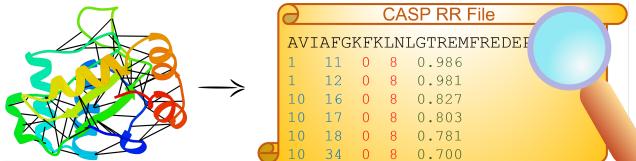


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Protein Contact Evaluation

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Section I Summary [job-dir](#)

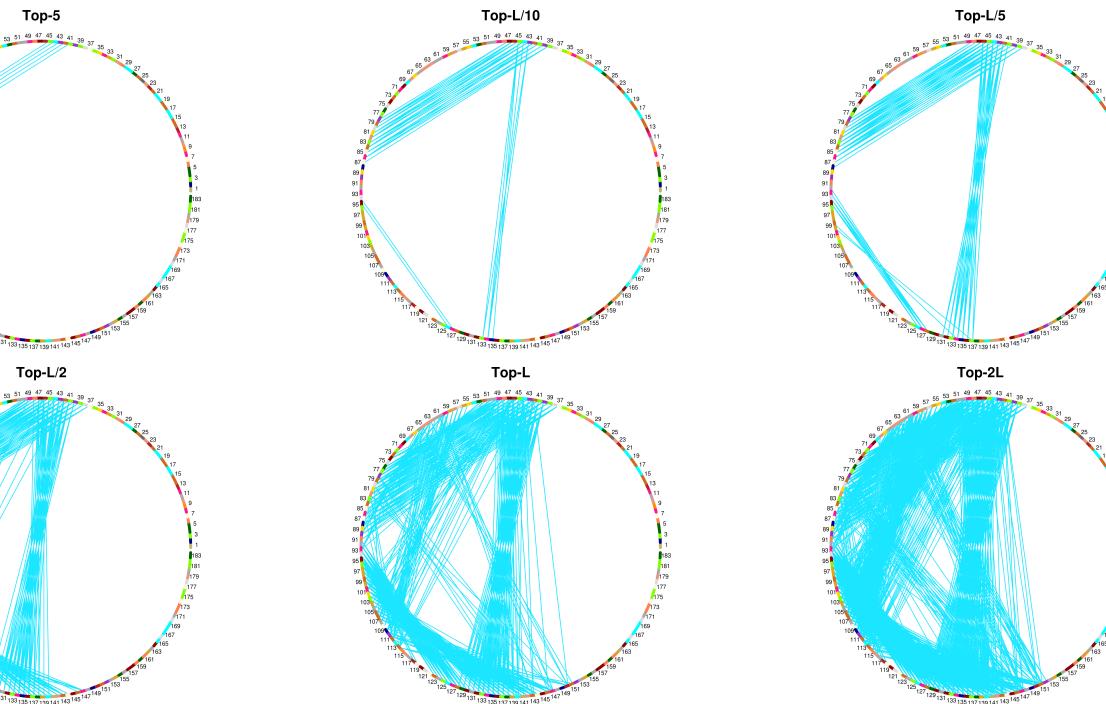
RR Input 866.rr.rtff
 PDB Input 5uw2.pdb [computed RR file](#)
 Sequence Length RR - 183 , Native - 152 [sequence comparison!](#)
 Contact Type Long-Range contacts with C_β atoms within 8 Å with minimum 24 residues sequence separation

Section II Contact Count [see description](#)

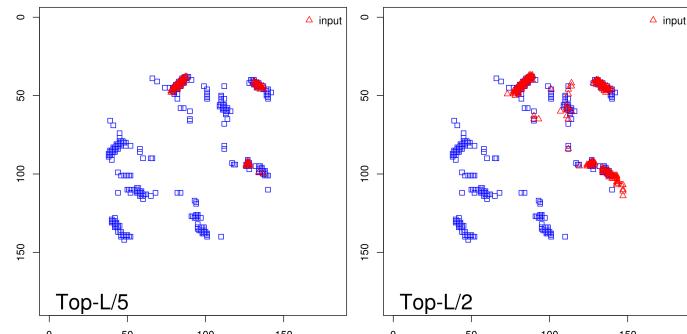
RR-File	Long-Range Contacts			L (= 332) from Native PDB (ignoring gaps)								
	Total	Not in Native	Remaining Total	Short-Range	Medium-Range	Long-Range	5	L/10	L/5	L/2	L	2L
all	15931	10036	4071	-	-	4071(100%)	5	33	66	166	332	664

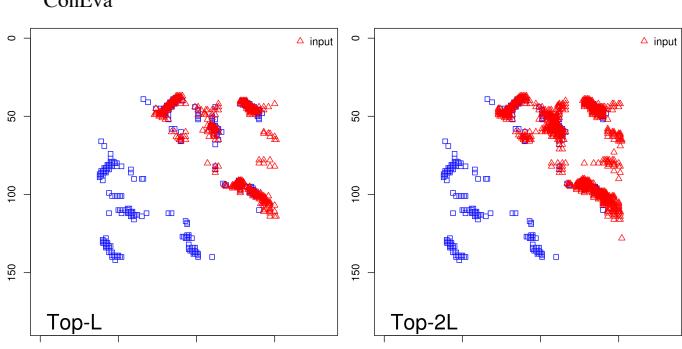
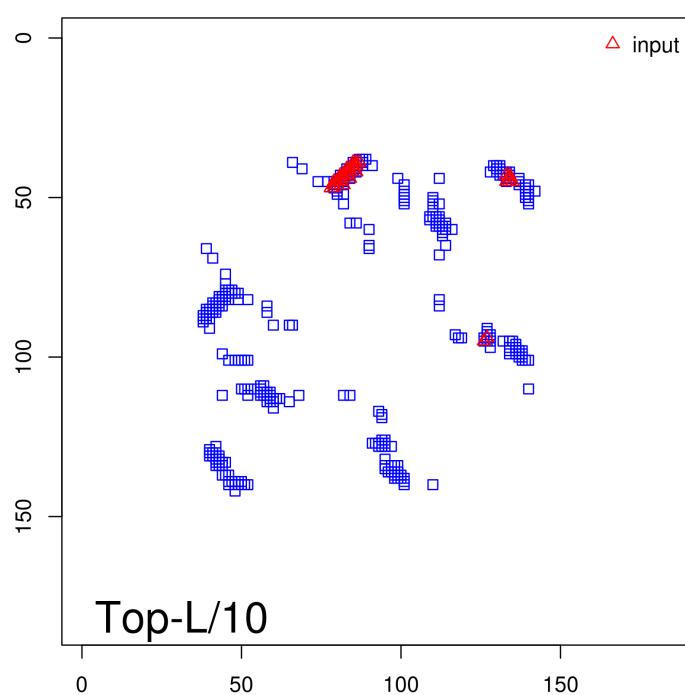
[How to visualize these contacts in UCSF Chimera?](#)

Section III Chord Diagrams [see description](#)



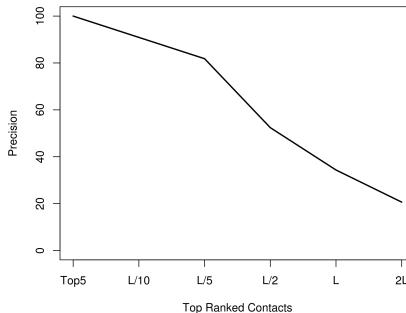
Section IV Contact Maps (with native in blue background)



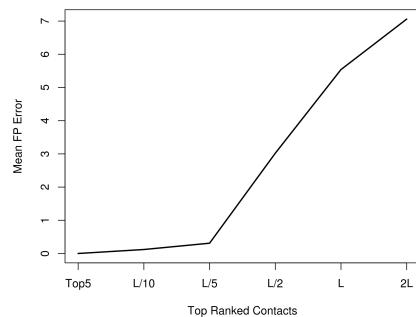


Section V Precision [see description](#)

RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
all	100.00	90.91	81.82	52.41	34.34	20.63



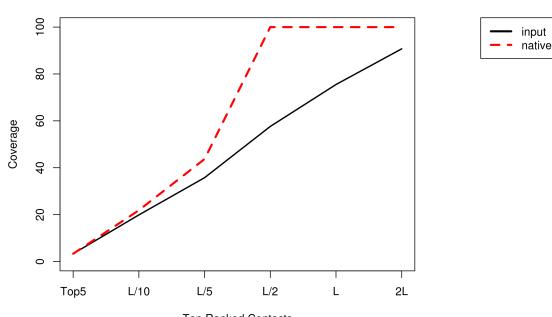
Section VI Mean False Positive Error [see description](#)



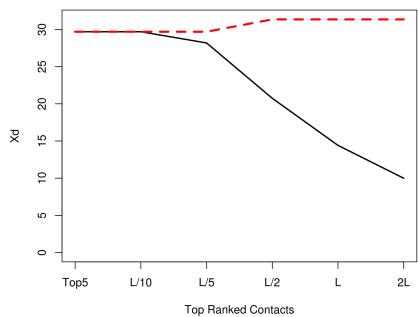
RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
all	0.00	0.12	0.31	3.02	5.54	7.06

Section VII Coverage [see description](#)

RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
input	3.31	19.87	35.76	57.62	75.50	90.73
native	3.31	21.85	43.71	100.00	100.00	100.00



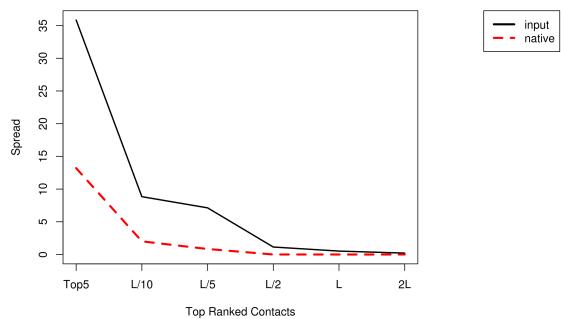
Section VIII X_d (Distance distribution) [see description](#)



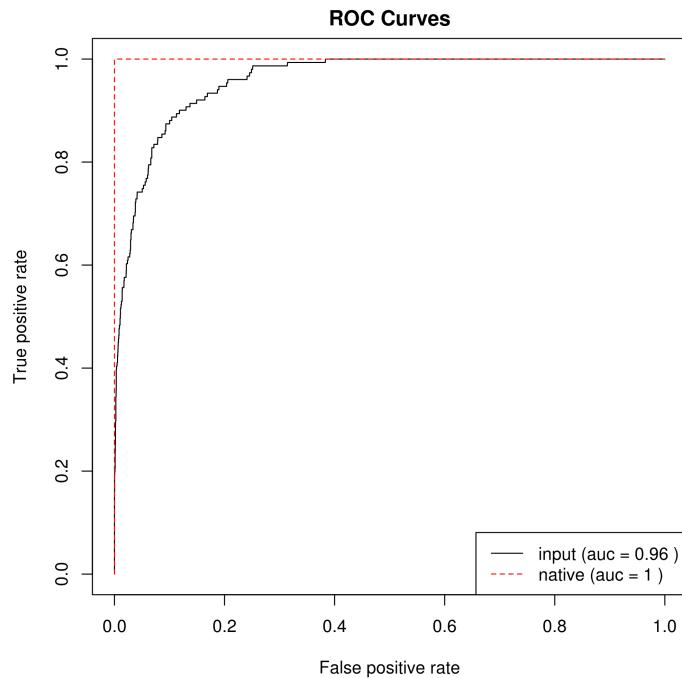
RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
input	29.69	29.69	28.18	20.74	14.41	9.99
native	29.69	29.69	29.69	31.35	31.35	31.35

Section IX Spread [see description](#)

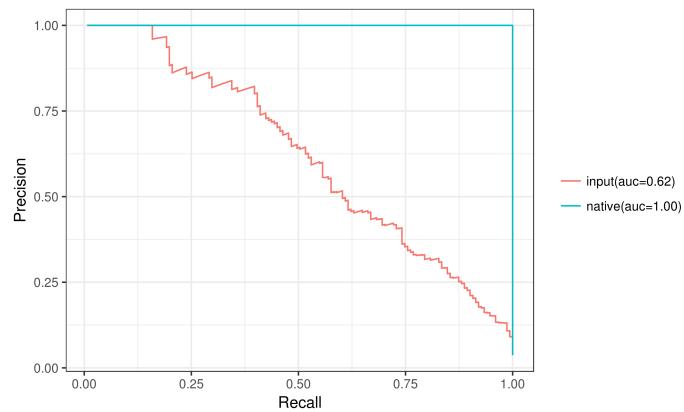
RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
input	35.84	8.84	7.13	1.14	0.52	0.21
native	13.20	2.01	0.84	0.00	0.00	0.00



Section X ROC Curves and AUC [see description](#)



Section XI Precision-Recall Curves and AUC-PR [see description](#)



Section XII Matthew's Correlation Coefficient (MCC) [see description](#)

RR-File	TP	FP	TN	FN	MCC
input	50	10	3910	101	0.52
native	151	0	3920	0	1.00

Section XIII Coordination Numbers [see description](#)

[Top-5](#)

[Top-L/10](#)

[Top-L/5](#)

[Top-L/2](#)

[Top-L](#)

[Top-2L](#)

```

      10          20          30          40          50          60          70          80          90          100
      |          |          |          |          |          |          |          |          |
MQTKKNEIWVGIFLLAALLAALFVCLKAANVTSIRTEPTYTLYATFDNIGGLKARSPVVSIGGVVVGRVADITLDPKTYLPRVTLEIEQRYNHIPDTSSLS [sequence]
-----56*****54598***9*5*6-21-2-65345*7*6*485*567**8*****8 [input: 664 pairs 109 residues]
-----3577*88873554351--4354411--22-11---1--1-3537364523132135613452 [native: 151 pairs 78 residues]

      110         120         130         140         150         160         170         180
      |          |          |          |          |          |          |          |
IRTSGLLGEQYLALNVGFEDPELGTAILKGDTIQDTKSAMVLEDLIGQFLYGSKGDDNKNSGDAPAAAPGNNETTEPVGTTK [sequence]
*****5*29123---55588*****3**2-**3----- [input: 664 pairs 109 residues]
9-----264944-1111----255134347146468-1----- [native: 151 pairs 78 residues]

```