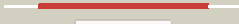



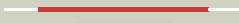
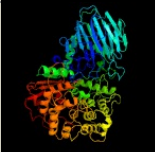

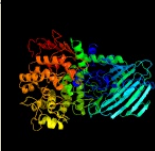









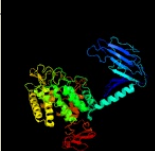

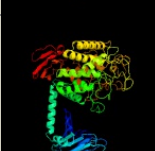

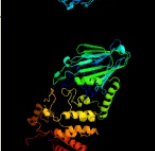
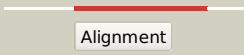



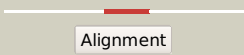

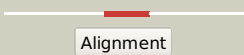

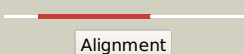



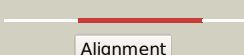







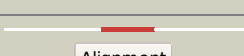
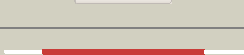
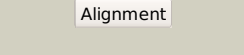


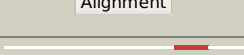


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0584 (-) _679232_681865
Date	Fri Jul 26 01:50:14 BST 2019
Unique Job ID	58723e80ff57f77e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wvyA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: alpha-1,2-mannosidase; PDBTitle: structure of the family gh92 inverting mannosidase bt21992 from bacteroides thetaiotaomicron vpi-5482
2	c6f92B_	 Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-1,2-mannosidase; PDBTitle: structure of the family gh92 alpha-mannosidase bt3965 from bacteroides2 thetaiotaomicron in complex with mannoimidazole (mani)
3	c2ww1B_	 Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-1,2-mannosidase; PDBTitle: structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
4	c6f90A_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: alpha-1,2-mannosidase, putative; PDBTitle: structure of the family gh92 alpha-mannosidase bt3130 from bacteroides2 thetaiotaomicron in complex with mannoimidazole (mani)
5	c2xsgB_	 Alignment		100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: ccman5; PDBTitle: structure of the gh92 family glycosyl hydrolase ccmn5
6	c5swiD_	 Alignment		100.0	26	PDB header: hydrolase Chain: D: PDB Molecule: sugar hydrolase; PDBTitle: crystal structure of spgh92 in complex with mannose
7	d1v7wa1	 Alignment		100.0	14	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyltransferase family 36 C-terminal domain
8	c1v7wA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: chitobiose phosphorylase; PDBTitle: crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
9	c4zlgA_	 Alignment		99.5	12	PDB header: transferase Chain: A: PDB Molecule: putative b-glycan phosphorylase; PDBTitle: cellobionic acid phosphorylase - gluconic acid complex
10	c2cqtA_	 Alignment		99.5	14	PDB header: transferase Chain: A: PDB Molecule: cellobiose phosphorylase; PDBTitle: crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
11	c3c67B_	 Alignment		98.6	17	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein ygjk; PDBTitle: escherichia coli k12 ygjk in a complexed with glucose

12	c6ggyA	 Alignment		98.1	17	PDB header: hydrolase Chain: A; PDB Molecule: laminaribiose phosphorylase; PDBTitle: paenibacillus sp. ym1 laminaribiose phosphorylase with sulphate bound
13	d2jg0a1	 Alignment		98.0	24	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Trehalase-like
14	c2jg0A	 Alignment		98.0	24	PDB header: hydrolase Chain: A; PDB Molecule: periplasmic trehalase; PDBTitle: family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin
15	c5m4aA	 Alignment		97.7	14	PDB header: hydrolase Chain: A; PDB Molecule: neutral trehalase; PDBTitle: neutral trehalase nth1 from saccharomyces cerevisiae in complex with2 trehalose
16	c1ug9A	 Alignment		97.6	17	PDB header: hydrolase Chain: A; PDB Molecule: glucodextranase; PDBTitle: crystal structure of glucodextranase from arthrobacter globiformis i42
17	c6i60B	 Alignment		97.6	10	PDB header: hydrolase Chain: B; PDB Molecule: alpha-rhamnosidase; PDBTitle: structure of alpha-l-rhamnosidase from dictyoglumus thermophilum
18	d1h54a1	 Alignment		97.4	10	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyltransferase family 36 C-terminal domain
19	c1h54B	 Alignment		97.3	10	PDB header: hydrolase Chain: B; PDB Molecule: maltose phosphorylase; PDBTitle: maltose phosphorylase from lactobacillus brevis
20	c5mhfA	 Alignment		97.3	11	PDB header: hydrolase Chain: A; PDB Molecule: mannosyl-oligosaccharide glucosidase; PDBTitle: murine endoplasmic reticulum alpha-glucosidase i with n-9'-2 methoxynonyl-1-deoxynojirimycin
21	c4ktrE	 Alignment	not modelled	97.2	13	PDB header: transferase Chain: E; PDB Molecule: glycoside hydrolase family 65 central catalytic; PDBTitle: crystal structure of 2-o-alpha-glucosylglycerol phosphorylase in2 complex with isofagomine and glycerol
22	c4j5tA	 Alignment	not modelled	97.2	11	PDB header: hydrolase Chain: A; PDB Molecule: mannosyl-oligosaccharide glucosidase; PDBTitle: crystal structure of processing alpha-glucosidase i
23	c5ohcB	 Alignment	not modelled	97.0	16	PDB header: hydrolase Chain: B; PDB Molecule: hydrolase; PDBTitle: crystal structure of mycolicibacterium hassiacum glucosylglycerate2 hydrolase (mhgh) in complex with glycerol
24	c5h42A	 Alignment	not modelled	96.7	10	PDB header: transferase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of 1,2-beta-oligoglucon phosphorylase from2 lachnoclostridium phytofermentans in complex with alpha-d-glucose-1-3 phosphate
25	c2z07A	 Alignment	not modelled	96.6	13	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein ttha0978; PDBTitle: crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
26	c1lf6A	 Alignment	not modelled	96.6	12	PDB header: hydrolase Chain: A; PDB Molecule: glucoamylase; PDBTitle: crystal structure of bacterial glucoamylase
27	d1w8oa1	 Alignment	not modelled	96.3	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
28	c5n6nC	 Alignment	not modelled	96.2	17	PDB header: signaling protein Chain: C; PDB Molecule: neutral trehalase;

28	c1bnc	Alignment	not modelled	90.2	17	PDBTitle: crystal structure of the 14-3-3:neutral trehalase nth1 complex PDB header: hydrolase
29	c5nz8A	Alignment	not modelled	96.2	13	Chain: A; PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase with cellotetraose2 and phosphate bound
30	c5mqrA	Alignment	not modelled	95.6	14	PDB header: hydrolase Chain: A; PDB Molecule: beta-l-arabinobiosidase; PDBTitle: sialidase bt_1020
31	c6gszA	Alignment	not modelled	95.4	14	PDB header: hydrolase Chain: A; PDB Molecule: alpha-l-rhamnosidase; PDBTitle: crystal structure of native alfa-l-rhamnosidase from aspergillus2 terreus
32	d1lf6a1	Alignment	not modelled	95.0	14	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Bacterial glucoamylase C-terminal domain-like
33	c2okxB	Alignment	not modelled	94.8	11	PDB header: hydrolase Chain: B; PDB Molecule: rhamnosidase b; PDBTitle: crystal structure of gh78 family rhamnosidase of bacillus sp. gl1 at2 1.9 a
34	c5nz7A	Alignment	not modelled	94.3	14	PDB header: hydrolase Chain: A; PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase ligand free form
35	c3w5mA	Alignment	not modelled	92.7	18	PDB header: hydrolase Chain: A; PDB Molecule: putative rhamnosidase; PDBTitle: crystal structure of streptomyces avermitilis alpha-l-rhamnosidase
36	c3cihA	Alignment	not modelled	91.7	10	PDB header: hydrolase Chain: A; PDB Molecule: putative alpha-rhamnosidase; PDBTitle: crystal structure of a putative alpha-rhamnosidase from2 bacteroides thetaiotaomicron
37	c5fjsB	Alignment	not modelled	86.1	14	PDB header: hydrolase Chain: B; PDB Molecule: glucosylceramidase; PDBTitle: bacterial beta-glucosidase reveals the structural and functional2 basis of genetic defects in human glucocerebrosidase 2 (gba2)3 disorders
38	c2gz6B	Alignment	not modelled	79.8	15	PDB header: isomerase Chain: B; PDB Molecule: n-acetyl-d-glucosamine 2-epimerase; PDBTitle: crystal structure of anabaena sp. ch1 n-acetyl-d-glucosamine 2-2 epimerase at 2.0 a
39	c4xhcB	Alignment	not modelled	73.4	11	PDB header: hydrolase Chain: B; PDB Molecule: alpha-l-rhamnosidase; PDBTitle: rhamnosidase from klebsiella oxytoca with rhamnose bound
40	c2rdyB	Alignment	not modelled	73.2	12	PDB header: hydrolase Chain: B; PDB Molecule: bh0842 protein; PDBTitle: crystal structure of a putative glycoside hydrolase family2 protein from bacillus halodurans
41	c2eacB	Alignment	not modelled	70.4	12	PDB header: hydrolase Chain: B; PDB Molecule: alpha-fucosidase; PDBTitle: crystal structure of 1,2-a-l-fucosidase from2 bifidobacterium bifidum in complex with3 deoxyfuconojirimycin
42	d1tg7a1	Alignment	not modelled	65.5	19	Fold: Beta-galactosidase LacA, domain 3 Superfamily: Beta-galactosidase LacA, domain 3 Family: Beta-galactosidase LacA, domain 3
43	c2mlbA	Alignment	not modelled	64.7	22	PDB header: de novo protein Chain: A; PDB Molecule: redesigned ubiquitin; PDBTitle: nmr solution structure of a computational designed protein based on2 template of human erythrocytic ubiquitin
44	c3wkgA	Alignment	not modelled	64.1	15	PDB header: isomerase Chain: A; PDB Molecule: cellobiose 2-epimerase; PDBTitle: crystal structure of cellobiose 2-epimerase in complex with2 glucosylmannose
45	d1nc5a	Alignment	not modelled	55.9	11	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Hypothetical protein YteR
46	c4q88B	Alignment	not modelled	48.0	18	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: glycosyl hydrolase family 88 from bacteroides vulgatus
47	c2yheD	Alignment	not modelled	45.2	28	PDB header: hydrolase Chain: D; PDB Molecule: sec-alkyl sulfatase; PDBTitle: structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp.
48	c2e7dA	Alignment	not modelled	44.2	13	PDB header: metal binding protein Chain: A; PDB Molecule: hypothetical protein isdh; PDBTitle: crystal structure of a neat domain from staphylococcus aureus
49	c3hx1B	Alignment	not modelled	43.7	14	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: slr1951 protein; PDBTitle: crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
50	c2l2rA	Alignment	not modelled	42.3	24	PDB header: antimicrobial protein Chain: A; PDB Molecule: antimicrobial peptide ecamp1; PDBTitle: helical hairpin structure of a novel antimicrobial peptide ecamp1 from2 seeds of barnyard grass (echinochloa crus-galli)
51	c4pdxB	Alignment	not modelled	37.3	26	PDB header: hydrolase Chain: B; PDB Molecule: putative alkyl/aryl-sulfatase yjcs; PDBTitle: crystal structure of escherchia coli uncharacterized protein yjcs
52	c6ccdA	Alignment	not modelled	37.0	20	PDB header: protein binding Chain: A; PDB Molecule: abc transporter atp-binding/permease protein rv1747; PDBTitle: the crystal structure of mycobacterium tuberculosis rv1747 fha-1
53	c1ttnA	Alignment	not modelled	36.5	10	PDB header: signaling protein Chain: A; PDB Molecule: dendritic cell-derived ubiquitin-like protein; PDBTitle: solution structure of the ubiquitin-like domain of human

						dc-2 ubp from dendritic cells
54	d1ttna1	Alignment	not modelled	36.5	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
55	d1wiaa_	Alignment	not modelled	34.0	8	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
56	d1ftx_	Alignment	not modelled	33.7	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
57	c1fx7C_	Alignment	not modelled	31.0	13	PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor iber; PDBTitle: crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis
58	d1ztda1	Alignment	not modelled	30.1	18	Fold: RNase III domain-like Superfamily: RNase III domain-like Family: PF0609-like
59	d1v2ya_	Alignment	not modelled	29.3	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
60	c2dd9C_	Alignment	not modelled	28.2	8	PDB header: luminescent protein Chain: C: PDB Molecule: green fluorescent protein; PDBTitle: a mutant of gfp-like protein from chironomid pupae
61	c4wu0B_	Alignment	not modelled	27.0	15	PDB header: hydrolase Chain: B: PDB Molecule: similar to yter (bacillus subtilis); PDBTitle: structural analysis of c. acetobutylicum atcc 824 glycoside hydrolase2 from family 105
62	c5zx9A_	Alignment	not modelled	26.9	18	PDB header: protein binding Chain: A: PDB Molecule: alanine and proline-rich secreted protein apa; PDBTitle: crystal structure of a protein from mycobacterium
63	c3rurB_	Alignment	not modelled	26.5	9	PDB header: metal transport Chain: B: PDB Molecule: iron-regulated surface determinant protein b; PDBTitle: staphylococcus aureus heme-bound selenomethionine-labeled isdb-n2
64	c5noaA_	Alignment	not modelled	26.3	18	PDB header: hydrolase Chain: A: PDB Molecule: family 88 glycosyl hydrolase; PDBTitle: polysaccharide lyase baccell_00875
65	d2j07a1	Alignment	not modelled	25.6	23	Fold: Cryptochrome/photolyase FAD-binding domain Superfamily: Cryptochrome/photolyase FAD-binding domain Family: Cryptochrome/photolyase FAD-binding domain
66	c5b68A_	Alignment	not modelled	24.9	12	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of apo amyloamylase from corynebacterium glutamicum
67	d1neia_	Alignment	not modelled	24.8	33	Fold: Hypothetical protein YoaG Superfamily: Hypothetical protein YoaG Family: Hypothetical protein YoaG
68	c3pmmA_	Alignment	not modelled	24.2	15	PDB header: hydrolase Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578
69	c1wwtA_	Alignment	not modelled	21.6	14	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase, cytoplasmic; PDBTitle: solution structure of the tgs domain from human threonyl-2 trna synthetase
70	c1cbyA_	Alignment	not modelled	21.4	15	PDB header: toxin Chain: A: PDB Molecule: delta-endotoxin cytB; PDBTitle: delta-endotoxin
71	d1cbya_	Alignment	not modelled	21.4	15	Fold: CytB endotoxin-like Superfamily: CytB endotoxin-like Family: CytB endotoxin-like
72	c2ndjA_	Alignment	not modelled	21.3	37	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 3; PDBTitle: structural basis for kcne3 and estrogen modulation of the kcnq12 channel
73	c4r1sB_	Alignment	not modelled	21.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: cinnamoyl coa reductase; PDBTitle: crystal structure of petunia hybrida cinnamoyl-coa reductase
74	c4w4tA_	Alignment	not modelled	20.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: mxaa; PDBTitle: the crystal structure of the terminal r domain from the myxalimid pks-2 nrps biosynthetic pathway
75	d2cfua2	Alignment	not modelled	20.7	12	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like
76	d2fbaa1	Alignment	not modelled	19.8	16	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glucoamylase
77	d1fp3a_	Alignment	not modelled	19.1	11	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: N-acylglucosamine (NAG) epimerase
78	c4xuvB_	Alignment	not modelled	19.0	13	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase family 105 protein; PDBTitle: crystal structure of a glycoside hydrolase family 105 (gh105) enzyme2 from thielavia terrestris
79	c2kk8A_	Alignment	not modelled	18.6	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein at4g05270; PDBTitle: nmr solution structure of a putative uncharacterized protein2 obtained from arabidopsis thaliana: northeast structural3

						genomics consortium target ar3449a
80	c4ce7B_	Alignment	not modelled	18.0	17	PDB header: hydrolase Chain: B: PDB Molecule: unsaturated 3s-rhamnoglycuronyl hydrolase; PDBTitle: crystal structure of a novel unsaturated beta-glucuronyl2 hydrolase enzyme, belonging to family gh105, involved in3 ulvan degradation
81	d1z2ma2	Alignment	not modelled	17.9	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
82	c2zmcW_	Alignment	not modelled	17.8	15	PDB header: luminescent protein Chain: C: PDB Molecule: fluorescent protein; PDBTitle: crystal structure of monomeric kusabira-orange (mko), orange-emitting2 gfp-like protein, at ph 6.0
83	c4jonA_	Alignment	not modelled	17.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: centrosomal protein of 170 kda; PDBTitle: crystal structure of a centrosomal protein 170kda, transcript variant2 beta (cep170) from homo sapiens at 2.15 a resolution (psi community3 target, sundstrom)
84	d1e6va1	Alignment	not modelled	17.6	35	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
85	c4d10H_	Alignment	not modelled	17.5	24	PDB header: signaling protein Chain: H: PDB Molecule: cop9 signalosome complex subunit 8; PDBTitle: crystal structure of the cop9 signalosome
86	d2g1la1	Alignment	not modelled	17.5	14	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
87	c3bg3B_	Alignment	not modelled	17.3	21	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
88	c2zo7A_	Alignment	not modelled	17.2	13	PDB header: luminescent protein Chain: A: PDB Molecule: cyan/green-emitting gfp-like protein, kusabira-cyan mutant PDBTitle: crystal structure of a kusabira-cyan mutant (kcy-r1), a cyan/green-2 emitting gfp-like protein
89	c1yceD_	Alignment	not modelled	16.7	25	PDB header: membrane protein Chain: D: PDB Molecule: subunit c; PDBTitle: structure of the rotor ring of f-type na+-atpase from ilyobacter2 tartaricus
90	d1z2ma1	Alignment	not modelled	16.6	8	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
91	c6b29B_	Alignment	not modelled	16.1	23	PDB header: protein binding Chain: B: PDB Molecule: sh3 and cysteine-rich domain-containing protein 3; PDBTitle: crystal structure of the second sh3 domain of stac3 (309-364)
92	c3nngA_	Alignment	not modelled	16.1	47	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the f5/8 type c domain of q5lfr2_bacfn protein2 from bacteroides fragilis. northeast structural genomics consortium3 target bfr258e
93	c2kanA_	Alignment	not modelled	15.8	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ar3433a; PDBTitle: solution nmr structure of ubiquitin-like domain of2 arabidopsis thaliana protein at2g32350. northeast3 structural genomics consortium target ar3433a
94	c2cfuA_	Alignment	not modelled	15.7	12	PDB header: hydrolase Chain: A: PDB Molecule: sdsa1; PDBTitle: crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
95	d1vdwa_	Alignment	not modelled	15.5	18	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
96	c2hbpA_	Alignment	not modelled	15.3	21	PDB header: endocytosis, protein binding Chain: A: PDB Molecule: cytoskeleton assembly control protein sla1; PDBTitle: solution structure of sla1 homology domain 1
97	c2y0nG_	Alignment	not modelled	14.8	29	PDB header: transcription Chain: G: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and msl3
98	c2y0nH_	Alignment	not modelled	14.8	29	PDB header: transcription Chain: H: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and msl3
99	c2ddcA_	Alignment	not modelled	14.5	19	PDB header: luminescent protein Chain: A: PDB Molecule: photoconvertible fluorescent protein; PDBTitle: unique behavior of a histidine responsible for an engineered green-to-2 red photoconversion process