

Bioinformatic Analysis of NEIL1 in Human

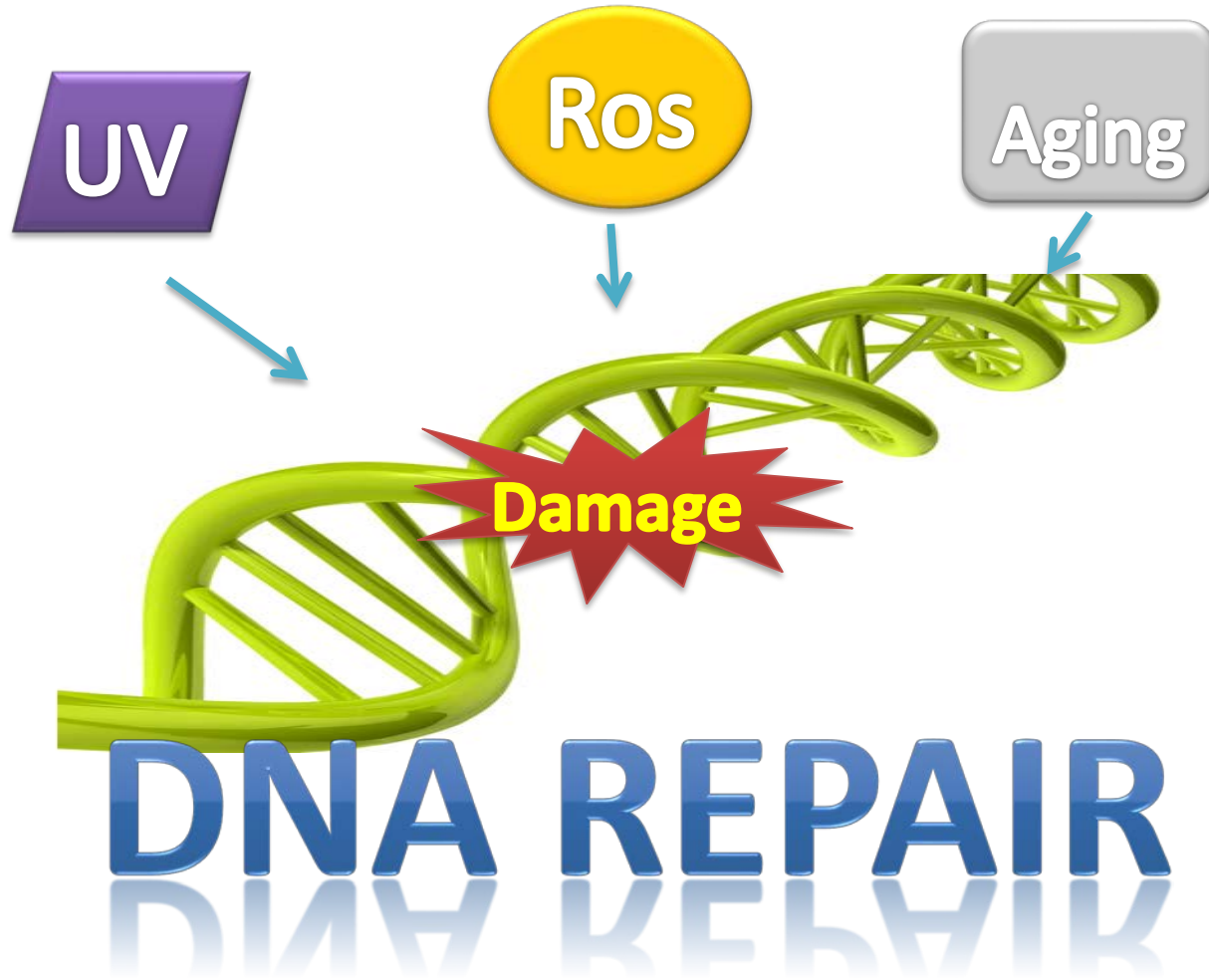
人NEIL 1蛋白的相关生物信息学分析

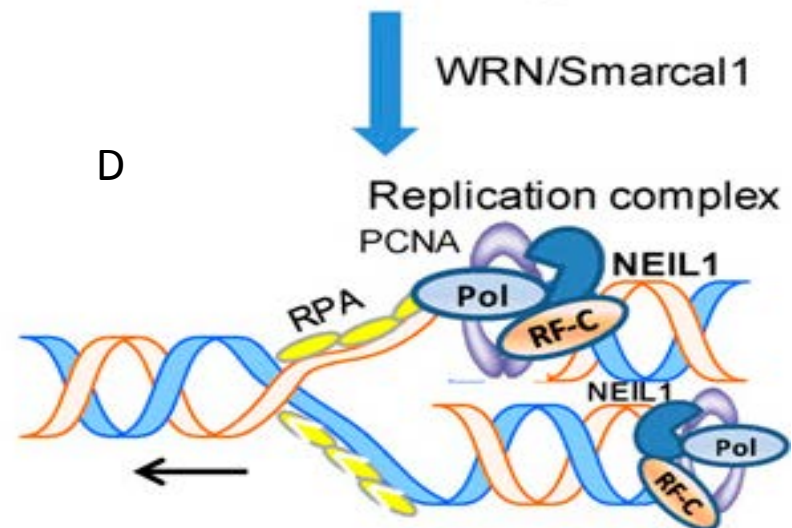
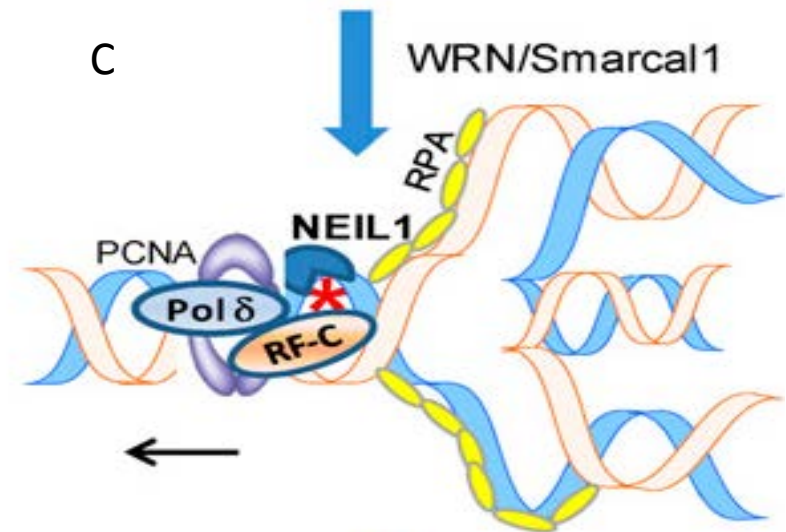
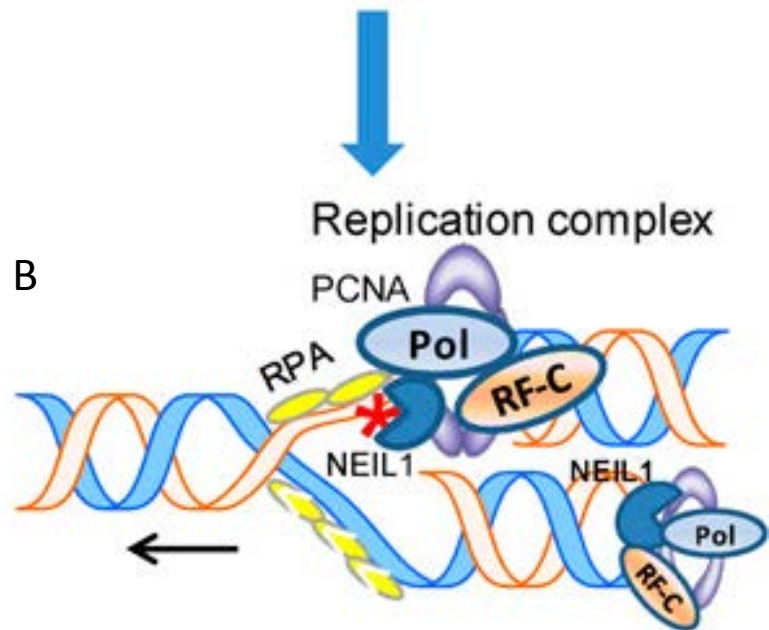
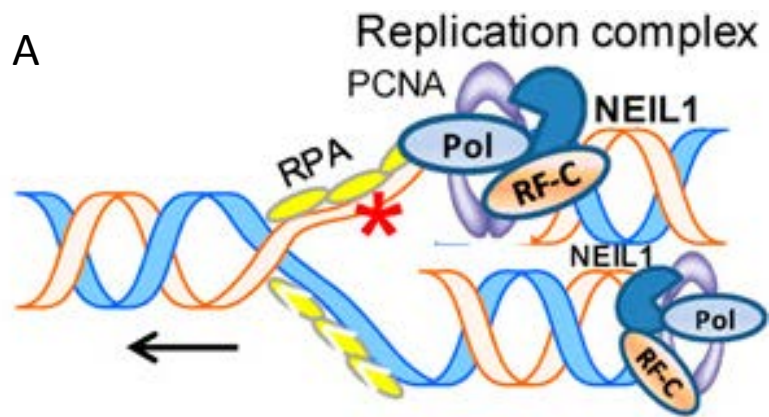
G09: 王奕蓉 田明洁 杨秋华 郑良珺

Outline

- Background
- Sequence analysis
- Structure analysis
- Molecular pathway

NEIL1- new component of BER system





Basic information

- Name: nei Endonuclease VIII-like 1
- Gene ID: 79661
- Sequence length: 389 AA
- Family: FPG family
- Orthologous: NEI (E.coli)
- Paralogous: NEIL2, NEIL3
- Ligand: DNA-binding
- Catalytic activity: Removes damaged bases from DNA, leaving an abasic site.

NEIL1	1	PEGPELHLASQFVNEACRALVFGGCVEKSSVSRNPEV	-PFESSAY	44			
NEIL2	1	PEGPLVRKFHHLVSP-F----	VGQQVVKTGSSKKLQ-PASLQSL	39			
NEIL3	1	VEGPGCTLNGEKIRARVL---	PGQAVTG--VRGSALR-SLQGRAL	39			
END8_	1	PEGPEIRRAADNLEAA----	IKGKPLTDVWFAPPQLK-PYQSQLI	40			
FPG_E	1	PELPEVETSRRGIEPHL---	VGATILHAVVRNGRLRW	41			
	1	* * : : *	: .	45			
NEIL1	45	R-----	ISASARGKELRL	57			
NEIL2	40	WLQ---	DTQVHGKKLFL	53			
NEIL3	40	RLAASTVVVSPQAAALNNDSSQNVLSL	FNGYVYSGVETL	GKELFM	84		
END8_	41	G---QH-----	VTHVETR	GKALLT	56		
FPG_E	42	RLSDQP-----	VLSVQRR	AKYLLL	60		
	46		. . * *	90			
NEIL1	72	-----	LALVFRFGMSGSFQLV	87			
NEIL2	99	GSSRSAELVPQGEDDSEYLERDAPAGDAG	RWLRVSFGLFGSVWVN	143			
NEIL3	90	-----	ALRIHF	GKGFIMIN	104		
END8_	62	-----	LTLYSHN	QLYGVWRVV	77		
FPG_E	66	-----	WIIH	LGMSGSLRIL	80		
	136		: : * :	180			
NEIL1	128	-WQPCRGPCVLQEQYQFRENVLRN--	LADKAFDRPICEALLDQRF	169			
NEIL2	186	SPVVTPTC	DILSE--K----FHRGQALEALGQAQPVCYTL	LLDQRY	224		
NEIL3	147	RMMKEL--DVCSP--EFS--	FLRAESEVKKQKGRMLGDV	LMQNV	185		
END8_	120	PFLQRVGPDVLDP--	NLTPEVVKERLLSPRFRNRQFAGLL	LDQAF	162		
FPG_E	123	NVLTHLGPEPLSD--	DFN--GEYLHQKCAKK-KTAIKPWLMDNKL	162			
	226		. . * * :	270			
NEIL1	170	FNGIGNYLRAEILYRLKIPPF	EKARSVLEALQQHRP	SPELTLSQK	214		
NEIL2	225	FSGLGNI	IKNEALYRAGIHP	LSGVSLSASRREVLV	-----	260	
NEIL3	186	LPGVGNI	IKNEALFDSGLHP	AVKVCQLTDEQ	IHHLM	-----	221
END8_	163	LAGLGN	YL	RVEILWQVGLTGNH	KAKDLNAAQLDALA	-----	198
FPG_E	163	VVGVGNI	YASESLFAAGIHP	DRLASSLSLAECELLA	-----	198	
	271	. * * * * :	: : .	315			



T-coffee

Sequence logo

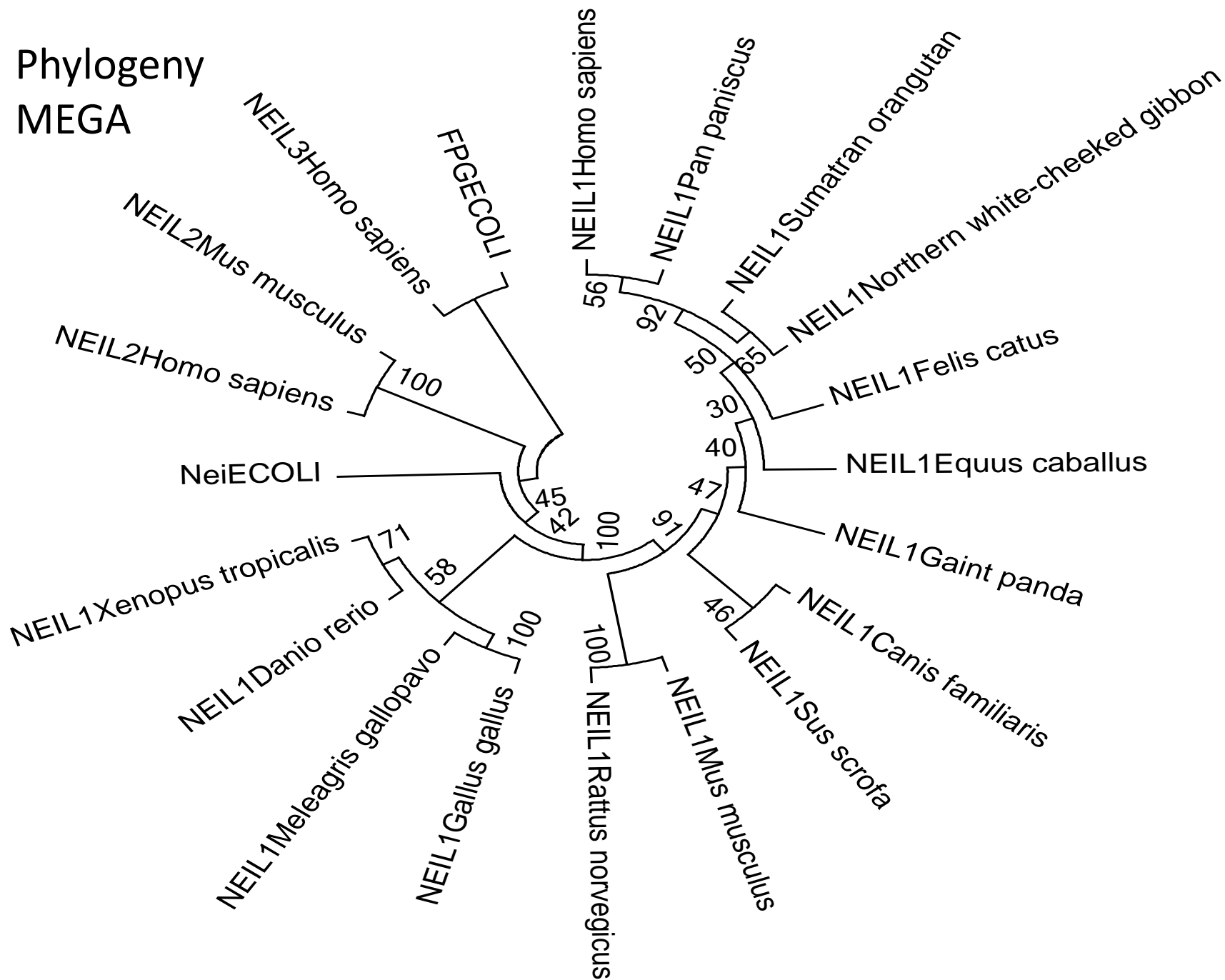
MEME



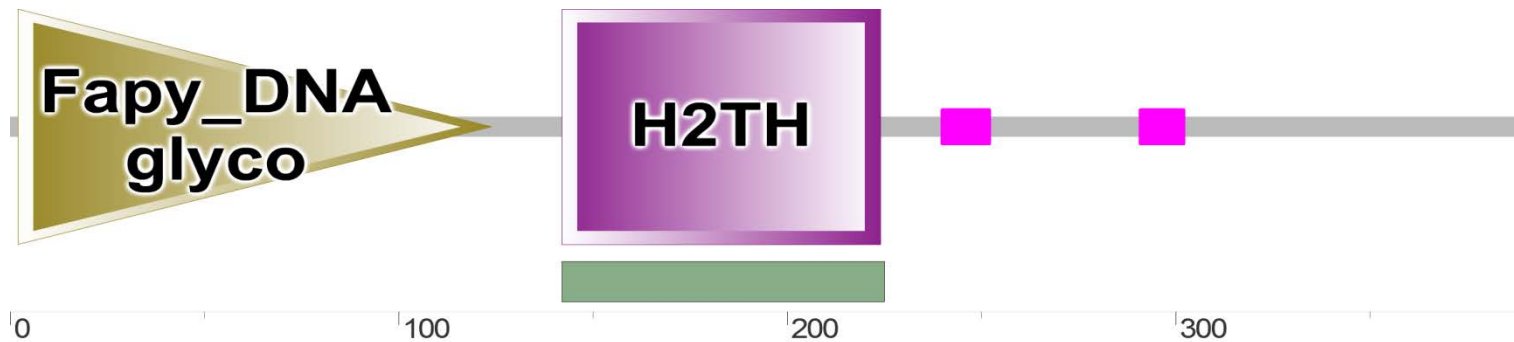
Helix-two turns-helix motif



Phylogeny MEGA



SMART



Fapy_DNA_glyco domain

This is a SMART **Fapy_DNA_glyco** domain ([full annotation](#)).

Position: 2 to 124

E-value: 5.12274901095688e-17 ([HMMER2](#))



H2TH domain

This is a SMART **H2TH** domain ([full annotation](#)).

Position: 142 to 224

E-value: 0.139273012466126 ([HMMER2](#))



 Low complicity region

Expasy GOR

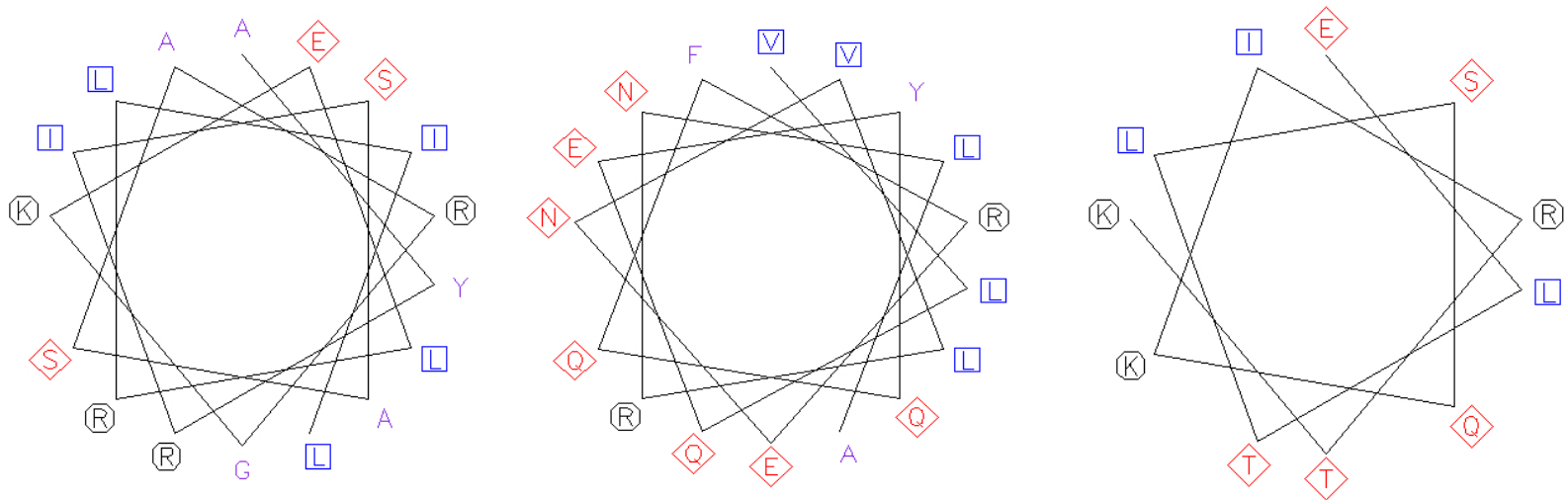
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      10      20      30      40      50      60      70
      |      |      |      |      |      |      |
PEGPELHLASQFVNEACRALVFGGCVEKSSVSRNPEVPPFESSAYRISASARGKELRLILSPLPGAQPQQE
cccccccchhhhhhhhhheeeeecccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
PLALVFRFGMGSFQLVPREELPRHAHLRFYTAPPGPRLALCFVDIRRFGRWDLGGKWQPGRGPCVLQEY
hhhhhhhcccccccceccccchhhhhhecccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
QQFRENVLRLNADKAFDRPICEALLDQRFNIGNYLRAEILYRLKIPPFKARSVLEALQQHRPSPELT
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ccccccccccccchhhhcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
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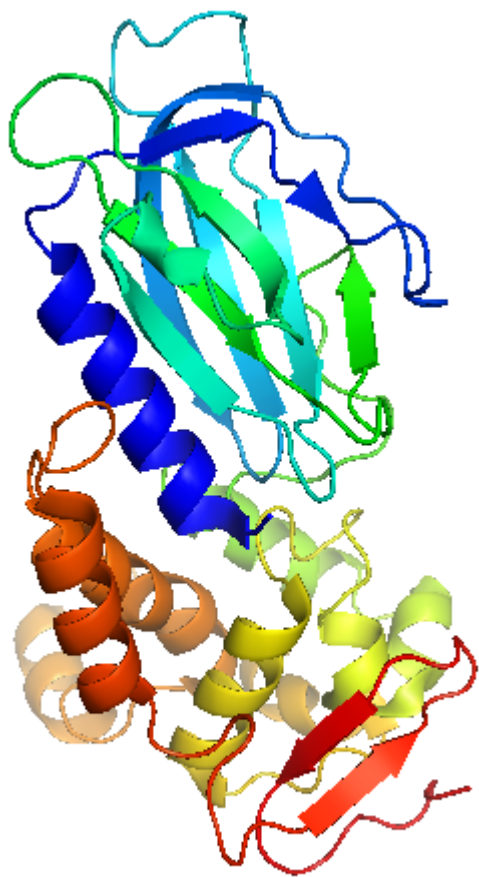
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Sequence length : 389

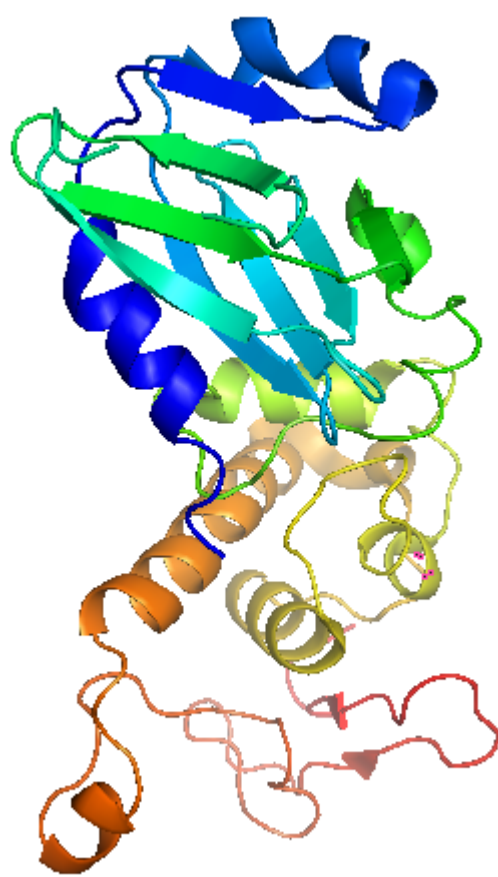
Pepwheels



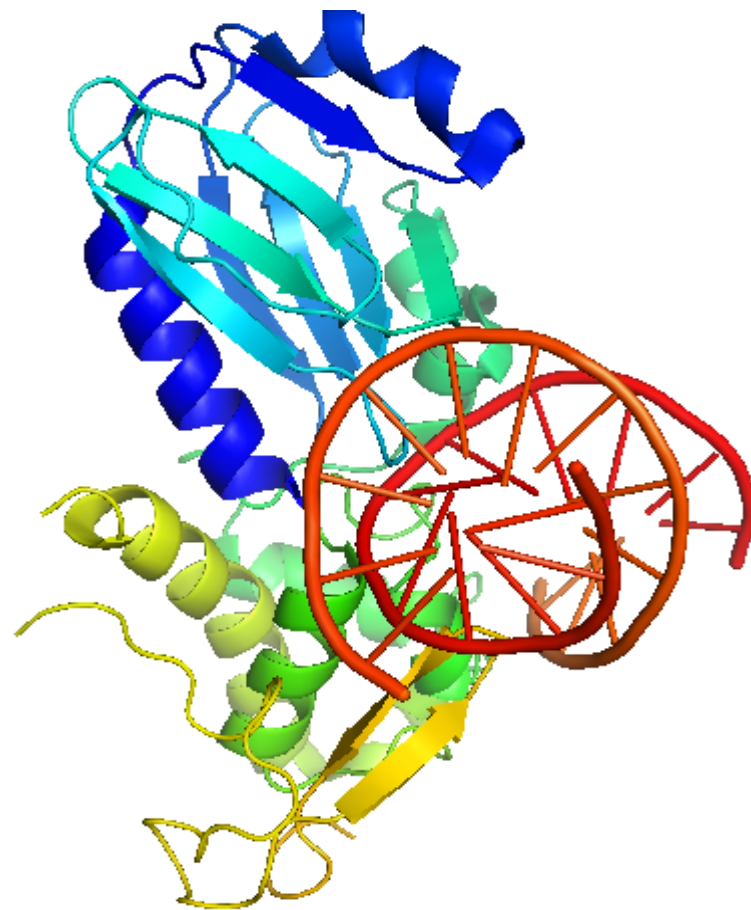
Pymol



NEIL1 (human)
1TDH



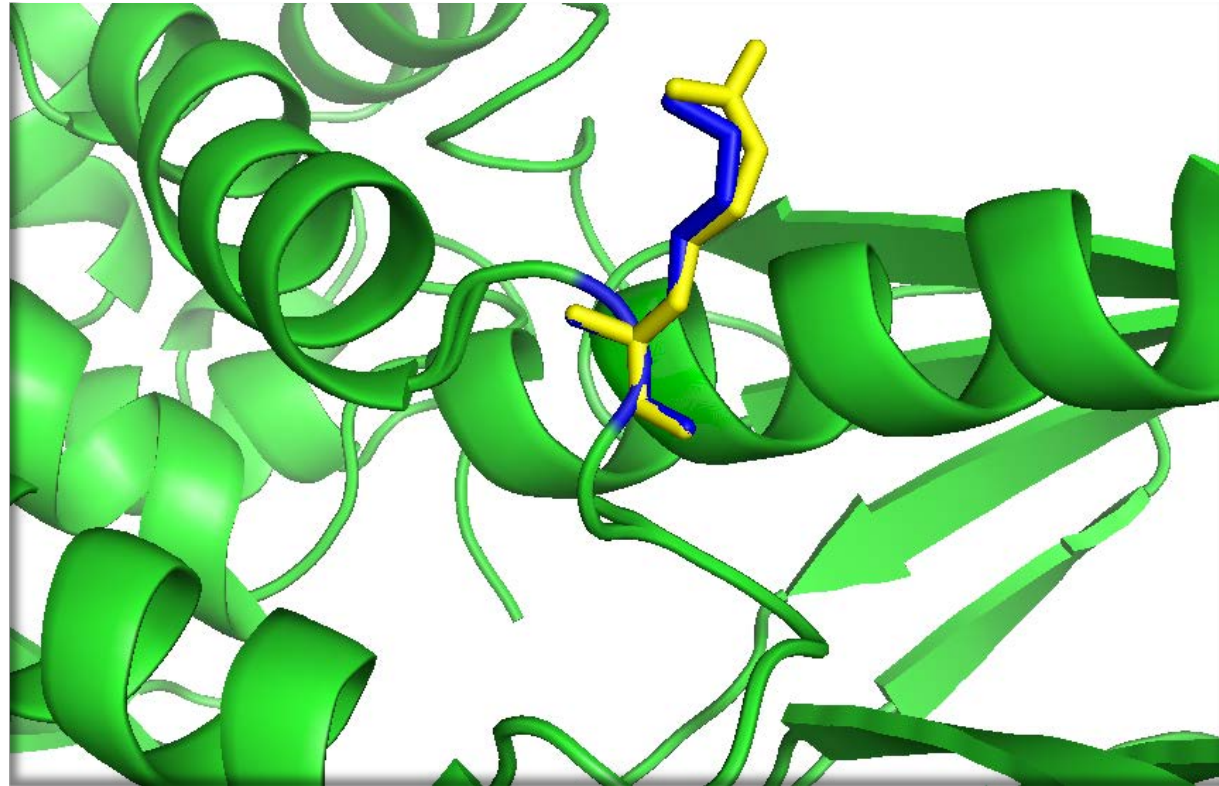
NEI (E.coli)
1Q39



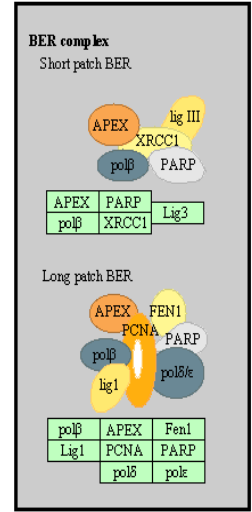
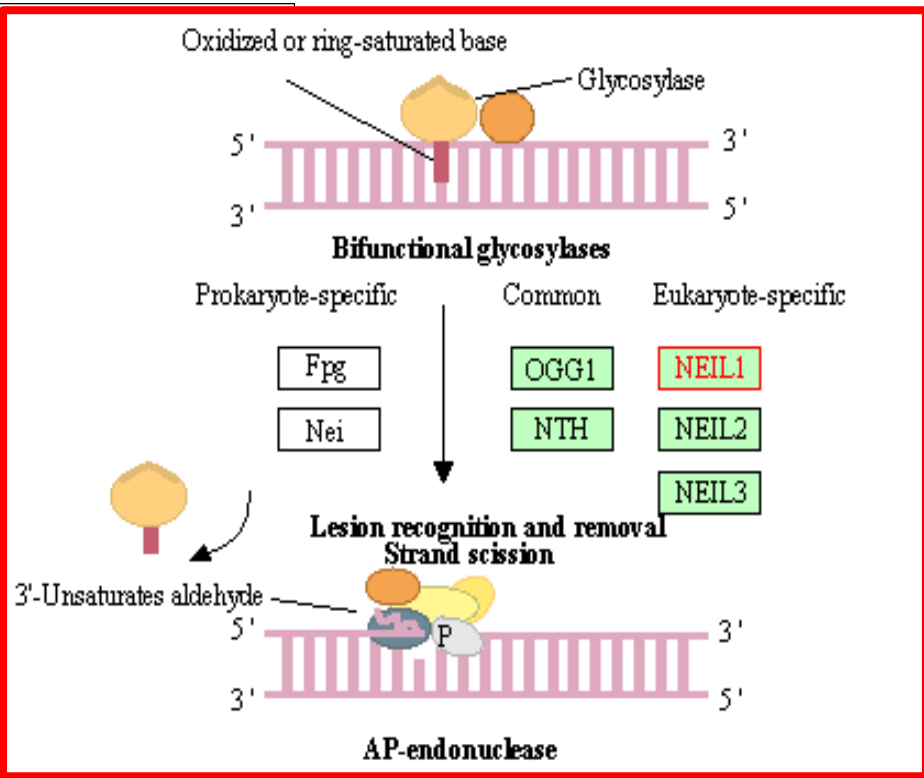
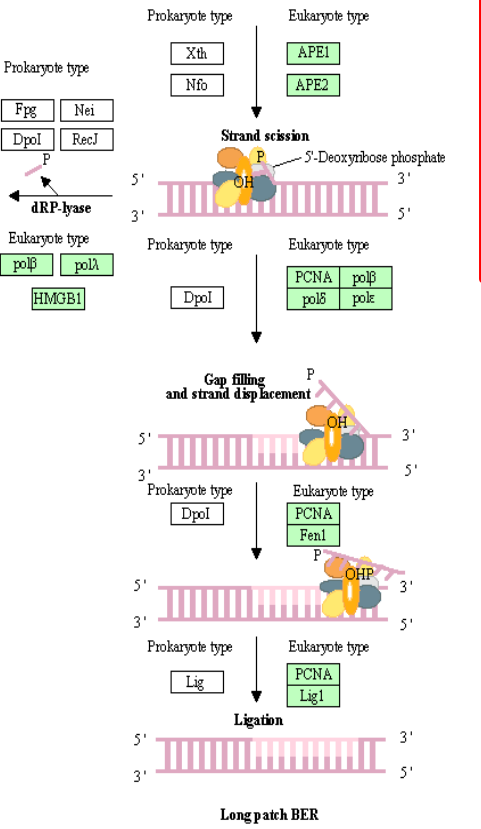
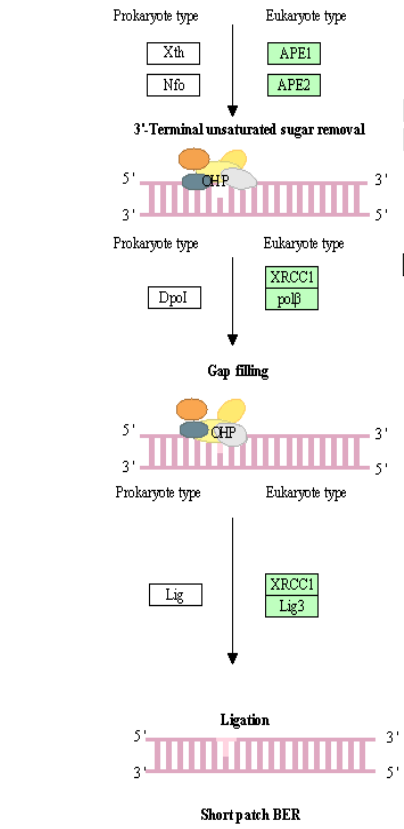
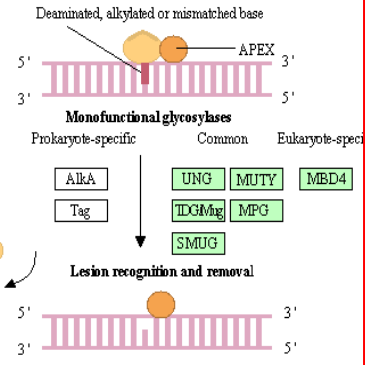
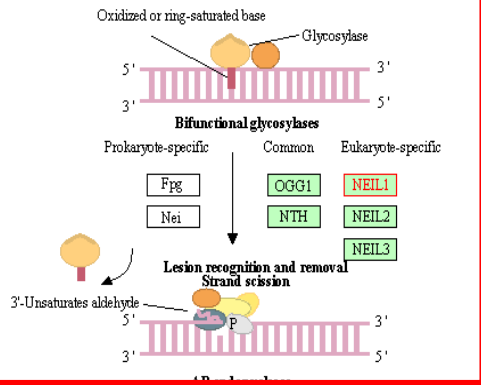
NEI binding with DNA (E.coli)
2EA0

Swiss-Model

RNA editing: K242—R242



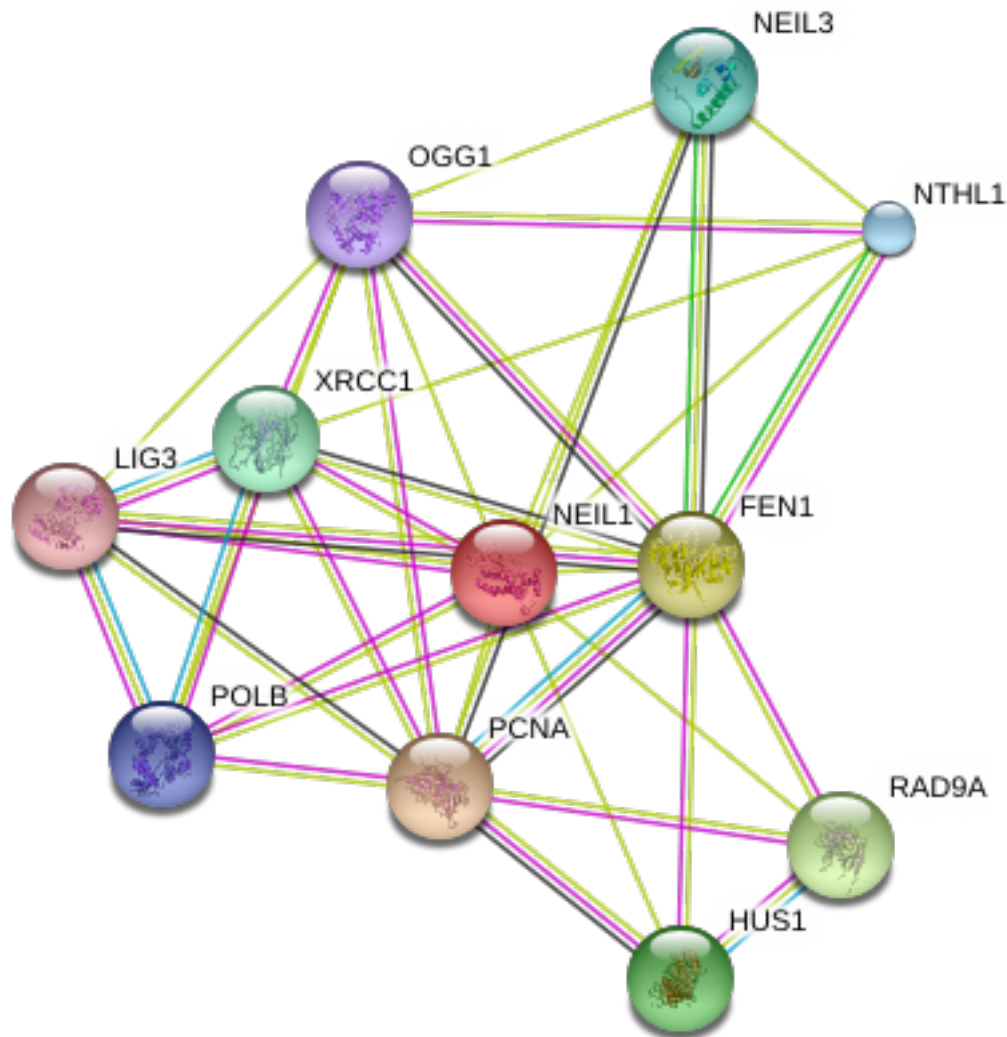
BASE EXCISION REPAIR



KEGG Pathway

Protein-Protein Interaction

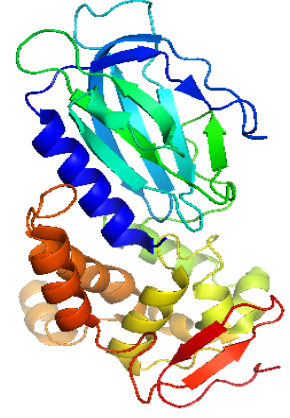
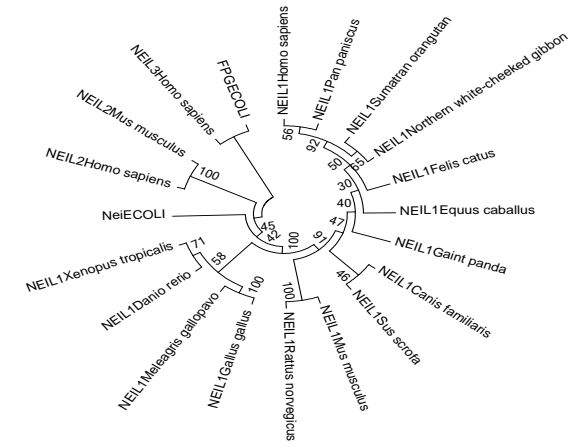
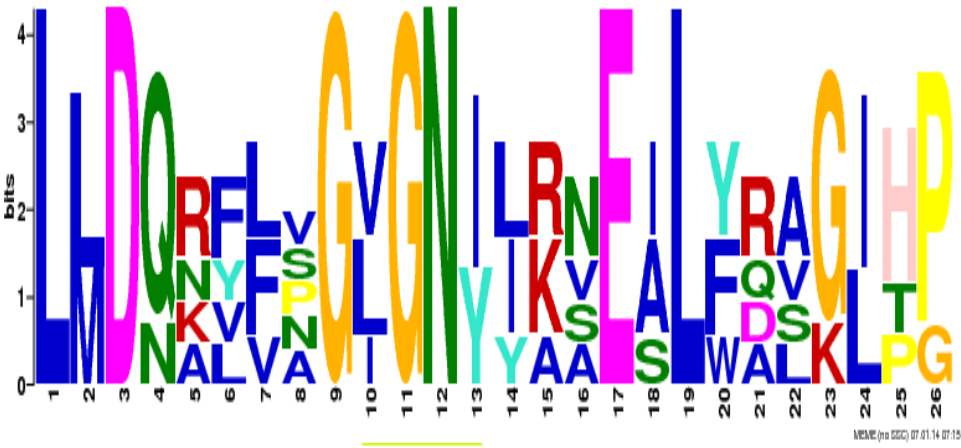
STRING



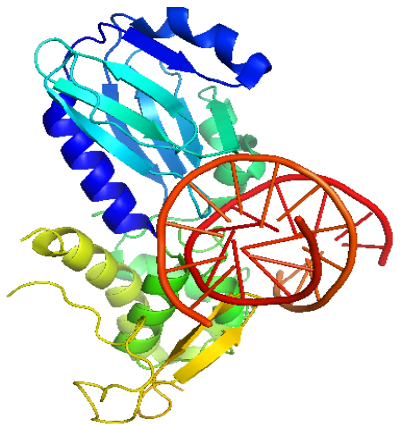
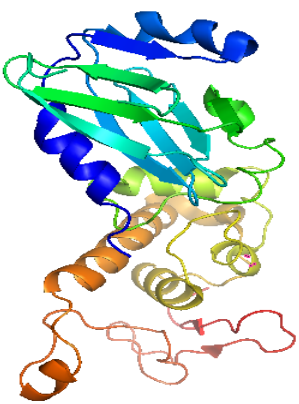
Neighborhood
 Gene Fusion
 Cooccurrence
 Coexpression
 Experiments
 Databases
 Textmining
 [Homology]

Score

●	PCNA						●	0.901
●	FEN1						●	0.878
●	RAD9A						●	0.851
●	HUS1						●	0.842
●	XRCC1					●	●	0.800
●	NEIL3						●	0.794
●	NTHL1						●	0.790
●	POLB					●	●	0.765
●	OGG1						●	0.752
●	LIG3					●	●	0.749



Integrate all clues and make a plan for bench works



NEIL1	128	-WQPGRGPCVLQEQ	QFRENVLRN	--LADKAFDRPICEALLDQRF	169
NEIL2	186	SPVVTPTCDILSE	--K---	FHRGQALEALGQAQPVCYTLLDQRY	224
NEIL3	147	RMMKEL	--DVCSP	--EFS--FLRAESEVKKKQGRMLGDVLMDDQNV	185
END8_E	120	PFLQRVGPDDVLDP	--NLTPEVVKERLLSPFRNRNQFAGLLLDQAF		162
FPG_E	123	NVLTHLGPPEPLSD	--DFN--GEYLHQKCAKK	-KTAIKPWLMDNKI	162
	226				270
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END8_E	163	LAGLGNYLRV EILWQVGLT	GNHKKAKDLNAAQLDALA	-----	198
FPG_E	163	VVGVGNIYASESLFAAGI	HPDRLASSLSLAECCELLA	-----	198
	271				315

Reference

- **Grin IR, Zharkov DO.** Eukaryotic endonuclease VIII-like proteins: new components of the base excision DNA repair system. *Biochemistry (Mosc)*. 2011 Jan;76(1):80-93.
- **Yeo J, Goodman RA, et al.** RNA editing changes the lesion specificity for the DNA repair enzyme NEIL1. *Proc Natl Acad Sci U S A*. 2010 Nov 30;107(48):20715-9.
- **Hegde ML, Hegde PM, et al.** Prereplicative repair of oxidized bases in the human genome is mediated by NEIL1 DNA glycosylase together with replication proteins. *Proc Natl Acad Sci U S A*. 2013 Aug 13;110(33):E3090-9.

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