

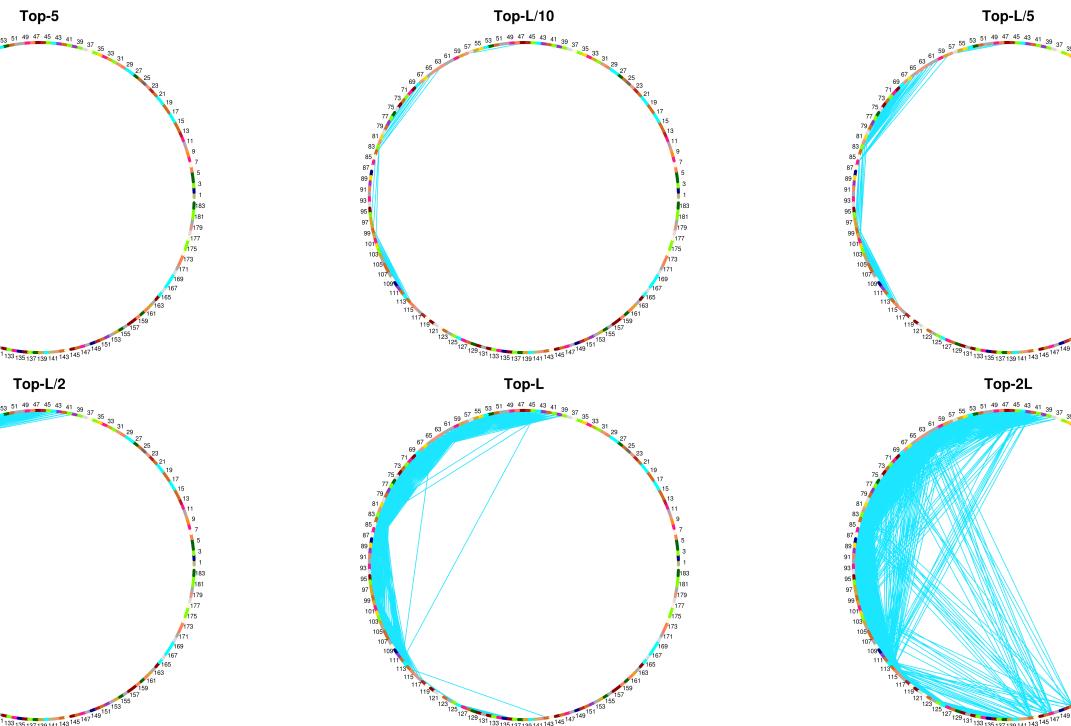
**Section I** Summary [job-dir](#)

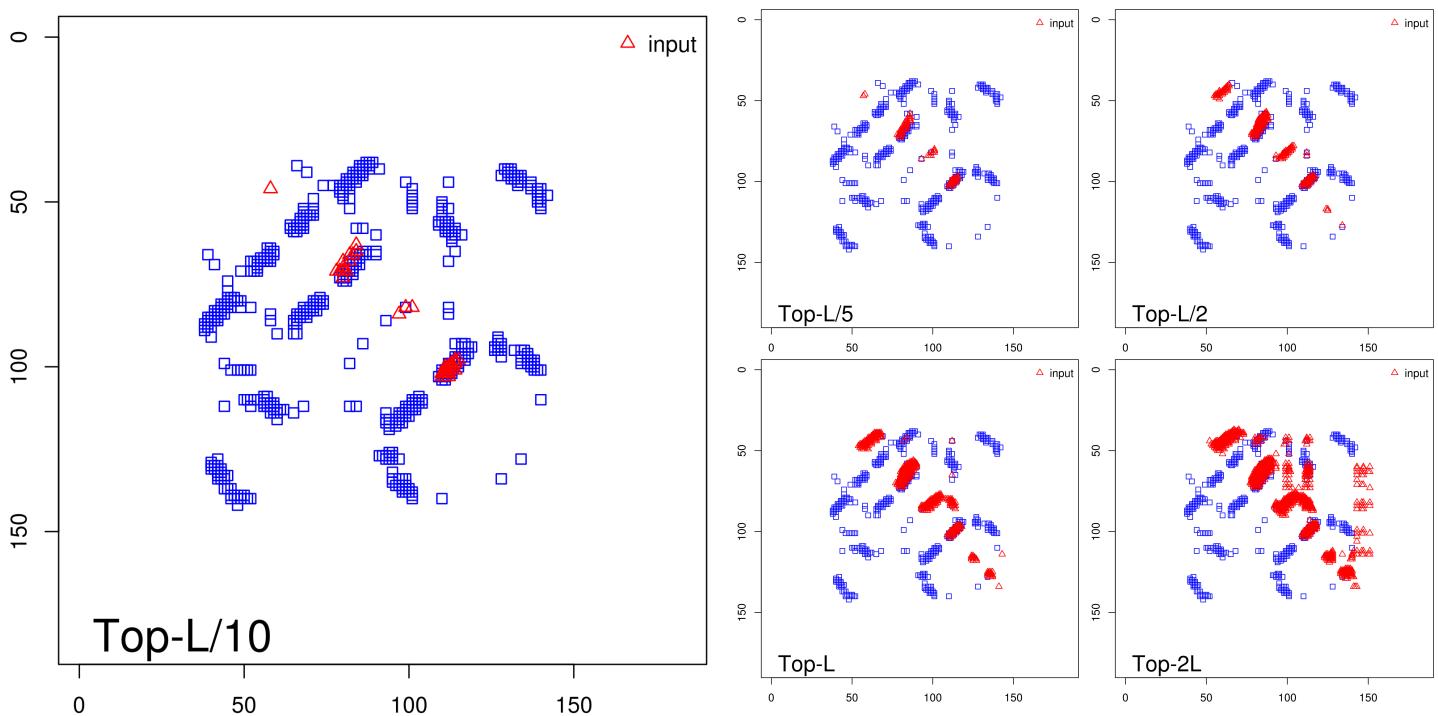
RR Input contact_map_T0866.txt
 PDB Input T0866_5uw2.pdb [computed RR file](#)
 Sequence Length RR - 183 , Native - 152 [sequence comparison!](#)
 Contact Type ALL contacts with C β atoms within 8 Å with minimum 6 residues sequence separation

Section II Contact Count [see description](#)

RR-File	ALL 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	15576	9890	5686	505 (9%)	1110 (20%)	4071 (72%)	5	33	66	166	332	664

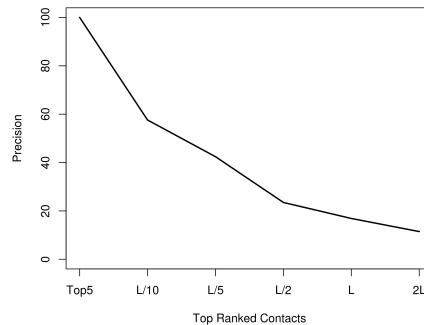
[How to visualize these contacts in UCSF Chimera?](#)

Section III Chord Diagrams [see description](#)**Section IV** Contact Maps (with native in blue background)

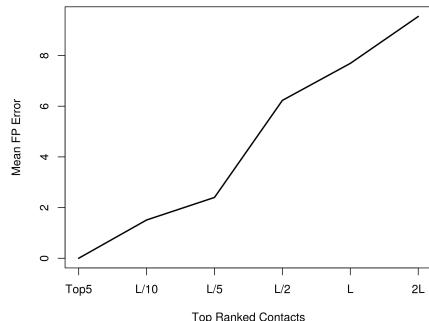


Section V Precision [see description](#)

RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
all	100.00	57.58	42.42	23.49	16.87	11.45



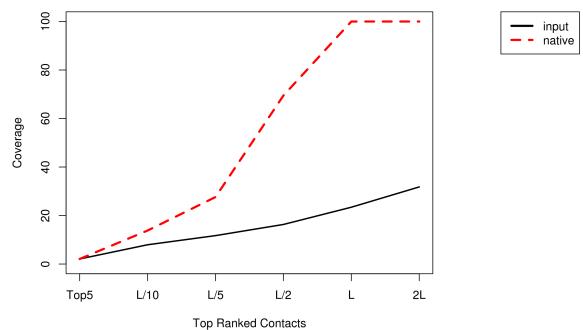
Section VI Mean False Positive Error [see description](#)



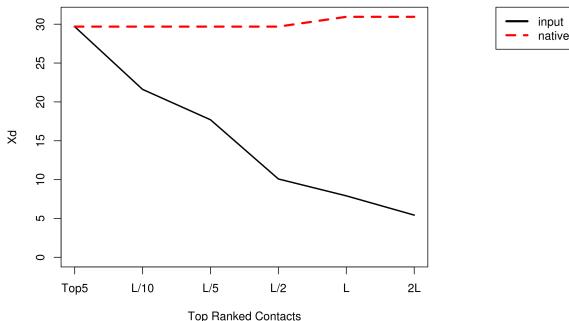
RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
all	0.00	1.51	2.40	6.23	7.69	9.54

Section VII Coverage [see description](#)

RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
input	2.09	7.95	11.72	16.32	23.43	31.80
native	2.09	13.81	27.62	69.46	100.00	100.00

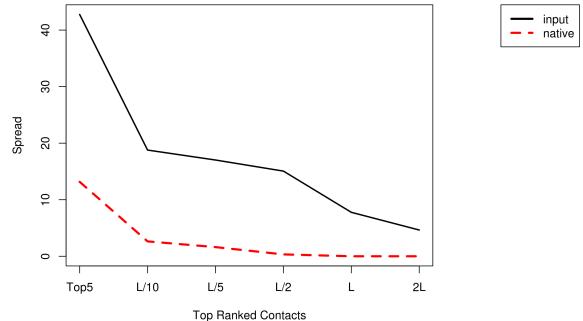


Section VIII X_d (Distance distribution) [see description](#)

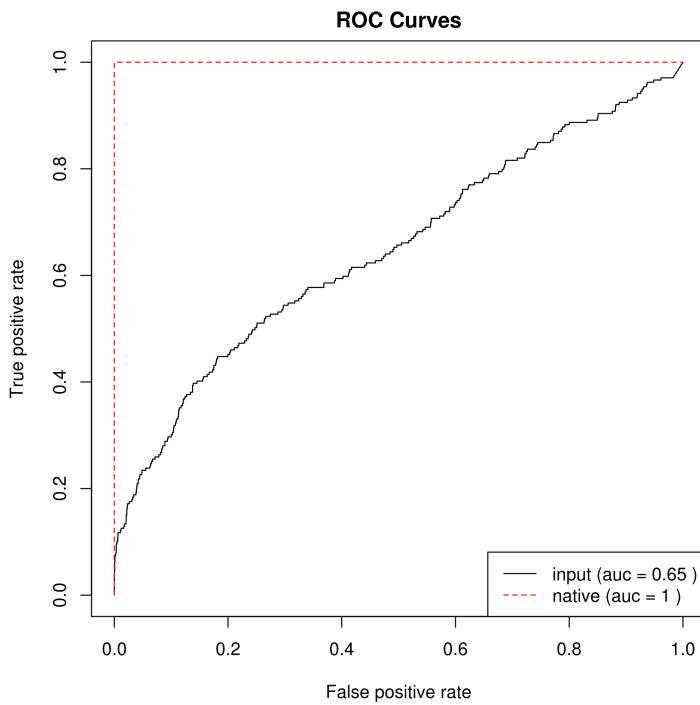


RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
input	29.69	21.61	17.70	10.08	7.91	5.43
native	29.69	29.69	29.69	29.69	30.95	30.95

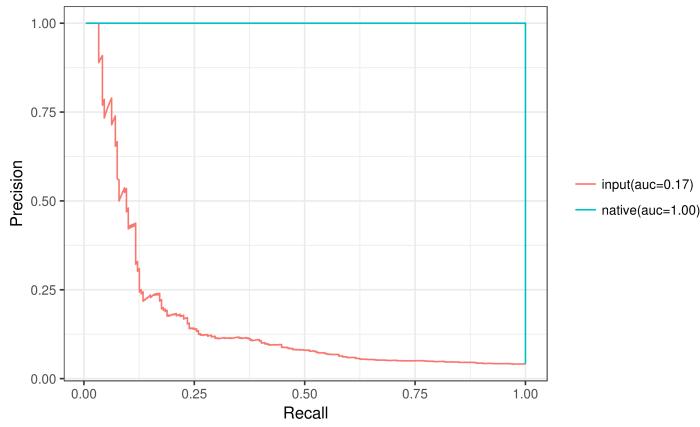
Section IX Spread [see description](#)



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	54	257	5294	185	0.16
native	239	0	5551	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
 | | | | | | | | |
 MQTKKNEIWVGIFLLAALLAALFVCLKAANVTSIRTEPTYTLYATFDNIGGLKARSPVSIIGGVVVGRVADITLDPKTYLPRVTLEIEQRYNHIPDTSSLS [sequence]
 -----25***8*****9662-4127*****6*-15*****22*59***** [input: 664 pairs 102 residues]

-----3577*888735643734267*6411-2696*538333--1-497*8*78431321676377*5 [native: 239 pairs 90 residues]

110 120 130 140 150 160 170 180

| | | | | | | |

IRTSGLLGEQYLALNVGFEDPELGTAILKDGDTIQDTKSAMVLEDLIGQFLYGSKGDDNKNSGDAPAAAPGNNETTEPVGTTK [sequence]

655647**81---6****2---3857757841---9*---28----- [input: 664 pairs 102 residues]

*432---3*8*8844521----256134348146468-1----- [native: 239 pairs 90 residues]