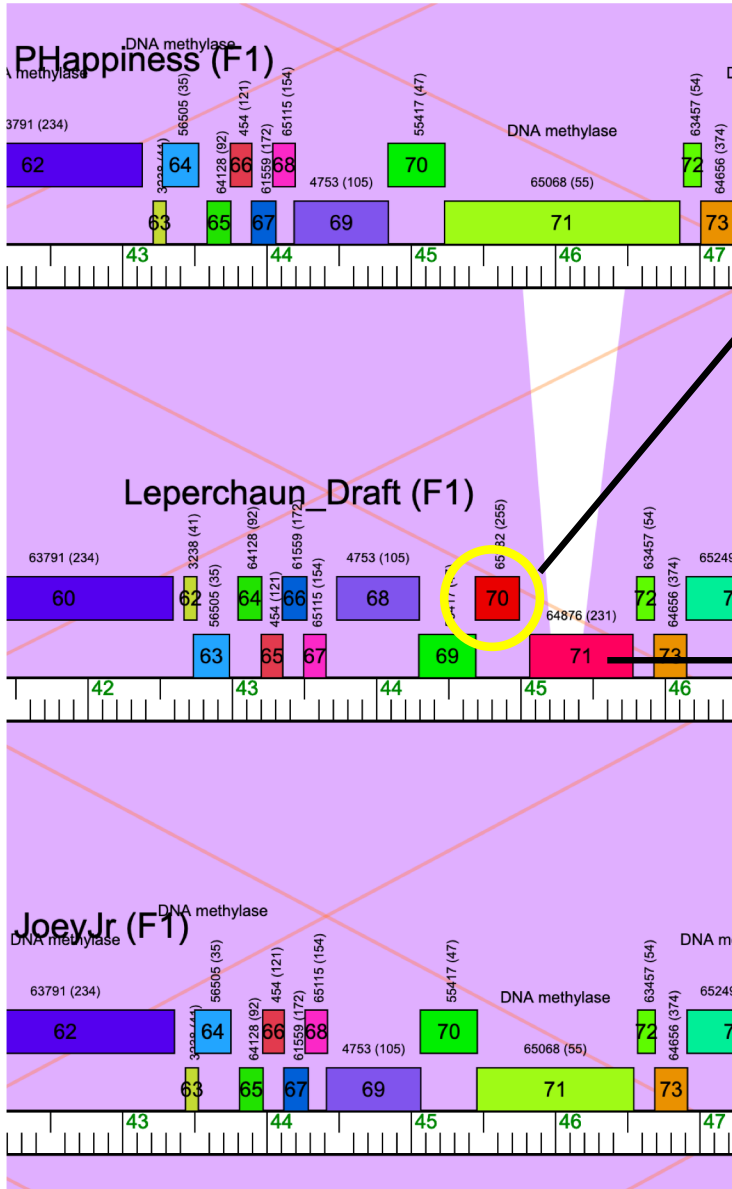


Leprechaun F1

Split methylase/methyltransferase



[Template alignment](#) | [Template 3D Structure](#) | [PDBe](#)

- ☐ L-5-HOMOCYSTEINE, COMPLEX (METHYLTRANSFERASE- DNA), transferase-DNA complex; HET: SO4, 3DR, SAH; 1.594A {Haemophilus parahaemolyticus}

Probability: 99.4%, E-value: 1.3e-11, Score: 71.3, Aligned cols: 90, Identities: 36%, Similarity: 0.617, Template Neff: 10.7

[illegible]

Q ss_pred		ccCcCCCCCCCc	
Q Q_3183860	81	RAGTAEGRHPLG	92 (102)
Q Consensus	81	+++ . + . + . +	92 (102)
		+++ . + . + . +	
T Consensus	90	+++ . + . + . +	101 (327)
T 5CIY_A	90	QKGFDSRGTLF	101 (327)
T ss_dssp		CGGGSGGGGHH	
T ss_psd		ccCCCCchhhHH	

N-terminal alignments
AA 1-92

[Template alignment](#) | [Template 3D Structure](#) | [PDBe](#)

- ☐ 2. L-HOMOCYSTEINE, COMPLEX (METHYLTRANSFERASE- DNA), transferase-DNA complex; HET: SO4, 3DR, SAH; 1.594A (Haemophilus parahaemolyticus)

Probability: 99.94%, E-value: 2.5e-26, Score: 208.66, Aligned cols: 242, Identities: 16%, Similarity: 0.13, Template Neff: 10.7

[illegible][illegible][illegible]

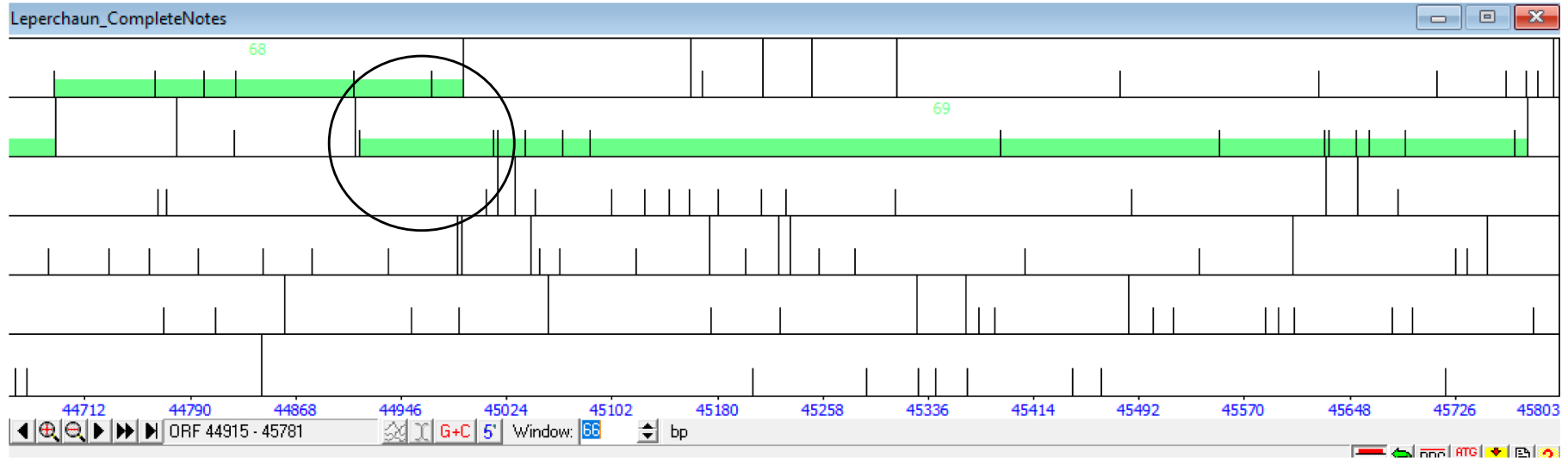
ss_pred		cCCCCcCcCCCCHHHHHHHhCccccCHHHHHHHHHHHHHHHhhhhh	
Q ss_128345_11	240	MGPAGMVTAVPGISRNDAIRICNGVCGPQAAYAAQLGLVYAAASHCV	286 (289)
Q Consensus	240	qGfP-----g-s-----T-GNaVpp--va-~---t---l-----	286 (289)
		+ . + . + . + + + + . + + + + . . . +	
T Consensus	283	qGfP-----T-GNav-----	326 (327)
T 5CIY_A	283	MGVPDSYKYNH--P-STSQAYKQGFGSVIVNLVGYIAYINIGSSLNFKFP	326 (327)
T ss_dssp		TTCTCTSCCC--S-CHHHHHHHHHHHcccCHHHHHHHHHHHHHHHHH	
T ss_pred		CccccCCCCc--C-ChHHHHHHhhccccCHHHHHHHHHHHHHhhccCCC	

Picks up @ AA83

This includes full
ORF with 80bp
overlap to previous
gene

Leprechaun F1

Split methylase/methyltransferase



Gene #67

GTGAAACTCGGTTTCGCTGTTCTCCGGCGCTGGCGGCCTCGACATCGCCGTCGAGCAGTTCTTCGGCGCCCGCACGGTGTGGCATTGCGAGCTGAACCCGGCCGCGTCCAAGGTGCTCGCGCAC
CGCTGGCCCGGTGTGCCGAACCTCGGCATATCACCGCGGTCGACTGGTCAGAAGTCGAGCCGGTCGACATTCTCGCTGGCGGATTTCCCTGCCAGGACGTGAGTGCCCGCGGTCTCGCGCC
GGCATCGCCGAGGGCAGGCACCCGCTCGGGCCTG**TG GGC** GCT GTT CGC CGA AGT CAT TAA

MKLGSLFSGAGGLDIAVEQFFGARTVWHCELNPAASKVLHRWPGVPNLGDITAVDWSEVEPVDILAGGFPCQDVSAAAGRRAGIAEGRHPLGPVGAVRRSH (highlight = HHpred alignments to PDB 5CIY_A)

Aligns 1-88 in PDB 5CIY_A

Gene #68 (green = overlapping sequence coding for matching amino acids)

GTGCCGCGCGGTTCGTCGCGCCCGCATCGCCGAGGGCAGGCACCCGCTCGGGCCTCTGGCGCTGTTTCGCCGAAGTCATTAACCAGCTGCGGCCGGGTGTCGTGGTGATCGAGAACGTAAGGGGG
TTGCTCAGTGCAAGGGCCTATCGCGCAATGGAATCCGAAGAGGCAGCTGTGGGAGACGGGGCAGATGGACCTGTTCTCCGGGCACTCGGTGCCGTACTCGGAGACCTTGCCGACCTCGGGTAT
GACGCGCAGTGGATCACTCTTGCCGCTTCCGACGTGCGCGCACCGCACCGGCGTGAACGCGTCTTCATCCTTGCTACTCCCGTCGCCAGTAGCGCATCCCTCGGGGAACCTCGCCGAGGCGCA
TCTGCGCAAGAAACCGGGACGACGCGAGTGACGGATCTGGCGATCATCGTCGAGAACAACCTGCTGGAGACAGCGACGGTCACCAGAACACGCTGCCGACCGTGCAGGATCTGCTGCCG
ACACCCCTCGGCGAGCGACGGGACCGCGCGGGCAGCATCCCGACCGGCGAGAGGGGCACTCGCGGCAGCTGTGCGACTATGCGCTGCTGGACGGCACCTCGCGCTGGGGCAAGTACGCCGCT
GCGATCGCACGCTGGGAGGCTGTGGCCGACCCGCGCCGTCGCCGACCGAGCCGAACAAGAACGGCAATCCCCGACTCACCGCCGCGTTCCCCGAGTGGATGATGGGCTGGCCCCGCGGCTGG
GTGACTGCGGTGCCGGGTATCTCGCGCAACGATGCGTTGCGCATCTGCGGGAACGGCGTATGCCCGCAACAGGCATACGCCGCACTCCAGATCCTCGTCAGGCTTTCGGCTTGCGAGGTGGCC
GAGTGA

**MPPVVAPASPRAGTRSGLWALFAEVINQLRPGVVVIENVRGLLSARAYRAMESEEAAGVDGADGPVLRALGAVLGDLDLGYDAQWITLAASDVGAPHRRRERVFILATPVASSASLGELARGA
SAQETGTQPSDGSQDHRREQAGDSQGHQNTLPQTVRDLPTPSASDGTGGGQHPDRREGHSRLCDYALLDGTSRWGKYAAAIAARWEAVAGPAPSPTEPNKGNPNRLTAAFPPEWMMGWPAW
VTAVPGISRNDALRICNGVCPQQAAYALQILVRVSACEVAE** (highlight = HHpred alignments to PDB 5CIY_A amino acids 83-326)