Phyre^2

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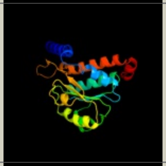
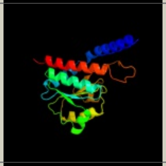
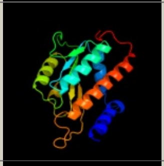
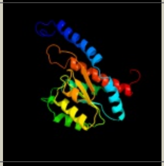
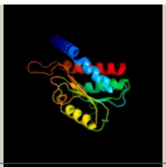
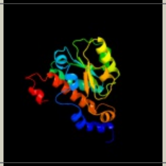
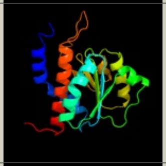
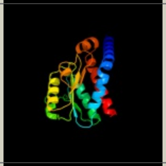
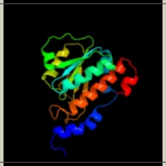
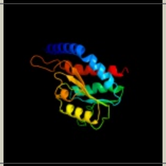
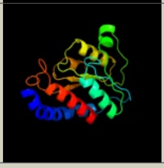
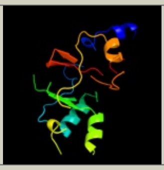
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3etnD_	Alignment		100.0	39	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative phosphosugar isomerase involved in capsule **PDBTitle:** crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
2	c3fxaA_	Alignment		100.0	33	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
3	c2xhzC_	Alignment		100.0	99	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
4	c3cvjB_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
5	d1vima_	Alignment		100.0	24	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
6	d1m3sa_	Alignment		100.0	21	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
7	c3shoA_	Alignment		99.9	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
8	d1jeoa_	Alignment		99.9	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
9	d1nria_	Alignment		99.9	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
10	c1nriA_	Alignment		99.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
11	c2yvaB_	Alignment		99.9	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa

12	d1x92a_	Alignment		99.9	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
13	c3fj1A_	Alignment		99.9	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
14	c2puwA_	Alignment		99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isomerase domain of glutamine-fructose-6-phosphate **PDBTitle:** the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
15	c2zj3A_	Alignment		99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate **PDBTitle:** isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
16	c2amlB_	Alignment		99.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
17	d1tk9a_	Alignment		99.9	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
18	d1moqa_	Alignment		99.9	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
19	c3trjC_	Alignment		99.9	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
20	c3hbaA_	Alignment		99.9	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
21	c3g68A_	Alignment	not modelled	99.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
22	d1j5xa_	Alignment	not modelled	99.9	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
23	c3tbfA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate aminotransferase **PDBTitle:** c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
24	c2x3yA_	Alignment	not modelled	99.9	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
25	c3fnaA_	Alignment		99.9	92	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**possible arabinose 5-phosphate isomerase; **PDBTitle:** crystal structure of the cbs pair of possible d-arabinose 5-phosphate2 isomerase yrbh from escherichia coli cft073
26	d1x94a_	Alignment	not modelled	99.9	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
27	c3knzA_	Alignment	not modelled	99.9	16	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative sugar binding protein; **PDBTitle:** crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a

						resolution
28	c2a3nA_	Alignment	not modelled	99.9	16	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative glucosamine-fructose-6-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
29	c3euaD_	Alignment	not modelled	99.9	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
30	c1jxaA_	Alignment	not modelled	99.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate synthase; **PDBTitle:** glucosamine 6-phosphate synthase with glucose 6-phosphate
31	c3fkjA_	Alignment	not modelled	99.8	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerases; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
32	d2yzia1	Alignment	not modelled	99.8	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
33	c1zfjA_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
34	c2qh1B_	Alignment	not modelled	99.8	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ta0289; **PDBTitle:** structure of ta289, a cbs-rubredoxin-like protein, in its fe+2-bound2 state
35	c2decA_	Alignment	not modelled	99.8	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**325aa long hypothetical protein; **PDBTitle:** crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
36	c3pc3A_	Alignment	not modelled	99.8	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cg1753, isoform a; **PDBTitle:** full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
37	d3ddja1	Alignment	not modelled	99.8	17	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
38	d1pbja3	Alignment	not modelled	99.8	25	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
39	d2d4za3	Alignment	not modelled	99.8	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
40	c2emqA_	Alignment	not modelled	99.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** hypothetical conserved protein (gk1048) from geobacillus kaustophilus
41	c3odpA_	Alignment	not modelled	99.8	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of a putative tagatose-6-phosphate ketose/aldose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution
42	c3hf7A_	Alignment	not modelled	99.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized cbs-domain protein; **PDBTitle:** the crystal structure of a cbs-domain pair with bound amp from2 klebsiella pneumoniae to 2.75a
43	d1yava3	Alignment	not modelled	99.8	17	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
44	d2o16a3	Alignment	not modelled	99.8	23	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
45	c3fwrB_	Alignment	not modelled	99.8	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**yqzb protein; **PDBTitle:** crystal structure of the cbs domains from the bacillus subtilis ccpn2 repressor complexed with adp
46	c3orgB_	Alignment	not modelled	99.8	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cmclc; **PDBTitle:** crystal structure of a eukaryotic clc transporter
47	c2qlvF_	Alignment	not modelled	99.8	17	**PDB header:**transferase/protein binding **Chain:** F: **PDB Molecule:**nuclear protein snf4; **PDBTitle:** crystal structure of the heterotrimer core of the s.2 cerevisiae ampk homolog snf1
48	d1y5ha3	Alignment	not modelled	99.8	19	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
49	d1x9ia_	Alignment	not modelled	99.8	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
50	c3lhhA_	Alignment	not modelled	99.8	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cbs domain protein; **PDBTitle:** the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
51	d1pvma4	Alignment	not modelled	99.8	20	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
52	d1vr9a3	Alignment	not modelled	99.8	20	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair

53	d2j9la1	Alignment	not modelled	99.8	12	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
54	c2qr1E_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** E: **PDB Molecule:**protein c1556.08c; **PDBTitle:** crystal structure of the adenylate sensor from amp-activated protein2 kinase in complex with adp
55	c2d4zB_	Alignment	not modelled	99.8	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride channel protein; **PDBTitle:** crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
56	c3lqnA_	Alignment	not modelled	99.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cbs domain protein; **PDBTitle:** crystal structure of cbs domain-containing protein of2 unknown function from bacillus anthracis str. ames ancestor
57	c1yavB_	Alignment	not modelled	99.8	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14130; **PDBTitle:** crystal structure of cbs domain-containing protein ykul2 from bacillus subtilis
58	c2ouxB_	Alignment	not modelled	99.8	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**magnesium transporter; **PDBTitle:** crystal structure of the soluble part of a magnesium transporter
59	c3i8nB_	Alignment	not modelled	99.8	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp2912; **PDBTitle:** a domain of a conserved functionally known protein from2 vibrio parahaemolyticus rimd 2210633.
60	d2rc3a1	Alignment	not modelled	99.8	19	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
61	c1vr9B_	Alignment	not modelled	99.7	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cbs domain protein/act domain protein; **PDBTitle:** crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution
62	c3ctuB_	Alignment	not modelled	99.7	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cbs domain protein; **PDBTitle:** crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
63	c3lfrB_	Alignment	not modelled	99.7	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative metal ion transporter; **PDBTitle:** the crystal structure of a cbs domain from a putative metal2 ion transporter bound to amp from pseudomonas syringae to3 1.55a
64	d2yzqa1	Alignment	not modelled	99.7	22	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
65	d2nyca1	Alignment	not modelled	99.7	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
66	c3i0zB_	Alignment	not modelled	99.7	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of putative putative tagatose-6-phosphate2 ketose/aldose isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution
67	c3jtfB_	Alignment	not modelled	99.7	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**magnesium and cobalt efflux protein; **PDBTitle:** the cbs domain pair structure of a magnesium and cobalt efflux protein2 from bordetella parapertussis in complex with amp
68	c2p9mD_	Alignment	not modelled	99.7	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0922; **PDBTitle:** crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
69	c3nqrD_	Alignment	not modelled	99.7	19	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**magnesium and cobalt efflux protein corc; **PDBTitle:** a putative cbs domain-containing protein from salmonella typhimurium2 lt2
70	c3lv9A_	Alignment	not modelled	99.7	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative transporter; **PDBTitle:** crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
71	c2v8qE_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** E: **PDB Molecule:**5'-amp-activated protein kinase subunit gamma-1; **PDBTitle:** crystal structure of the regulatory fragment of mammalian2 ampk in complexes with amp
72	d1o50a3	Alignment	not modelled	99.7	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
73	c3ocmA_	Alignment	not modelled	99.7	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
74	d2ef7a1	Alignment	not modelled	99.7	27	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
75	c2pfiA_	Alignment	not modelled	99.7	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**chloride channel protein clc-ka; **PDBTitle:** crystal structure of the cytoplasmic domain of the human2 chloride channel clc-ka
76	c3kpbA_	Alignment	not modelled	99.7	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj0100; **PDBTitle:** crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
77	d2v8qe2	Alignment	not modelled	99.7	12	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair

78	d2ouxa2	Alignment	not modelled	99.7	23	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
79	c3gbyA_	Alignment	not modelled	99.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ct1051; **PDBTitle:** crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
80	c3c3jA_	Alignment	not modelled	99.7	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
81	c2yvxD_	Alignment	not modelled	99.7	23	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
82	d2ooxe2	Alignment	not modelled	99.7	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
83	c3fhmD_	Alignment	not modelled	99.7	23	**PDB header:**structural genomics, unknown function, n **Chain:** D: **PDB Molecule:**uncharacterized protein atu1752; **PDBTitle:** crystal structure of the cbs-domain containing protein atu1752 from2 agrobacterium tumefaciens
84	c2yvzA_	Alignment	not modelled	99.7	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
85	c3kh5A_	Alignment	not modelled	99.7	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein mj1225; **PDBTitle:** crystal structure of protein mj1225 from methanocaldococcus2 jannaschii, a putative archaeal homolog of g-ampk.
86	c3kxrA_	Alignment	not modelled	99.7	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**magnesium transporter, putative; **PDBTitle:** structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.
87	d2ooxe1	Alignment	not modelled	99.7	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
88	c3ocoB_	Alignment	not modelled	99.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hemolysin-like protein containing cbs domains; **PDBTitle:** the crystal structure of a hemolysin-like protein containing cbs2 domain of oenococcus oeni psu
89	d2v8qe1	Alignment	not modelled	99.7	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
90	c3ocmB_	Alignment	not modelled	99.7	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**putative membrane protein; **PDBTitle:** the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
91	d2riha1	Alignment	not modelled	99.7	20	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
92	c3l31B_	Alignment	not modelled	99.7	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable manganase-dependent inorganic **PDBTitle:** crystal structure of the cbs and drtgg domains of the2 regulatory region of clostridium perfringens3 pyrophosphatase complexed with the inhibitor, amp
93	d3ddja2	Alignment	not modelled	99.6	21	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
94	d1zfja4	Alignment	not modelled	99.6	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
95	c3oi8B_	Alignment	not modelled	99.6	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of functionally unknown conserved protein domain2 from neisseria meningitidis mc58
96	c2yzqA_	Alignment	not modelled	99.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1780; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii
97	c3ddjA_	Alignment	not modelled	99.6	18	**PDB header:**amp-binding protein **Chain:** A: **PDB Molecule:**cbs domain-containing protein; **PDBTitle:** crystal structure of a cbs domain-containing protein in complex with2 amp (sso3205) from sulfolobus solfataricus at 1.80 a resolution
98	d2yzqa2	Alignment	not modelled	99.5	19	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
99	d2yvxa2	Alignment	not modelled	99.5	22	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
100	c3fioB_	Alignment	not modelled	99.1	16	**PDB header:**nucleotide binding protein, metal bindin **Chain:** B: **PDB Molecule:**a cystathionine beta-synthase domain protein **PDBTitle:** crystal structure of a fragment of a cystathionine beta-2 synthase domain protein fused to a zn-ribbon-like domain
101	d1jcna4	Alignment	not modelled	98.5	21	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
102	c1zzgB	Alignment	not modelled	98.3	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase;

102	c1zzgB_	Alignment	not modelled	98.[illegible]	22	**PDBTitle:** crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
103	d1c7qa_	Alignment	not modelled	98.1	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
104	c2q8nB_	Alignment	not modelled	98.1	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
105	c3ff1B_	Alignment	not modelled	98.0	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structure of glucose 6-phosphate isomerase from staphylococcus aureus
106	d1jr1a4	Alignment	not modelled	97.6	21	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
107	d1gzda_	Alignment	not modelled	97.4	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
108	c3jx9B_	Alignment	not modelled	97.2	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution
109	c2wu8A_	Alignment	not modelled	97.2	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
110	d1u0fa_	Alignment	not modelled	97.2	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
111	c3hjbA_	Alignment	not modelled	97.2	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
112	c3ljkA_	Alignment	not modelled	97.1	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** glucose-6-phosphate isomerase from francisella tularensis.
113	d1hm5a_	Alignment	not modelled	97.1	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
114	c3ujhB_	Alignment	not modelled	97.1	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
115	d1q50a_	Alignment	not modelled	97.0	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
116	d1iata_	Alignment	not modelled	96.9	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
117	c1t10A_	Alignment	not modelled	96.6	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
118	c2o2cB_	Alignment	not modelled	96.6	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase, glycosomal; **PDBTitle:** crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
119	c3nbuC_	Alignment	not modelled	96.5	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of pgi glucosephosphate isomerase
120	c3pr3B_	Alignment	not modelled	96.3	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate