

Usavi_draft_70: potentially ribbon-helix-helix?

Currently 7 members of pham call ribbon-helix-helix DNA binding domain protein.

Usavi_draft_70:

Phages DB: https://phagesdb.org/genes/Usavi_CDS_70/

HHpred results:

- ✓ 64 Start: 55,460 Stop: 55,104 Reverse (NKF)
- ✓ 65 Start: 55,932 Stop: 55,573 Reverse (NKF)
- ✗ 66 Start: 56,267 Stop: 55,929 Reverse ()
- ✓ 67 Start: 56,481 Stop: 56,609 Forward (NKF)
- ✓ 68 Start: 56,688 Stop: 57,449 Forward (NKF)
- ✗ (Not Included) Start: 57,057 Stop: 57,449 Forward ()
- ✓ 69 Start: 57,555 Stop: 57,734 Forward (ribbon-helix-helix DNA binding domain)
- ✓ 70 Start: 57,766 Stop: 57,948 Forward (NKF)
- ✓ 71 Start: 58,009 Stop: 58,716 Forward (helix-turn-helix DNA binding domain)
- ✓ 72 Start: 58,709 Stop: 59,281 Forward (NKF)
- ✓ 73 Start: 59,278 Stop: 59,700 Forward (NKF)
- ✓ 74 Start: 59,741 Stop: 59,869 Forward (NKF)

2BNH_B
1TRQ_B
4AAT_A
2K10_B
6SBM_A
2H10_G
2BSQ_H
7BY3_A
2AN7_B
4HV0_B
2K6L_A
5XE3_E
4ME7_E
1P94_A
3FT7_A
6A6X_D
3Q0Q_A
1NLA_B
2MDV_B
1BAZ_B
6XRW_D
2KEL_A
2K29_B
1U9P_A
2K5J_B
1MNT_A
4Q2U_G
1X93_B
7AK7_D
5X3T_E

Nr	Hit	Name	Probability	E-value	Score	SS	Aligned cols	Target Length
<input type="checkbox"/> 1	2BNW_B	ORF OMEGA; DNA-BINDING-REGULATORY PROTEIN COMPLEX, RIBBON-HELIX-HELIX, RHH, METJ/ARC SUPERFAMILY, COOPERATIVE DNA BINDIN	98.99	3.3e-9	53.79	5.7	41	53
<input type="checkbox"/> 2	1IRQ_B	omega transcriptional repressor; transcriptional repressor, ribbon-helix-helix, GENE REGULATION; 1.5A {Streptococcus pyo	98.88	1.3e-8	55.03	5.7	41	71
<input type="checkbox"/> 3	4AAI_A	ORF E73; VIRAL PROTEIN, EXTREMOPHILE, ARCHAEA, RIBBON-HELIX-HELIX PROTEINS, DNA-BINDING PROTEINS; NMR {SULFOLOBUS VIRUS	98.54	4.1e-7	48.41	5.2	39	73
<input type="checkbox"/> 4	2K1O_B	Putative; Helicobacter pylori, repressor, transcriptional regulator, DNA-binding, ribbon-helix-helix, HP0564, JHP0511, U	98.51	3.1e-7	49.07	4.2	45	66
<input type="checkbox"/> 5	6SBW_A	CdbA; nucleoid ribbon-helix-helix, DNA BINDING PROTEIN; 2.24A {Myxococcus xanthus DK 1622}	98.47	9.5e-7	45.68	5.4	41	67
<input type="checkbox"/> 6	2H1O_G	Trafficking protein A; PIN domain, RHH protein, DNA binding, tetramer of dimers, GENE REGULATION-DNA COMPLEX COMPLEX; HE	98.41	0.0000016	44.89	5.3	40	68
<input type="checkbox"/> 7	2BSQ_H	TRAFFICKING PROTEIN A; TRANSCRIPTION, TRANSCRIPTION REGULATION COMPLEX, PIN DOMAIN, RIBBON-HELIX-HELIX, DNA BINDING, HET	98.32	0.0000028	45.37	5.1	38	77

Both 2BNW and 1IRQ link to manuscripts that discuss RHH.

PDB: <https://www.rcsb.org/structure/2BNW>

PDB: <https://www.rcsb.org/structure/1IRQ>

*I don't see any HHpred hits that line up with the evidence entries for the example RHH genes, Chorkpop_70.

Chorkpop_70 HHpred: https://toolkit.tuebingen.mpg.de/jobs/Chorkpop_70

Phareon_67 HHpred: https://toolkit.tuebingen.mpg.de/jobs/Chorkpop_71