Phyre^2

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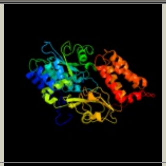
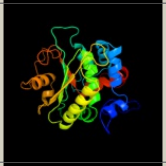
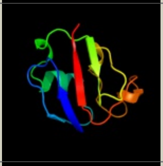
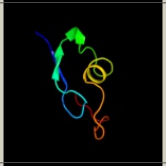
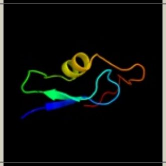
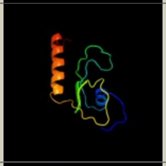
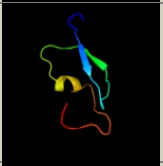
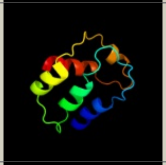
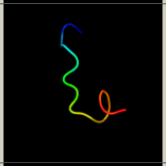
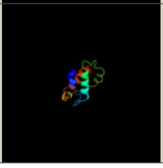
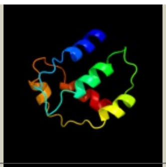
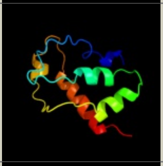
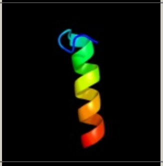
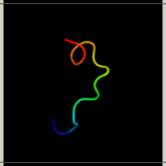
Description	P31979
Date	Thu Jan 5 11:48:55 GMT 2012
Unique Job ID	6055bc112678ce3b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fugA_	Alignment		100.0	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-quinone oxidoreductase chain 1; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
2	d2fug12	Alignment		100.0	54	**Fold:**Nqo1 FMN-binding domain-like **Superfamily:**Nqo1 FMN-binding domain-like **Family:**Nqo1 FMN-binding domain-like
3	d2fug11	Alignment		100.0	32	**Fold:**Bromodomain-like **Superfamily:**Nqo1C-terminal domain-like **Family:**Nqo1C-terminal domain-like
4	d2fug13	Alignment		99.9	43	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Nqo1 middle domain-like **Family:**Nqo1 middle domain-like
5	c2w8iG_	Alignment		93.2	18	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**putative outer membrane lipoprotein wza; **PDBTitle:** crystal structure of wza24-345.
6	c2j58G_	Alignment		91.9	18	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**outer membrane lipoprotein wza; **PDBTitle:** the structure of wza
7	c1c4cA_	Alignment		78.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (fe-only hydrogenase); **PDBTitle:** binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
8	c3p42D_	Alignment		65.8	13	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**predicted protein; **PDBTitle:** structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
9	d2bs2b1	Alignment		46.1	20	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
10	c3swrA_	Alignment		44.3	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 1; **PDBTitle:** structure of human dnmt1 (601-1600) in complex with sinefungin
11	c2b76N_	Alignment		43.9	16	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation

12	c2bs2E_	Alignment		42.1	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
13	d1kf6b1	Alignment		41.3	17	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
14	c3bqqB_	Alignment		37.7	7	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**proactivator polypeptide; **PDBTitle:** crystal structure of human saposin d (triclinic)
15	c1ffuA_	Alignment		36.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cuts, iron-sulfur protein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
16	c2h89B_	Alignment		36.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
17	c3bl5E_	Alignment		35.9	19	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**queuosine biosynthesis protein quec; **PDBTitle:** crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
18	d1nkla_	Alignment		35.3	12	**Fold:**Saposin-like **Superfamily:**Saposin **Family:**NKL-like
19	c3pt6B_	Alignment		32.4	36	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna (cytosine-5)-methyltransferase 1; **PDBTitle:** crystal structure of mouse dnmt1(650-1602) in complex with dna
20	d1zxia1	Alignment		28.2	21	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
21	d1of9a_	Alignment	not modelled	28.2	13	**Fold:**Saposin-like **Superfamily:**Saposin **Family:**Ameobapore A
22	c3thdD_	Alignment	not modelled	25.2	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
23	d1n62a1	Alignment	not modelled	24.3	20	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
24	c3cf4A_	Alignment	not modelled	23.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetyl-coa decarboxylase/synthase alpha subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
25	c1dgjA_	Alignment	not modelled	22.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
26	c3d3aA_	Alignment	not modelled	22.3	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
27	c1w59B_	Alignment	not modelled	21.7	27	**PDB header:**cell division **Chain:** B: **PDB Molecule:**cell division protein ftsz homolog 1; **PDBTitle:** ftsz dimer, empty (m. jannaschii)
28	c3b9jI_	Alignment	not modelled	21.6	22	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine

29	d2gtga1	Alignment	not modelled	20.0	12	**Fold:**Saposin-like **Superfamily:**Saposin **Family:**NKL-like
30	d1nekb1	Alignment	not modelled	19.9	14	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
31	d1t3qa1	Alignment	not modelled	18.7	21	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
32	d1v97a1	Alignment	not modelled	18.4	22	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
33	c2he3A_	Alignment	not modelled	18.0	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 2; **PDBTitle:** crystal structure of the selenocysteine to cysteine mutant of human2 glutathionine peroxidase 2 (gpx2)
34	d1o8xa_	Alignment	not modelled	18.0	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
35	d1z6na1	Alignment	not modelled	17.9	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
36	c1n60D_	Alignment	not modelled	17.7	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**carbon monoxide dehydrogenase small chain; **PDBTitle:** crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
37	c3eubJ_	Alignment	not modelled	16.8	22	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
38	d1ujsa_	Alignment	not modelled	16.1	26	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
39	d2pg3a1	Alignment	not modelled	16.1	44	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
40	d1deca_	Alignment	not modelled	16.1	36	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
41	c1nekB_	Alignment	not modelled	15.9	18	**PDB header:**oxidoreductase/electron transport **Chain:** B: **PDB Molecule:**succinate dehydrogenase iron-sulfur protein; **PDBTitle:** complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
42	d1l9la_	Alignment	not modelled	15.6	6	**Fold:**Saposin-like **Superfamily:**Saposin **Family:**NKL-like
43	c1rm6F_	Alignment	not modelled	15.5	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
44	d1uufa1	Alignment	not modelled	15.1	55	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
45	d1i5ga_	Alignment	not modelled	15.0	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
46	d1jqoa_	Alignment	not modelled	14.8	35	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
47	c1jqoA_	Alignment	not modelled	14.8	35	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
48	c3nsjA_	Alignment	not modelled	14.6	24	**PDB header:**immune system **Chain:** A: **PDB Molecule:**perforin-1; **PDBTitle:** the x-ray crystal structure of lymphocyte perforin
49	d1rm6c1	Alignment	not modelled	14.2	18	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
50	c3o2qB_	Alignment	not modelled	13.6	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
51	c3l23A_	Alignment	not modelled	13.6	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
52	c2w3rG_	Alignment	not modelled	13.4	15	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
53	d1ejba_	Alignment	not modelled	13.0	24	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
54	c2ds8A_	Alignment	not modelled	12.9	35	**PDB header:**metal binding protein, protein binding **Chain:** A: **PDB Molecule:**atp-dependent clp protease atp-binding subunit

						PDBTitle: structure of the zbd-xb complex
55	c3mk3L_	Alignment	not modelled	12.9	21	**PDB header:**transferase **Chain:** L: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase; **PDBTitle:** crystal structure of lumazine synthase from salmonella typhimurium lt2
56	c3qmhA_	Alignment	not modelled	12.8	64	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**cpg-binding protein; **PDBTitle:** structural basis of selective binding of non-methylated cpg islands2 (dna-tcga) by the cxxc domain of cfp1
57	d1c2ya_	Alignment	not modelled	12.7	11	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
58	c2jyiA_	Alignment	not modelled	12.7	64	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein hrx; **PDBTitle:** solution structure of mll cxxc domain
59	c3fdfA_	Alignment	not modelled	12.5	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fr253; **PDBTitle:** crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
60	c3ogrA_	Alignment	not modelled	12.1	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** complex structure of beta-galactosidase from trichoderma reesei with2 galactose
61	d1ffva1	Alignment	not modelled	11.8	17	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
62	d1cdoa1	Alignment	not modelled	11.8	36	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
63	c1t3qD_	Alignment	not modelled	11.7	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
64	c2l3xA_	Alignment	not modelled	11.7	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ablim2 protein; **PDBTitle:** villin head piece domain of human ablim2
65	d1rvv1_	Alignment	not modelled	11.7	17	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
66	c2bm0A_	Alignment	not modelled	11.1	15	**PDB header:**elongation factor **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
67	c2kvgA_	Alignment	not modelled	11.0	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32; **PDBTitle:** structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
68	d2fa8a1	Alignment	not modelled	11.0	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
69	c3hrdH_	Alignment	not modelled	10.7	22	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
70	c3p04B_	Alignment	not modelled	10.6	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
71	c2j2sA_	Alignment	not modelled	10.6	64	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**zinc finger protein hrx; **PDBTitle:** solution structure of the nonmethyl-cpg-binding cxxc domain2 of the leukaemia-associated mll histone methyltransferase
72	d1yu5x1	Alignment	not modelled	10.3	13	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
73	c2ojlB_	Alignment	not modelled	10.2	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
74	c1ovxB_	Alignment	not modelled	10.2	35	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** nmr structure of the e. coli clpx chaperone zinc binding domain dimer
75	d2ds5a1	Alignment	not modelled	10.2	35	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**ClpX chaperone zinc binding domain
76	d1nqua_	Alignment	not modelled	10.2	15	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
77	d2vapa1	Alignment	not modelled	10.1	26	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
78	c3o2sB_	Alignment	not modelled	9.9	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72 complex
79	c2p0gB_	Alignment	not modelled	9.7	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**selenoprotein w-related protein; **PDBTitle:** crystal structure of selenoprotein w-related protein from2 vibrio cholerae. northeast structural genomics target vcr75

80	c1xc6A_	Alignment	not modelled	9.6	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
81	d1mmca_	Alignment	not modelled	9.6	0	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant lectins/antimicrobial peptides **Family:**Antimicrobial peptide 2, AC-AMP2
82	c1ogpD_	Alignment	not modelled	9.3	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**sulfite oxidase; **PDBTitle:** the crystal structure of plant sulfite oxidase provides2 insight into sulfite oxidation in plants and animals
83	d1lbua2	Alignment	not modelled	8.9	12	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**Muramoyl-pentapeptide carboxypeptidase
84	d1c41a_	Alignment	not modelled	8.8	17	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
85	d1v9wa_	Alignment	not modelled	8.8	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Txnl5-like
86	d1o73a_	Alignment	not modelled	8.7	27	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
87	c2obkE_	Alignment	not modelled	8.5	20	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**selt/selw/selh selenoprotein domain; **PDBTitle:** x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
88	c3p04A_	Alignment	not modelled	8.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
89	d1qzpa_	Alignment	not modelled	8.5	18	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
90	c2h9gS_	Alignment	not modelled	8.4	25	**PDB header:**immune system/apoptosis **Chain:** S: **PDB Molecule:**tumor necrosis factor receptor superfamily member 10b **PDBTitle:** crystal structure of phage derived fab bdf1 with human death receptor2 5 (dr5)
91	c3fkfC_	Alignment	not modelled	8.4	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol-disulfide oxidoreductase; **PDBTitle:** thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
92	c1zr6A_	Alignment	not modelled	8.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucooligosaccharide oxidase; **PDBTitle:** the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
93	c2obxH_	Alignment	not modelled	8.1	15	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh2 from mesorhizobium loti (gene mll7281, swiss-2 prot entry q986n2) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
94	c3dexA_	Alignment	not modelled	8.1	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sav_2001; **PDBTitle:** crystal structure of sav_2001 protein from streptomyces2 avermitilis, northeast structural genomics consortium3 target svr107.
95	c1zlgA_	Alignment	not modelled	8.0	31	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**anosmin 1; **PDBTitle:** solution structure of the extracellular matrix protein2 anosmin-1
96	d2fzwa1	Alignment	not modelled	7.9	36	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
97	d1di0a_	Alignment	not modelled	7.8	17	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
98	c3l0aA_	Alignment	not modelled	7.8	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative exonuclease; **PDBTitle:** crystal structure of putative exonuclease (rer070207002219) from2 eubacterium rectale at 2.19 a resolution
99	d2f9wa1	Alignment	not modelled	7.7	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**CoaX-like