



Alignment Window: 1ITU

1ITU Chain_A	(1)	----	DFFRDEAERIMRDS	PVIDG	----	HNDLPWQLDMFNNRLQDERANLTTLAGTHTNIPKLRA	FVGGQFWSVYTPQ	EDT									
1ITU_model_Chain_A	(1)	----	DFFRDEAERIMRDS	PVIDG	----	HNDLPWQLDMFNNRLQDERANLTTLAGTHTNIPKLRA	FVGGQFWSVYTPQ	EDT									
Sec. Struct. Model			~~~~~	~~~~~		~~~~~	~~~~~	~~~~~									
Slvmt Access.			~~~~~	~~~~~		~~~~~	~~~~~	~~~~~									
Crystal Contacts																	
Ligand Contacts																	
Water Contacts																	
B-factors			~~~~~	~~~~~		~~~~~	~~~~~	~~~~~									
Human	(1)	----	MUSGWW	WSLVAV	CTADFFRDEAERIMRDS	PVIDG	----	HNDLPWQLDMFNNRLQDERANLTTLAGTHTNIPKLRA	FVGGQFWSVYTPQ	EDT							
Macaque	(1)	----						MFNNRLQDTRAN	TTTLAGTHTNIPKLRA	FVGGQFWSVYTPQ	EDT						
Cat	(1)	----	MGTSWW	WTLVAV	CTGQDFRDEAERIMRGT	PVIDG	----	HNDLPWQLDMFNNRLQDERANLTTLAGTHTNIPKLRA	FVGGQFWSVYTPQ	EDT							
Horse	(1)	----			MAQGCPERWRQPG	ACGLPNLAFVT	TAPE	HNDLPWQLDMFNNRLQDERANLTTLAGTHTNIPKLRA	FVGGQFWSVYTPQ	EDT							
Rabbit	(1)	----	MWTSWW	WPLVAV	CTADSFLDQAVQILRV	TPVIDG	----	HNDLPWQLDMFNNRLQDERANLTTLAGTHTNIPKLRA	FVGGQFWSVYTPQ	EDT							
Chicken	(1)	----			MDCTRS	LPQEGGNS	GSSTAQNEAC	VSG	----	HNDLPVLRMRFPQNRIS	----	KVNIREINKTHTNLLKLRA	FVGAQFWSVYVLES	A			
Zebrafish	(1)	----	MEWVKILCLV	LVFSPFS	SEADELMDRA	LKLMDET	PLIDG	----	HNDLPWQMRNLFNNQLN	----	DVDLRLNLS	THNIEIKYQRLSAGFNA	FVPD	EDT			
Tetraodon	(1)	----					ALRLMAET	PLIDG	----	HNDLPWQLRKR	FNNQLN	----	AVDLYQLNT	THNIPKLRA	FVKE	RLGAFWSVYTPQ	EDT
Consensus																	

41 46 51 56 61 66 71 76 81 86 91 96 101 106 111 116 121 126 131 136 141 146 151 156 161

DLPWQLDMFNNRLQDERANLTTLAGTHTNIPKLRAQFVGGQFWSVYTPQCDTONKDAVRRTLEQMDVVHRMCRMPETFLVYTSSAGIRQAFREGKVASLIGVEGGHSIDSSLGVLRLALYQLGMRV

ACE ACD



Human_BC

Construct Design

Construct ID	Construct Name	Mutations	N-Term	Construct	C-Term
4871	Human_BC_1_411		1		411
6559	Human_BC_1_411_I40ACE		1		411
6567	Human_BC_1_411_E24A	A	1		411
6697	Human_BC_17_411_I40ACE		17		411
6698	Human_BC_17_385_I40ACE		17		385
6700	Human_BC_17_411_E24A	A	17		411
6701	Human_BC_17_385_E24A	A	17		385

Sequences

- 1ITU_model_Chain_A
 - HeAtoms
 - CIL 452 (CLASTATIN)
 - CIL 451 (CLASTATIN)
 - CZN B 412 (ZINC ION)
 - CZN B 411 (ZINC ION)
 - CZN A 402 (ZINC ION)
 - CZN A 401 (ZINC ION)
 - NAG B 464 (N-ACETYL...)
 - NAG A 463 (N-ACETYL...)
 - NAG B 462 (N-ACETYL...)
 - NAG A 461 (N-ACETYL...)
 - Water Atoms
 - Space Group: P1211
 - Secondary Structures

Residue Information

- Residue: V
- Residue Short Name: TRP
- Residue Long Name: TRYPTOPHAN
- Residue Number: 25
- Original Position: 25
- Align Position: 48
- Conservation: None
- Secondary Structure Model: Right ...
- Solvent Accessibility (%): 7.58
- Crystal Contact: no
- B Factor: 14.68
- Ligand Contacts
 - Atom: CIL 451 Distance: 3.88
 - Atom: CIL 451 Distance: 3.89
- Water Contacts
- Crystal Contacts
- Protein-Protein Contacts
- Atoms