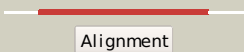

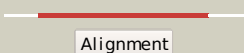

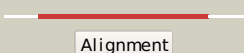

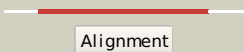

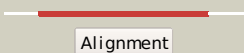

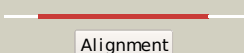

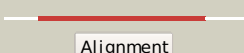

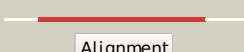

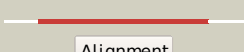

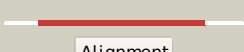

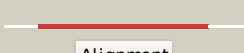



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2arza1</a>	 Alignment		100.0	20	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
2	<a href="#">c3gasA</a>	 Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> heme oxygenase; <b>PDBTitle:</b> crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
3	<a href="#">c3dnhB</a>	 Alignment		99.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein atu2129; <b>PDBTitle:</b> the crystal structure of the protein atu2129 (unknown function) from <i>Agrobacterium tumefaciens</i> str. c58
4	<a href="#">d1vl7a</a>	 Alignment		99.9	16	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
5	<a href="#">d1xhna1</a>	 Alignment		99.9	11	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
6	<a href="#">d1rfea</a>	 Alignment		99.9	16	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
7	<a href="#">d2htia1</a>	 Alignment		99.9	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
8	<a href="#">c2htiA</a>	 Alignment		99.9	14	<b>PDB header:</b> fmN-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bh0577 protein; <b>PDBTitle:</b> crystal structure of a flavin-nucleotide-binding protein (bh_0577)2 from <i>Bacillus halodurans</i> at 2.50 Å resolution
9	<a href="#">c3db0B</a>	 Alignment		99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lin2891 protein; <b>PDBTitle:</b> crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from <i>Listeria innocua</i> at 2.00 Å resolution
10	<a href="#">c3f7eB</a>	 Alignment		99.9	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmN- <b>PDBTitle:</b> msmeg_3380 f420 reductase
11	<a href="#">d2fhqa1</a>	 Alignment		99.9	11	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like

12	<a href="#">c2ig6B_</a>	Alignment		99.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nimc/nima family protein; <b>PDBTitle:</b> crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution
13	<a href="#">d2asfa1</a>	Alignment		99.8	11	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
14	<a href="#">c3ec6A_</a>	Alignment		99.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> general stress protein 26; <b>PDBTitle:</b> crystal structure of the general stress protein 26 from bacillus2 anthracis str. sterne
15	<a href="#">d2i02a1</a>	Alignment		99.8	9	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
16	<a href="#">c3fkhB_</a>	Alignment		99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution
17	<a href="#">c2re7A_</a>	Alignment		99.8	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase related2 protein (psyc_0186) from psychrobacter arcticus 273-4 at 2.50 a3 resolution
18	<a href="#">d2fg9a1</a>	Alignment		99.8	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
19	<a href="#">d2hq7a1</a>	Alignment		99.8	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
20	<a href="#">d2hq9a1</a>	Alignment		99.8	9	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
21	<a href="#">c2hhzA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
22	<a href="#">c2iabB_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a protein with fmN-binding split barrel fold2 (np_828636.1) from streptomyces avermitilis at 2.00 a resolution
23	<a href="#">d1w9aa_</a>	Alignment	not modelled	99.8	8	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
24	<a href="#">c3dmbA_</a>	Alignment	not modelled	99.8	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative general stress protein 26 with a pnp-oxidase like <b>PDBTitle:</b> crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
25	<a href="#">d2fura1</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
26	<a href="#">c3cp3A_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae
27	<a href="#">d1flma_</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like

28	<a href="#">d2vpaa1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
29	<a href="#">c2htdB</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted flavin-nucleotide-binding protein from cog3576 <b>PDBTitle:</b> crystal structure of a putative pyridoxamine 5'-phosphate oxidase2 (ldb0262) from lactobacillus delbrueckii subsp. at 1.60 a resolution
30	<a href="#">c2q9kA</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution
31	<a href="#">d1nrga</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
32	<a href="#">c1nrgA</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxine 5'-phosphate oxidase; <b>PDBTitle:</b> structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
33	<a href="#">c2qeaB</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative general stress protein 26; <b>PDBTitle:</b> crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution
34	<a href="#">c2ou5B</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn-binding; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related fmn-2 binding protein (jann_0254) from jannaschia sp. ccs1 at 1.60 a3 resolution
35	<a href="#">d1t9ma</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
36	<a href="#">d1ty9a</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
37	<a href="#">c2ol5B</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> pai 2 protein; <b>PDBTitle:</b> crystal structure of a protease synthase and sporulation negative2 regulatory protein pai 2 from bacillus stearothermophilus
38	<a href="#">d1dnla</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
39	<a href="#">c2a2iA</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
40	<a href="#">d2a2ja1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
41	<a href="#">c2i51B</a>	Alignment	not modelled	99.5	9	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein of cog5135; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related, fmn2 binding protein (npun_f5749) from nostoc punctiforme pcc 73102 at3 1.40 a resolution
42	<a href="#">d1ci0a</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
43	<a href="#">c3ba3A</a>	Alignment	not modelled	99.2	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-like protein; <b>PDBTitle:</b> crystal structure of pyridoxamine 5'-phosphate oxidase-like protein2 (np_783940.1) from lactobacillus plantarum at 1.55 a resolution
44	<a href="#">c3h96B</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> f420-h2 dependent reductase a; <b>PDBTitle:</b> msmeg_3358 f420 reductase
45	<a href="#">d2imla1</a>	Alignment	not modelled	90.6	7	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
46	<a href="#">d2ptfa1</a>	Alignment	not modelled	90.0	9	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
47	<a href="#">c2ptfB</a>	Alignment	not modelled	87.1	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein mth_863; <b>PDBTitle:</b> crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn
48	<a href="#">d2nr4a1</a>	Alignment	not modelled	82.2	8	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
49	<a href="#">d1ejea</a>	Alignment	not modelled	81.3	10	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> NADH:FMN oxidoreductase-like
50	<a href="#">c3b5mD</a>	Alignment	not modelled	74.0	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
51	<a href="#">c3hmrA</a>	Alignment	not modelled	61.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase domain protein, fmn-binding; <b>PDBTitle:</b> crystal structure of a fmn-binding domain of flavin reductases-like2 enzyme (sbal_0626) from shewanella baltica

						os155 at 1.50 a resolution
52	<a href="#">d1rz0a_</a>	Alignment	not modelled	42.5	12	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> NADH:FMN oxidoreductase-like
53	<a href="#">c3e4vA_</a>	Alignment	not modelled	42.5	8	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> nadh:fmn oxidoreductase like protein; <b>PDBTitle:</b> crystal structure of nadh:fmn oxidoreductase like protein in complex2 with fmh (yp_544701.1) from methylobacillus flagellatus kt at 1.40 a3 resolution
54	<a href="#">c2r6vA_</a>	Alignment	not modelled	40.9	10	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ph0856; <b>PDBTitle:</b> crystal structure of fmh-binding protein (np_142786.1) from pyrococcus2 horikoshii at 1.35 a resolution
55	<a href="#">d1wgbA_</a>	Alignment	not modelled	35.3	7	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> NADH:FMN oxidoreductase-like
56	<a href="#">c3cb0B_</a>	Alignment	not modelled	31.7	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxyphenylacetate 3-monooxygenase; <b>PDBTitle:</b> cibr
57	<a href="#">c3fgeA_</a>	Alignment	not modelled	31.3	3	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative flavin reductase with split barrel domain; <b>PDBTitle:</b> crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution
58	<a href="#">c2r0xA_</a>	Alignment	not modelled	27.7	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> possible flavin reductase; <b>PDBTitle:</b> crystal structure of a putative flavin reductase (ycdh, hs_1225) from2 haemophilus somnus 129pt at 1.06 a resolution
59	<a href="#">c3bnkB_</a>	Alignment	not modelled	26.8	6	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> flavoredoxin; <b>PDBTitle:</b> x-ray crystal structure of flavoredoxin from methanosarcina2 acetivorans
60	<a href="#">c3pftA_</a>	Alignment	not modelled	23.9	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase; <b>PDBTitle:</b> crystal structure of untagged c54a mutant flavin reductase (dszd) in2 complex with fmh from mycobacterium goodii
61	<a href="#">c2d5mA_</a>	Alignment	not modelled	20.1	8	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> flavoredoxin; <b>PDBTitle:</b> flavoredoxin of desulfovibrio vulgaris (miyazaki f)
62	<a href="#">d1i0rA_</a>	Alignment	not modelled	19.7	8	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> NADH:FMN oxidoreductase-like
63	<a href="#">c2ytyA_</a>	Alignment	not modelled	18.0	6	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cold shock domain-containing protein e1; <b>PDBTitle:</b> solution structure of the fourth cold-shock domain of the human2 kiaa0885 protein (unr protein)
64	<a href="#">c3hfoC_</a>	Alignment	not modelled	17.9	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> ssr3341 protein; <b>PDBTitle:</b> crystal structure of an hfq protein from synechocystis sp.
65	<a href="#">c2d38A_</a>	Alignment	not modelled	14.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical nadh-dependent fmh oxidoreductase; <b>PDBTitle:</b> the crystal structure of flavin reductase hpac complexed with nadp+
66	<a href="#">c3nfwB_</a>	Alignment	not modelled	13.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitrilotriacetate monooxygenase component b; <b>PDBTitle:</b> crystal structure of nitrilotriacetate monooxygenase component b2 (a0r521 homolog) from mycobacterium thermoresistibile
67	<a href="#">c2ecrA_</a>	Alignment	not modelled	12.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase component (hpac) of 4-hydroxyphenylacetate <b>PDBTitle:</b> crystal structure of the ligand-free form of the flavin reductase2 component (hpac) of 4-hydroxyphenylacetate 3-monooxygenase
68	<a href="#">c2qckA_</a>	Alignment	not modelled	12.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase domain protein; <b>PDBTitle:</b> crystal structure of flavin reductase domain protein (yp_831077.1)2 from arthrobacter sp. fb24 at 1.90 a resolution
69	<a href="#">c3hfnA_</a>	Alignment	not modelled	11.3	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> asl2047 protein; <b>PDBTitle:</b> crystal structure of an hfq protein from anabaena sp.
70	<a href="#">c1ykaA_</a>	Alignment	not modelled	10.8	21	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin ydhg; <b>PDBTitle:</b> solution structure of grx4, a monothiol glutaredoxin from2 e. coli.
71	<a href="#">d1aisa2</a>	Alignment	not modelled	9.3	8	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
72	<a href="#">c2wwaj_</a>	Alignment	not modelled	8.5	35	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 60s ribosomal protein l19; <b>PDBTitle:</b> cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
73	<a href="#">c3k87B_</a>	Alignment	not modelled	8.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> chlorophenol-4-monooxygenase component 1; <b>PDBTitle:</b> crystal structure of nadh:fad oxidoreductase (tfct) - fad2 complex
74	<a href="#">c2wulB_</a>	Alignment	not modelled	7.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin related protein 5; <b>PDBTitle:</b> crystal structure of the human glutaredoxin 5 with bound2 glutathione in an fes cluster
75	<a href="#">c3bpkB_</a>	Alignment	not modelled	6.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitrilotriacetate monooxygenase component b;

						<b>PDBTitle:</b> crystal structure of nitrilotriacetate monooxygenase2 component b from bacillus cereus
76	<a href="#">c3hy4A_</a>	Alignment	not modelled	6.8	63	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-formyltetrahydrofolate cyclo-ligase; <b>PDBTitle:</b> structure of human mthfs with n5-iminium phosphate
77	<a href="#">d1sbqa_</a>	Alignment	not modelled	6.5	63	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> Methenyltetrahydrofolate synthetase
78	<a href="#">c1u3fA_</a>	Alignment	not modelled	6.4	63	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> 5,10-methenyltetrahydrofolate synthetase; <b>PDBTitle:</b> structural and functional characterization of a 5,10-2 methenyltetrahydrofolate synthetase from mycoplasma3 pneumoniae (gi: 13508087)
79	<a href="#">c1ydmC_</a>	Alignment	not modelled	5.5	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein yqgn; <b>PDBTitle:</b> x-ray structure of northeast structural genomics target sr44