

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	clct9D_	 Alignment		100.0	100	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from <i>Escherichia coli</i>
2	clq15A_	 Alignment		100.0	22	PDB header: biosynthetic protein Chain: A: PDB Molecule: cara; PDBTitle: carbapenam synthetase
3	clmlzB_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
4	dlct9a1	 Alignment		100.0	99	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
5	dljgtal	 Alignment		100.0	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
6	dlq15a1	 Alignment		100.0	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
7	dlct9a2	 Alignment		100.0	99	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
8	dlq15a2	 Alignment		100.0	18	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
9	clgph1_	 Alignment		100.0	27	PDB header: transferase(glutamine amidotransferase) Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
10	clecjB_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
11	cljxaA_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: glucosamine 6-phosphate synthase; PDBTitle: glucosamine 6-phosphate synthase with glucose 6-phosphate

12	dljga2	Alignment		100.0	24	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
13	dlgph12	Alignment		100.0	27	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
14	dlecfa2	Alignment		100.0	27	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
15	dlxffa_	Alignment		100.0	29	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
16	dlxnga1	Alignment		99.9	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
17	dlofda3	Alignment		99.8	23	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
18	dlte5a_	Alignment		99.8	22	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
19	dlea0a3	Alignment		99.8	26	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
20	c3mdnD_	Alignment		99.6	21	PDB header: transferase Chain: D: PDB Molecule: glutamine aminotransferase class-ii domain protein; PDBTitle: structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
21	c2e18B_	Alignment	not modelled	99.5	18	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of project ph0182 from pyrococcus horikoshii ot3
22	c3fiuD_	Alignment	not modelled	99.5	18	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmh synthetase from francisella tularensis
23	c3p52B_	Alignment	not modelled	99.4	19	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
24	d2pg3a1	Alignment	not modelled	99.3	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
25	c3bl5E_	Alignment	not modelled	99.2	18	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
26	c3k32D_	Alignment	not modelled	99.1	25	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein mj0690; PDBTitle: the crystal structure of predicted subunit of trna2 methyltransferase from methanocaldococcus jannaschii dsm
27	dlgpma1	Alignment	not modelled	99.0	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
28	dlk92a1	Alignment	not modelled	99.0	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
						PDB header: oxidoreductase

29	c1lm1A_	Alignment	not modelled	98.9	25	Chain: A: PDB Molecule: ferredoxin-dependent glutamate synthase; PDBTitle: structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
30	d1wy5a1	Alignment	not modelled	98.9	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
31	d1j20a1	Alignment	not modelled	98.9	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
32	c3dpiA_	Alignment	not modelled	98.8	16	PDB header: ligase Chain: A: PDB Molecule: nad+ synthetase; PDBTitle: crystal structure of nad+ synthetase from burkholderia pseudomallei
33	c3q4gA_	Alignment	not modelled	98.8	12	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad synthetase from vibrio cholerae
34	c2ywcC_	Alignment	not modelled	98.8	16	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
35	c1gpmD_	Alignment	not modelled	98.8	16	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
36	d1kqpa_	Alignment	not modelled	98.7	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
37	c1k97A_	Alignment	not modelled	98.7	19	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
38	c2hmaA_	Alignment	not modelled	98.7	17	PDB header: transferase Chain: A: PDB Molecule: probable trna (5-methylaminomethyl-2-thiouridylate)- PDBTitle: the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trnu from streptococcus pneumoniae
39	d1vl2a1	Alignment	not modelled	98.7	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
40	d2c5sa1	Alignment	not modelled	98.6	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
41	c2derA_	Alignment	not modelled	98.6	19	PDB header: transferase/rna Chain: A: PDB Molecule: trna-specific 2-thiouridylase mnma; PDBTitle: cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
42	c3tqiB_	Alignment	not modelled	98.6	16	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
43	c2vdcF_	Alignment	not modelled	98.5	23	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadph] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
44	c2e21A_	Alignment	not modelled	98.5	11	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
45	c3n05B_	Alignment	not modelled	98.5	17	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
46	c2nz2A_	Alignment	not modelled	98.5	20	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
47	c2vxoB_	Alignment	not modelled	98.5	18	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
48	d1ni5a1	Alignment	not modelled	98.4	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
49	c1kh2D_	Alignment	not modelled	98.4	21	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
50	d1wxia1	Alignment	not modelled	98.4	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
51	c2dplA_	Alignment	not modelled	98.3	16	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from pyrococcus horikoshii ot3
52	c2c5sA_	Alignment	not modelled	98.3	18	PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
53	c3dlaD_	Alignment	not modelled	98.3	20	PDB header: ligase Chain: D: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and

					don
54	c3uowB_	Alignment	not modelled	98.3	15 PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
55	c3a2kB_	Alignment	not modelled	98.3	13 PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
56	c1vl2C_	Alignment	not modelled	98.2	18 PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
57	c1ni5A_	Alignment	not modelled	98.0	12 PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
58	d1sura_	Alignment	not modelled	97.9	11 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
59	c3ilvA_	Alignment	not modelled	97.5	17 PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
60	c2o8vA_	Alignment	not modelled	97.5	11 PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: paps reductase in a covalent complex with thioredoxin c35a
61	d1zuna1	Alignment	not modelled	97.5	8 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
62	d1ru8a_	Alignment	not modelled	97.3	13 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
63	c1zunA_	Alignment	not modelled	97.2	8 PDB header: transferase Chain: A: PDB Molecule: sulfate adenyllyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
64	c2oq2B_	Alignment	not modelled	97.1	13 PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
65	c2goyC_	Alignment	not modelled	97.1	15 PDB header: oxidoreductase Chain: C: PDB Molecule: adenosine phosphosulfate reductase; PDBTitle: crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
66	d1vbka1	Alignment	not modelled	96.2	19 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
67	d2d13a1	Alignment	not modelled	95.9	14 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
68	c3g59A_	Alignment	not modelled	95.1	8 PDB header: transferase Chain: A: PDB Molecule: fmn adenyllyltransferase; PDBTitle: crystal structure of candida glabrata fmn2 adenyllyltransferase in complex with atp
69	c2wsiA_	Alignment	not modelled	94.8	10 PDB header: transferase Chain: A: PDB Molecule: fad synthetase; PDBTitle: crystal structure of yeast fad synthetase (fad1) in complex2 with fad
70	c1vbka_	Alignment	not modelled	90.0	15 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
71	c2cb1A_	Alignment	not modelled	70.5	14 PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
72	c3o1lB_	Alignment	not modelled	65.6	10 PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
73	c2j0eA_	Alignment	not modelled	37.6	13 PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
74	d1dv5a_	Alignment	not modelled	37.1	19 Fold: Acyl carrier protein-like Superfamily: ACP-like Family: apo-D-alanyl carrier protein
75	c3sbtB_	Alignment	not modelled	37.0	13 PDB header: splicing Chain: B: PDB Molecule: a1 cistron-splicing factor aar2; PDBTitle: crystal structure of a aar2-prp8 complex
76	c3nwpA_	Alignment	not modelled	36.2	11 PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
77	c3kx6C_	Alignment	not modelled	35.4	17 PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose-1,6-bisphosphate aldolase from babesia2 bovis at 2.1a resolution
78	c3n0vD_	Alignment	not modelled	35.4	12 PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
					PDB header: lyase Chain: A: PDB Molecule: fructose-bisphosphate aldolase;

79	c3mbfA_	Alignment	not modelled	32.8	16	PDBTitle: crystal structure of fructose bisphosphate aldolase from2 encephalitozoon cuniculi, bound to fructose 1,6-bisphosphate
80	d1md6a_	Alignment	not modelled	29.4	26	Fold: beta-Trefoil Superfamily: Cytokine Family: Interleukin-1 (IL-1)
81	c2b8tA_	Alignment	not modelled	27.8	13	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from u.urealyti cum in2 complex with thymidine
82	d2b8ta1	Alignment	not modelled	27.2	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
83	c3icoA_	Alignment	not modelled	25.7	14	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of 6-phosphogluconolactonase from2 mycobacterium tuberculosis
84	d1qo5b_	Alignment	not modelled	25.5	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
85	d1hkoa_	Alignment	not modelled	24.7	24	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
86	c3mmtC_	Alignment	not modelled	24.6	25	PDB header: hydrolase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose bisphosphate aldolase from bartonella2 henselae, bound to fructose bisphosphate
87	c3lhiA_	Alignment	not modelled	24.5	19	PDB header: hydrolase Chain: A: PDB Molecule: putative 6-phosphogluconolactonase; PDBTitle: crystal structure of putative 6-2 phosphogluconolactonase(y_p_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
88	d1b4ub_	Alignment	not modelled	24.3	26	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
89	d1mj4a_	Alignment	not modelled	23.5	6	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
90	c3rfuC_	Alignment	not modelled	23.3	21	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
91	d1zaia1	Alignment	not modelled	22.9	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
92	d1iccc_	Alignment	not modelled	22.6	18	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
93	c3hn6D_	Alignment	not modelled	21.7	14	PDB header: isomerase Chain: D: PDB Molecule: glucosamine-6-phosphate deaminase; PDBTitle: crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
94	d1fdja_	Alignment	not modelled	21.7	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
95	d1f2ja_	Alignment	not modelled	21.7	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
96	c1x3xA_	Alignment	not modelled	21.5	24	PDB header: electron transport Chain: A: PDB Molecule: cytochrome b5; PDBTitle: crystal structure of cytochrome b5 from ascaris suum
97	d2qapa1	Alignment	not modelled	21.4	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
98	c2qapC_	Alignment	not modelled	21.4	19	PDB header: lyase Chain: C: PDB Molecule: fructose-1,6-bisphosphate aldolase; PDBTitle: fructose-1,6-bisphosphate aldolase from leishmania mexicana
99	c3ndnC_	Alignment	not modelled	21.2	11	PDB header: lyase Chain: C: PDB Molecule: o-succinylhomoserine sulfhydrylase; PDBTitle: crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
100	d1kbia2	Alignment	not modelled	21.0	24	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
101	c9paiB_	Alignment	not modelled	20.9	14	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: protein (plasminogen activator inhibitor-1) residues 365- PDBTitle: cleaved substrate variant of plasminogen activator inhibitor-1
102	c2pc4B_	Alignment	not modelled	20.8	20	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
103	d1m2ia_	Alignment	not modelled	20.7	24	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
104	d1vk9a_	Alignment	not modelled	20.7	12	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Hypothetical protein TM1506

105	c3lwdA_	 Alignment	not modelled	20.4	15	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
106	d1a5ca_	 Alignment	not modelled	20.4	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
107	d1cxya_	 Alignment	not modelled	20.3	18	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5