PolyPhen-2 prediction of functional effects of human nsSNPs

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PolyPhen-2 report for WNV72739.1 K15S

Query

Protein Acc	Position	AA_1	AA_2	Description
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WNV72739.1 15 K S PDC1 [Saccharomyces cerevisiae synthetic construct]

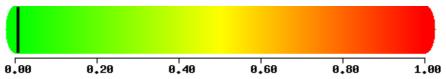
Results

Prediction/Confidence

PolyPhen-2 v2.2.3r406

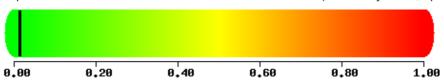
HumDiv

This mutation is predicted to be **BENIGN** with a score of **0.007** (sensitivity: **0.96**; specificity: **0.75**)



HumVar

This mutation is predicted to be **BENIGN** with a score of **0.014** (sensitivity: **0.95**; specificity: **0.53**)



Details

Multiple sequence alignment

UniProtKB/UniRef100 Release 2011 12 (14-Dec-2011)

sp G0WA30#1			MRWAGNANELI
sp A5DIS4#1	MTEITLGRYLFERL S Q-	-LNVNSIFGVPGDFNLSLLDKIYEVD	G M RWAGNANELI
sp UPI000151BD5C#1		-LNVNSIFGVPGDFNLSLLDKIYEVD	
sp G3B6D2#1		-LDVNTVFGLPGDFNLSLLDKIYDVE	
sp E7Q427#1		-VNVNTIFGLPGDFNLSLLDKIYEVD	
sp C4Y6M9#1		-LSVQTIFGLPGDFNLSLLDKIYEVD	
sp G3AGU2#1		-LEVQTIFGL P GDFNLSLLDKIYEVEDVHGH	
sp A3GGL8#1		-LQVQTIFGVPGDFNLSLLDKIYEVEDAHGH	
sp 043106#1		-LQVQTIFGVPGDFNLSLLDKIYEVEDAHGH	
sp Q6FTF3#1		-IHIDTIFGLPGDFNLTLLDKIYEVE	
sp Q6BHI3#1		-VEVSTIFGLPGDFNLTLLDKIYEVE	
sp P83779#1		-LKVDTVFGLPGDFNLALLDKIYEVE	
sp G3AEG2#1		-LEVNTIFGLPGDFNLSLLDKIYEVE	
sp B9WGU5#1	MSEITLGRFFFERL H Q-	-LQVDTVFGLPGDFNLALLDKIYEVE	G M RWAGNANELI
	M CETTI COVECEDI IIO	LIVETTECH BODENI OLI DIVIVETE	CMPLIACHANELI

Shown are 75 amino acids surrounding the mutation position (marked with a black box)

3D Visualization

PDB/DSSP Snapshot 25-May-2021 (178229 Structures)

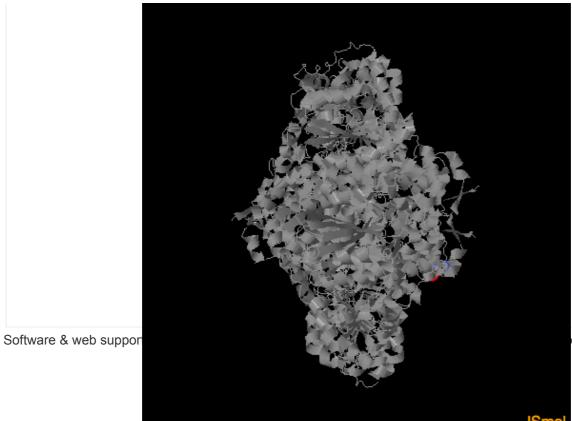
EntryID: 2W93

ChainID: D

Residue: Lys15

Identity: 99.3%

Overlap: 99.8% (562 a



ment: biobyte solutions