Phyre^2

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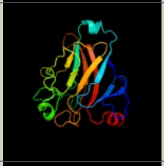
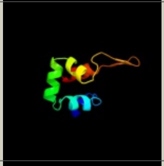
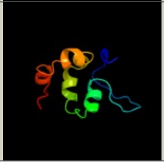
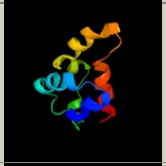
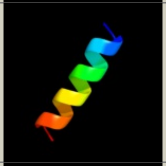
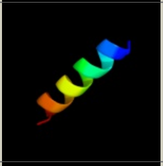
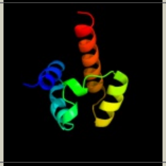
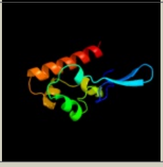
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t4wa_	Alignment		100.0	100	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
2	c2rp5A_	Alignment		100.0	100	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative uncharacterized protein cep-1; **PDBTitle:** solution structure of the oligomerization domain in cep-1
3	c2j1xA_	Alignment		99.8	20	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** human p53 core domain mutant m133l-v203a-y220c-n239y-n268d
4	d2ac0a1	Alignment		99.8	22	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
5	c2xipA_	Alignment		99.8	23	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**tumour protein p73; **PDBTitle:** crystal structure of the dna binding domain of human tp732 refined at 1.8 a resolution
6	d1hu8a_	Alignment		99.8	23	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**p53 DNA-binding domain-like
7	c3q06B_	Alignment		99.7	23	**PDB header:**cell cycle/dna **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** an induced fit mechanism regulates p53 dna binding kinetics to confer2 sequence specificity
8	c2rmnA_	Alignment		99.5	27	**PDB header:**cell cycle, antitumor protein **Chain:** A: **PDB Molecule:**tumor protein 63; **PDBTitle:** the solution structure of the p63 dna-binding domain
9	d1b0xa_	Alignment		61.9	27	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
10	c1b0xA_	Alignment		61.9	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (epha4 receptor tyrosine kinase); **PDBTitle:** the crystal structure of an eph receptor sam domain reveals2 a mechanism for modular dimerization.
11	c3bq7A_	Alignment		57.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase delta; **PDBTitle:** sam domain of diacylglycerol kinase delta1 (e35g)

12	c2kg5A_	Alignment		48.3	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**arf-gap, rho-gap domain, ank repeat and ph **PDBTitle:** nmr solution structure of arap3-sam
13	c2dl0A_	Alignment		44.5	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sam-domain of the sam and sh32 domain containing protein 1
14	c2k4pA_	Alignment		43.4	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**phosphatidylinositol-3,4,5-trisphosphate 5- **PDBTitle:** solution structure of ship2-sam
15	d1kx5d_	Alignment		41.5	53	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
16	d1eqzb_	Alignment		39.7	59	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
17	d1s32d_	Alignment		38.2	53	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
18	c3k1rB_	Alignment		37.9	22	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**usher syndrome type-1g protein; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
19	c3hilB_	Alignment		37.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** sam domain of human ephrin type-a receptor 1 (epha1)
20	c3bs7A_	Alignment		37.5	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein aveugle; **PDBTitle:** crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle
21	d1ucva_	Alignment	not modelled	36.4	22	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
22	d1rg6a_	Alignment	not modelled	34.3	16	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
23	d1v38a_	Alignment	not modelled	34.2	17	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
24	c2eaoA_	Alignment	not modelled	32.9	24	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**ephrin type-b receptor 1; **PDBTitle:** solution structure of the c-terminal sam-domain of mouse2 ephrin type-b receptor 1 precursor (ec 2.7.1.112)
25	d1coka_	Alignment	not modelled	29.9	21	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
26	d1q2ha_	Alignment	not modelled	29.9	63	**Fold:**Dimerisation interlock **Superfamily:**Phenylalanine zipper **Family:**Adapter protein APS, dimerisation domain
27	d1sgga_	Alignment	not modelled	28.5	21	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
28	d1jixa_	Alignment	not modelled	28.1	50	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**beta-Glucosyltransferase (DNA-modifying)
29	d1x40a1	Alignment	not modelled	27.2	23	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain

						Family:SAM (sterile alpha motif) domain
30	c2gleA_	Alignment	not modelled	24.5	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**neurabin-1; **PDBTitle:** solution structure of neurabin sam domain
31	d2f3na1	Alignment	not modelled	23.6	17	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
32	d2ccqa1	Alignment	not modelled	23.2	20	**Fold:**PUG domain-like **Superfamily:**PUG domain-like **Family:**PUG domain
33	c1vjqB_	Alignment	not modelled	22.4	30	**PDB header:**structural genomics, de novo protein **Chain:** B: **PDB Molecule:**designed protein; **PDBTitle:** designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
34	c2ke7A_	Alignment	not modelled	21.6	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin repeat and sterile alpha motif domain- **PDBTitle:** nmr structure of the first sam domain from aida1
35	c2jssA_	Alignment	not modelled	21.5	48	**PDB header:**chaperone/nuclear protein **Chain:** A: **PDB Molecule:**chimera of histone h2b.1 and histone h2a.z; **PDBTitle:** nmr structure of chaperone chz1 complexed with histone2 h2a.z-h2b
36	c1tmxA_	Alignment	not modelled	21.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyquinol 1,2-dioxygenase; **PDBTitle:** crystal structure of hydroxyquinol 1,2-dioxygenase from2 nocardioides simplex 3e
37	d1imhc2	Alignment	not modelled	20.9	15	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**Rel/Dorsal transcription factors, DNA-binding domain
38	d1pdaa2	Alignment	not modelled	19.6	24	**Fold:**dsRBD-like **Superfamily:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain **Family:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
39	c3kkaD_	Alignment	not modelled	19.6	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** co-crystal structure of the sam domains of epha1 and epha2
40	c2e8nA_	Alignment	not modelled	19.4	19	**PDB header:**transferase, signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** solution structure of the c-terminal sam-domain of ephaa2:2 ephrin type-a receptor 2 precursor (ec 2.7.10.1)
41	c2eamA_	Alignment	not modelled	19.2	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative 47 kda protein; **PDBTitle:** solution structure of the n-terminal sam-domain of a human2 putative 47 kda protein
42	d1tzyb_	Alignment	not modelled	19.1	59	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
43	d1wwva1	Alignment	not modelled	18.5	26	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
44	c2v2gC_	Alignment	not modelled	18.4	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxiredoxin 6; **PDBTitle:** crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
45	c3okzB_	Alignment	not modelled	18.2	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein gbs0355; **PDBTitle:** crystal structure of protein gbs0355 from streptococcus agalactiae,2 northeast structural genomics consortium target sar127
46	c2kncB_	Alignment	not modelled	18.0	23	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
47	d1ow5a_	Alignment	not modelled	17.8	18	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
48	c1ow5A_	Alignment	not modelled	17.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase ste11; **PDBTitle:** nmr structure of the saccharomyces cerevisiae sam (sterile2 alpha motif) domain
49	c3s88J_	Alignment	not modelled	17.7	46	**PDB header:**immune system/viral protein **Chain:** J: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** crystal structure of sudan ebolavirus glycoprotein (strain gulu) bound2 to 16f6
50	d1p7hl2	Alignment	not modelled	17.6	14	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**Rel/Dorsal transcription factors, DNA-binding domain
51	c3suiB_	Alignment	not modelled	17.5	83	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**transient receptor potential cation channel subfamily v **PDBTitle:** crystal structure of ca2+-calmodulin in complex with a trpv1 c-2 terminal peptide
52	c2qkqA_	Alignment	not modelled	17.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-b receptor 4; **PDBTitle:** structure of the sam domain of human ephrin type-b receptor2 4
53	c2jynA_	Alignment	not modelled	17.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0368 protein ypl225w; **PDBTitle:** a novel solution nmr structure of protein yst0336 from2 saccharomyces cerevisiae. northeast structural genomics3 consortium target yt51/ontario centre for structural4 proteomics target yst0336
						PDB header:cell adhesion

54	c1s4xA_	Alignment	not modelled	17.4	25	**Chain:** A: **PDB Molecule:**integrin beta-3; **PDBTitle:** nmr structure of the integrin b3 cytoplasmic domain in dpc2 micelles
55	d2r7ka1	Alignment	not modelled	17.1	35	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**PurP N-terminal domain-like
56	c4g5sE_	Alignment	not modelled	17.1	54	**PDB header:**cell cycle/signaling protein **Chain:** E: **PDB Molecule:**g-protein-signaling modulator 2; **PDBTitle:** structure of lgn gl3/galphai3 complex
57	c4g5sF_	Alignment	not modelled	17.1	54	**PDB header:**cell cycle/signaling protein **Chain:** F: **PDB Molecule:**g-protein-signaling modulator 2; **PDBTitle:** structure of lgn gl3/galphai3 complex
58	c2lcyA_	Alignment	not modelled	17.0	38	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**virion spike glycoprotein; **PDBTitle:** nmr structure of the complete internal fusion loop from ebolavirus gp22 at ph 5.5
59	c1oxjA_	Alignment	not modelled	16.6	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-binding protein smaug; **PDBTitle:** crystal structure of the smaug rna binding domain
60	d1d8ba_	Alignment	not modelled	16.4	9	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
61	c2ddiA_	Alignment	not modelled	15.7	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**wap, follistatin/kazal, immunoglobulin, kunitz **PDBTitle:** nmr structure of the second kunitz domain of human wfikkn1
62	c2l01A_	Alignment	not modelled	14.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bvu3908 from bacteroides vulgatus,2 northeast structural genomics consortium target bvr153
63	c3ukzC_	Alignment	not modelled	14.3	100	**PDB header:**protein transport/protein binding **Chain:** C: **PDB Molecule:**nuclear cap-binding protein subunit 1; **PDBTitle:** mouse importin alpha: mouse cbp80 cnls complex
64	d1jmsa3	Alignment	not modelled	14.1	18	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**DNA polymerase beta-like, second domain
65	d2f9zc1	Alignment	not modelled	13.9	28	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**CheD-like
66	d1rvga_	Alignment	not modelled	13.8	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
67	d1id3d_	Alignment	not modelled	13.5	65	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
68	d1gtka2	Alignment	not modelled	13.4	24	**Fold:**dsRBD-like **Superfamily:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain **Family:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
69	c2l02B_	Alignment	not modelled	13.4	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
70	c1k09B_	Alignment	not modelled	13.3	50	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**core module ii; **PDBTitle:** solution structure of betacore, a designed water soluble2 four-stranded antiparallel b-sheet protein
71	d1oxja1	Alignment	not modelled	13.3	16	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
72	c4g5sG_	Alignment	not modelled	13.2	63	**PDB header:**cell cycle/signaling protein **Chain:** G: **PDB Molecule:**g-protein-signaling modulator 2; **PDBTitle:** structure of lgn gl3/galphai3 complex
73	c2kn8A_	Alignment	not modelled	13.1	30	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**dna cleavage and packaging protein large subunit, ul89; **PDBTitle:** nmr structure of the c-terminal domain of pul89
74	d1gjia2	Alignment	not modelled	12.9	50	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**Rel/Dorsal transcription factors, DNA-binding domain
75	d1v54g_	Alignment	not modelled	12.8	50	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIa **Family:**Mitochondrial cytochrome c oxidase subunit VIa
76	d1doqa_	Alignment	not modelled	12.8	13	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
77	d1gvfa_	Alignment	not modelled	12.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
78	d1yela1	Alignment	not modelled	12.7	15	**Fold:**DNA-binding pseudobarrel domain **Superfamily:**DNA-binding pseudobarrel domain **Family:**B3 DNA binding domain
79	c2opiB_	Alignment	not modelled	12.5	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
						PDB header:lyase

80	c3qm3C_	Alignment	not modelled	12.2	16	**Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from campylobacter jejuni
81	c3lvgD_	Alignment	not modelled	12.0	16	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**clathrin light chain b; **PDBTitle:** crystal structure of a clathrin heavy chain and clathrin light chain2 complex
82	c3csyJ_	Alignment	not modelled	12.0	38	**PDB header:**immune system/viral protein **Chain:** J: **PDB Molecule:**envelope glycoprotein gp2; **PDBTitle:** crystal structure of the trimeric prefusion ebola virus glycoprotein2 in complex with a neutralizing antibody from a human survivor
83	c2lmrA_	Alignment	not modelled	11.9	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ankyrin repeat and sam domain-containing protein 1a; **PDBTitle:** solution structure of the first sam domain of odin
84	d1hd2a_	Alignment	not modelled	11.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
85	c2xhfA_	Alignment	not modelled	11.8	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin 5; **PDBTitle:** crystal structure of peroxiredoxin 5 from alvinella pompejana
86	c3d3rA_	Alignment	not modelled	11.8	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
87	d1miua4	Alignment	not modelled	11.8	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
88	c2o1uA_	Alignment	not modelled	11.5	36	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound
89	d1a66a_	Alignment	not modelled	11.5	15	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**Rel/Dorsal transcription factors, DNA-binding domain
90	c3n9tA_	Alignment	not modelled	11.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pnpc; **PDBTitle:** cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4
91	c3au9A_	Alignment	not modelled	10.8	23	**PDB header:**isomerase/isomerase inhibitor **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of the quaternary complex-1 of an isomerase
92	c3q94B_	Alignment	not modelled	10.8	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
93	c1m8oB_	Alignment	not modelled	10.7	25	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**platele integrin beta3 subunit: cytoplasmic **PDBTitle:** platelet integrin alfaiib-beta3 cytoplasmic domain
94	c3ihtB_	Alignment	not modelled	10.6	44	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosyl-l-methionine methyl transferase; **PDBTitle:** crystal structure of s-adenosyl-l-methionine methyl transferase2 (yp_165822.1) from silicibacter pomeroyi dss-3 at 1.80 a resolution
95	c4de8A_	Alignment	not modelled	10.5	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cps2a; **PDBTitle:** lytr-cps2a-psr family protein with bound octaprenyl monophosphate2 lipid
96	d1b4fa_	Alignment	not modelled	10.5	19	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
97	c2cqtA_	Alignment	not modelled	9.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cellobiose phosphorylase; **PDBTitle:** crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
98	d1ooaa2	Alignment	not modelled	9.7	29	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**Rel/Dorsal transcription factors, DNA-binding domain
99	c2iswB_	Alignment	not modelled	9.7	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate