






















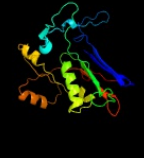






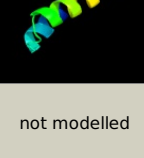


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2394_(ggtB)_2688020_2689951
Date	Mon Aug 5 13:25:55 BST 2019
Unique Job ID	c20c392ffd1fc78d


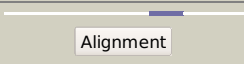
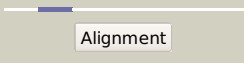
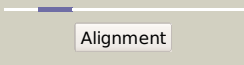
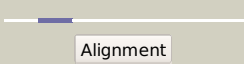
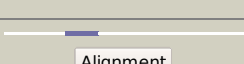
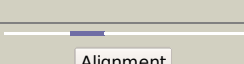
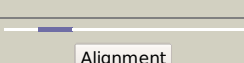
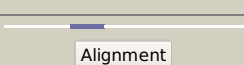
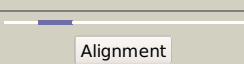
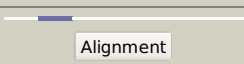
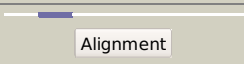
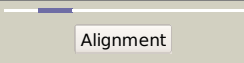
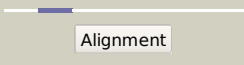
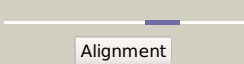
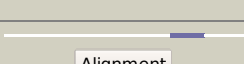

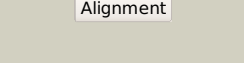
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4y23A_	 Alignment		100.0	35	PDB header: transferase Chain: A: PDB Molecule: gamma glutamyl transpeptidase,gamma-glutamyltranspeptidase; PDBTitle: crystal structure of t399a precursor mutant protein of gamma-glutamyl2 transpeptidase from bacillus licheniformis
2	d2nlza1	 Alignment		100.0	27	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Gamma-glutamyltranspeptidase-like
3	d2i3oa1	 Alignment		100.0	25	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Gamma-glutamyltranspeptidase-like
4	c2e0wA_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: t391a precursor mutant protein of gamma-glutamyltranspeptidase from2 escherichia coli
5	c2v36A_	 Alignment		100.0	35	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase large chain; PDBTitle: crystal structure of gamma-glutamyl transferase from bacillus subtilis
6	c2qm6C_	 Alignment		100.0	33	PDB header: transferase Chain: C: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of helicobacter pylori gamma-glutamyltranspeptidase2 in complex with glutamate
7	c2z8jA_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of escherichia coli gamma-glutamyltranspeptidase in2 complex with azaserine prepared in the dark
8	c4gdxA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase 1 heavy chain; PDBTitle: crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex
9	c5zjgC_	 Alignment		100.0	31	PDB header: transferase Chain: C: PDB Molecule: gamma-glutamyltransferase 1 threonine peptidase. merops PDBTitle: gamma-glutamyltranspeptidase from pseudomonas nitroreducens complexed2 with gly-gly
10	c3g9kD_	 Alignment		100.0	30	PDB header: hydrolase Chain: D: PDB Molecule: capsule biosynthesis protein capd; PDBTitle: crystal structure of bacillus anthracis transpeptidase enzyme capd
11	c5zjgD_	 Alignment		100.0	32	PDB header: transferase Chain: D: PDB Molecule: gamma-glutamyltransferase 1 threonine peptidase. merops PDBTitle: gamma-glutamyltranspeptidase from pseudomonas nitroreducens complexed2 with gly-gly

12	c2e0yB_	Alignment		100.0	39	PDB header: transferase Chain: B; PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of the samarium derivative of mature gamma-2 glutamyltranspeptidase from escherichia coli
13	c4gdxB_	Alignment		100.0	34	PDB header: hydrolase Chain: B; PDB Molecule: gamma-glutamyltranspeptidase 1 light chain; PDBTitle: crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex
14	c2v36D_	Alignment		100.0	36	PDB header: transferase Chain: D; PDB Molecule: gamma-glutamyltranspeptidase small chain; PDBTitle: crystal structure of gamma-glutamyl transferase from bacillus subtilis
15	c2nqoB_	Alignment		100.0	35	PDB header: transferase Chain: B; PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of helicobacter pylori gamma-glutamyltranspeptidase
16	c3ga9S_	Alignment		100.0	30	PDB header: hydrolase Chain: S; PDB Molecule: capsule biosynthesis protein capd; PDBTitle: crystal structure of bacillus anthracis transpeptidase enzyme capd,2 crystal form ii
17	c1p4vA_	Alignment		95.0	33	PDB header: hydrolase Chain: A; PDB Molecule: n(4)-(beta-n-acetylglucosaminy)l-asparaginase PDBTitle: crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine
18	c1t3mA_	Alignment		94.7	26	PDB header: hydrolase Chain: A; PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
19	c1apyA_	Alignment		94.5	42	PDB header: hydrolase Chain: A; PDB Molecule: aspartylglucosaminidase; PDBTitle: human aspartylglucosaminidase
20	c2gezE_	Alignment		94.0	24	PDB header: hydrolase Chain: E; PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-independent plant asparaginase
21	c3cuqA_	Alignment	not modelled	94.0	26	PDB header: protein transport Chain: A; PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
22	c4pu6A_	Alignment	not modelled	93.9	21	PDB header: hydrolase Chain: A; PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with k+ cations
23	c2zmeA_	Alignment	not modelled	93.5	26	PDB header: protein transport Chain: A; PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
24	c2zakB_	Alignment	not modelled	93.4	26	PDB header: hydrolase Chain: B; PDB Molecule: l-asparaginase precursor; PDBTitle: orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
25	c1u5tA_	Alignment	not modelled	93.2	21	PDB header: transport protein Chain: A; PDB Molecule: appears to be functionally related to snf7; PDBTitle: structure of the escrt-ii endosomal trafficking complex
26	c4gduB_	Alignment	not modelled	93.1	37	PDB header: hydrolase Chain: B; PDB Molecule: l-asparaginase; PDBTitle: crystal structure of sulfate-bound human l-asparaginase protein
27	c2a8lB_	Alignment	not modelled	92.0	37	PDB header: hydrolase Chain: B; PDB Molecule: threonine aspartase 1; PDBTitle: crystal structure of human taspase1 (t234a mutant)
28	c2gacA_	Alignment	not modelled	91.9	37	PDB header: hydrolase Chain: A; PDB Molecule: glycosylasparaginase; PDBTitle: t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum

29	c1apzB	Alignment	not modelled	85.8	28	PDB header: complex (hydrolase/peptide) Chain: B: PDB Molecule: aspartylglucosaminidase; PDBTitle: human aspartylglucosaminidase complex with reaction product
30	d1u5ta1	Alignment	not modelled	78.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
31	c2zalD	Alignment	not modelled	78.1	36	PDB header: hydrolase Chain: D: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
32	c1w7pD	Alignment	not modelled	76.9	25	PDB header: protein transport Chain: D: PDB Molecule: vps36p, ylr417w; PDBTitle: the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
33	c2zmeB	Alignment	not modelled	75.9	6	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein-sorting-associated protein 36; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
34	c1u5tB	Alignment	not modelled	75.1	25	PDB header: transport protein Chain: B: PDB Molecule: defective in vacuolar protein sorting; vps36p; PDBTitle: structure of the escrt-ii endosomal trafficking complex
35	c2zalB	Alignment	not modelled	73.3	29	PDB header: hydrolase Chain: B: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
36	c1k2xD	Alignment	not modelled	70.1	36	PDB header: hydrolase Chain: D: PDB Molecule: putative l-asparaginase; PDBTitle: crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
37	c1k2xB	Alignment	not modelled	70.1	36	PDB header: hydrolase Chain: B: PDB Molecule: putative l-asparaginase; PDBTitle: crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
38	c1jn9D	Alignment	not modelled	70.1	36	PDB header: hydrolase Chain: D: PDB Molecule: putative l-asparaginase; PDBTitle: structure of putative asparaginase encoded by escherichia coli ybik2 gene
39	c2gacD	Alignment	not modelled	68.6	31	PDB header: hydrolase Chain: D: PDB Molecule: glycosylasparaginase; PDBTitle: t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
40	c1t3mB	Alignment	not modelled	61.4	28	PDB header: hydrolase Chain: B: PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
41	c1t3mD	Alignment	not modelled	61.4	28	PDB header: hydrolase Chain: D: PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
42	c1jn9B	Alignment	not modelled	61.4	28	PDB header: hydrolase Chain: B: PDB Molecule: putative l-asparaginase; PDBTitle: structure of putative asparaginase encoded by escherichia coli ybik2 gene
43	c5loyD	Alignment	not modelled	59.5	13	PDB header: hydrolase Chain: D: PDB Molecule: designed anbu protein; PDBTitle: helical assembly of a designed anbu protein
44	c2gezF	Alignment	not modelled	58.0	38	PDB header: hydrolase Chain: F: PDB Molecule: l-asparaginase beta subunit; PDBTitle: crystal structure of potassium-independent plant asparaginase
45	c5nywT	Alignment	not modelled	52.1	19	PDB header: unknown function Chain: T: PDB Molecule: proteasome subunit; PDBTitle: anbu (ancestral beta-subunit) from yersinia bercovieri
46	c4pv3D	Alignment	not modelled	51.1	33	PDB header: hydrolase Chain: D: PDB Molecule: l-asparaginase beta subunit; PDBTitle: crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with na+ cations
47	d1u5tb1	Alignment	not modelled	37.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
48	c5xugB	Alignment	not modelled	36.0	28	PDB header: hydrolase Chain: B: PDB Molecule: endo-1,4-beta-mannanase; PDBTitle: complex structure(rmman134a-m5).
49	c5nygF	Alignment	not modelled	33.8	13	PDB header: hydrolase Chain: F: PDB Molecule: anbu; PDBTitle: anbu (gly-1) mutant from hyphomicrobium sp. strain mc1 - sg p2(1)2(1)2 2(1)
50	c5jtsA	Alignment	not modelled	32.4	33	PDB header: hydrolase Chain: A: PDB Molecule: beta-1,4-mannanase; PDBTitle: structure of a beta-1,4-mannanase, ssgH134.
51	c5yvmA	Alignment	not modelled	30.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq
52	c6d6rF	Alignment	not modelled	28.4	23	PDB header: hydrolase Chain: F: PDB Molecule: exosome complex component mtr3; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
53	d1v6ta	Alignment	not modelled	28.0	50	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
54	c2x5eA	Alignment	not modelled	28.0	67	PDB header: unknown function Chain: A: PDB Molecule: upf0271 protein pa4511; PDBTitle: crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa

55	d1xw8a_	Alignment	not modelled	27.4	50	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
56	d2dfaa1	Alignment	not modelled	27.3	50	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
57	d1u2ka_	Alignment	not modelled	27.1	25	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
58	d2ccaa1	Alignment	not modelled	26.6	27	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
59	d2fi0a1	Alignment	not modelled	25.6	21	Fold: SP0561-like Superfamily: SP0561-like Family: SP0561-like
60	d1a0da_	Alignment	not modelled	25.0	21	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
61	c3kzwD_	Alignment	not modelled	24.3	17	PDB header: hydrolase Chain: D: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
62	c3wrbB_	Alignment	not modelled	24.1	17	PDB header: oxidoreductase Chain: B: PDB Molecule: gallate dioxygenase; PDBTitle: crystal structure of the anaerobic h124f desb-gallate complex
63	c3gxqB_	Alignment	not modelled	21.5	27	PDB header: dna binding protein/dna Chain: B: PDB Molecule: putative regulator of transfer genes arta; PDBTitle: structure of arta and dna complex
64	d1o7ea_	Alignment	not modelled	20.2	22	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
65	c5i8iD_	Alignment	not modelled	19.8	23	PDB header: hydrolase Chain: D: PDB Molecule: urea amidolyase; PDBTitle: crystal structure of the k. lactis urea amidolyase
66	c2nn6F_	Alignment	not modelled	19.8	47	PDB header: hydrolase/transferase Chain: F: PDB Molecule: exosome component 6; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
67	c1udsA_	Alignment	not modelled	19.3	28	PDB header: transferase Chain: A: PDB Molecule: ribonuclease ph; PDBTitle: crystal structure of the trna processing enzyme rnase ph r126a mutant2 from aquifex aeolicus
68	c3hkmB_	Alignment	not modelled	19.1	26	PDB header: hydrolase Chain: B: PDB Molecule: os03g0854200 protein; PDBTitle: crystal structure of rice(oryza sativa) rrp46
69	c2ccaA_	Alignment	not modelled	18.8	27	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxidase/catalase t; PDBTitle: crystal structure of the catalase-peroxidase (katg) and2 s315t mutant from mycobacterium tuberculosis
70	c3ij3A_	Alignment	not modelled	18.3	29	PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
71	d2qalk1	Alignment	not modelled	18.0	30	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
72	c5loxH_	Alignment	not modelled	17.7	18	PDB header: hydrolase Chain: H: PDB Molecule: peptidase; PDBTitle: helical assembly of the anbu complex from pseudomonas aeruginosa
73	d1oj7a_	Alignment	not modelled	17.2	20	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
74	c3bt3B_	Alignment	not modelled	17.1	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: glyoxalase-related enzyme, arac type; PDBTitle: crystal structure of a glyoxalase-related enzyme from clostridium2 phytofermentans
75	d1jq5a_	Alignment	not modelled	16.8	19	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
76	c3iraA_	Alignment	not modelled	16.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
77	d1r6la1	Alignment	not modelled	16.2	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
78	c3va7A_	Alignment	not modelled	16.2	18	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
79	c1itkB_	Alignment	not modelled	16.1	24	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase-peroxidase; PDBTitle: crystal structure of catalase-peroxidase from haloarcula2 marismortui
80	d1ro0a_	Alignment	not modelled	16.0	24	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: Bifunctional DNA primase/polymerase N-terminal domain
81	c2nn6D_	Alignment	not modelled	15.9	32	PDB header: hydrolase/transferase Chain: D: PDB Molecule: exosome complex exonuclease rrp46; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40

82	c2zkqk	 Alignment	not modelled	15.8	17	PDB header: ribosomal protein/rna Chain: K: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
83	d2uubk1	 Alignment	not modelled	15.6	17	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
84	d2nn6f1	 Alignment	not modelled	15.6	44	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
85	c4ifdC	 Alignment	not modelled	15.5	22	PDB header: hydrolase/rna Chain: C: PDB Molecule: exosome complex component rrp43; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
86	c3b4tC	 Alignment	not modelled	15.4	32	PDB header: transferase Chain: C: PDB Molecule: ribonuclease ph; PDBTitle: crystal structure of mycobacterium tuberculosis rnase ph, the2 mycobacterium tuberculosis structural genomics consortium target3 rv1340
87	c1u2jC	 Alignment	not modelled	15.3	21	PDB header: oxidoreductase Chain: C: PDB Molecule: peroxidase/catalase hpi; PDBTitle: crystal structure of the c-terminal domain from the2 catalase-peroxidase katg of escherichia coli (p21 21 21)
88	d1wg8a1	 Alignment	not modelled	15.2	24	Fold: SAM domain-like Superfamily: Putative methyltransferase TM0872, insert domain Family: Putative methyltransferase TM0872, insert domain
89	d2nn6b1	 Alignment	not modelled	15.2	33	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
90	d1huwa	 Alignment	not modelled	15.0	18	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Long-chain cytokines
91	d1udsa1	 Alignment	not modelled	14.8	28	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
92	d2nn6a1	 Alignment	not modelled	14.7	33	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
93	d2je6b1	 Alignment	not modelled	14.5	11	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
94	d2nn6e1	 Alignment	not modelled	14.4	33	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
95	c4ifdE	 Alignment	not modelled	13.9	11	PDB header: hydrolase/rna Chain: E: PDB Molecule: exosome complex component rrp42; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
96	c5kpeA	 Alignment	not modelled	13.7	32	PDB header: de novo protein Chain: A: PDB Molecule: de novo beta sheet design protein or664; PDBTitle: solution nmr structure of denovo beta sheet design protein, northeast2 structural genomics consortium (nesg) target or664
97	c6bwsA	 Alignment	not modelled	13.6	17	PDB header: unknown function Chain: A: PDB Molecule: glycolate utilization protein; PDBTitle: crystal structure of efga from methylobacterium extorquens
98	c1wg8B	 Alignment	not modelled	13.2	22	PDB header: transferase Chain: B: PDB Molecule: predicted s-adenosylmethionine-dependent PDBTitle: crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.
99	d2ba0g1	 Alignment	not modelled	13.0	33	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like