

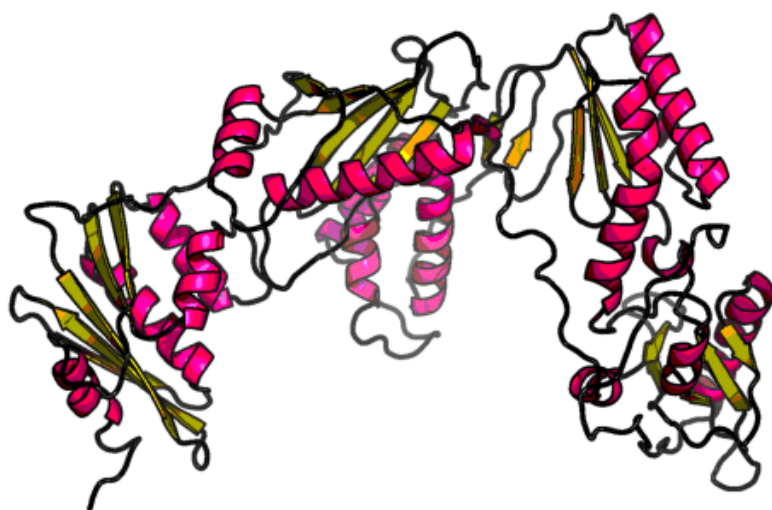
RT1 | rt1

Section I. Input Sequence and Domain Partition ([help](#))

1	11	21	31	41	51	61	71	81	91
PISPIETVPV	KLKPGMDGPK	VKQWPLTEEK	IKALVEICTE	MEKEGKISKI	GPENPYNTPV	FAIKKDKSTK	WRKLVDFREL	NKRTQDFWEV	QLGIPHPAGL
1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111
101	111	121	131	141	151	161	171	181	191
KKKKSVTVLD	VGDAYFSVPL	DEDFRKYTAF	TIPSINNETP	GIRYQYNVLP	QGWKGSPAIF	QSSMTKILEP	FRKQNPDIVI	YQYMDLTVVG	SDLEIGQHRT
1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111
201	211	221	231	241	251	261	271	281	291
KIEELRQHLL	RWGLTTPDKK	HQKEPPFLWM	GYELHPDKWT	VQPIVLPEKD	SWTVNDIQKL	VGKLNWASQI	YPGIKVRQLC	KLLRGTKALT	EVIPLTEEAE
1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111
301	311	321	331	341	351	361	371	381	391

Section II. Summary Prediction Results

The predicted model for the whole sequence. Left click for an image of higher quality; right click to save.

Summary ([help](#))

- The input predicted as **1** domain(s)
- Best template: **3drrA**, p-value **1.96e-15**
- Overall uGDT (GDT): **466 (83)**
- 560 (100%)** residues are modeled
- 6 (1%)** positions predicted as disordered
- Secondary struct: **30% H, 20% E, 48% C**
- Solvent access: **30% E, 37% M, 32% B**

Download

the predicted model as PDB file.

detailed prediction results.

To open .zip files, you may use [7-zip](#) for **Windows** or unzip for **Linux/Unix/MacOS**.

Status

Current status: *Complete*
 Submitted on: *2017-10-22 14:34*
 Scheduled on: *2017-10-22 14:35*
 Finished on: *2017-10-22 15:05*

Section III. Detailed Prediction Results ([you can see each result entry by clicking on it](#))

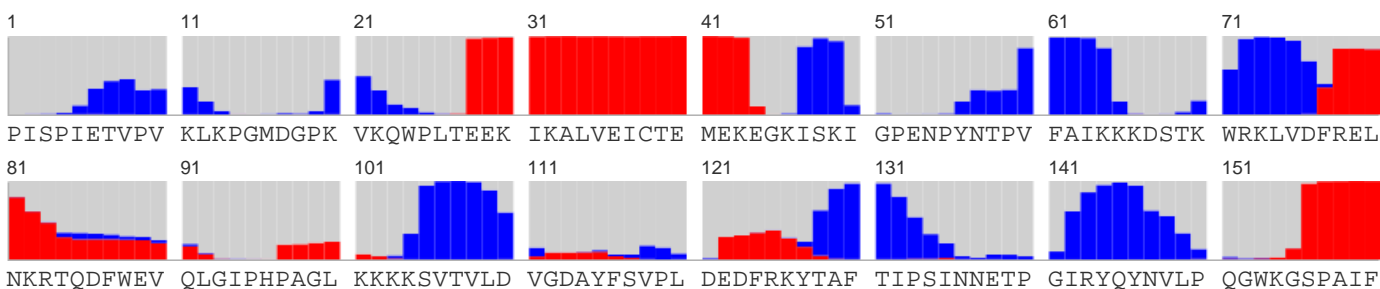
[\[-\]](#) Click to view the predicted structure property for the whole sequence

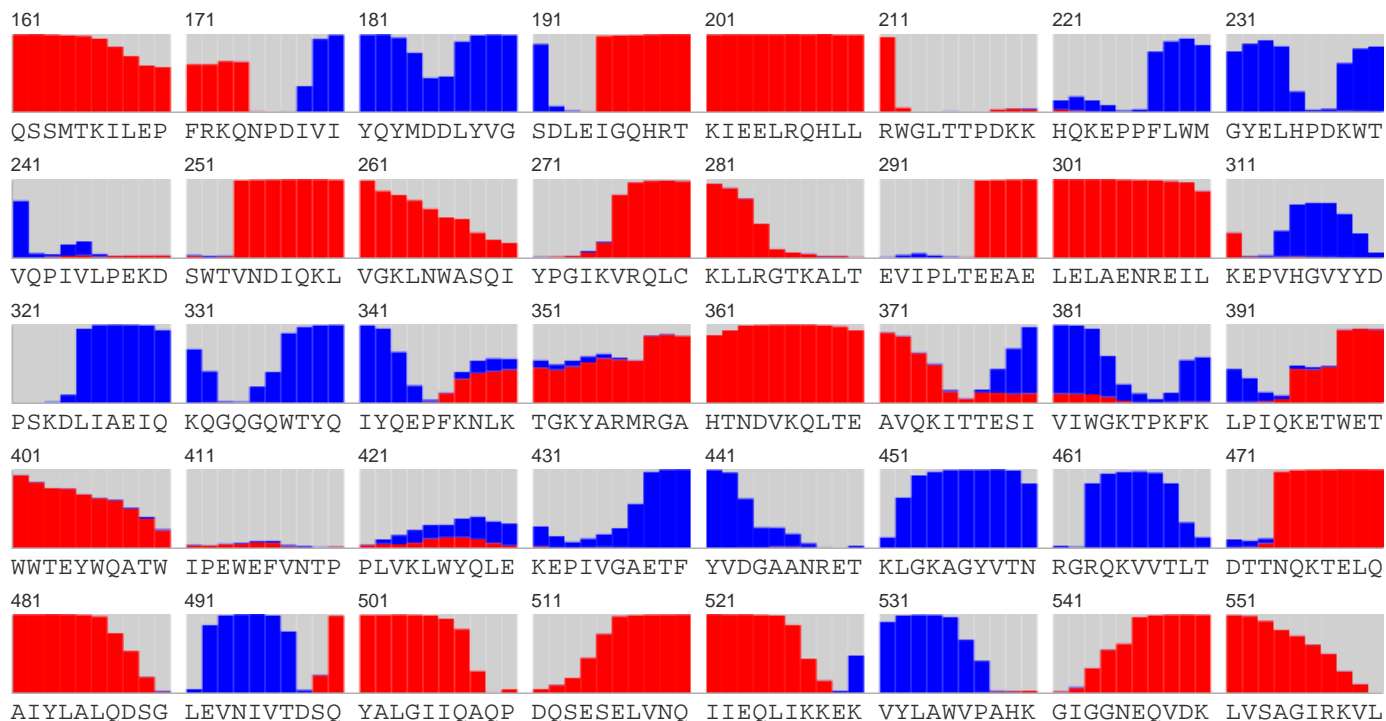
Loading site_media/jsmol/23_core/package.js...

Disorder

Legend for 3-class secondary structure (*hovering over a residue will display the predicted distribution for that residue*)

■ Helix ■ Beta ■ Coil





[-] Click to view 3D model(s) for domain 1 [1, 560] P-value:1.96e-15

View Alternative Model

Template: [3drr:A](#)

Rank: 1 P-value: 1.96e-15 uGDT(GDT): 466(83) uSeqId(SeqId): 556(99) Score: 484

Jsmol viewer quick guide

- Left-click+drag to rotate the structure.
- Use the middle-scroller to zoom.
- Right-click the structure for more options.
- Hover over a target residue in the sequence alignment box to see it highlighted in the structure.
- Visit the [Jmol mouse manual wiki](#)

Rotation

- spin on/off
- spin on/off
- fast
- slow
- fast
- slow

Coloring

- color AAs
- color SSs
- color AAs
- color SSs

Display

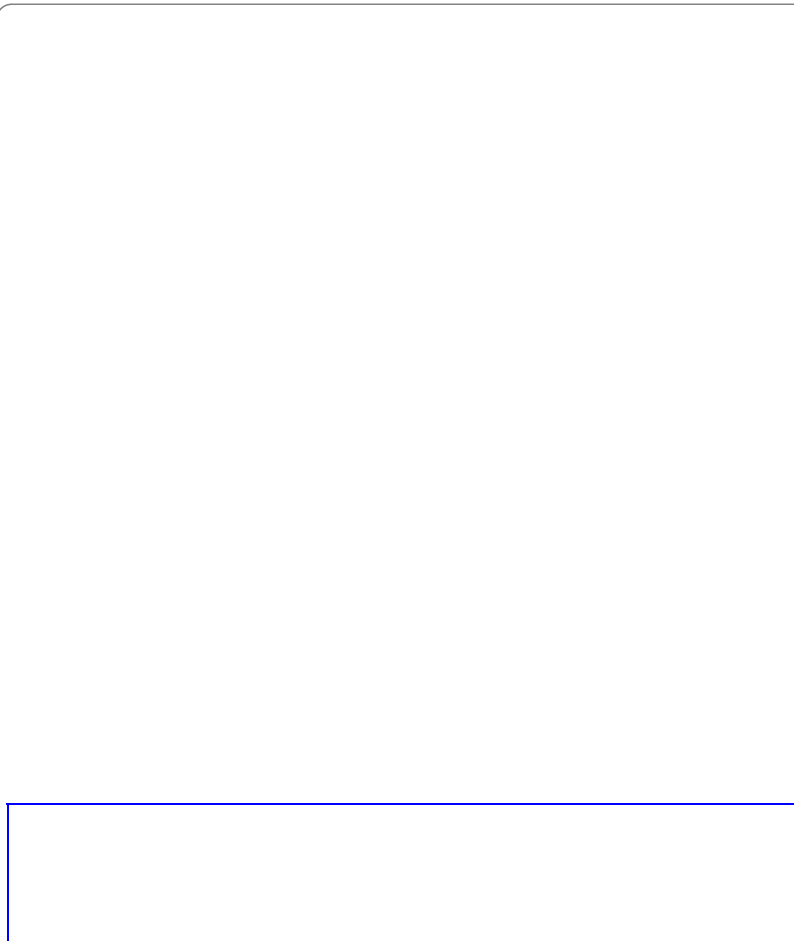
- side chain
- back bone
- cartoon
- side chain
- back bone
- cartoon

Zoom

Show Quality

- low
- high low
- high

Save





Click to see help for this sequence alignment box. The sequences are arranged in the order of query, 3drrA

G	10	20	30	40	50	60		
-	PISPIETVP	VKLKPGMDGP	KVKQWPLTEE	KIKALVEICT	EMEKEGKISK	IGPENPYNTP	VFAIKKDKST	
S	PISPIETVP	VKLKPGMDGP	KVKQWPLTEE	KIKALVEICT	EMEKEGKISK	IGPENPYNTP	VFAIKKDKST	
-	000000000	000000000	000000000	000000000	000000000	000000000	000000000	
70	80	90	100	110	120	130		
K	WRKLVDFRE	LNKRTQDFWE	VQLGIPHPAG	LKKKKSVTVL	DVGDAYFSVP	LDEDFRKYTA	FTIPSINNET	
K	WRKLVDFRE	LNKRTQDFWE	VQLGIPHPAG	LKKKKSVTVL	DVGDAYFSVP	LDEDFRKYTA	FTIPSINNET	
0	000000000	000000000	000000000	000000000	000000000	000000000	000000000	
140	150	160	170	180	190	200		
P	GIRYQYNVL	PQGWKGSPAIF	QSSMTKILE	PFRKQNPDI	IYQYMDDL	YVGS	DLEIGQHR	TKIEELRQHL
P	GIRYQYNVL	PQGWKGSPAIF	QSSMTKILE	PFRKQNPDI	ICQYMDDL	YVGS	DLEIGQHR	TKIEELRQHL
0	000000000	000000000	000000000	000000000	000000000	000000000	000000000	
210	220	230	240	250	260	270		
L	RWGLTTPDK	KHQKEPPFLW	MGYELHPDKW	TVQP	IVLPEK	DSWTVNDI	QKLVGKLNWASQ	IYPGIKVRQL
L	RWGLTTPDK	KHQKEPPFLW	MGYELHPDKW	TVQP	IVLPEK	DSWTVNDI	QKLVGKLNWASQ	IYPGIKVRQL
0	000000000	000000000	000000000	000000000	000000000	000000000	000000000	
280	290	300	310	320	330	340		
C	KLLRGT	KALTEVIPLTEEA	ELELAENREI	LKEPVHGVY	YDPSKDLIAEI	QKQGQGW	TYQIYQEPFKNL	
C	KLLRGT	KALTEVIPLTEEA	ELELAENREI	LKEPVHGVY	YDPSKDLIAEI	QKQGQGW	TYQIYQEPFKNL	

Please cite the following server and method papers:

1. Morten Källberg, Haipeng Wang, Sheng Wang, Jian Peng, Zhiyong Wang, Hui Lu, and Jinbo Xu. [Template-based protein structure modeling using the RaptorX web server. Nature Protocols 7, 1511-1522, 2012.](#)
2. Jianzhu Ma, Sheng Wang, Feng Zhao, and Jinbo Xu. [Protein threading using context-specific alignment potential. Bioinformatics \(Proceedings of ISMB 2013\), Vol. 29, Issue 13, pp. i257-i265.](#)
3. Jian Peng and Jinbo Xu. [A multiple-template approach to protein threading. PROTEINS, 2011 Jun;79\(6\):1930-9. doi: 10.1002/prot.23016. Epub 2011 Apr 4.](#)
4. Jian Peng and Jinbo Xu. [RaptorX: exploiting structure information for protein alignment by statistical inference. PROTEINS, 2011, Vol 79, Issue S10, pp. 161-171.](#)