	not modelled	12.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
69	d1qr5a_	Alignment	not modelled	11.9	7	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
70	c3shrA_	Alignment	not modelled	11.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cgmp-dependent protein kinase 1; **PDBTitle:** crystal structure of cgmp-dependent protein kinase reveals novel site2 of interchain communication
71	c2i34B_	Alignment	not modelled	11.8	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** the crystal structure of class c acid phosphatase from bacillus2 anthracis with tungstate bound
72	c3rbuA_	Alignment	not modelled	11.7	19	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** n-terminally avitev-tagged human glutamate carboxypeptidase ii in2 complex with 2-pmpa
73	d1k3xa1	Alignment	not modelled	11.4	30	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
74	c2ootA_	Alignment	not modelled	10.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii
75	d1ka5a_	Alignment	not modelled	10.7	8	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
76	c3c9fB_	Alignment	not modelled	10.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase from candida albicans sc5314
77	d1wosa2	Alignment	not modelled	10.5	21	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**Aminomethyltransferase folate-binding domain
78	d1nowa1	Alignment	not modelled	10.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
79	d1qbaa3	Alignment	not modelled	10.4	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
80	c3of1A_	Alignment	not modelled	10.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**camp-dependent protein kinase regulatory subunit; **PDBTitle:** crystal structure of bcy1, the yeast regulatory subunit of

						pka
81	c1cx8F_	Alignment	not modelled	10.2	16	**PDB header:**metal transport **Chain:** F: **PDB Molecule:**transferrin receptor protein; **PDBTitle:** crytal structure of the ectodomain of human transferrin receptor
82	d1vr6a1	Alignment	not modelled	9.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
83	c3fgeA_	Alignment	not modelled	9.7	23	**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
84	d2o5aa1	Alignment	not modelled	9.7	18	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
85	d1cgme_	Alignment	not modelled	9.6	19	**Fold:**Four-helical up-and-down bundle **Superfamily:**TMV-like viral coat proteins **Family:**TMV-like viral coat proteins
86	d1tdza1	Alignment	not modelled	9.6	40	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
87	c1worA_	Alignment	not modelled	9.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of t-protein of the glycine cleavage2 system
88	d1ei7a_	Alignment	not modelled	9.4	36	**Fold:**Four-helical up-and-down bundle **Superfamily:**TMV-like viral coat proteins **Family:**TMV-like viral coat proteins
89	c3kmlB_	Alignment	not modelled	9.1	36	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**coat protein; **PDBTitle:** circular permutant of the tobacco mosaic virus
90	c3iyuY_	Alignment	not modelled	9.1	19	**PDB header:**virus **Chain:** Y: **PDB Molecule:**outer capsid protein vp4; **PDBTitle:** atomic model of an infectious rotavirus particle
91	c1ps9A_	Alignment	not modelled	9.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
92	c1qbaA_	Alignment	not modelled	9.0	33	**PDB header:**glycosyl hydrolase **Chain:** A: **PDB Molecule:**chitobiase; **PDBTitle:** bacterial chitobiase, glycosyl hydrolase family 20
93	d1ee8a1	Alignment	not modelled	8.8	40	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
94	c2jroA_	Alignment	not modelled	8.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of so0334 from shewanella oneidensis. northeast2 structural genomics target sor75
95	d1vh8a_	Alignment	not modelled	8.5	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
96	c2wk1A_	Alignment	not modelled	8.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**novp; **PDBTitle:** structure of the o-methyltransferase novp
97	d1k82a1	Alignment	not modelled	8.1	30	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
98	c3gveB_	Alignment	not modelled	8.0	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yfkn protein; **PDBTitle:** crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
99	c2ylaA_	Alignment	not modelled	8.0	23	**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