Phyre^2

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Description	P0A6W5
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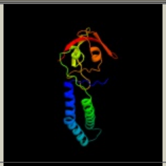
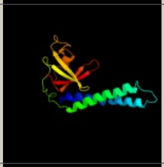
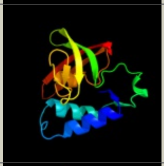
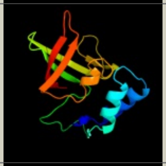
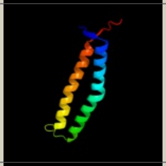
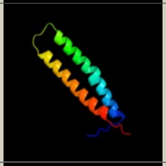
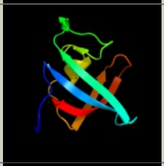
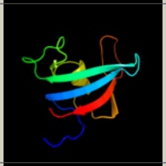
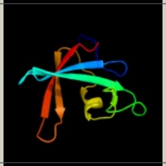
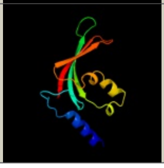
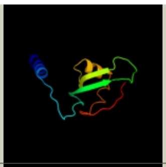
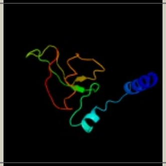
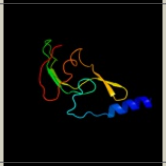
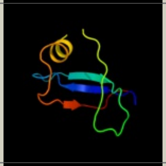
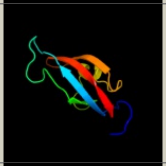
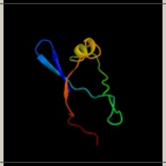
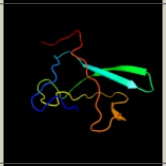
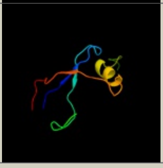
Unique Job ID	a4d97c8714225dbd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2p4vA_	Alignment		100.0	35	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
2	c1grjA_	Alignment		100.0	100	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**grea protein; **PDBTitle:** grea transcript cleavage factor from escherichia coli
3	c2etnA_	Alignment		100.0	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
4	c3bmbB_	Alignment		100.0	25	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
5	c2pn0D_	Alignment		100.0	29	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
6	d1grja1	Alignment		99.9	100	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
7	d2f23a1	Alignment		99.9	26	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
8	d2f23a2	Alignment		99.9	28	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
9	d1grja2	Alignment		99.9	100	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
10	d2etna2	Alignment		99.9	28	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
11	c3gtyX_	Alignment		95.2	22	**PDB header:**chaperone/ribosomal protein **Chain:** X: **PDB Molecule:**trigger factor; **PDBTitle:** promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone

12	d1t11a3	Alignment		88.4	11	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
13	d1w26a3	Alignment		86.9	12	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
14	c1w26B_	Alignment		82.9	16	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
15	c1t11A_	Alignment		79.0	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor
16	d1krha1	Alignment		78.6	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
17	d1l1pa_	Alignment		73.8	16	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
18	d1qx4a1	Alignment		63.5	13	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
19	d1ndha1	Alignment		59.5	8	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
20	d2cnda1	Alignment		58.3	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
21	c1zeqX_	Alignment	not modelled	47.4	7	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
22	c2kw8A_	Alignment	not modelled	45.6	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**lpxtg-site transpeptidase family protein; **PDBTitle:** solution structure of bacillus anthracis sortase a (srta)2 transpeptidase
23	d1e32a3	Alignment	not modelled	45.5	21	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
24	c2gpjA_	Alignment	not modelled	43.9	17	**PDB header:**fad-binding protein **Chain:** A: **PDB Molecule:**siderophore-interacting protein; **PDBTitle:** crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
25	c2kfwA_	Alignment	not modelled	41.9	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
26	d1tvca1	Alignment	not modelled	41.8	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
27	d1umka1	Alignment	not modelled	41.6	11	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
28	c2dq0A_	Alignment	not modelled	40.1	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog

29	c3fn5B_	Alignment	not modelled	39.3	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sortase a; **PDBTitle:** crystal structure of sortase a (spy1154) from streptococcus2 pyogenes serotype m1 strain sf370
30	c3shwA_	Alignment	not modelled	38.5	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3-sh3-guk supramodule complex with2 connexin-45 peptide
31	c3g5oA_	Alignment	not modelled	38.5	26	**PDB header:**toxin/antitoxin **Chain:** A: **PDB Molecule:**uncharacterized protein rv2865; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
32	d1hxva_	Alignment	not modelled	37.3	8	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
33	c1hxvA_	Alignment	not modelled	37.3	8	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** ppiase domain of the mycoplasma genitalium trigger factor
34	d1t2wa_	Alignment	not modelled	36.2	11	**Fold:**Sortase **Superfamily:**Sortase **Family:**Sortase
35	d1st6a4	Alignment	not modelled	34.3	29	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
36	c2krgA_	Alignment	not modelled	33.9	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**na(+)/h(+) exchange regulatory cofactor nhe-rf1; **PDBTitle:** solution structure of human sodium/ hydrogen exchange2 regulatory factor 1(150-358)
37	c3shuB_	Alignment	not modelled	33.5	26	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3
38	d1fdra1	Alignment	not modelled	33.2	14	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
39	d1gvha2	Alignment	not modelled	32.7	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
40	c3o0pA_	Alignment	not modelled	32.5	14	**PDB header:**transferase , hydrolase **Chain:** A: **PDB Molecule:**sortase family protein; **PDBTitle:** pilus-related sortase c of group b streptococcus
41	c3re9A_	Alignment	not modelled	31.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sortase-like protein; **PDBTitle:** crystal structure of sortasec1 from streptococcus suis
42	c2l55A_	Alignment	not modelled	31.0	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**silb,silver efflux protein, mfp component of the three **PDBTitle:** solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
43	c3cgnA_	Alignment	not modelled	30.8	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd
44	c2pjhB_	Alignment	not modelled	30.4	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
45	d1st6a3	Alignment	not modelled	30.0	28	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
46	c3pr9A_	Alignment	not modelled	29.2	8	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
47	c2kr7A_	Alignment	not modelled	29.1	0	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd; **PDBTitle:** solution structure of helicobacter pylori slyd
48	c2w1kB_	Alignment	not modelled	28.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative sortase; **PDBTitle:** crystal structure of sortase c-3 (srtc-3) from2 streptococcus pneumoniae
49	d1dm9a_	Alignment	not modelled	26.9	14	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
50	c1dm9A_	Alignment	not modelled	26.9	14	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
51	d2piaa1	Alignment	not modelled	26.9	23	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
52	c2k8iA_	Alignment	not modelled	26.8	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of e.coli slyd
53	c2xwgA_	Alignment	not modelled	26.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sortase; **PDBTitle:** crystal structure of sortase c-1 from actinomyces oris (formerly2 actinomyces naeslundii)
54	d2f5ya1	Alignment	not modelled	26.5	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
						PDB header:structural protein

55	c3k1rA_	Alignment	not modelled	26.0	12	**Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
56	c3g66A_	Alignment	not modelled	25.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sortase c; **PDBTitle:** the crystal structure of streptococcus pneumoniae sortase c2 provides novel insights into catalysis as well as pilin3 substrate specificity
57	d2gp4a1	Alignment	not modelled	24.7	11	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
58	d1t9fa_	Alignment	not modelled	23.9	10	**Fold:**beta-Trefoil **Superfamily:**MIR domain **Family:**MIR domain
59	d1ep3b1	Alignment	not modelled	23.4	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
60	d1uita_	Alignment	not modelled	23.4	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
61	d1y7na1	Alignment	not modelled	22.8	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
62	c3rccl_	Alignment	not modelled	22.7	7	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**sortase srta; **PDBTitle:** crystal structure of the streptococcus agalactiae sortase a
63	c1cz5A_	Alignment	not modelled	21.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vcp-like atpase; **PDBTitle:** nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
64	c3prdA_	Alignment	not modelled	20.8	8	**PDB header:**chaperone, isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
65	c3u5cG_	Alignment	not modelled	20.3	14	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**40s ribosomal protein s6-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
66	d1pina2	Alignment	not modelled	20.3	12	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
67	d1fnda1	Alignment	not modelled	19.3	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
68	c2piaA_	Alignment	not modelled	18.1	12	**PDB header:**reductase **Chain:** A: **PDB Molecule:**phthalate dioxygenase reductase; **PDBTitle:** phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]
69	d2iv2x1	Alignment	not modelled	18.0	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
70	c2vn1A_	Alignment	not modelled	17.9	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**70 kda peptidylprolyl isomerase; **PDBTitle:** crystal structure of the fk506-binding domain of plasmodium2 falciparum fkbp35 in complex with fk506
71	d1ix5a_	Alignment	not modelled	17.9	17	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
72	d1sm4a1	Alignment	not modelled	17.2	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
73	d2a6qa1	Alignment	not modelled	16.9	21	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
74	c2xznY_	Alignment	not modelled	16.8	17	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**rps6e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
75	d2jioa1	Alignment	not modelled	16.7	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
76	c1krhA_	Alignment	not modelled	16.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
77	c2gp4A_	Alignment	not modelled	16.0	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
78	c2eehA_	Alignment	not modelled	15.8	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pdz domain-containing protein 7; **PDBTitle:** solution structure of first pdz domain of pdz domain2 containing protein 7
79	c2z17A_	Alignment	not modelled	15.7	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pleckstrin homology sec7 and coiled-coil domains- **PDBTitle:** crystal sturcture of pdz domain from human pleckstrin2 homology, sec7
80	d1vloa1	Alignment	not modelled	15.3	15	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain

81	c3rbjB_	Alignment	not modelled	15.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sortase family protein; **PDBTitle:** crystal structure of the lid-mutant of streptococcus agalactiae2 sortase c1
82	d1kshb_	Alignment	not modelled	14.5	5	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
83	c2l66B_	Alignment	not modelled	14.4	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
84	d1seta1	Alignment	not modelled	13.6	16	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Seryl-tRNA synthetase (SerRS)
85	d1qbea_	Alignment	not modelled	13.6	22	**Fold:**RNA bacteriophage capsid protein **Superfamily:**RNA bacteriophage capsid protein **Family:**RNA bacteriophage capsid protein
86	d1kwaa_	Alignment	not modelled	13.3	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
87	d1ogya1	Alignment	not modelled	13.0	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
88	c2fug4_	Alignment	not modelled	12.8	10	**PDB header:**oxidoreductase **Chain:** 4: **PDB Molecule:**nadh-quinone oxidoreductase chain 4; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
89	d2fug41	Alignment	not modelled	12.8	10	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nqo4-like
90	d1gawa1	Alignment	not modelled	12.7	33	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
91	d1qfja1	Alignment	not modelled	12.7	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
92	d1q1ca1	Alignment	not modelled	12.2	16	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
93	c2w1jB_	Alignment	not modelled	12.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative sortase; **PDBTitle:** crystal structure of sortase c-1 (srtc-1) from2 streptococcus pneumoniae
94	c2d90A_	Alignment	not modelled	11.9	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pdz domain containing protein 1; **PDBTitle:** solution structure of the third pdz domain of pdz domain2 containing protein 1
95	c2xzrA_	Alignment	not modelled	11.4	32	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**immunoglobulin-binding protein eibd; **PDBTitle:** escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
96	d1vlfm1	Alignment	not modelled	11.4	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
97	d1a8pa1	Alignment	not modelled	11.3	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
98	d2bmwa1	Alignment	not modelled	11.2	30	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
99	d1nbwa1	Alignment	not modelled	10.6	62	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Swiveling domain of dehydratase reactivase alpha subunit **Family:**Swiveling domain of dehydratase reactivase alpha subunit