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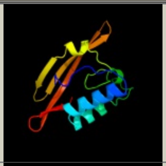
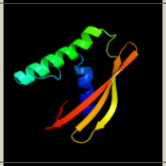
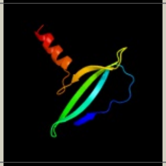
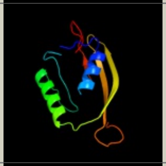
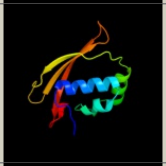
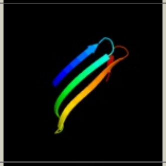
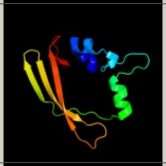
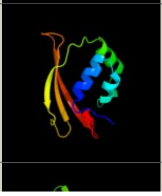
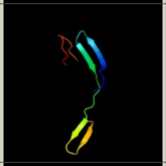
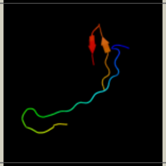
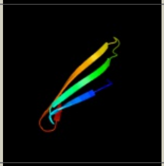
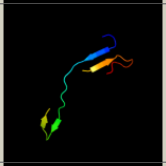
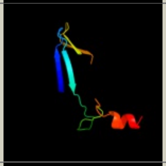
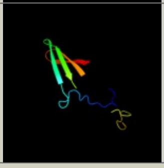
Description	Q46858
Date	Thu Jan 5 12:35:18 GMT 2012
Unique Job ID	842eabe67540a359

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kztB_	Alignment		98.3	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (np_812423.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
2	c3k7cC_	Alignment		97.3	15	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**putative ntf2-like transpeptidase; **PDBTitle:** crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from campylobacter jejuni at 2.00 a resolution
3	c2qguA_	Alignment		96.3	14	**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
4	c3gwrA_	Alignment		92.9	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative calcium/calmodulin-dependent protein kinase type **PDBTitle:** crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution
5	c2i9wA_	Alignment		92.8	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution
6	d3b7ca1	Alignment		90.9	19	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SO0125-like
7	d3blza1	Alignment		88.7	20	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Sbal0622-like
8	c2jq5A_	Alignment		88.0	15	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**sec-c motif; **PDBTitle:** solution structure of rpa3114, a sec-c motif containing2 protein from rhodopseudomonas palustris; northeast3 structural genomics consortium target rpt5 / ontario4 center for structural proteomics target rp3097
9	d1vqqa1	Alignment		87.8	12	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Penicillin binding protein 2a (PBP2A), N-terminal domain
10	c3dukD_	Alignment		87.0	15	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
11	d2i9wa1	Alignment		85.9	15	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SEC-C associated NTF2-like domain

12	c3fkaD_	Alignment		79.8	14	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized ntf-2 like protein; **PDBTitle:** crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
13	d3ebya1	Alignment		74.3	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ring hydroxylating beta subunit
14	d2rgqa1	Alignment		72.5	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Rv3472-like
15	d3ef8a1	Alignment		72.3	11	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
16	c3a76B_	Alignment		71.6	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**gamma-hexachlorocyclohexane dehydrochlorinase; **PDBTitle:** the crystal structure of lina
17	d3e99a1	Alignment		71.1	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ring hydroxylating beta subunit
18	d2rfra1	Alignment		69.7	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
19	d3cu3a1	Alignment		67.0	18	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
20	d1idpa_	Alignment		65.9	19	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Scytalone dehydratase
21	d3b8la1	Alignment	not modelled	64.3	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
22	d3stda_	Alignment	not modelled	63.9	20	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Scytalone dehydratase
23	d3cnxa1	Alignment	not modelled	58.1	14	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SAV4671-like
24	d2owpa1	Alignment	not modelled	52.1	20	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BxeB1374-like
25	c2gbxF_	Alignment	not modelled	45.5	7	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**biphenyl 2,3-dioxygenase beta subunit; **PDBTitle:** crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
26	d1gpca_	Alignment	not modelled	41.1	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
27	c2jqvA_	Alignment	not modelled	39.5	13	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**aig2 protein-like; **PDBTitle:** solution structure at3g28950.1 from arabidopsis thaliana
28	c3gzrA_	Alignment	not modelled	39.4	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein with a ntf2-like fold; **PDBTitle:** crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution
						Fold: Cystatin-like

29	d2chca1	Alignment	not modelled	36.2	13	**Superfamily:**NTF2-like **Family:**Rv3472-like
30	c1mwuA_	Alignment	not modelled	34.5	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 2a; **PDBTitle:** structure of methicillin acyl-penicillin binding protein 2a2 from methicillin resistant staphylococcus aureus strain3 27r at 2.60 a resolution.
31	d1twfc2	Alignment	not modelled	32.9	14	**Fold:**Insert subdomain of RNA polymerase alpha subunit **Superfamily:**Insert subdomain of RNA polymerase alpha subunit **Family:**Insert subdomain of RNA polymerase alpha subunit
32	c2hx6A_	Alignment	not modelled	32.8	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
33	c3f7sA_	Alignment	not modelled	31.8	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution
34	c3fh1A_	Alignment	not modelled	30.7	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function (mll8193)2 from mesorhizobium loti at 1.60 a resolution
35	d3ejva1	Alignment	not modelled	30.7	28	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
36	d1y74a1	Alignment	not modelled	29.9	24	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
37	c1fuiB_	Alignment	not modelled	29.4	25	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
38	d1zl8a1	Alignment	not modelled	29.0	37	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
39	d2a1ka1	Alignment	not modelled	27.3	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
40	d2f86b1	Alignment	not modelled	23.0	24	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
41	c3h51A_	Alignment	not modelled	22.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative calcium/calmodulin dependent protein kinase ii **PDBTitle:** crystal structure of putative calcium/calmodulin dependent protein2 kinase ii association domain (np_636218.1) from xanthomonas3 campestris at 1.70 a resolution
42	d2b1xb1	Alignment	not modelled	21.1	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ring hydroxylating beta subunit
43	d2rcda1	Alignment	not modelled	19.4	25	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BxeB1374-like
44	d2bbya_	Alignment	not modelled	18.8	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding domain from rap30
45	c3ibzA_	Alignment	not modelled	16.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative tellurium resistant like protein terd; **PDBTitle:** crystal structure of putative tellurium resistant like protein (terd)2 from streptomyces coelicolor a3(2)
46	c2jmkA_	Alignment	not modelled	16.1	35	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hypothetical protein ta0956; **PDBTitle:** solution structure of ta0956
47	d2axti1	Alignment	not modelled	16.0	22	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
48	c3bb9D_	Alignment	not modelled	15.5	28	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**putative orphan protein; **PDBTitle:** crystal structure of a putative ketosteroid isomerase (sfri_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
49	d2bmob1	Alignment	not modelled	15.5	11	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ring hydroxylating beta subunit
50	d2ux0a1	Alignment	not modelled	15.3	18	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
51	c3efhB_	Alignment	not modelled	14.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
52	c3ke7A_	Alignment	not modelled	14.1	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative ketosteroid isomerase; **PDBTitle:** crystal structure of a putative ketosteroid isomerase (yp_001303366.1)2 from parabacteroides distasonis atcc 8503 at 1.45 a resolution
53	d2r4ia1	Alignment	not modelled	13.9	6	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**CHU142-like
						Fold: Cystatin-like

54	d3ec9a1	Alignment	not modelled	13.9	22	**Superfamily:**NTF2-like **Family:**PhzA/PhzB-like
55	c3iu0A_	Alignment	not modelled	13.6	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-glutamine gamma-glutamyltransferase; **PDBTitle:** structural basis for zymogen activation and substrate binding of2 transglutaminase from streptomyces mobaraense
56	d1iu4a_	Alignment	not modelled	13.6	35	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Microbial transglutaminase
57	d1dqaa1	Alignment	not modelled	13.3	18	**Fold:**Ferredoxin-like **Superfamily:**NAD-binding domain of HMG-CoA reductase **Family:**NAD-binding domain of HMG-CoA reductase
58	c3kspA_	Alignment	not modelled	13.1	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**calcium/calmodulin-dependent kinase ii association domain; **PDBTitle:** crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution
59	d2evra1	Alignment	not modelled	12.4	14	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**Spr N-terminal domain-like
60	c1x4qA_	Alignment	not modelled	12.4	23	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u4/u6 small nuclear ribonucleoprotein prp3; **PDBTitle:** solution structure of pwi domain in u4/u6 small nuclear2 ribonucleoprotein prp3(hprp3)
61	c3hx8A_	Alignment	not modelled	11.6	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative ketosteroid isomerase; **PDBTitle:** crystal structure of putative ketosteroid isomerase2 (np_103587.1) from mesorhizobium loti at 1.45 a resolution
62	d2ezwa1	Alignment	not modelled	11.5	50	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
63	d3bb9a1	Alignment	not modelled	10.4	22	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SO0125-like
64	d1hkxa_	Alignment	not modelled	10.3	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
65	c1bm4A_	Alignment	not modelled	10.1	17	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (moloney murine leukemia virus capsid); **PDBTitle:** momlv capsid protein major homology region peptide analog
66	d1ulib_	Alignment	not modelled	9.4	9	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ring hydroxylating beta subunit
67	d1kh0a_	Alignment	not modelled	9.4	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
68	c3robC_	Alignment	not modelled	9.3	14	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776
69	c2htbB_	Alignment	not modelled	9.3	29	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative enzyme related to aldose 1-epimerase; **PDBTitle:** crystal structure of a putative mutarotase (yead) from2 salmonella typhimurium in monoclinic form
70	c3kkfA_	Alignment	not modelled	9.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative antibiotic biosynthesis monooxygenase; **PDBTitle:** crystal structure of putative antibiotic biosynthesis2 monooxygenase (np_810307.1) from bacteriodes3 thetaiotaomicron vpi-5482 at 1.30 a resolution
71	d1v5ra1	Alignment	not modelled	8.7	50	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GAS2 domain-like **Family:**GAS2 domain
72	d2icwg1	Alignment	not modelled	7.5	35	**Fold:**Superantigen MAM **Superfamily:**Superantigen MAM **Family:**Superantigen MAM
73	c3gzxB_	Alignment	not modelled	7.5	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**biphenyl dioxygenase subunit beta; **PDBTitle:** crystal structure of the biphenyl dioxygenase in complex with biphenyl2 from comamonas testosteroni sp. strain b-356
74	c2vkzH_	Alignment	not modelled	6.7	14	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
75	d1cida1	Alignment	not modelled	6.7	35	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
76	c3sjrB_	Alignment	not modelled	6.6	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved unkown function protein cv_1783 from2 chromobacterium violaceum atcc 12472
77	d2cxaa1	Alignment	not modelled	6.6	40	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**LFTR-like
						PDB header:transferase **Chain:** A: **PDB Molecule:**leucyl/phenylalanyl-trna-protein

78	c2cxaA_	Alignment	not modelled	6.6	40	transferase; **PDBTitle:** crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
79	c3rh0A_	Alignment	not modelled	6.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
80	c1p81A_	Alignment	not modelled	6.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of the d181e variant of catalase hpii2 from e. coli
81	d2imja1	Alignment	not modelled	6.3	53	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PFL3262-like
82	c3dkzA_	Alignment	not modelled	6.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thioesterase superfamily protein; **PDBTitle:** crystal structure of the q7w9w5_borpa protein from2 bordetella parapertussis. northeast structural genomics3 consortium target bpr208c.
83	d1eyha_	Alignment	not modelled	6.1	19	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**ENTH domain
84	c3soyA_	Alignment	not modelled	6.1	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ntf2-like superfamily protein; **PDBTitle:** nuclear transport factor 2 (ntf2-like) superfamily protein from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
85	d1u9ya2	Alignment	not modelled	6.1	29	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
86	c3r8kB_	Alignment	not modelled	6.1	26	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul protein (hexagonal form)
87	d1nekc_	Alignment	not modelled	5.8	22	**Fold:**Heme-binding four-helical bundle **Superfamily:**Fumarate reductase respiratory complex transmembrane subunits **Family:**Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
88	c3g9hA_	Alignment	not modelled	5.8	32	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**suppressor of yeast profilin deletion; **PDBTitle:** crystal structure of the c-terminal mu homology domain of2 syp1
89	c2wtkB_	Alignment	not modelled	5.7	17	**PDB header:**transferase/metal-binding protein **Chain:** B: **PDB Molecule:**ste20-related kinase adapter protein alpha; **PDBTitle:** structure of the heterotrimeric lkb1-stradalpha-mo25alpha2 complex
90	c3mjdA_	Alignment	not modelled	5.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
91	d2fcla1	Alignment	not modelled	5.5	24	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**TM1012-like
92	d1inza_	Alignment	not modelled	5.5	19	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**ENTH domain
93	c2k85A_	Alignment	not modelled	5.5	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glucocorticoid receptor dna-binding factor 1; **PDBTitle:** p190-a rhogap ff1 domain
94	c3qk9B_	Alignment	not modelled	5.3	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**mitochondrial import inner membrane translocase subunit **PDBTitle:** yeast tim44 c-terminal domain complexed with cymal-3
95	d1zbma1	Alignment	not modelled	5.2	8	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
96	d1q8ba_	Alignment	not modelled	5.1	8	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Hypothetical protein YjcS
97	c2kklA_	Alignment	not modelled	5.1	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mb1858; **PDBTitle:** solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
98	d1o7nb_	Alignment	not modelled	5.1	11	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Ring hydroxylating beta subunit