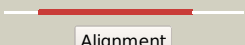

















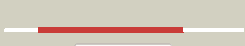





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0202c_(mmpL11)_238392_241292
Date	Tue Jul 23 14:50:25 BST 2019
Unique Job ID	2b76001d87b74d48

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ajjA_	 Alignment		100.0	23	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
2	c5khnB_	 Alignment		100.0	19	PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
3	c5lq3F_	 Alignment		100.0	15	PDB header: transport protein Chain: F: PDB Molecule: cmeb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
4	c6dmoA_	 Alignment		100.0	14	PDB header: protein binding Chain: A: PDB Molecule: protein patched homolog 1; PDBTitle: cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l
5	c4mt1A_	 Alignment		100.0	15	PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
6	c6owsB_	 Alignment		100.0	14	PDB header: membrane protein Chain: B: PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
7	c3jd8A_	 Alignment		100.0	15	PDB header: membrane protein Chain: A: PDB Molecule: niemann-pick c1 protein; PDBTitle: cryo-em structure of the full-length human npc1 at 4.4 angstrom
8	c3k07A_	 Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
9	c2v50A_	 Alignment		100.0	18	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein mexb; PDBTitle: the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb
10	c5xamA_	 Alignment		100.0	16	PDB header: membrane protein Chain: A: PDB Molecule: protein translocase subunit secdf; PDBTitle: crystal structure of secdf in i form at 4 a resolution
11	c3aqpB_	 Alignment		100.0	15	PDB header: membrane protein Chain: B: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: crystal structure of secdf, a translocon-associated membrane protein,2 from thermus throphilus

12	c1oy8A_	Alignment		100.0	19	PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
13	c4k0eA_	Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
14	c4k0eC_	Alignment		100.0	15	PDB header: transport protein Chain: C: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
15	c6csxA_	Alignment		100.0	19	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb; PDBTitle: single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom
16	c5mg3F_	Alignment		99.9	16	PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon
17	c5mg3D_	Alignment		99.9	18	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
18	d1iwga7	Alignment		99.9	19	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
19	d1iwga8	Alignment		99.9	12	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
20	c4y0IA_	Alignment		98.6	100	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein mmp11; PDBTitle: mycobacterial membrane protein mmp11d2
21	c2yvxD_	Alignment	not modelled	81.0	10	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
22	c6gctA_	Alignment	not modelled	79.1	20	PDB header: membrane protein Chain: A: PDB Molecule: neutral amino acid transporter b(0); PDBTitle: cryo-em structure of the human neutral amino acid transporter asct2
23	d1iwga3	Alignment	not modelled	70.2	11	Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
24	c2zxeG_	Alignment	not modelled	52.3	23	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: phospholemmman-like protein; PDBTitle: crystal structure of the sodium - potasslum pump in the e2.2k+.pi2 state
25	c2cooA_	Alignment	not modelled	43.5	28	PDB header: transferase Chain: A: PDB Molecule: lipoamide acyltransferase component of branched- PDBTitle: solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
26	d1t4za_	Alignment	not modelled	42.9	63	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: KaiB-like
27	c4ky0B_	Alignment	not modelled	42.3	12	PDB header: transport protein, membrane protein Chain: B: PDB Molecule: proton/glutamate symporter, sdf family; PDBTitle: crystal structure of a substrate-free glutamate transporter homologue2 from thermococcus kodakarensis
28	c4p6vE_	Alignment	not modelled	37.5	22	PDB header: oxidoreductase Chain: E: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit e;

						PDBTitle: crystal structure of the na ⁺ -translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
29	c4ml9A_	Alignment	not modelled	37.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized tim barrel protein with the2 conserved phosphate binding site fromsebaldeella termitidis
30	c6bc0D_	Alignment	not modelled	36.4	15	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of trpm4 in atp bound state with short coiled coil2 at 2.9 angstrom resolution
31	c1zwvA_	Alignment	not modelled	35.8	29	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase component of branched- PDBTitle: solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
32	c3d0fA_	Alignment	not modelled	33.6	14	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
33	c2eq8C_	Alignment	not modelled	31.5	31	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
34	c6b2zf_	Alignment	not modelled	29.1	27	PDB header: membrane protein Chain: F: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
35	c6b8ht_	Alignment	not modelled	28.6	27	PDB header: membrane protein Chain: T: PDB Molecule: atp synthase subunit 9, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
36	c5et0B_	Alignment	not modelled	28.6	56	PDB header: protein binding/motor protein Chain: B: PDB Molecule: myosin-iiib; PDBTitle: crystal structure of myo3b-arb2 in complex with espin1-ar
37	c5et0D_	Alignment	not modelled	28.6	56	PDB header: protein binding/motor protein Chain: D: PDB Molecule: myosin-iiib; PDBTitle: crystal structure of myo3b-arb2 in complex with espin1-ar
38	c1w3dA_	Alignment	not modelled	28.1	21	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: nmr structure of the peripheral-subunit binding domain of bacillus2 stearothermophilus e2p
39	c2mwiA_	Alignment	not modelled	27.6	29	PDB header: protein binding Chain: A: PDB Molecule: deoxynucleotidyltransferase terminal-interacting protein 1; PDBTitle: the structure of the carboxy-terminal domain of dnttip1
40	c6bcqB_	Alignment	not modelled	24.4	15	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of trpm4 in atp bound state with long coiled coil at2 3.3 angstrom resolution
41	c5n9yB_	Alignment	not modelled	21.6	16	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
42	d2yvxa3	Alignment	not modelled	20.3	10	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
43	c2gp4A_	Alignment	not modelled	19.6	17	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
44	d1w85j_	Alignment	not modelled	18.3	21	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
45	c4ev6E_	Alignment	not modelled	18.1	10	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
46	c1w4kA_	Alignment	not modelled	17.3	26	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase e2; PDBTitle: peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
47	c6nr3B_	Alignment	not modelled	17.1	11	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium
48	c6nr3D_	Alignment	not modelled	17.1	11	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium
49	c6nr3A_	Alignment	not modelled	17.1	11	PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium
50	c6nr3C_	Alignment	not modelled	17.1	11	PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium

51	d2cyua1	Alignment	not modelled	16.2	19	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
52	d1wkta_	Alignment	not modelled	15.9	50	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like Family: Yeast killer toxin
53	c2eq7C_	Alignment	not modelled	15.9	23	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate dehydrogenase e2 component; PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
54	c5ibyA_	Alignment	not modelled	14.9	17	PDB header: ligase,transferase Chain: A: PDB Molecule: lipooate--protein ligase; PDBTitle: crystal structure of enterococcus faecalis lipooate-protein ligase a2 (lpla-2) in complex with lipoic acid
55	d2eiaa1	Alignment	not modelled	14.0	17	Fold: Acyl carrier protein-like Superfamily: Retrovirus capsid dimerization domain-like Family: Retrovirus capsid protein C-terminal domain
56	c3dv0I_	Alignment	not modelled	13.9	21	PDB header: oxidoreductase/transferase Chain: I: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
57	c2eq9C_	Alignment	not modelled	13.6	21	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
58	c3lrcC_	Alignment	not modelled	12.7	11	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
59	c4qoyE_	Alignment	not modelled	12.3	29	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyl)transacetylase PDBTitle: novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydrolipoyl acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
60	d1iyxa1	Alignment	not modelled	12.2	17	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
61	c6hwhb_	Alignment	not modelled	12.2	16	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
62	d1f61a_	Alignment	not modelled	12.0	28	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
63	c2l81A_	Alignment	not modelled	11.9	12	PDB header: cell adhesion Chain: A: PDB Molecule: enhancer of filamentation 1; PDBTitle: solution nmr structure of the serine-rich domain of hef1 (enhancer of2 filamentation 1) from homo sapiens, northeast structural genomics3 consortium target hr5554a
64	c5wujB_	Alignment	not modelled	11.8	20	PDB header: motor protein Chain: B: PDB Molecule: flagellar motor switch protein flig; PDBTitle: crystal structure of flif-flig complex from h. pylori
65	c4n71A_	Alignment	not modelled	11.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: predicted hd phosphohydrolase phnz; PDBTitle: x-ray crystal structure of 2-amino-1-hydroxyethylphosphonate-bound2 phnz
66	c2na9A_	Alignment	not modelled	11.7	7	PDB header: signaling protein Chain: A: PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta
67	c2na8A_	Alignment	not modelled	11.5	7	PDB header: membrane protein Chain: A: PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the cytokine receptor common subunit beta
68	d1xpu3	Alignment	not modelled	11.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
69	d1igna2	Alignment	not modelled	11.1	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: DNA-binding domain of rap1
70	d2qtva4	Alignment	not modelled	11.0	26	Fold: Gelsolin-like Superfamily: C-terminal, gelsolin-like domain of Sec23/24 Family: C-terminal, gelsolin-like domain of Sec23/24
71	c4aqzA_	Alignment	not modelled	11.0	27	PDB header: transport protein Chain: A: PDB Molecule: type iv pilus biogenesis and competence protein pilq; PDBTitle: b2 domain of neisseria meningitidis pilus assembly protein pilq
72	c4w8oA_	Alignment	not modelled	10.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: luciferase-like enzymeamp-coa-ligase; PDBTitle: structure of the luciferase-like enzyme from the nonluminescent2 zophobas morio mealworm
73	d2qfia1	Alignment	not modelled	10.9	12	Fold: Alpha-lytic protease prodomain-like Superfamily: Cation efflux protein cytoplasmic domain-like Family: Cation efflux protein cytoplasmic domain-like
74	c6bpqA_	Alignment	not modelled	10.8	11	PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m

						PDBTitle: structure of the cold- and menthol-sensing ion channel trpm8
75	c6bpgB_	Alignment	not modelled	10.8	11	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: structure of the cold- and menthol-sensing ion channel trpm8
76	c6bpgC_	Alignment	not modelled	10.8	11	PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: structure of the cold- and menthol-sensing ion channel trpm8
77	c6bpgD_	Alignment	not modelled	10.8	11	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: structure of the cold- and menthol-sensing ion channel trpm8
78	c3i4eA_	Alignment	not modelled	10.8	30	PDB header: lyase Chain: A: PDB Molecule: isocitrate lyase; PDBTitle: crystal structure of isocitrate lyase from burkholderia2 pseudomallei
79	c5dckA_	Alignment	not modelled	10.8	25	PDB header: viral protein Chain: A: PDB Molecule: capsid c-terminal domain; PDBTitle: crystal structure of fiv capsid c-terminal domain
80	c5ij6A_	Alignment	not modelled	10.6	19	PDB header: ligase,transferase Chain: A: PDB Molecule: lipoate--protein ligase; PDBTitle: crystal structure of enterococcus faecalis lipoate-protein ligase a2 (lpla-1) in complex with lipoic acid
81	c1bajA_	Alignment	not modelled	10.3	29	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: hiv-1 capsid protein c-terminal fragment plus gag p2 domain
82	c5zvs2_	Alignment	not modelled	10.3	33	PDB header: viral protein Chain: 2: PDB Molecule: vp2; PDBTitle: structure of rna polymerase complex and genome within a dsrna virus2 provides insights into the mechanisms of transcription and assembly
83	c2jysA_	Alignment	not modelled	10.2	18	PDB header: hydrolase Chain: A: PDB Molecule: protease/reverse transcriptase; PDBTitle: solution structure of simian foamy virus (mac) protease
84	d1hl9a1	Alignment	not modelled	10.2	23	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: Putative alpha-L-fucosidase C-terminal domain
85	c5tseA_	Alignment	not modelled	10.1	23	PDB header: lipid binding protein Chain: A: PDB Molecule: lps-assembly lipoprotein lpte; PDBTitle: 2.35 angstrom crystal structure minor lipoprotein from acinetobacter2 baumannii.
86	c4mcjC_	Alignment	not modelled	10.0	18	PDB header: transferase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative nucleoside deoxyribosyltransferase2 (bdi_0649) from parabacteroides distasonis atcc 8503 at 2.40 a3 resolution
87	c2e5aA_	Alignment	not modelled	9.9	31	PDB header: ligase Chain: A: PDB Molecule: lipoyltransferase 1; PDBTitle: crystal structure of bovine lipoyltransferase in complex2 with lipoyl-amp
88	c2yy0D_	Alignment	not modelled	9.9	8	PDB header: transcription Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
89	c2plxB_	Alignment	not modelled	9.9	38	PDB header: hydrolase Chain: B: PDB Molecule: peptide inhibitor; PDBTitle: trypsin complexed to a synthetic peptide from veronica hederifolia
90	c3sohB_	Alignment	not modelled	9.8	20	PDB header: motor protein Chain: B: PDB Molecule: flagellar motor switch protein flig; PDBTitle: architecture of the flagellar rotor
91	d1q92a_	Alignment	not modelled	9.6	11	Fold: HAD-like Superfamily: HAD-like Family: 5'(3')-deoxyribonucleotidase (dnt-2)
92	c2bbjB_	Alignment	not modelled	9.5	19	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
93	d1ut7a_	Alignment	not modelled	9.2	20	Fold: NAC domain Superfamily: NAC domain Family: NAC domain
94	c3jlzP_	Alignment	not modelled	9.1	16	PDB header: metal transport Chain: P: PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
95	d1bala_	Alignment	not modelled	9.0	16	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
96	c2v9vA_	Alignment	not modelled	9.0	18	PDB header: transcription Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of moorella thermoacetica selb(377-511)
97	c3h6gA_	Alignment	not modelled	8.9	38	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: macrocyprin 1a; PDBTitle: macrocyprin, a beta-trefoil cysteine protease inhibitor
98	c4b1xM_	Alignment	not modelled	8.9	32	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpel-2 bound to g-actin
						Fold: TIM beta/alpha-barrel

99	d2fyma1	Alignment	not modelled	8.8	21	Superfamily: Enolase C-terminal domain-like Family: Enolase
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