

Forum: <https://seaphages.org/forums/topic/4391/>

**Usavi\_draft\_58** (stop @ 49093): DNA Primase/Polymerase/Helicase?

Currently Pham 84: <https://phagesdb.org/phams/84/>

Tricky functional call. Pham includes numerous inconsistent calls: DNA primase/helicase; DNA primase/polymerase/helicase; DNA primase/polymerase; RepA-like helicase; DNA helicase.

### Usavi\_draft\_58:

```
MLGSTPITAILGAGIDNRDPEAVRAFVQRQAADIGLSIMFIAPDSKAPVDLRTPQKKKADDKAAQEAAREAGRRDWARVKSPAGLTLATSDKAVLDRLKRYL
TLYAERYPEGVPVNVAVEVGGSSALVVVDCDTAAQLQRFYEALPEDIGIDDVPPPTVVTGPHAGKGDGLADPSSWAHSDGGHFYFTVPDEILPTLPRNLG
AMTWGGEDGFVAVLWDKRYLVIPPSTRPEGAYEVVGRDYPITDAPWLLDAIREAAAARRAERTERAHRDSEAGELSEAIDGWAEATPWSAILEPLGWTAPPR
ADACGCPVWTAPGVHASPKSATAHDTGCALGRYTEVNAPLHIWTDNPGEPFEAWISDKGTKLSKLQAVALIDYEGNIGKAMDEIGLTPDLAVEVDPIAP
KQVDPDHAMTGDGDFELPAPEPETTSTPDEPPFCVCDTEAGAFVVDADGDMWHMPEGGSEGDEHLAEPAPATYAHDASCNTAHTAGPEPCPTPTS
ADDLSLDPADFGKAEPADPEPSYAAADPEQTDPDVYDPSHSGVPRIAPFSHWRDMPPEYVIEGLLEHGGLTSIIGPPGIGKSSVVLDMACHIAVGKRWQ
GRRTLKTKVLYLPGEGLAGAVQRLRAWEANHDVLDLNDLMLGDSIILIKASNEAWGDLAAYIARHEIGLVVFDTFARQSSGLEENSATDVGVAVRRYDKLR
ELTGAGVCVVHHTSKAHTDQGRGSSALNGALDSELVVRATWDTESAMIDGRLPGRPMEVMTTKQKNAEALAEALMMVSYEDEDAGIKAPLITGPNG
SVDPMQGEIVLARPRPEAVIETAVRIRQFVNDLPTQGATRAEILTAVQADAYARRRDSAAVWKLHIQRAVDMGLRFNLIETLTGTASGSRYIPGQVIGIEQAR
TLAAAEVIDGD
```

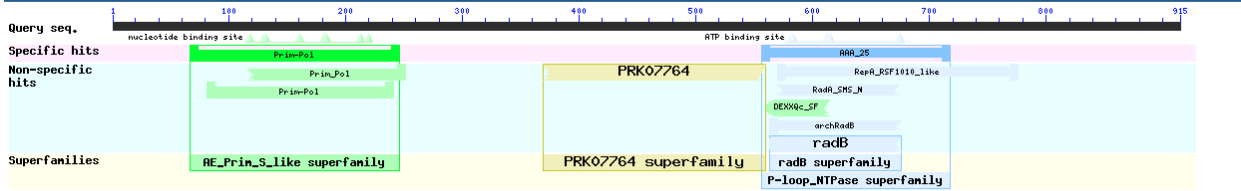
HHpred results: [https://toolkit.tuebingen.mpg.de/jobs/usavi\\_58](https://toolkit.tuebingen.mpg.de/jobs/usavi_58)

### Visualization



CDD Results:

**Graphical summary**  Zoom to residue level [show extra options >](#)



[Search for similar domain architectures](#) [Refine search](#)

**List of domain hits**

Name	Accession	Description	Interval	E-value
RepA_RSF1010_like	cd01125	Hexameric Replicative Helicase RepA of plasmid RSF1010 and related proteins; This family ...	570-776	8.54e-43
AAA_25	pfam13481	AAA domain; This AAA domain is found in a wide variety of presumed DNA repair proteins.	556-718	5.05e-30
Prim_Pol	cd04859	Prim_Pol: Primase-polymerase (primpol) domain of the type found in bifunctional replicases ...	116-251	5.82e-11
Prim-Pol	smart00943	Bifunctional DNA primase/polymerase, N-terminal; Members of this family adopt a structure ...	81-241	1.25e-08
Prim-Pol	pfam09250	Bifunctional DNA primase/polymerase, N-terminal; Members of this family adopt a structure ...	67-246	1.38e-08
RadA_SMS_N	cd01121	bacterial RadA DNA repair protein; Sms or bacterial RadA is a DNA repair protein that plays a ...	570-674	7.57e-05
DEXXQc_SF1	cd18043	DEXXQ-box helicase domain of Superfamily 1 helicases; Superfamily 1 (SF1) helicases are ...	560-614	3.10e-04
archRadB	cd01394	archaeal RadB; The archaeal protein RadB shares similarity RadA, the archaeal functional ...	563-676	4.83e-04
radB	PRK09361	DNA repair and recombination protein RadB; Provisional	563-676	2.54e-03
PRK07764	PRK07764	DNA polymerase III subunits gamma and tau; Validated	369-560	8.00e-03

**Blast search parameters**

Data Source: Live blast search RID = X5V0ARAM013  
 User Options: Database: CDSEARCH/ctdd Low complexity filter: no Composition Based Adjustment: yes E-value threshold: 0.01 Maximum number of hits: 500