Phyre2

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Description	P76149
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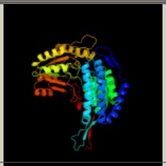
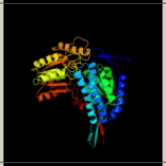
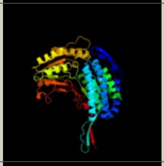
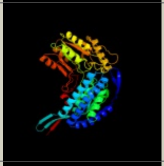
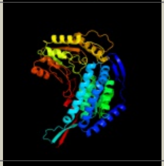
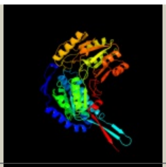
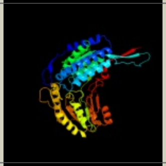
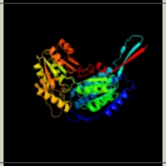
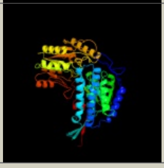
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3efvC_	Alignment		100.0	80	**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
2	d1a4sa_	Alignment		100.0	30	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
3	c3ed6B_	Alignment		100.0	27	**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
4	c2jg7G_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**antiquitin; **PDBTitle:** crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
5	d1bxsa_	Alignment		100.0	30	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
6	c2ve5H_	Alignment		100.0	32	**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	28	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
8	c3iwkB_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aminoaldehyde dehydrogenase; **PDBTitle:** crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)
9	c3rosA_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent aldehyde dehydrogenase; **PDBTitle:** crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
10	c2d4eB_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**5-carboxymethyl-2-hydroxymuconate semialdehyde **PDBTitle:** crystal structure of the hpcc from thermus thermophilus hb8
11	c2w8qA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase, **PDBTitle:** the crystal structure of human ssadh in complex with ssa.

12	c3r31A_	Alignment		100.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
13	c2o2qA_	Alignment		100.0	29	**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
14	c3rh9A_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nad(p)(+)); **PDBTitle:** the crystal structure of oxidoreductase from marinobacter aquaeolei
15	c3ifgH_	Alignment		100.0	35	**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
16	d1ag8a_	Alignment		100.0	30	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
17	c3k2wD_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**betaine-aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
18	d1o04a_	Alignment		100.0	30	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
19	c3qanB_	Alignment		100.0	30	**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
20	c3b4wA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
21	c3jz4C_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate-semialdehyde dehydrogenase [nadp+]; **PDBTitle:** crystal structure of e. coli nadp dependent enzyme
22	d1uzba_	Alignment	not modelled	100.0	28	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
23	d1wnda_	Alignment	not modelled	100.0	30	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
24	c1t90B_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable methylmalonate-semialdehyde **PDBTitle:** crystal structure of methylmalonate semialdehyde2 dehydrogenase from bacillus subtilis
25	c3ek1C_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
26	d1euha_	Alignment	not modelled	100.0	30	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
27	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
28	c3hazA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of bifunctional proline utilization a2 (puta) protein
						PDB header:oxidoreductase

29	c2hg2A_	Alignment	not modelled	100.0	33	**Chain:** A: **PDB Molecule:**aldehyde dehydrogenase a; **PDBTitle:** structure of lactaldehyde dehydrogenase
30	d1ky8a_	Alignment	not modelled	100.0	28	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
31	c3prlD_	Alignment	not modelled	100.0	30	**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
32	c3ju8B_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinylglutamic semialdehyde dehydrogenase; **PDBTitle:** crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
33	c3pqaA_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lactaldehyde dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
34	d1bi9a_	Alignment	not modelled	100.0	31	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
35	c2vroB_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
36	d1ad3a_	Alignment	not modelled	100.0	23	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
37	c3r64A_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad dependent benzaldehyde dehydrogenase; **PDBTitle:** crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
38	d1ez0a_	Alignment	not modelled	100.0	22	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
39	c3lnsD_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**benzaldehyde dehydrogenase; **PDBTitle:** benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
40	c3v4cB_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
41	c3k9dD_	Alignment	not modelled	100.0	18	**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	18	**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	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
46	c1vluB_	Alignment	not modelled	100.0	18	**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	98.4	17	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
48	d2bona1	Alignment	not modelled	61.3	17	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
49	d1a9xa2	Alignment	not modelled	60.9	20	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
50	c2yvqA_	Alignment	not modelled	60.1	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
51	c2qyxB_	Alignment	not modelled	46.2	5	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein mj0159; **PDBTitle:** crystal structure of uncharacterized protein mj0159 from2 methanocaldococcus jannaschii
52	d1uz5a3	Alignment	not modelled	42.5	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
53	d2jgra1	Alignment	not modelled	37.5	17	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
						PDB header:de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein;

54	c2l69A_	Alignment	not modelled	36.9	14	**PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
55	d2p1ra1	Alignment	not modelled	34.5	17	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
56	d1wo8a1	Alignment	not modelled	30.2	10	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
57	d1u0ta_	Alignment	not modelled	28.3	18	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
58	c2bonB_	Alignment	not modelled	28.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipid kinase; **PDBTitle:** structure of an escherichia coli lipid kinase (yegs)
59	d1ycga1	Alignment	not modelled	25.7	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
60	d1k99a_	Alignment	not modelled	21.8	8	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
61	d2ioja1	Alignment	not modelled	21.4	8	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**DRTGG domain
62	c2crjA_	Alignment	not modelled	20.3	11	**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	c1uz5A_	Alignment	not modelled	19.9	18	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
64	c3fghA_	Alignment	not modelled	19.8	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor a, mitochondrial; **PDBTitle:** human mitochondrial transcription factor a box b
65	c3v4gA_	Alignment	not modelled	19.6	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
66	c2co9A_	Alignment	not modelled	19.0	8	**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
67	c3jtpB_	Alignment	not modelled	18.8	17	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**adapter protein meca 1; **PDBTitle:** crystal structure of the c-terminal domain of meca
68	c2ec4A_	Alignment	not modelled	18.7	10	**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
69	d1j3xa_	Alignment	not modelled	18.5	8	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
70	c1j3xA_	Alignment	not modelled	18.5	8	**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
71	c2g4rB_	Alignment	not modelled	17.9	12	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
72	c2eqzA_	Alignment	not modelled	17.8	8	**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
73	c2q9uB_	Alignment	not modelled	17.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
74	d1xxaa_	Alignment	not modelled	17.0	30	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
75	d2g2ca1	Alignment	not modelled	16.7	12	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
76	c2ze3A_	Alignment	not modelled	16.3	15	**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
77	d1mkza_	Alignment	not modelled	15.9	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
78	d1wu2a3	Alignment	not modelled	15.8	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
79	c2cs1A_	Alignment	not modelled	15.8	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
80	d1t95a1	Alignment	not modelled	15.6	35	**Fold:**RuvA C-terminal domain-like **Superfamily:**Hypothetical protein AF0491, middle domain

						Family: Hypothetical protein AF0491, middle domain
81	c2yukA_	Alignment	not modelled	15.2	15	**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
82	d1j46a_	Alignment	not modelled	15.0	8	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
83	c3fa4D_	Alignment	not modelled	14.7	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase; **PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
84	d1xi8a3	Alignment	not modelled	14.0	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
85	d1s7ia_	Alignment	not modelled	13.8	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
86	d1hsma_	Alignment	not modelled	13.4	16	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
87	d2lefa_	Alignment	not modelled	13.4	11	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
88	d1y5ea1	Alignment	not modelled	13.4	22	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
89	c3labA_	Alignment	not modelled	13.3	16	**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
90	d2ftsa3	Alignment	not modelled	12.9	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
91	c2is8A_	Alignment	not modelled	12.6	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
92	d1lwma_	Alignment	not modelled	12.5	8	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
93	c3u2bC_	Alignment	not modelled	12.3	3	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription factor sox-4; **PDBTitle:** structure of the sox4 hmg domain bound to dna
94	d1v64a_	Alignment	not modelled	11.8	5	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
95	d2nqra3	Alignment	not modelled	11.8	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
96	c3lo3E_	Alignment	not modelled	11.5	16	**PDB header:**structure genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown2 protein from colwellia psychrerythraea 34h.
97	c2qiwA_	Alignment	not modelled	11.5	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pep phosphonomutase; **PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
98	c1hmfA_	Alignment	not modelled	11.5	14	**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
99	d1hmfa_	Alignment	not modelled	11.5	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box