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Description	P77674
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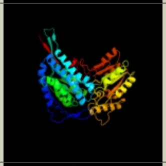
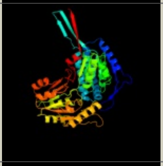
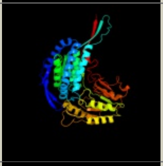
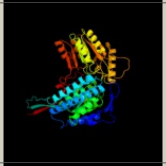
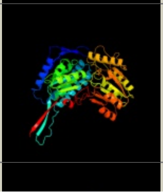
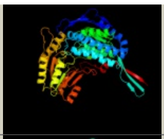
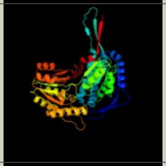
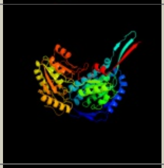
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wnda_	Alignment		100.0	100	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
2	c3ed6B_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
3	d1a4sa_	Alignment		100.0	37	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
4	d1bxsa_	Alignment		100.0	37	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
5	c2o2qA_	Alignment		100.0	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formyltetrahydrofolate dehydrogenase; **PDBTitle:** crystal structure of the c-terminal domain of rat2 10'formyltetrahydrofolate dehydrogenase in complex with nadp
6	c2ve5H_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
7	d1o9ja_	Alignment		100.0	38	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
8	c2jg7G_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**antiquitin; **PDBTitle:** crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
9	c3rh9A_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nad(p)(+)); **PDBTitle:** the crystal structure of oxidoreductase from marinobacter aquaeolei
10	d1o04a_	Alignment		100.0	38	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
11	d1ag8a_	Alignment		100.0	38	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like

12	c2d4eB_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**5-carboxymethyl-2-hydroxymuconate semialdehyde **PDBTitle:** crystal structure of the hpcc from thermus thermophilus hb8
13	c3ifgH_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of succinate-semialdehyde dehydrogenase from2 burkholderia pseudomallei, part 1 of 2
14	c3iwkB_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aminoaldehyde dehydrogenase; **PDBTitle:** crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)
15	c3r31A_	Alignment		100.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
16	c3ek1C_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
17	c3k2wD_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**betaine-aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
18	c3qanB_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-pyrroline-5-carboxylate dehydrogenase 1; **PDBTitle:** crystal structure of 1-pyrroline-5-carboxylate dehydrogenase from2 bacillus halodurans
19	c1t90B_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable methylmalonate-semialdehyde **PDBTitle:** crystal structure of methylmalonate semialdehyde2 dehydrogenase from bacillus subtilis
20	c3jz4C_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate-semialdehyde dehydrogenase [nadp+]; **PDBTitle:** crystal structure of e. coli nadp dependent enzyme
21	c2w8qA_	Alignment	not modelled	100.0	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase, **PDBTitle:** the crystal structure of human ssadh in complex with ssa.
22	d1uzba_	Alignment	not modelled	100.0	29	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
23	c3b4wA_	Alignment	not modelled	100.0	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
24	c3i44A_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
25	d1euha_	Alignment	not modelled	100.0	30	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
26	c2hg2A_	Alignment	not modelled	100.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase a; **PDBTitle:** structure of lactaldehyde dehydrogenase
27	c3prlD_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadp-dependent glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of nadp-dependent glyceraldehyde-3-phosphate2 dehydrogenase from bacillus halodurans c-125
28	d1ky8a_	Alignment	not modelled	100.0	29	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
						PDB header:oxidoreductase **Chain:** B: **PDB Molecule:**succinylglutamic semialdehyde

29	c3ju8B_	Alignment	not modelled	100.0	29	dehydrogenase; **PDBTitle:** crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
30	d1bi9a_	Alignment	not modelled	100.0	36	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
31	c3hazA_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of bifunctional proline utilization a2 (puta) protein
32	c3rosA_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent aldehyde dehydrogenase; **PDBTitle:** crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
33	c2vroB_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
34	c3efvC_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative succinate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of a putative succinate-semialdehyde dehydrogenase2 from salmonella typhimurium lt2 with bound nad
35	c3r64A_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad dependent benzaldehyde dehydrogenase; **PDBTitle:** crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
36	c3pqaA_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lactaldehyde dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
37	d1ad3a_	Alignment	not modelled	100.0	25	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
38	c3v4cB_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
39	d1ez0a_	Alignment	not modelled	100.0	19	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
40	c3lnsD_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**benzaldehyde dehydrogenase; **PDBTitle:** benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
41	c3k9dD_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of probable aldehyde dehydrogenase from listeria2 monocytogenes egd-e
42	d1o20a_	Alignment	not modelled	100.0	15	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
43	c3my7A_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alcohol dehydrogenase/acetaldehyde dehydrogenase; **PDBTitle:** the crystal structure of the acdh domain of an alcohol dehydrogenase2 from vibrio parahaemolyticus to 2.25a
44	c2h5gA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**delta 1-pyrroline-5-carboxylate synthetase; **PDBTitle:** crystal structure of human pyrroline-5-carboxylate synthetase
45	d1vlua_	Alignment	not modelled	100.0	17	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
46	c1vluB_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gamma-glutamyl phosphate reductase; **PDBTitle:** crystal structure of gamma-glutamyl phosphate reductase (yor323c) from2 saccharomyces cerevisiae at 2.40 a resolution
47	d1k75a_	Alignment	not modelled	98.3	16	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
48	c3oqbF_	Alignment	not modelled	25.6	8	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
49	d1h6da1	Alignment	not modelled	23.9	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	d2ioja1	Alignment	not modelled	21.9	14	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**DRTGG domain
51	c2ec4A_	Alignment	not modelled	20.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fas-associated factor 1; **PDBTitle:** solution structure of the uas domain from human fas-2 associated factor 1
52	c1sazA_	Alignment	not modelled	19.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable butyrate kinase 2; **PDBTitle:** membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
53	d1lc0a1	Alignment	not modelled	15.9	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

54	c2yukA_	Alignment	not modelled	15.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**myeloid/lymphoid or mixed-lineage leukemia **PDBTitle:** solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog
55	d1t0tv_	Alignment	not modelled	15.5	7	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
56	d1wo8a1	Alignment	not modelled	15.2	14	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
57	d1vdha_	Alignment	not modelled	15.0	21	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
58	d1k99a_	Alignment	not modelled	14.4	6	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
59	c1j3xA_	Alignment	not modelled	14.3	6	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**high mobility group protein 2; **PDBTitle:** solution structure of the n-terminal domain of the hmgb2
60	d1j3xa_	Alignment	not modelled	14.3	6	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
61	c2eqzA_	Alignment	not modelled	14.2	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**high mobility group protein b3; **PDBTitle:** solution structure of the first hmg-box domain from high2 mobility group protein b3
62	c2crjA_	Alignment	not modelled	13.8	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the hmg domain of mouse hmg domain2 protein hmgx2
63	c2yvqA_	Alignment	not modelled	12.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
64	c3fd8A_	Alignment	not modelled	12.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
65	c3fghA_	Alignment	not modelled	12.6	3	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor a, mitochondrial; **PDBTitle:** human mitochondrial transcription factor a box b
66	c3jtpB_	Alignment	not modelled	12.5	17	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**adapter protein meca 1; **PDBTitle:** crystal structure of the c-terminal domain of meca
67	c2co9A_	Alignment	not modelled	12.1	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**thymus high mobility group box protein tox; **PDBTitle:** solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse
68	c1vjtA_	Alignment	not modelled	11.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
69	c2iswB_	Alignment	not modelled	11.3	8	**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
70	c2qguA_	Alignment	not modelled	11.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable signal peptide protein; **PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
71	d1sgva1	Alignment	not modelled	11.1	26	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
72	c3cxjB_	Alignment	not modelled	10.9	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
73	c3e7hA_	Alignment	not modelled	10.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** the crystal structure of the beta subunit of the dna-2 directed rna polymerase from vibrio cholerae o1 biovar3 eltor
74	c3ec7C_	Alignment	not modelled	10.5	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
75	d2lefa_	Alignment	not modelled	10.5	8	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
76	d1vkna1	Alignment	not modelled	10.4	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
77	c3evnA_	Alignment	not modelled	10.4	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
78	c3tfwB_	Alignment	not modelled	10.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative o-methyltransferase; **PDBTitle:** crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae

79	c3db2C_	Alignment	not modelled	9.9	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative nadph-dependent oxidoreductase; **PDBTitle:** crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
80	d1s7ia_	Alignment	not modelled	9.8	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
81	d1ydwa1	Alignment	not modelled	9.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
82	d1ryda1	Alignment	not modelled	9.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
83	c2p2sA_	Alignment	not modelled	9.4	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
84	d2dlxa1	Alignment	not modelled	9.1	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**UAS domain
85	c2q4eB_	Alignment	not modelled	8.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable oxidoreductase at4g09670; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
86	d1lwma_	Alignment	not modelled	8.8	11	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
87	c2cs1A_	Alignment	not modelled	8.7	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pms1 protein homolog 1; **PDBTitle:** solution structure of the hmg domain of human dna mismatch2 repair protein
88	c2ze3A_	Alignment	not modelled	8.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dfa0005; **PDBTitle:** crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
89	c2ixaA_	Alignment	not modelled	8.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
90	d1saza2	Alignment	not modelled	8.5	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
91	d1hsma_	Alignment	not modelled	8.3	18	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
92	c3labA_	Alignment	not modelled	8.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate) **PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
93	d1zh8a1	Alignment	not modelled	8.2	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
94	c3nt5B_	Alignment	not modelled	8.2	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
95	c2vxhF_	Alignment	not modelled	8.0	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**chlorite dismutase; **PDBTitle:** the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
96	c3mtjA_	Alignment	not modelled	7.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
97	d1v64a_	Alignment	not modelled	7.8	8	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
98	d1hmfa_	Alignment	not modelled	7.6	17	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
99	c1hmfA_	Alignment	not modelled	7.6	17	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**high mobility group protein fragment-b; **PDBTitle:** structure of the hmg box motif in the b-domain of hmg1