Phyre2

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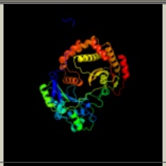
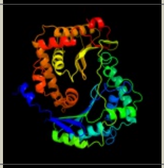
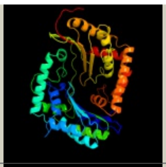
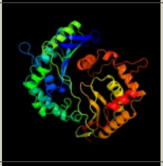
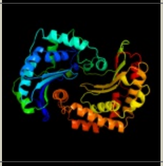
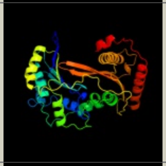
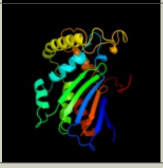
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3go9A_	Alignment		100.0	60	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**insulinase family protease; **PDBTitle:** predicted insulinase family protease from yersinia pestis
2	c1sqpA_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome-c reductase complex core protein i, **PDBTitle:** crystal structure analysis of bovine bc1 with myxothiazol
3	c1hr9D_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mitochondrial processing peptidase beta subunit; **PDBTitle:** yeast mitochondrial processing peptidase beta-e73q mutant2 complexed with malate dehydrogenase signal peptide
4	c1nu1A_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase complex core protein i, **PDBTitle:** crystal structure of mitochondrial cytochrome bc1 complexed with 2-2 nonyl-4-hydroxyquinoline n-oxide (nqno)
5	c1q2lA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease iii; **PDBTitle:** crystal structure of pitrilysin
6	c2wk3A_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**insulin degrading enzyme; **PDBTitle:** crystal structure of human insulin-degrading enzyme in2 complex with amyloid-beta (1-42)
7	c2jbuB_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**insulin-degrading enzyme; **PDBTitle:** crystal structure of human insulin degrading enzyme2 complexed with co-purified peptides.
8	c1hr6C_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mitochondrial processing peptidase alpha subunit; **PDBTitle:** yeast mitochondrial processing peptidase
9	c3hdiA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**processing protease; **PDBTitle:** crystal structure of bacillus halodurans metallo peptidase
10	c3amiB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zinc peptidase; **PDBTitle:** the crystal structure of the m16b metallopeptidase subunit from2 sphingomonas sp. a1
11	c3eoqB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc protease; **PDBTitle:** the crystal structure of putative zinc protease beta-2 subunit from thermus thermophilus hb8

12	c3gwbA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m16 inactive domain family protein; **PDBTitle:** crystal structure of peptidase m16 inactive domain from pseudomonas2 fluorescens. northeast structural genomics target plr293l
13	c2fgeA_	Alignment		100.0	11	**PDB header:**hydrolase, plant protein **Chain:** A: **PDB Molecule:**zinc metalloprotease (insulinase family); **PDBTitle:** crystal structure of presequence protease prep from2 arabidopsis thaliana
14	c3amjB_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zinc peptidase inactive subunit; **PDBTitle:** the crystal structure of the heterodimer of m16b peptidase from2 sphingomonas sp. a1
15	c1l0lB_	Alignment		100.0	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ubiquinol-cytochrome c reductase complex core protein 2; **PDBTitle:** structure of bovine mitochondrial cytochrome bc1 complex with a bound2 fungicide famoxadone
16	c3cx5L_	Alignment		100.0	12	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**cytochrome b-c1 complex subunit 1, mitochondrial; **PDBTitle:** structure of complex iii with bound cytochrome c in reduced2 state and definition of a minimal core interface for3 electron transfer.
17	c3d3yA_	Alignment		100.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a conserved protein from enterococcus faecalis2 v583
18	c3cxhM_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**cytochrome b-c1 complex subunit 2, mitochondrial; **PDBTitle:** structure of yeast complex iii with isoform-2 cytochrome c2 bound and definition of a minimal core interface for3 electron transfer.
19	d1ppja1	Alignment		100.0	19	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
20	d1hr6b1	Alignment		100.0	19	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
21	d1bcca1	Alignment	not modelled	100.0	18	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
22	d2fgea4	Alignment	not modelled	100.0	9	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
23	d1hr6a1	Alignment	not modelled	100.0	17	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
24	d1q2la4	Alignment	not modelled	100.0	19	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
25	d1ppjb1	Alignment	not modelled	100.0	15	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
26	d1bccb1	Alignment	not modelled	100.0	15	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
27	d3cx5b1	Alignment	not modelled	100.0	15	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
28	d3cx5a1	Alignment	not modelled	100.0	14	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
29	d1hr6b2	Alignment	not modelled	99.9	12	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase

						Family:MPP-like
30	c3ivlA_	Alignment	not modelled	99.9	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative zinc protease; **PDBTitle:** the crystal structure of the inactive peptidase domain of a putative2 zinc protease from bordetella parapertussis to 2.2a
31	d1bcca2	Alignment	not modelled	99.8	8	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
32	d1ppjb2	Alignment	not modelled	99.8	6	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
33	d1q2la1	Alignment	not modelled	99.8	9	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
34	d1ppja2	Alignment	not modelled	99.8	8	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
35	d1hr6a2	Alignment	not modelled	99.8	9	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
36	d3cx5a2	Alignment	not modelled	99.8	9	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
37	d1bccb2	Alignment	not modelled	99.8	6	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
38	d2fgea3	Alignment	not modelled	99.7	11	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
39	d2fgea2	Alignment	not modelled	99.6	6	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
40	d1q2la2	Alignment	not modelled	98.8	7	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
41	d2fgea1	Alignment	not modelled	98.5	10	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
42	d1q2la3	Alignment	not modelled	98.4	11	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
43	c1g6uB_	Alignment	not modelled	60.1	28	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**domain swapped dimer; **PDBTitle:** crystal structure of a domain swapped dimer
44	c3fhkF_	Alignment	not modelled	56.1	18	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**upf0403 protein yphp; **PDBTitle:** crystal structure of apc1446, b.subtilis yphp disulfide2 isomerase
45	d1g5ta_	Alignment	not modelled	21.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
46	c3l7vA_	Alignment	not modelled	20.1	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1377c; **PDBTitle:** crystal structure of a hypothetical protein smu.1377c from2 streptococcus mutans ua159
47	d2rdea1	Alignment	not modelled	16.0	4	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain
48	d1q5ma_	Alignment	not modelled	15.5	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
49	c2qruA_	Alignment	not modelled	13.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
50	d1tuza_	Alignment	not modelled	13.9	5	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
51	d1g64b_	Alignment	not modelled	13.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
52	c2bh7A_	Alignment	not modelled	13.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms
53	d1fe0a_	Alignment	not modelled	13.1	4	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
54	c3gnnA_	Alignment	not modelled	12.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
55	c2yw3E_	Alignment	not modelled	11.9	15	**PDB header:**lyase **Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- **PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate

						aldolase from tthb1
56	d1yira1	Alignment	not modelled	11.9	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase C-terminal domain
57	c2x3dC_	Alignment	not modelled	11.4	5	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**sso6206; **PDBTitle:** crystal structure of sso6206 from sulfolobus solfataricus p2
58	c1d2fB_	Alignment	not modelled	11.4	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**maly protein; **PDBTitle:** x-ray structure of maly from escherichia coli: a pyridoxal-5'-2 phosphate-dependent enzyme acting as a modulator in mal gene3 expression
59	d1d2fa_	Alignment	not modelled	11.3	21	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
60	c2pbrB_	Alignment	not modelled	11.1	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of thymidylate kinase (aq_969) from aquifex aeolicus2 vf5
61	c3lv8A_	Alignment	not modelled	10.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate kinase; **PDBTitle:** 1.8 angstrom resolution crystal structure of a thymidylate kinase2 (tmk) from vibrio cholerae o1 biovar eltor str. n16961 in complex3 with tmp, thymidine-5'-diphosphate and adp
62	c3pajA_	Alignment	not modelled	10.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
63	c1x1oC_	Alignment	not modelled	9.8	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
64	c1qapA_	Alignment	not modelled	9.7	16	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
65	d1pn0a3	Alignment	not modelled	9.7	11	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**PHBH-like
66	c1i5kD_	Alignment	not modelled	9.5	23	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**m protein; **PDBTitle:** structure and binding determinants of the recombinant kringle-2 domain2 of human plasminogen to an internal peptide from a group a3 streptococcal surface protein
67	c1i5kC_	Alignment	not modelled	9.5	23	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**m protein; **PDBTitle:** structure and binding determinants of the recombinant kringle-2 domain2 of human plasminogen to an internal peptide from a group a3 streptococcal surface protein
68	c3ostA_	Alignment	not modelled	8.5	10	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase kcc4; **PDBTitle:** structure of the kinase associated-1 (ka1) from kcc4p
69	c2kj4B_	Alignment	not modelled	8.4	23	**PDB header:**blood clotting **Chain:** B: **PDB Molecule:**vek-30; **PDBTitle:** solution structure of the complex of vek-30 and plasminogen2 kringle 2
70	d2raqa1	Alignment	not modelled	8.3	18	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
71	c3qspB_	Alignment	not modelled	8.1	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** analysis of a new family of widely distributed metal-independent alpha2 mannosidases provides unique insight into the processing of n-linked3 glycans, streptococcus pneumoniae sp_2144 non-productive substrate4 complex with alpha-1,6-mannobiose
72	c2h18A_	Alignment	not modelled	8.1	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**adp-ribosylation factor-like protein 8a; **PDBTitle:** structure of human adp-ribosylation factor-like 10b (arl10b)
73	d1geha2	Alignment	not modelled	8.1	13	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
74	c2doiB_	Alignment	not modelled	8.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**plasminogen-binding group a streptococcal m-like protein **PDBTitle:** the x-ray crystallographic structure of the angiogenesis inhibitor,2 angiostatin, bound to a peptide from the group a streptococcus3 protein pam
75	c2do6A_	Alignment	not modelled	7.9	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of rsgi ruh-065, a uba domain from human2 cdna
76	c3iwdC_	Alignment	not modelled	7.7	23	**PDB header:**lyase **Chain:** C: **PDB Molecule:**s-adenosylmethionine decarboxylase; **PDBTitle:** t. maritima adometdc complex with 5'-deoxy-5'-dimethyl2 thioadenosine
77	c2adbA_	Alignment	not modelled	7.7	14	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**polypyrimidine tract-binding protein 1; **PDBTitle:** solution structure of polypyrimidine tract binding protein2 rbd2 complexed with cucucu rna
						PDB header:transferase

78	c3ihjA_	Alignment	not modelled	7.7	15	**Chain:** A: **PDB Molecule:**alanine aminotransferase 2; **PDBTitle:** human alanine aminotransferase 2 in complex with plp
79	d1wxia1	Alignment	not modelled	7.6	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
80	c3tl4X_	Alignment	not modelled	7.6	12	**PDB header:**ligase **Chain:** X: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of the trna binding domain of glutaminyl-trna2 synthetase from saccharomyces cerevisiae
81	c2d9sA_	Alignment	not modelled	7.5	6	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase; **PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
82	c1z65A_	Alignment	not modelled	7.5	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**prion-like protein doppel; **PDBTitle:** mouse doppel 1-30 peptide
83	d1k8kd1	Alignment	not modelled	7.5	24	**Fold:**Secretion chaperone-like **Superfamily:**Arp2/3 complex subunits **Family:**Arp2/3 complex subunits
84	c1yueA_	Alignment	not modelled	7.4	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**head vertex protein gp24; **PDBTitle:** bacteriophage t4 capsid vertex protein gp24
85	d1bxna2	Alignment	not modelled	7.4	10	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
86	c2i38A_	Alignment	not modelled	7.4	22	**PDB header:**rna binding protein/chimera **Chain:** A: **PDB Molecule:**fusion protein consists of immunoglobin g- **PDBTitle:** solution structure of the rrm of srp20
87	c2hvzA_	Alignment	not modelled	7.3	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor, arginine/serine-rich 7; **PDBTitle:** solution structure of the rrm domain of sr rich factor 9g8
88	d1c7na_	Alignment	not modelled	7.3	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
89	d2cq2a1	Alignment	not modelled	7.2	7	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
90	c3l0gD_	Alignment	not modelled	7.1	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
91	c2r47C_	Alignment	not modelled	7.1	17	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein mth_862; **PDBTitle:** crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
92	c3llkA_	Alignment	not modelled	7.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfhydryl oxidase 1; **PDBTitle:** sulfhydryl oxidase fragment of human qsox1
93	c2e5iA_	Alignment	not modelled	6.9	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein l-like; **PDBTitle:** solution structure of rna binding domain 2 in heterogeneous2 nuclear ribonucleoprotein l-like
94	d1h0ca_	Alignment	not modelled	6.6	7	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
95	d1t3ta3	Alignment	not modelled	6.6	14	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**FGAM synthase PurL, PurS-like domain
96	c1w89E_	Alignment	not modelled	6.5	17	**PDB header:**electron transport **Chain:** E: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of the reduced form of human thioredoxin 2
97	d8ruca2	Alignment	not modelled	6.5	8	**Fold:**Ferredoxin-like **Superfamily:**RuBisCO, large subunit, small (N-terminal) domain **Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase
98	d1nh2b_	Alignment	not modelled	6.4	15	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
99	d1nvpb_	Alignment	not modelled	6.3	19	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain