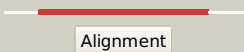

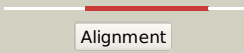

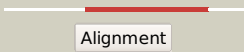

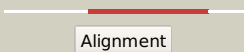

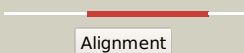

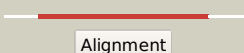

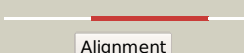


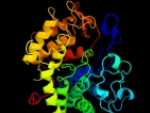


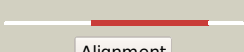

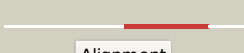
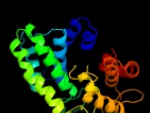


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2402_(-)_2698539_2700467
Date	Wed Aug 7 12:50:01 BST 2019
Unique Job ID	4ed0302e73f67bf3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1lf6A_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: glucoamylase; PDBTitle: crystal structure of bacterial glucoamylase
2	d1ulva1	 Alignment		100.0	19	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Bacterial glucoamylase C-terminal domain-like
3	d1lf6a1	 Alignment		100.0	19	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Bacterial glucoamylase C-terminal domain-like
4	c5z3dA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase 15-related protein; PDBTitle: glycosidase f290y
5	d2fbaa1	 Alignment		100.0	19	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glucoamylase
6	c1ug9A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: glucodextranase; PDBTitle: crystal structure of glucodextranase from arthrobacter globiformis i42
7	d1gaia_	 Alignment		100.0	21	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glucoamylase
8	c2vn4A_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: glucoamylase; PDBTitle: glycoside hydrolase family 15 glucoamylase from hypocrea jecorina
9	c6fhvA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: glucoamylase; PDBTitle: crystal structure of penicillium oxalicum glucoamylase
10	c6fhwB_	 Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: glucoamylase p; PDBTitle: structure of hormoconis resinae glucoamylase
11	c5hopA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: lmo0182 protein; PDBTitle: 1.65 angstrom resolution crystal structure of lmo0182 (residues 1-245)2 from listeria monocytogenes egd-e

12	c1v7wA_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: chitobiose phosphorylase; PDBTitle: crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
13	c4zlgA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: putative b-glycan phosphorylase; PDBTitle: cellobionic acid phosphorylase - gluconic acid complex
14	c5gorE_	Alignment		100.0	17	PDB header: hydrolase Chain: E: PDB Molecule: alkaline invertase; PDBTitle: crystal structure of alkaline invertase inva from anabaena sp. pcc2 7120
15	c3c67B_	Alignment		100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein ygjk; PDBTitle: escherichia coli k12 ygjk in a complexed with glucose
16	c5z73A_	Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: alr0819 protein; PDBTitle: crystal structure of alkaline/neutral invertase invb from anabaena sp.2 pcc 7120
17	c2cqtA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: cellobiose phosphorylase; PDBTitle: crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
18	c2z07A_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ttha0978; PDBTitle: crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
19	d1v7wa1	Alignment		99.9	14	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyltransferase family 36 C-terminal domain
20	c5fjsB_	Alignment		99.9	12	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
21	c5ohcB_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: crystal structure of mycolicibacterium hassiacum glucosylglycerate2 hydrolase (mhggh) in complex with glycerol
22	c3qspB_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: analysis of a new family of widely distributed metal-independent alpha2 mannosidases provides unique insight into the processing of n-linked3 glycans, streptococcus pneumoniae sp_2144 non-productive substrate4 complex with alpha-1,6-mannobiose
23	c5d0fB_	Alignment	not modelled	99.8	16	PDB header: sugar binding protein Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the candida glabrata glycogen debranching enzyme2 (e564q) in complex with maltopentaose
24	c5h42A_	Alignment	not modelled	99.8	10	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of 1,2-beta-oligoglucan phosphorylase from2 lachnoclostridium phytofermentans in complex with alpha-d-glucose-1-3 phosphate
25	d2jg0a1	Alignment	not modelled	99.8	15	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Trehalase-like
26	c2jg0A_	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: periplasmic trehalase; PDBTitle: family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin
27	c5nz7A_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase ligand free form
						PDB header: hydrolase

28	c4j5tA_	Alignment	not modelled	99.8	13	Chain: A: PDB Molecule: mannosyl-oligosaccharide glucosidase; PDBTitle: crystal structure of processing alpha-glucosidase i
29	d2nvpa1	Alignment	not modelled	99.7	13	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: CPF0428-like
30	c6i60B_	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: B: PDB Molecule: alpha-rhamnosidase; PDBTitle: structure of alpha-l-rhamnosidase from dictyoglumus thermophilum
31	c4xhcB_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: alpha-l-rhamnosidase; PDBTitle: rhamnosidase from klebsiella oxytoxa with rhamnose bound
32	c5m4aA_	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: neutral trehalase; PDBTitle: neutral trehalase nth1 from saccharomyces cerevisiae in complex with2 trehalose
33	d2p0va1	Alignment	not modelled	99.7	14	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: CPF0428-like
34	c2p0vA_	Alignment	not modelled	99.7	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein bt3781; PDBTitle: crystal structure of bt3781 protein from bacteroides thetaiotaomicron,2 northeast structural genomics target btr58
35	c5mhfA_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: mannosyl-oligosaccharide glucosidase; PDBTitle: murine endoplasmic reticulum alpha-glucosidase i with n-9'-2 methoxynonyl-1-deoxynojirimycin
36	c6gszA_	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha-l-rhamnosidase; PDBTitle: crystal structure of native alfa-l-rhamnosidase from aspergillus2 terreus
37	c5nz8A_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase with cellotetraose2 and phosphate bound
38	c2okxB_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: B: PDB Molecule: rhamnosidase b; PDBTitle: crystal structure of gh78 family rhamnosidase of bacillus sp. gl1 at2 1.9 a
39	c3w5mA_	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: A: PDB Molecule: putative rhamnosidase; PDBTitle: crystal structure of streptomyces avermitilis alpha-l-rhamnosidase
40	c6ggvA_	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: A: PDB Molecule: laminaribiose phosphorylase; PDBTitle: paenibacillus sp. ym1 laminaribiose phosphorylase with sulphate bound
41	c3cihA_	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: A: PDB Molecule: putative alpha-rhamnosidase; PDBTitle: crystal structure of a putative alpha-rhamnosidase from2 bacteroides thetaiotaomicron
42	c5n6nC_	Alignment	not modelled	99.4	17	PDB header: signaling protein Chain: C: PDB Molecule: neutral trehalase; PDBTitle: crystal structure of the 14-3-3:neutral trehalase nth1 complex
43	c4ufcA_	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: A: PDB Molecule: gh95; PDBTitle: crystal structure of the gh95 enzyme bacova_03438
44	c4ktrE_	Alignment	not modelled	98.9	12	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
45	c2rdyB_	Alignment	not modelled	98.7	13	PDB header: hydrolase Chain: B: PDB Molecule: bh0842 protein; PDBTitle: crystal structure of a putative glycoside hydrolase family2 protein from bacillus halodurans
46	d1h54a1	Alignment	not modelled	98.6	14	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyltransferase family 36 C-terminal domain
47	c1w6kA_	Alignment	not modelled	98.6	14	PDB header: isomerase Chain: A: PDB Molecule: lanosterol synthase; PDBTitle: structure of human osc in complex with lanosterol
48	c1o79A_	Alignment	not modelled	98.5	14	PDB header: isomerase Chain: A: PDB Molecule: squalene--hopene cyclase; PDBTitle: structures of human oxidosqualene cyclase inhibitors bound to an2 homologous enzyme
49	d2sqca1	Alignment	not modelled	98.4	13	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
50	c1h54B_	Alignment	not modelled	98.3	13	PDB header: hydrolase Chain: B: PDB Molecule: maltose phosphorylase; PDBTitle: maltose phosphorylase from lactobacillus brevis
51	c2eacB_	Alignment	not modelled	98.2	13	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
52	c5zhbB_	Alignment	not modelled	97.8	11	PDB header: isomerase Chain: B: PDB Molecule: cellobiose 2-epimerase; PDBTitle: structure of cellobiose 2-epimerase from bacillus thermoamylovorans2 b4167
53	d1w6ka1	Alignment	not modelled	97.4	15	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
54	c5hn8A_	Alignment	not modelled	97.1	16	PDB header: isomerase Chain: A: PDB Molecule: ent-copalyl diphosphate synthase;

54	c3up6A	Alignment	not modelled	97.1	10	PDBTitle: ent-copalyl diphosphate synthase from streptomyces platensis
55	c5mqrA	Alignment	not modelled	96.8	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-l-arabinobiosidase; PDBTitle: sialidase bt_1020
56	c3wkgA	Alignment	not modelled	96.7	15	PDB header: isomerase Chain: A: PDB Molecule: cellobiose 2-epimerase; PDBTitle: crystal structure of cellobiose 2-epimerase in complex with2 glucosylmannose
57	d2afaa1	Alignment	not modelled	92.6	14	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: N-acylglucosamine (NAG) epimerase
58	c4mu9B	Alignment	not modelled	92.5	14	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase family 73; PDBTitle: crystal structure of a putative glycosylhydrolase (bt_3782) from2 bacteroides thetaiotaomicron vpi-5482 at 1.89 a resolution
59	d2sqca2	Alignment	not modelled	92.4	10	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
60	c5zigD	Alignment	not modelled	91.5	12	PDB header: isomerase Chain: D: PDB Molecule: cellobiose 2-epimerase; PDBTitle: the structure of cellobiose 2-epimerase from spirochaeta thermophila2 dsm 6192
61	c3vw5B	Alignment	not modelled	90.7	14	PDB header: isomerase Chain: B: PDB Molecule: cellobiose 2-epimerase; PDBTitle: crystal structure of sugar epimerase from ruminal bacterium
62	d2d5ja1	Alignment	not modelled	90.6	16	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyl Hydrolase Family 88
63	c3gt5A	Alignment	not modelled	90.1	15	PDB header: isomerase Chain: A: PDB Molecule: n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of an n-acetylglucosamine 2-epimerase family protein2 from xylella fastidiosa
64	c4c1oA	Alignment	not modelled	88.9	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-xylosidase; PDBTitle: geobacillus thermoglucosidasius gh family 52 xylosidase
65	c4z4IA	Alignment	not modelled	85.8	11	PDB header: isomerase Chain: A: PDB Molecule: cellobiose 2-epimerase; PDBTitle: crystal structure of cellobiose 2-epimerase from caldicellulosiruptor2 saccharolyticus dsm 8903
66	c2zzrA	Alignment	not modelled	85.7	13	PDB header: hydrolase Chain: A: PDB Molecule: unsaturated glucuronyl hydrolase; PDBTitle: crystal structure of unsaturated glucuronyl hydrolase from2 streptococcus agalactiae
67	c3wiwA	Alignment	not modelled	80.9	14	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase family 88; PDBTitle: crystal structure of unsaturated glucuronyl hydrolase specific for2 heparin
68	d1qqfa	Alignment	not modelled	79.9	9	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Complement components
69	d1fp3a	Alignment	not modelled	77.3	14	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: N-acylglucosamine (NAG) epimerase
70	c5x32B	Alignment	not modelled	74.4	9	PDB header: isomerase Chain: B: PDB Molecule: n-acylglucosamine 2-epimerase; PDBTitle: crystal structure of d-mannose isomerase
71	c3renB	Alignment	not modelled	74.0	9	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase, family 8; PDBTitle: cpf_2247, a novel alpha-amylase from clostridium perfringens
72	d1c3da	Alignment	not modelled	70.2	10	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Complement components
73	d1gxma	Alignment	not modelled	68.7	12	Fold: alpha/alpha toroid Superfamily: Family 10 polysaccharide lyase Family: Family 10 polysaccharide lyase
74	c4q2bA	Alignment	not modelled	68.5	14	PDB header: hydrolase Chain: A: PDB Molecule: endo-1,4-beta-d-glucanase; PDBTitle: the crystal structure of an endo-1,4-d-glucanase from pseudomonas2 putida kt2440
75	c4v1sA	Alignment	not modelled	62.6	10	PDB header: hydrolase Chain: A: PDB Molecule: alpha-1,6-mannanase; PDBTitle: structure of the gh76 alpha-mannanase bt2949 from2 bacteroides thetaiotaomicron
76	c4maIB	Alignment	not modelled	59.7	15	PDB header: unknown function Chain: B: PDB Molecule: motility protein fimv; PDBTitle: tpr3 of fimv from p. aeruginosa (pao1)
77	c3s9vD	Alignment	not modelled	59.5	17	PDB header: lyase, isomerase Chain: D: PDB Molecule: abietadiene synthase, chloroplastic; PDBTitle: abietadiene synthase from abies grandis
78	c4qk0C	Alignment	not modelled	59.4	13	PDB header: hydrolase Chain: C: PDB Molecule: gh127 beta-l-arabinofuranoside; PDBTitle: crystal structure of ara127n-se, a gh127 beta-l-arabinofuranosidase2 from geobacillus stearothermophilus t6
79	c3p5rB	Alignment	not modelled	54.1	18	PDB header: lyase Chain: B: PDB Molecule: taxadiene synthase; PDBTitle: crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
80	c3wkkA	Alignment	not modelled	53.7	18	PDB header: hydrolase Chain: A: PDB Molecule: non-reducing end beta-l-arabinofuranosidase; PDBTitle: crystal structure of gh127 beta-l-arabinofuranosidase

						hypba1 from2 bifidobacterium longum arabinose complex form
81	d1hzfa_	Alignment	not modelled	52.0	18	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Complement components
82	c1hzfA_	Alignment	not modelled	52.0	18	PDB header: immune system Chain: A: PDB Molecule: complement factor c4a; PDBTitle: c4adg fragment of human complement factor c4a
83	c3saeA_	Alignment	not modelled	51.2	19	PDB header: lyase Chain: A: PDB Molecule: alpha-bisabolene synthase; PDBTitle: structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production
84	c4n2sA_	Alignment	not modelled	50.0	13	PDB header: splicing/rna Chain: A: PDB Molecule: tha8 rna binding protein; PDBTitle: crystal structure of tha8 in complex with zm1a-6 rna
85	d1r76a_	Alignment	not modelled	46.2	12	Fold: alpha/alpha toroid Superfamily: Family 10 polysaccharide lyase Family: Family 10 polysaccharide lyase
86	c4a5wA_	Alignment	not modelled	41.4	13	PDB header: immune system Chain: A: PDB Molecule: complement c5; PDBTitle: crystal structure of c5b6
87	c4wslA_	Alignment	not modelled	38.8	36	PDB header: de novo protein Chain: A: PDB Molecule: pentatricopeptide repeat protein; PDBTitle: crystal structure of designed cppr-polyc protein
88	c3nqpB_	Alignment	not modelled	38.7	9	PDB header: sugar binding protein Chain: B: PDB Molecule: susd superfamily protein; PDBTitle: crystal structure of a susd superfamily protein (bf1802) from2 bacteroides fragilis nctc 9343 at 1.90 a resolution
89	c3jwgA_	Alignment	not modelled	36.9	21	PDB header: transferase Chain: A: PDB Molecule: methyltransferase type 12; PDBTitle: crystal structure analysis of the methyltransferase domain of2 bacterial-cthen1-c
90	c5iwwD_	Alignment	not modelled	35.6	31	PDB header: rna binding protein Chain: D: PDB Molecule: pls9-ppr; PDBTitle: crystal structure of rna editing factor of designer pls-type ppr/9r2 protein in complex with morf9/rip9
91	c6r2mB_	Alignment	not modelled	33.1	12	PDB header: hydrolase Chain: B: PDB Molecule: glycoside transferase; PDBTitle: crystal structure of pssz from listeria monocytogenes
92	c5swiD_	Alignment	not modelled	31.6	11	PDB header: hydrolase Chain: D: PDB Molecule: sugar hydrolase; PDBTitle: crystal structure of spgh92 in complex with mannose
93	c3pybB_	Alignment	not modelled	30.7	15	PDB header: isomerase Chain: B: PDB Molecule: ent-copalyl diphosphate synthase, chloroplastic; PDBTitle: crystal structure of ent-copalyl diphosphate synthase from arabidopsis2 thaliana in complex with 13-aza-13,14-dihydrocopalyl diphosphate
94	d1tj1a1	Alignment	not modelled	28.3	20	Fold: N-terminal domain of bifunctional PutA protein Superfamily: N-terminal domain of bifunctional PutA protein Family: N-terminal domain of bifunctional PutA protein
95	c4ayqA_	Alignment	not modelled	27.2	8	PDB header: hydrolase Chain: A: PDB Molecule: mannosyl-oligosaccharide 1,2-alpha-mannosidase; PDBTitle: structure of the gh47 processing alpha-1,2-mannosidase from2 caulobacter strain k31 in complex with mannoimidazole
96	c3g6jB_	Alignment	not modelled	26.5	11	PDB header: immune system Chain: B: PDB Molecule: complement c3 alpha chain; PDBTitle: c3b in complex with a c3b specific fab
97	c3qxqD_	Alignment	not modelled	26.3	14	PDB header: hydrolase Chain: D: PDB Molecule: endoglucanase; PDBTitle: structure of the bacterial cellulose synthase subunit z in complex2 with cellopentaose
98	c4bojC_	Alignment	not modelled	24.6	14	PDB header: hydrolase Chain: C: PDB Molecule: alpha-1,6-mannanase; PDBTitle: crystal structure of bacillus circulans tn-31 aman6 in2 complex with mannobiose
99	d2pqrB1	Alignment	not modelled	22.2	25	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
100	c5mqoA_	Alignment	not modelled	21.8	13	PDB header: hydrolase Chain: A: PDB Molecule: non-reducing end beta-l-arabinofuranosidase; PDBTitle: glycoside hydrolase bt 1003
101	c1slyA_	Alignment	not modelled	21.7	24	PDB header: glycosyltransferase Chain: A: PDB Molecule: 70-kda soluble lytic transglycosylase; PDBTitle: complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
102	d3dssb1	Alignment	not modelled	21.5	14	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Protein prenyltransferases
103	c5izwA_	Alignment	not modelled	20.9	24	PDB header: rna binding protein Chain: A: PDB Molecule: pls9-ppr; PDBTitle: crystal structure of rna editing specific factor of designer pls-type2 ppr-9r protein