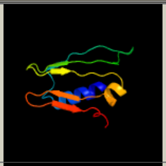
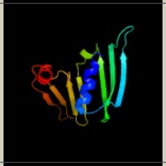
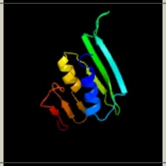
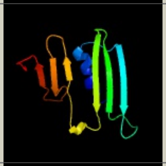
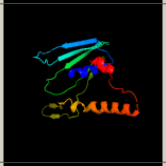
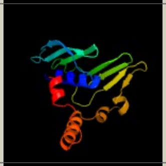
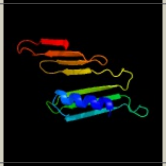
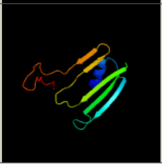
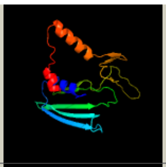
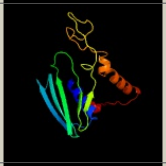
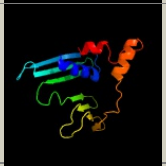
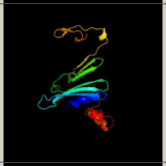
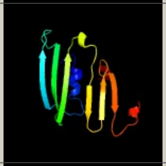
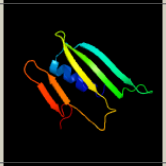
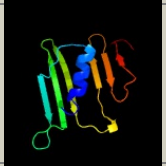
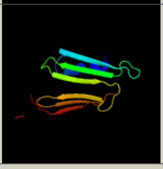
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1752_(-)_1981137_1981586
Date	Fri Aug 2 13:30:35 BST 2019
Unique Job ID	bea43feaf16c4cf1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ydwa2	Alignment		99.6	33	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
2	c3evnA_	Alignment		99.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
3	c3oqbF_	Alignment		99.4	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
4	c3e9mC_	Alignment		99.4	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
5	d1h6da2	Alignment		99.4	19	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
6	c4miyB_	Alignment		99.4	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol dehydrogenase from lactobacillus2 casei in complex with nad and myo-inositol
7	d1zh8a2	Alignment		99.3	21	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
8	c2o48X_	Alignment		99.3	25	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**dimeric dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of mammalian dimeric dihydrodiol dehydrogenase
9	c2glxD_	Alignment		99.3	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1,5-anhydro-d-fructose reductase; **PDBTitle:** crystal structure analysis of bacterial 1,5-af reductase
10	d2nvwa2	Alignment		99.3	7	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
11	c3ezyB_	Alignment		99.3	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from thermotoga2 maritima

12	c4mkzA_	Alignment		99.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inositol dehydrogenase; **PDBTitle:** crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k
13	c6norB_	Alignment		99.3	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nad dependent dehydrogenase; **PDBTitle:** crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
14	c2p2sA_	Alignment		99.2	17	**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
15	c3e18A_	Alignment		99.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
16	c3q2kB_	Alignment		99.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaca
17	c3rbvA_	Alignment		99.2	25	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sugar 3-ketoreductase; **PDBTitle:** crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
18	c3nt5B_	Alignment		99.2	14	**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
19	c3dtyA_	Alignment		99.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from pseudomonas2 syringae
20	c2nvwB_	Alignment		99.2	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal sctucture of transcriptional regulator gal80p from2 kluyveromymes lactis
21	c2ho3D_	Alignment	not modelled	99.2	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
22	c1evjC_	Alignment	not modelled	99.2	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
23	c6a3fB_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** levoglucosan dehydrogenase, apo form
24	c5a06E_	Alignment	not modelled	99.1	23	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**aldose-aldose oxidoreductase; **PDBTitle:** crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol
25	c3ec7C_	Alignment	not modelled	99.1	7	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
26	c3ceaA_	Alignment	not modelled	99.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**myo-inositol 2-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
27	c5uibA_	Alignment	not modelled	99.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase protein; **PDBTitle:** crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium
28	c5yabD_	Alignment	not modelled	99.1	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**scyllo-inositol dehydrogenase with l-glucose dehydrogenase **PDBTitle:** crystal structure of scyllo-inositol dehydrogenase with l-

						glucose2 dehydrogenase activity
29	c1h6dL_	Alignment	not modelled	99.1	22	**PDB header:**protein translocation **Chain:** L: **PDB Molecule:**precursor form of glucose-fructose **PDBTitle:** oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
30	c1ofgF_	Alignment	not modelled	99.1	22	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
31	c4hktA_	Alignment	not modelled	99.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inositol 2-dehydrogenase; **PDBTitle:** crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312)
32	c4gqaC_	Alignment	not modelled	99.0	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad binding oxidoreductase; **PDBTitle:** crystal structure of nad binding oxidoreductase from klebsiella2 pneumoniae
33	c4h3vA_	Alignment	not modelled	99.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**oxidoreductase domain protein; **PDBTitle:** crystal structure of oxidoreductase domain protein from kribbella2 flavida
34	c2q4eB_	Alignment	not modelled	99.0	21	**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
35	c3ip3D_	Alignment	not modelled	99.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** structure of putative oxidoreductase (tm_0425) from thermotoga2 maritima
36	c3euwB_	Alignment	not modelled	99.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
37	c4fb5A_	Alignment	not modelled	99.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable oxidoreductase protein; **PDBTitle:** crystal structure of a probable oxidoreduxtase protein
38	c1tltB_	Alignment	not modelled	99.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase (virulence factor mvim homolog); **PDBTitle:** crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
39	c3btuD_	Alignment	not modelled	98.9	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
40	c6jnkA_	Alignment	not modelled	98.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-arabinose 1-dehydrogenase (nad(p)(+)); **PDBTitle:** crystal structure of azospirillum brasilense l-arabinose 1-2 dehydrogenase (nadp-bound form)
41	c3u3xJ_	Alignment	not modelled	98.9	22	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021
42	c3v5nA_	Alignment	not modelled	98.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of oxidoreductase from sinorhizobium meliloti
43	c1zh8B_	Alignment	not modelled	98.8	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
44	c4ew6A_	Alignment	not modelled	98.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-galactose-1-dehydrogenase protein; **PDBTitle:** crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli
45	c4hadD_	Alignment	not modelled	98.8	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**probable oxidoreductase protein; **PDBTitle:** crystal structure of probable oxidoreductase protein from rhizobium2 etli cfn 42
46	c5b3uB_	Alignment	not modelled	98.8	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**biliverdin reductase; **PDBTitle:** crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
47	c3fd8A_	Alignment	not modelled	98.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
48	c3m2tA_	Alignment	not modelled	98.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
49	c3db2C_	Alignment	not modelled	98.7	14	**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
50	c3gfgB_	Alignment	not modelled	98.7	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized oxidoreductase yvaa; **PDBTitle:** structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
51	c1lc3A_	Alignment	not modelled	98.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biliverdin reductase a; **PDBTitle:** crystal structure of a biliverdin reductase enzyme-cofactor2 complex
52	c3kuxA_	Alignment	not modelled	98.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis
						PDB header:oxidoreductase

53	c3fhlC_	Alignment	not modelled	98.6	18	**Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
54	c3c1aB_	Alignment	not modelled	98.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
55	c3f4lF_	Alignment	not modelled	98.6	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative oxidoreductase yhhx; **PDBTitle:** crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
56	c3e82A_	Alignment	not modelled	98.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
57	c3uuwB_	Alignment	not modelled	98.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase with nad(p)-binding rossmann-fold **PDBTitle:** 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
58	c4oo3A_	Alignment	not modelled	98.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative oxidoreductase (parmer_00841) from2 parabacteroides merdae atcc 43184 at 2.23 a resolution
59	d1tlta2	Alignment	not modelled	98.5	16	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
60	c3oa0B_	Alignment	not modelled	98.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lipopolysaccaride biosynthesis protein wbpb; **PDBTitle:** crystal structure of the wlba (wbpb) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcnaca
61	c3moiA_	Alignment	not modelled	98.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
62	d1xeaa2	Alignment	not modelled	98.3	7	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
63	c3oa2B_	Alignment	not modelled	98.2	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**wbpb; **PDBTitle:** crystal structure of the wlba (wbpb) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
64	c2ixaA_	Alignment	not modelled	98.1	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
65	c1xeaD_	Alignment	not modelled	98.1	7	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
66	c4gmfD_	Alignment	not modelled	95.5	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**yersiniabactin biosynthetic protein ybtu; **PDBTitle:** apo structure of a thiazolinyl imine reductase from yersinia2 enterocolitica (irp3)
67	c1j5pA_	Alignment	not modelled	92.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate dehydrogenase; **PDBTitle:** crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
68	c6g1mA_	Alignment	not modelled	91.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** amine dehydrogenase from petrotoga mobilis; open and closed form
69	c6iaqA_	Alignment	not modelled	90.5	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase n-terminus domain-containing **PDBTitle:** structure of amine dehydrogenase from mycobacterium smegmatis
70	c2e12B_	Alignment	not modelled	28.7	14	**PDB header:**translation **Chain:** B: **PDB Molecule:**hypothetical protein xcc3642; **PDBTitle:** the crystal structure of xc5848 from xanthomonas campestris2 adopting a novel variant of sm-like motif
71	d1xsza2	Alignment	not modelled	14.8	23	**Fold:**TBP-like **Superfamily:**RalF, C-terminal domain **Family:**RalF, C-terminal domain
72	c2c55A_	Alignment	not modelled	11.9	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein p6; **PDBTitle:** solution structure of the human immunodeficiency virus type2 1 p6 protein
73	c5lnbB_	Alignment	not modelled	11.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ubiquitin-like-specific protease 2; **PDBTitle:** crystal structure of the de-sumoylating protease
74	c3eayA_	Alignment	not modelled	11.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sentrin-specific protease 7; **PDBTitle:** crystal structure of the human senp7 catalytic domain
75	c6iauB_	Alignment	not modelled	8.9	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amine dehydrogenase; **PDBTitle:** amine dehydrogenase from cystobacter fuscus in complex with nadp+ and2 cyclohexylamine
76	c3fm2A_	Alignment	not modelled	7.6	11	**PDB header:**heme-binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein, distantly related to a heme **PDBTitle:** crystal structure of a putative heme-binding protein (ava_4353) from2 anabaena variabilis atcc 29413 at 1.80 a resolution
						PDB header:hydrolase

77	c5hagA_	Alignment	not modelled	7.0	14	**Chain:** A: **PDB Molecule:**deubiquitinase and deneddylase dub1; **PDBTitle:** structure of chlamydia trachomatis effector protein chladub1
78	c5iroD_	Alignment	not modelled	6.7	19	**PDB header:**immune system/transcription **Chain:** D: **PDB Molecule:**e3 19 kda protein; **PDBTitle:** crystal structure of a complex between the human adenovirus type 4 e3-2 19k protein and mhc class molecule hla-a2/tax
79	d2bkra1	Alignment	not modelled	6.5	23	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
80	c4z92A_	Alignment	not modelled	6.5	27	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid subunit vp1; **PDBTitle:** crystal structure of parechovirus-1 virion
81	d1slqa_	Alignment	not modelled	6.2	16	**Fold:**VP4 membrane interaction domain **Superfamily:**VP4 membrane interaction domain **Family:**VP4 membrane interaction domain
82	d1n0ea_	Alignment	not modelled	5.9	10	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Hypothetical protein MraZ
83	c6m9yD_	Alignment	not modelled	5.6	13	**PDB header:**fluorescent protein **Chain:** D: **PDB Molecule:**fluorescent protein lanfp6a; **PDBTitle:** x-ray structure of branchiostoma floridae fluorescent protein lanfp6a
84	c6h9iB_	Alignment	not modelled	5.3	29	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**csf5; **PDBTitle:** csf5, crispr-cas type iv cas6 crrna endonuclease
85	c6dg4A_	Alignment	not modelled	5.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ulp1-like sumo protease; **PDBTitle:** structure of the chaetomium thermophilum ulp1-like sumo protease2 catalytic domain