

Mutant X- Exercise

Sequence 2

gtgttgttgc gcccattatgag ccgcctgagg ttggctctga ctgtaccacc atccactacaactacatgtg
taacagtcc tcatggcg gcatgaaccg gaggccccatc ctcaccatca

Part 1:

- 1) This mutation is located at nucleotide 82; the mutated query skipped the nucleotide (G) and is a *deletion mutation*.

size of nucleotide: 2,561 bp

Part 2:

- 1) I would expect to see more introns than exons.
- 2) There are ____ introns and ____ exons in the first transcript listed.
- 3) The mRNA transcript is 2,561 bp.
- 4) There are 393 amino acids in the protein.
- 5) The molecular weight of the protein is 43539.

Part 3:

- 1) The gene mutation was initially mapped by *McBride et al. (1985, 1986), then analyzed by Benchimol et al. (1985) and finally assigned to chromosome 17 by Isobe et al. (1986)*.
- 2) This mutated gene, *p53*, can be found in the following diseases:
 - a) bone marrow failure syndrome 5
 - b) somatic breast cancer
 - c) somatic hepatocellular carcinoma
 - d) Li-Fraumeni syndrome
 - e) somatic nasopharyngeal carcinoma
 - f) somatic pancreatic cancer
- 3) This gene is located on chromosome 17.
- 4) The normal gene is supposed to *bind the dimers present at the binding site; only 1 copy is not enough for p53 binding and any alteration of the motif/dimer will also result in the inability to bind*.

Sequence 12

aatataaagtg gaggcgctcg gctggccggc attccctgaag ctgacagcat tcggggccgag 61
atgtctcgct ccgtggcctt agctgtgctc ccgctactct ctctttctgg cctggaggct 121
atccaaatcgta ctccaaatggat tcagggttac tcacgtcatc cagcagagaa tggaaatgtca 181
aatttcctga attgttatgt gtctgggttt catccatccg acatgtttt tgacttactg 241
aagaatggag agagaatttgaaaatggag cattcagact tgtctttcag caaggactgg 301
tctttctatc tcttgacta cactgaattc accccccactg aaaaagatgtca gtatgcctgc 361
cgtgtgaacc atgtgacttt gtcacagccc aagatgttta agtgggatgtc agacatgtaa 421
gcagcatcat ggagggttga agatgccca ttggatgg atgaattcca aattctgctt 481
gcttgcttt taatattgtat atgcattatac acttacactt tatgcacaaa atgttagggtt 541
ataataatgt taacatggac atgatcttct ttataattct actttgagtg ctgtcccat 601
gtttgatgtta tctgagcagg ttgctccaca ggttagctta ggaggctgg caacttagag 661

gtggggagca gagaattctc ttatccaaca tcaacatctt ggtcagattt gaactttca 721
atctctgca ctc当地aaagctt gtaagatag ttaagcggtc ataagttac ttccaattt 781
catactctgc ttagaattt gggaaaatt tagaaatata attgacagga ttattggaaa 841
tttgttataa tgaatgaaac atttgtcat ataagattca tatttacttc ttatacattt 901
gataaaagtaa ggc当地atggtg tggttaatct ggtttattt tggccacaa gtaaataaaa 961
tcataaaact tggatgttta tctctta

- A. Position 91 from C to G (substitution); and there's a gap from the nucleotide 674 to 677 (insertion: AATT)
Length: 1007 bp
Protein length: 119 aa
Calculated_mol_wt=13583 ; 11.6 kD

B. I would expect both introns and exons.

C. 1. How was the gene mutation initially identified? Beta-2-microglobulin had been found in the serum of normal individuals and in the urine in elevated amounts in patients with Wilson disease ([277900](#)), cadmium poisoning, and other conditions leading to renal tubular dysfunction. Immunodeficiency 43 was identified because of a homozygous missense mutation in the B2M gene.

2. State which diseases you can find this mutated gene.

Immunodeficiency 43

Amyloidosis, familial visceral

3. What chromosome is this gene located on? chromosome 15 and 1

4. What is the function of the normal gene?

Sequence 13

gagaactctt gagaccggga gcccagctgc ccaccctctg gacattcacc cagccaggta
61 gtctcgac ctc当地agggct cc当地ccagact cctgcccagg ccaggactga ggcaaggcctc
121 aaggcacttc taggacctgc ct当地tctcac caagatgaac tcactggttt ct当地gcagct
181 actgc当地ttc ct当地gtgccca cccactttgg ggagccatta gaaaagggtgg cctctgtggg
241 gaattctaga cccacaggcc agcagctaga atccctggc ctccctggcc cc当地gggagca
301 gagcctgccc tgccaccgaga ggaaggccagg tgctactgccc aggctgagcc gtc当地ggggac
361 ct当地gttcc cc当地ccccccg agagctccgg gagcccccagg cagccgggccc tgtccccc
421 ccacagccgc cagatccccg caccccaaggc cgccgtgctg gtgcagcggg agaaggac
481 gacgaactac aactggaact ccttcggcct ggc当地tccggc aagcgggagg cggcaccagg

Part 1

1. The mutation is located at nucleotide 482, and it is a substitution.

Part 2

1. I would expect to see both introns and exons, the reason why is because introns have the purpose of acting like “hot spots” for recombination in the formation of new combinations (exons). And since there was a mutation we would expect to have both exons and introns.

2. How many introns and exons are in the first transcript listed?

3 exons ????

3. The length is 714 bp

4. 138 aa

5. Calculated weight: 12542

Part 3

1. The gene mutation was initially identified by *Lee and Welch in 1997*. As for us it was more initially identified just comparing the query and subject brackets.
2. This mutated gene, *KISS1*, can be found to have suppressed the ability to metastasis in athymic nude mice by at least 95 percent, without affecting the tumorigenicity of the cells.
3. The gene is located on chromosome 6
4. KISS1 is a factor of GnRH secretion and puberty onset.

MSA Analysis

Part 1

- P0AER2.1 is a glycerol uptake facilitator protein and *is* an aquaglyceroporin (AQP)
- Fasta's:

>WP_000084268.1 MULTISPECIES: glycerol uptake facilitator protein GlpF [Enterobacteriaceae]
MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLVAMAIYLTAGVSGAHLNPAVTIALWLFA
C
FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAIL
M
GLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
P
IVGAIVGAFAYRKLIAGRHLPCDICVVEEKETTTPSEQKASL
>EII23566.1 aquaglyceroporin [Escherichia coli 9.0111]
MDAFANGMRSYNPIMSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLVAMAIYLTAGVSGA
H
LNPAVTIALWLFA
FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAIL
V
QAFAVEMVITAILMGLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFT
G
GRDIPYFLVPLFGPIVGAIVGAFAYRKLIAGRHLPCDICVVEEKETTTPSEQKASL
>EFC4002950.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLVAMAIYLTAGVSGAHLNPAVTIALWLFA
C
FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAIL
M
GLILALTDDGNGVPRGPLAPLLVGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
P
IVGAIVGAFAYRKLIAGRHLPCDICVVEEKETTTPSEQKASL
>HCJ9303534.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLVAMAIYLTAGVSGAHLNPAVTIALWLFA
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAIL
M
GLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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IVGAVVGA
IVGAIVGAFAYRKLIAGRHLPCDICVVEEKETTTPSEQKASL
>WP_069906191.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKIAGASFGQWEISVIWGLVAMAIYLTAGVSGAHLNPAVTIALWLFA
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAIL
M
GLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
P
IVGAIVGAFAYRKLIAGRHLPCDICVVEEKETTTPSEQKASL
>WP_032330355.1 glycerol uptake facilitator protein GlpF [Escherichia coli]

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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPFLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_000084261.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
M
GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPFLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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IVGAIVGAFAYRKLIAGRHLPCDICVVEEKETTTPSEQKASL
>WP_139968770.1 MULTISPECIES: glycerol uptake facilitator protein GlpF
[Escherichia]
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPFLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_097433134.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPFLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>EFY9945837.1 glycerol uptake facilitator protein GlpF [Shigella boydii]
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FDKRKVIPFIISQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPFLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_069905124.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
M
GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPFLTGFAMNPARDGPKVFAWLAGWGNIAFTGGRDIPYFLVPLFG
P
IVGAIVGAFAYRKLIAGRHLPCDICVVEEKETTTPSEQKASL
>WP_256025592.1 glycerol uptake facilitator protein GlpF [Escherichia coli]

MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAAALKVAGASFGQWEISVIWGLVAMAIYLTAGVSGAHLNPAVTIALWLFA
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
M
GLILALTDDGNGIPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_228607197.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
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GLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKIFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_089591748.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
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GLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_104208942.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAIEMVITAIL
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GLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_222694967.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
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GLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_096152078.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAAALKVAGASFGQWEISIIWGLVAMAIYLTAGVSGAHLNPAVTIALWLFA
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
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GLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>MCN2556330.1 glycerol uptake facilitator protein GlpF [Escherichia coli]

MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAAALKVAGASFGQWEISVIWGLGVAMAIYLTAGVSGAHLNPAVTIALWLFA
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>HAI3832658.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>EGK6101618.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSIESVDSLADTFSTYPNPHINFVQAFAVEMVITAIL
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_001460178.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_100286854.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>HCN4653144.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAAALKVAGASFGQWEISVIWGLGVAMAIYLTAGVSGAHLNPAVTIALWLFA
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_061349307.1 glycerol uptake facilitator protein GlpF [Escherichia coli]

MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAAALKVAGASFGQWEISVIWGLVAMAIYLTAGVSGAHLNPAVTIALWLFA
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
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>EGI4428924.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>EFH5736458.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>EFJ1993816.1 glycerol uptake facilitator protein GlpF [Escherichia coli]

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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>EET5188252.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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FDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAIL
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GLILALTDDNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFG
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>WP_110826319.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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[Enterobacteriaceae]
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>EFK5514385.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>EEV7655455.1 glycerol uptake facilitator protein GlpF [Escherichia coli]

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>EFW0987407.1 glycerol uptake facilitator protein GlpF [Shigella sonnei]
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>WP_148871274.1 glycerol uptake facilitator protein GlpF [Escherichia coli]

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>EFL6097435.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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[Enterobacteriaceae]
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>WP_262018857.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>HCN2910968.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>EET4585203.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>HAW2312700.1 glycerol uptake facilitator protein GlpF [Escherichia coli]

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 >HAN3763063.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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Part 2

- Alignments:
 - Clustal Omega

>WP_097292524.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_280948396.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>HAN3763063.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>EET4585203.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>HCN2910968.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_262018857.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_000084263.1 MULTISPECIES: glycerol uptake facilitator protein GlpF [Enterobacteriaceae]
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>EFL6097435.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>HAZ7426195.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_148871274.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>HAW1880889.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_100662000.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEEKETTTPSEQKASL-----

>WP_137518125.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EFW0987407.1 glycerol uptake facilitator protein GlpF [Shigella sonnei]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>MCN4029060.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EEV7655455.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EES5072902.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEEKETTTPSEQKASL-----

>WP_137576966.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAGIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_052896116.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAGIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_094171713.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAGIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>HAN4091877.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAGIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EFO0185315.1 aquaporin [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAGIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_024213621.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAGIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EFK5514385.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAGIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_021293120.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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LYYNLFFDFEQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITAILMGLILAL
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GRDIPYFLVPLFGPIVGAILGAFAYRKLRHLPCDICVVEEKETTTPSEQKASL-----

>WP_074481225.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPIVGAIVGAFAYRKLRHLPCDICVVEEKETTTPSKQKASL-----

>WP_175127226.1 unnamed protein product [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_268065270.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EFA7471174.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>MBS8586580.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPIVGAIVGAFAYRKLRHLPCDICVVEEKETTTPSEQKASL-----

>WP_220401377.1 MIP/aquaporin family protein [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPIVGAIVGAFAYRKLRHLPCDICVVEKKETTTPSEQKASL-----

>WP_000084269.1 MULTISPECIES: glycerol uptake facilitator protein GlpF [Enterobacteriaceae]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EHD0879349.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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LYYNLFFDFKQTHHIVRGSVESVLAGTFSTYPNPHINFVQAFAVEMVITLMLILAL
TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEEKETTPSEQKASL----

>WP_096846969.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEEKETTPSEQKASL----

>WP_053886403.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVSFTG
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>EFQ2098627.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EEZ1780650.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_228613580.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>HAV8830186.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_024234723.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_021568910.1 glycerol uptake facilitator protein GlpF [Escherichia coli]

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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_175055721.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EJD7677529.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>QMS38848.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_166431906.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>MJJ04982.1 aquaporin [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EFN9220058.1 aquaporin [Escherichia coli]
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>EEZ9818133.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_032167137.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAGASMPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_085314107.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAGASMPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_089589682.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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GRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEEKETTPSEQKASL----

>WP_180759910.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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LYYNLFFDFEQTHHIVRGSVESVDSLADGTFSTYPNPINVFQAFAVEMVITAILMGLILAL
TDDGNGVPRGPLAPLLIGLLIAGASMPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEEKETTPSEQKASL----

>EJR3852918.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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GRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEEKETTPSEQKASL----

>EJA2249138.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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IWGLGVAMAIYLTAGVSGAHLNPAVTIALWLFCFDKRKVIPFIVSQVAGAFCAAALVYG
LYYNLFFDFEQTHHIVRGSVESVDSLADGTFSTYPNPINVFQAFAVEMVITAILMGLILAL
TDDGNGVPRGPLAPLLIGLLIAGASMPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEEKETTPSEQKASL----

>HCO7194178.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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GRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEEKETTPSEQKASL----

>EFA2153050.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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IWGLGVAMAIYLTAGVSGAHLNPAVTIALWLFCFDKRKVIPFIVSQVAGAFCAAALVYG
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEERETTPSEQKASL----

>EFC1460127.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_267657475.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>EGJ7727869.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_110826319.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPLVGAIVGAFAYRKLIGRHLPCDICVVEEKETTPSEQKASL----

>EET5188252.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
GRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHLPCDICVVEEKETTPSEQKASL----

>EJJ2206110.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EFJ1993816.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EFH5736458.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EFG5971915.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>EES4073774.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_062903386.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPMAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>EGI4428924.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTG
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>WP_061349307.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>HCN4653144.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_100286854.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_001460178.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>EGK6101618.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>MCN2556330.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_096152078.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_222694967.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_104208942.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>WP_089591748.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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---->WP_256025592.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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---->WP_069905124.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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---->EFY9945837.1 glycerol uptake facilitator protein GlpF [Shigella boydii]
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---->WP_097433134.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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---->WP_139968770.1 MULTISPECIES: glycerol uptake facilitator protein GlpF [Escherichia]
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---->WP_000084261.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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---->WP_032330355.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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---->WP_069906191.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>HCJ9303534.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>EFC4002950.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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>HAI3832658.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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TIKHD

>WP_000084268.1 MULTISPECIES: glycerol uptake facilitator protein GlpF [Enterobacteriaceae]
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>EII23566.1 aquaglyceroporin [Escherichia coli 9.0111]
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>EGX7149627.1 glycerol uptake facilitator protein GlpF [Escherichia coli]
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The PRALINE alignment process was completed in 50.0 seconds.

Alignment score = 25559706.00
 Alignment score per aligned residue pair = 18.38
 Sequence identities = 1381270
 Percent sequence identity = 0.99
 Number of sequences = 100
 Alignment length = 305
 Number of residues = 28124
 Number of gaps = 2376

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[Download Secondary structure prediction files](#)

Results colour-coded for amino acid conservation

The current colourscheme of the alignment is for **amino acid conservation**.

Residue Type Hydrophobicity Sec.Structure Make PDF

The conservation scoring is performed by PRALINE. The scoring scheme works from 0 for the least conserved alignment. The colour assignments are:

Unconserved 0 1 2 3 4 5 6 7 8 9 10 Conserved

	10	20	30	40	50
WP_000084268_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
EII23566_1_aqua	MDAFANGMRS	YNPIIMSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
HAI3832658_1_g1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
EFC4002950_1_g1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
HCJ9303534_1_g1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_069906191_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKIAG
WP_032330355_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_000084261_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_139968770_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_097433134_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
EFY9945837_1_g1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_069905124_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_256025592_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_228607197_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_089591748_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_104208942_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_222694967_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_096152078_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
MCN2556330_1_g1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
EGK6101618_1_g1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
WP_001460178_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
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WP_166431906_1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
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EGJ7727869_1_g1	-----	MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
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WP_024234723_1-----	-----MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
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WP_262018857_1-----	-----MSQTST	LKGQCIAEFL	GTGLLIFFGV	GCVAALKVAG
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Consistency	00000000000	0000*99***	*****9*	***9*9***9
			*****99***	*****9*99*

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WP_139968770_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPATVIALW	LFACFDKRKV					
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EFY9945837_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPATVIALW	LFACFDKRKV					
WP_069905124_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPATVIALW	LFACFDKRKV					
WP_256025592_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPATVIALW	LFACFDKRKV					
WP_228607197_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPATVIALW	LFACFDKRKV					
WP_08861740_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPATVIALW	LFACFDKRKV					

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EJJ2206110_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
EET5188252_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
EFC1460127_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LYACFDKRKV
EFA2153050_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
HC07194178_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
EJR3852918_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
WP_085314107_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
WP_032167137_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFSCFDKRKV
EEZ9818133_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
MJJ04982_1_aqua	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
WP_021568910_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
WP_024234723_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
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EEZ1780650_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
WP_053886403_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
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HAN2312700_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
EFA7471174_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
WP_021293120_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
WP_024213621_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
HAN4091877_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
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WP_262018857_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
WP_074481225_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
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EIZ1217478_1_g1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
WP_160187104_1	ASFGQWEISV	IWGLGVAMAI	YLTAGVSGAH	LNPARTIALW	LFACFDKRKV
Consistency	****9*9***9	*****9***9	**99*9****	*****99**	999*****99

		110.....	120.....	130.....	140.....	150
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HAI3832658_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFDFE	QTHHIVRGSV	ESVDLAGTFS		
EFC4002950_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFDFE	QTHHIVRGSV	ESVDLAGTFS		
HCJ9303534_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFDFE	QTHHIVRGSV	ESVDLAGTFS		
WP_069906191_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFDFE	QTHHIVRGSV	ESVDLAGTFS		
WP_032330355_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFDFE	QTHHIVRGSV	ESVDLAGTFS		
WP_000084261_1	IPFIVSQIAG	AFCAAALVYG	LYYNLFFDFE	QTHHIVRGSV	ESVDLAGTFS		
WP_139968770_1	IPFVVVSQVAG	AFCAAALVYG	LYYNLFFDFE	QTHHIVRGSV	ESVDLAGTFS		
WP_097433134_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFDFE	QTHHIIIRGSV	ESVDLAGTFS		
EFY9945837_1_g1	IPFIISQVAG	AFCAAALVYG	LYYNLFFDFE	QTHHIVRGSV	ESVDLAGTFS		
WP_069905124_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFDFE	QTHHIVRGSV	ESVDLAGTFS		

EFQ2098627_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
MBS8586580_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
MCS1251213_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_137576966_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EGX7149627_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EGI4428924_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EES4073774_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EFG5971915_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EJJ2206110_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EET5188252_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EFC1460127_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EFA2153050_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
HCO7194178_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDSLGTFS
EJR3852918_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_085314107_1	IPFIVSQVAG	AFCAAASLVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_032167137_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EEZ9818133_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
MJJ04982_1_aqua	IPFIVSQVSG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_021568910_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_024234723_1	IPFIVSQVAG	AFCASALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
HAV8830186_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_228613580_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EEZ1780650_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_053886403_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_096846969_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
HAW2312700_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EFA7471174_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_021293120_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_024213621_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGNV	ESVDLAGTFS
HAN4091877_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_000084263_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_094171713_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_137518125_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EES5072902_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
MCN4029060_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EFW0987407_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
HAW1880889_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_148871274_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
HCN2910968_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EET4585203_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_052896116_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_262018857_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_074481225_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
HAZ7426195_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EFL6097435_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_072693170_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_280948396_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_100662000_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_000084269_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_220401377_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EFH5736458_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QSHHIVRGSV	ESVDLAGTFS
WP_267657475_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EJA2249138_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EHD0879349_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_268065270_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
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EFK5514385_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EFO0185315_1_aq	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EEV7655455_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	KSVDLAGTFS
EFN4732685_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
HBC1484665_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
HAN3763063_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_097292524_1	IPFIVSQVAG	AFCAAALVYG	LYYNFFFDFE	QTHHIVRGSV	ESVDLAGTFS
EIZ1217478_1_g1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
WP_160187104_1	IPFIVSQVAG	AFCAAALVYG	LYYNLFFFDFE	QTHHIVRGSV	ESVDLAGTFS
Consistency	***99***99*	***9*9*****	***9*****9	*9***99***99	9*9*99*****

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WP_000084268_1	TYPNPHINFV	QAFAVEMVIT	AILMGLILAL	TDDGNGVPRG	PLAPLLIGLL
EII23566_1_aqua	TYPNPHINFV	QAFAVEMVIT	AILMGLILAL	TDDGNGVPRG	PLAPLLIGLL
HAI3832658_1_g1	TYPNPHINFV	QAFAVEMVIT	AILMGLILAL	TDDGNGVPRG	PLAPLLIGLL
EFC4002950_1_g1	TYPNPHINFV	QAFAVEMVIT	AILMGLILAL	TDDGNGVPRG	PLAPLLVGLL
HCJ9303534_1_g1	TYPNPHINFV	QAFAVEMVIT	AILMGLILAL	TDDGNGVPRG	PLAPLLIGLL

		AIAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
WP_089589682_1	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
EFN9220058_1_aq	TYPNPHINFV	QAFAVEMVLT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
QMS38848_1_glyc	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
EJD7677529_1_g1	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
WP_175055721_1	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
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EJJ2206110_1_g1	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
EET5188252_1_g1	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
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HC07194178_1_g1	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
EJR3852918_1_g1	TYPNPHINFV	QAFS VEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
WP_085314107_1	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
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EEZ9818133_1_g1	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
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WP_097292524_1	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
EIZ1217478_1_g1	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
WP_160187104_1	TYPNPHINFV	QAFAVEMVIT	AILMGLLAL	TDDGNGVPRG	PLAPLLIGLL
Consistency	*****9***	***99***9*	9****99***	*****9***	*9****9***

..... 210 220 230 240 250

WP_159908770_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
WP_097433134_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
EFY9945837_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
WP_069905124_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNIAFTG	GRDIPYFLVP
WP_256025592_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
WP_228607197_1	IAVIGASMGP	LTGFAMNPAR	DFGPKIFAWL	AGWGNVAFTG	GRDIPYFLVP
WP_089591748_1	IAIIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
WP_104208942_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
WP_222694967_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
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MCN2556330_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
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WP_001460178_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
WP_100286854_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
WP_166431906_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
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WP_061349307_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWM	AGWGNVAFTG	GRDIPYFLVP
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EFJ1993816_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
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EGJ7727869_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
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EFN9220058_1_aq	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
QMS38848_1_glyc	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
EJD7677529_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFMVP
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EFG5971915_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
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HC07194178_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
EJR3852918_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
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EEZ9818133_1_g1	IAVIGASMGP	LTGFSMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
MJJ04982_1_aqua	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
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HAV8830186_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
WP_228613580_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
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WP_096846969_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
HAW2312700_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
EFA7471174_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
WP_021293120_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
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HAN4091877_1_g1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
WP_000084263_1	IAVIGASMGP	LTGFAMNPAR	DFGPKVFAWL	AGWGNVAFTG	GRDIPYFLVP
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Consistency **00000**

- Muscle

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Results for job muscle-l20230606-130620-0763-75526820-p2n

Alignments	Result Summary	Phylogenetic Tree	Results Viewers	Submission Details
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CLUSTAL multiple sequence alignment by MUSCLE (3.8)

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HAW1880889.1 -----MNQTSTLKGQCIAEFLGTGLLIFFGVGCVAAALKVAGASFGQWEISV
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WP_085314107.1	-----	-----	-----
WP_089589682.1	-----	-----	-----
WP_180759910.1	-----	-----	-----
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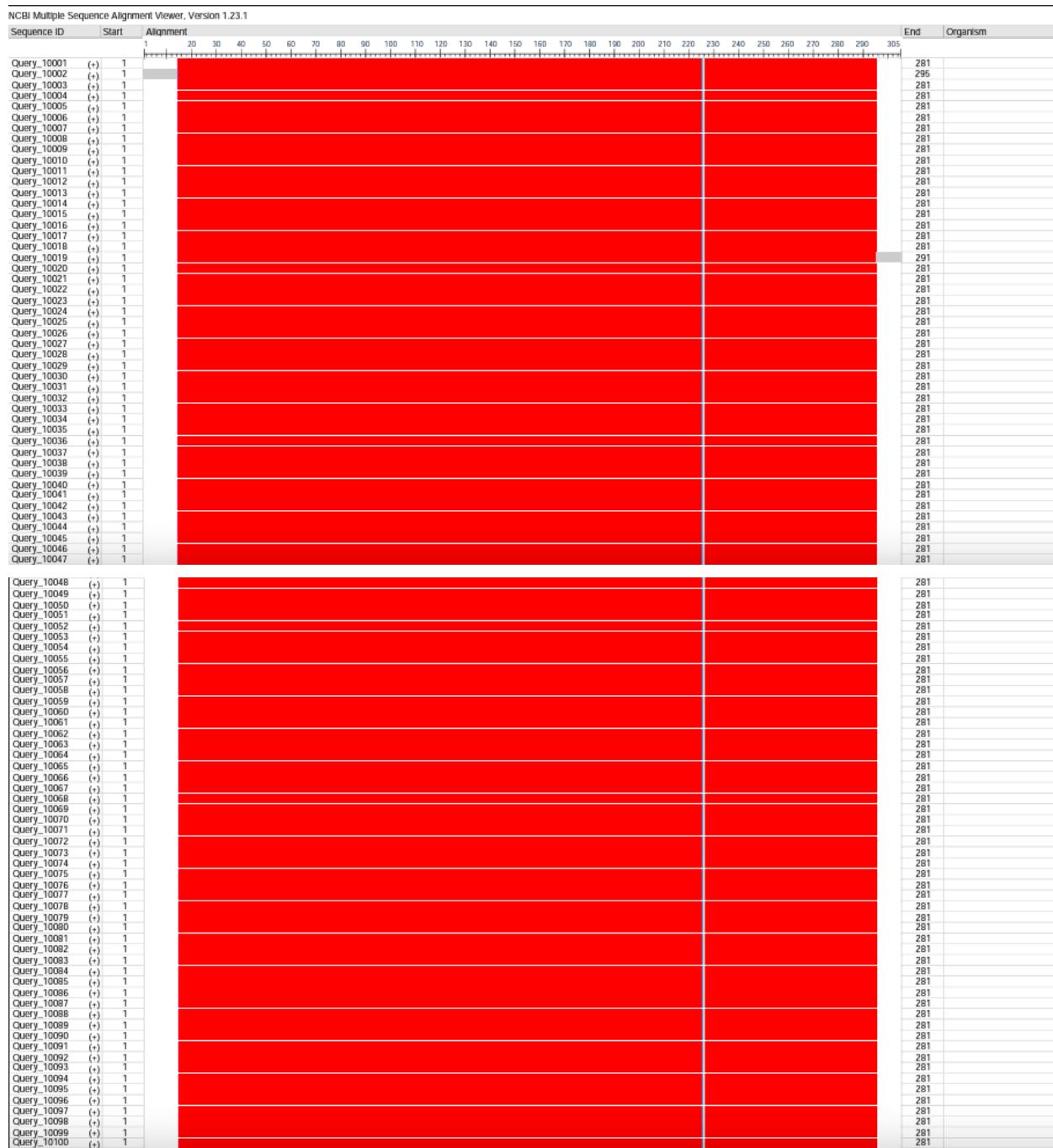
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EIZ1217478.1	-----		
WP_262018857.1	-----		
HAN3763063.1	-----		
WP_072693170.1	-----		
WP_280948396.1	-----		
WP_097292524.1	-----		
WP_000084268.1	-----		
HAI3832658.1	TIKHD		

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○ COBALT



Part 2 continuation : Alignment Visualization

COME BACK

Part 3

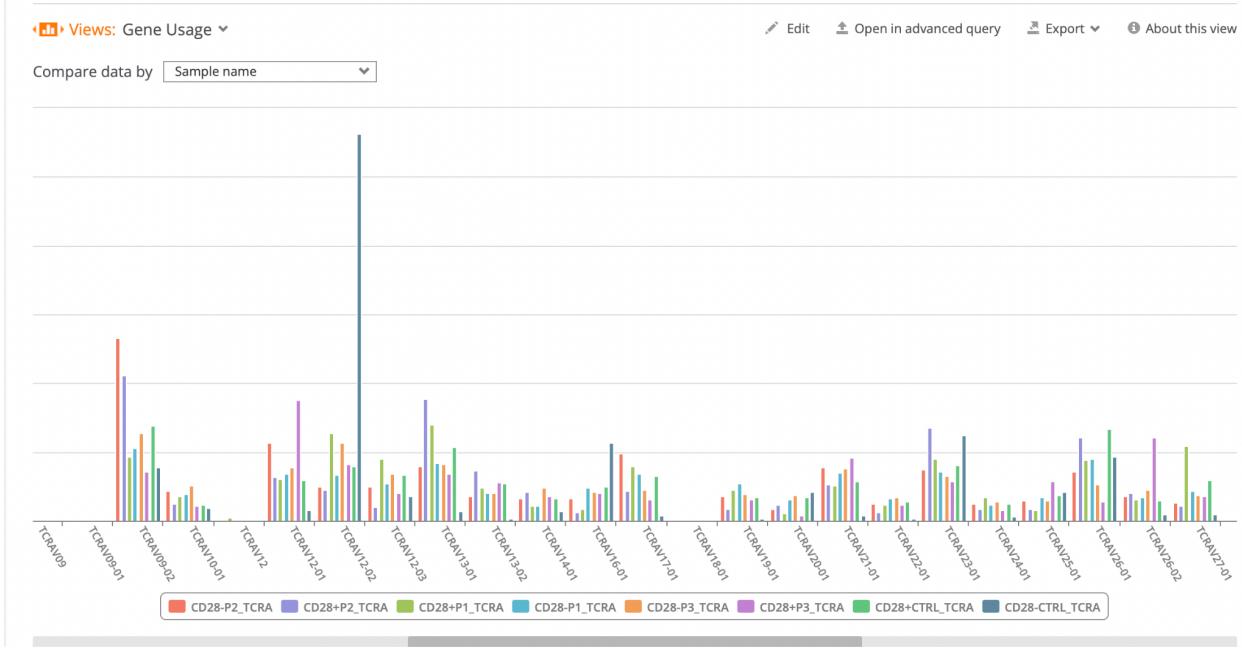
GEO Dataset/DAVID

- choice of disorder: rheumatoid arthritis
 - GEO dataset: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE136052>
 - DAVID clusters:

ImmunoSeq

<https://doi.org/10.21417/VB2021C>

1. Gene usage



2. CDR3 length

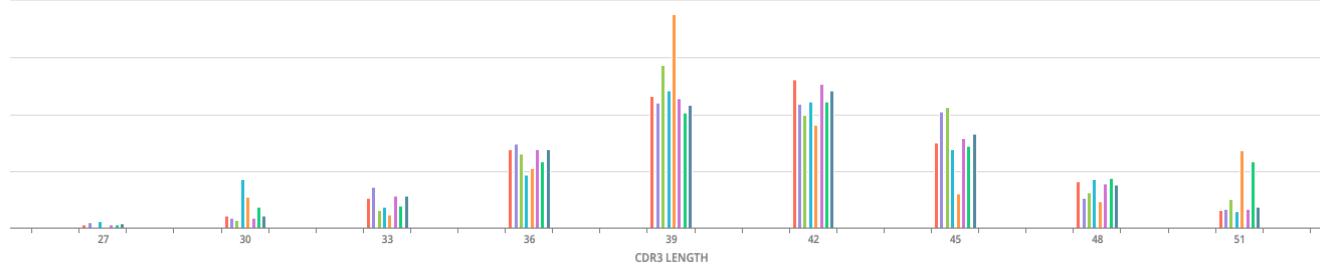
Analysis 1

Filters (2) Notes Duplicate

Views: CDR3 Length ▾

Edit Open in advanced query Export About this view

Compare data by Sample name ▾



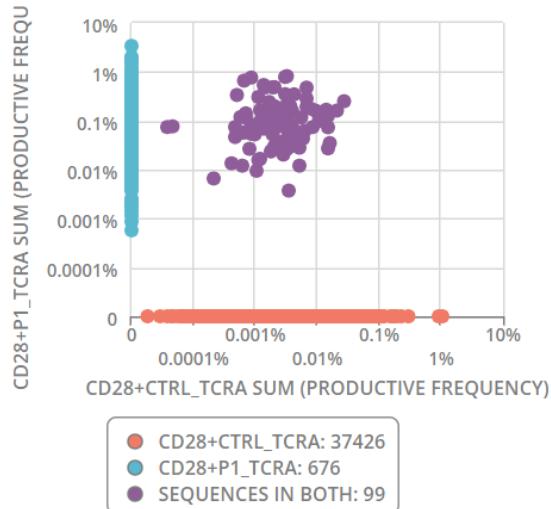
3. Pairwise scatterplot

Analysis 1

Views: Pair-wise Scatter Plot ▾

Edit

Open in advar



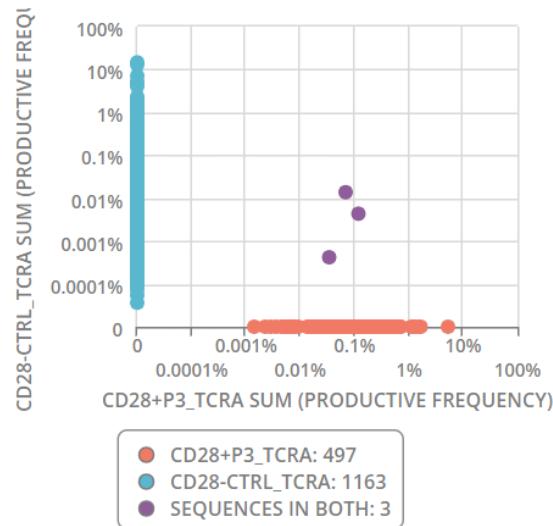
(first two)

Analysis 3

Views: Pair-wise Scatter Plot ▾

Edit

Open in advar

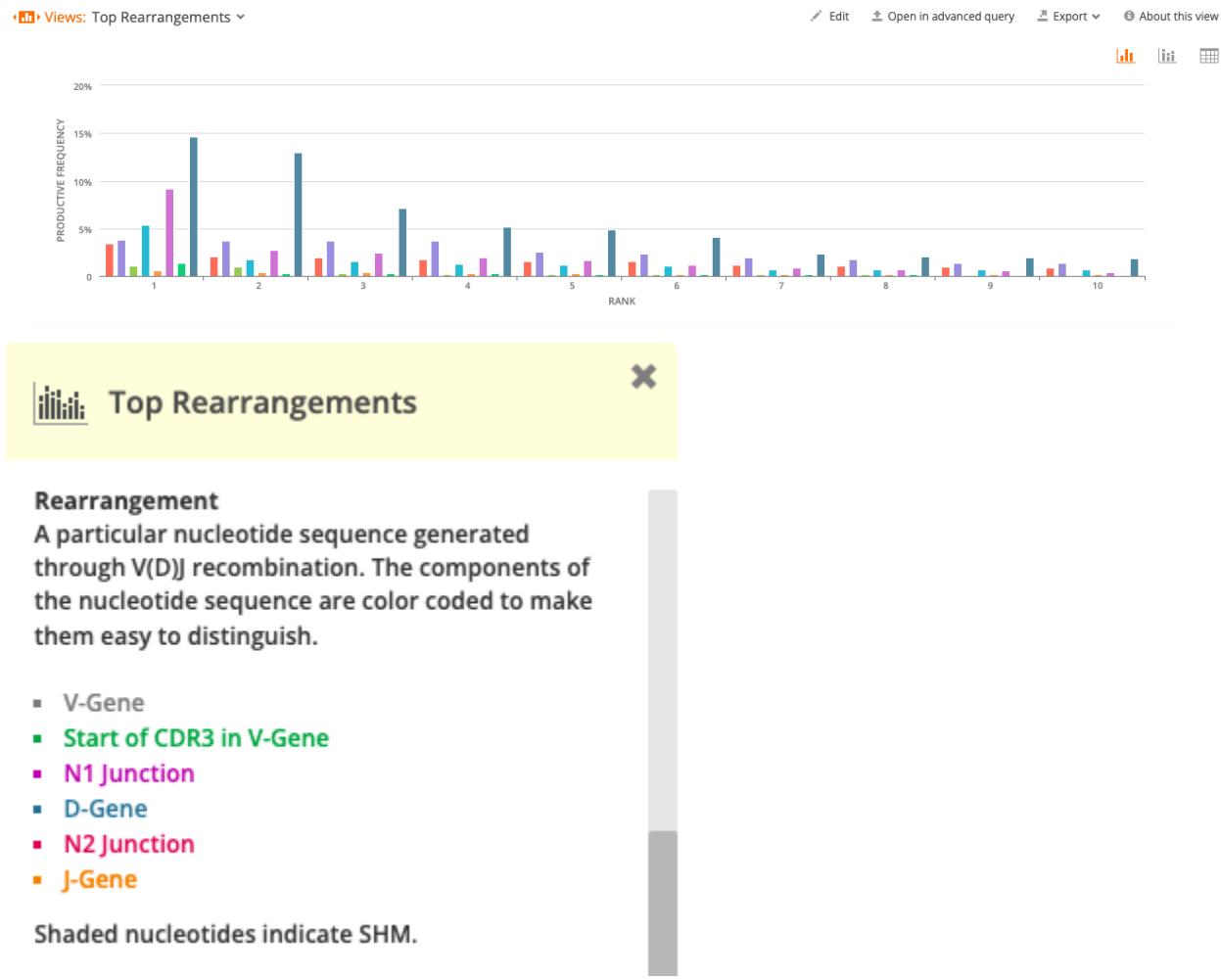


(Three and four)

4. Combined rearrangements

https://universityofdallas-my.sharepoint.com/:t/g/personal/nvegaortiz_udallas_edu/Eb2rQW4G4P1No4ALftcv4HcBecAc7HuOku469uImK59itg?e=p5GOmd

5. Top rearrangements



Advanced features

Clonality

Diversity