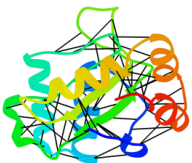


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Protein Contact Evaluation

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CASP RR File

AVIAFGKFKLNLTREMFREDEP

1	11	0	8	0.986
1	12	0	8	0.981
10	16	0	8	0.827
10	17	0	8	0.803
10	18	0	8	0.781
10	34	0	8	0.700

Section I Summary [job-dir](#)

PDB Input5z82.pdb [computed RR file](#)

Sequence LengthRR - 276 , Native - 270 [sequence comparison!](#)

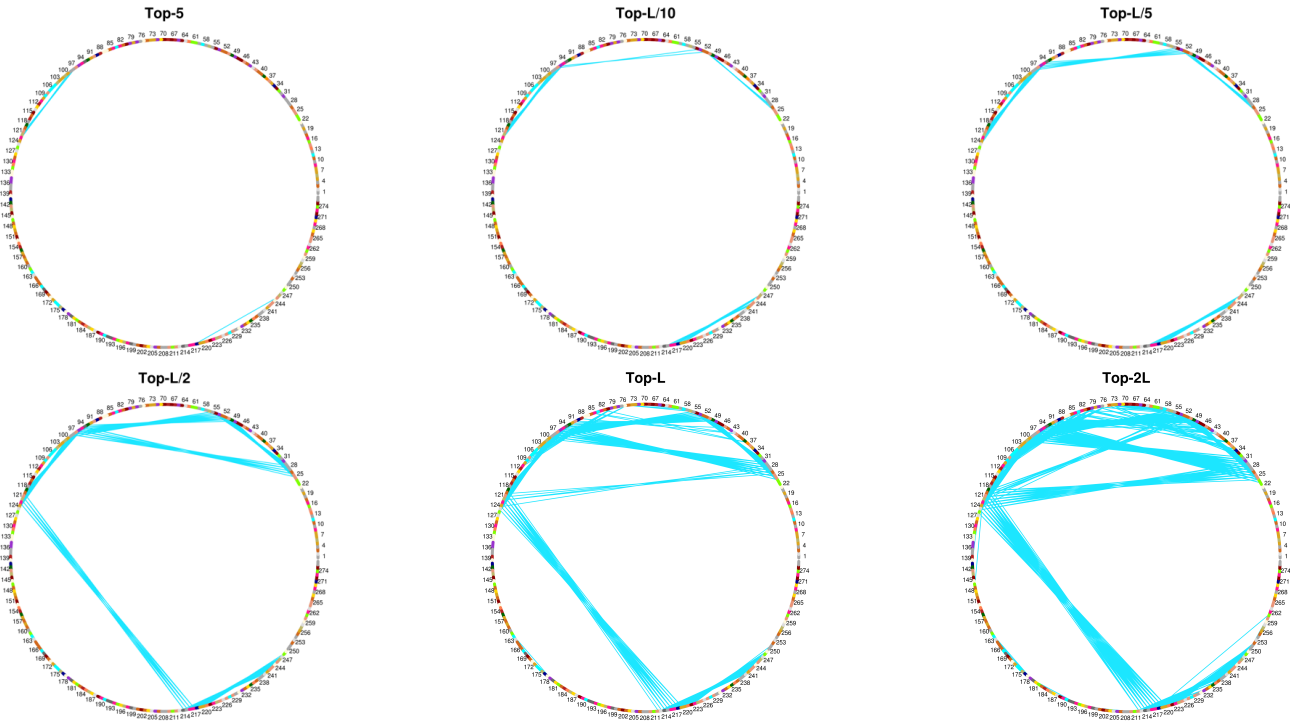
Contact TypeALL contacts with C β atoms within 8 Å with minimum 6 residues sequence separation

Section II Contact Count [see description](#)

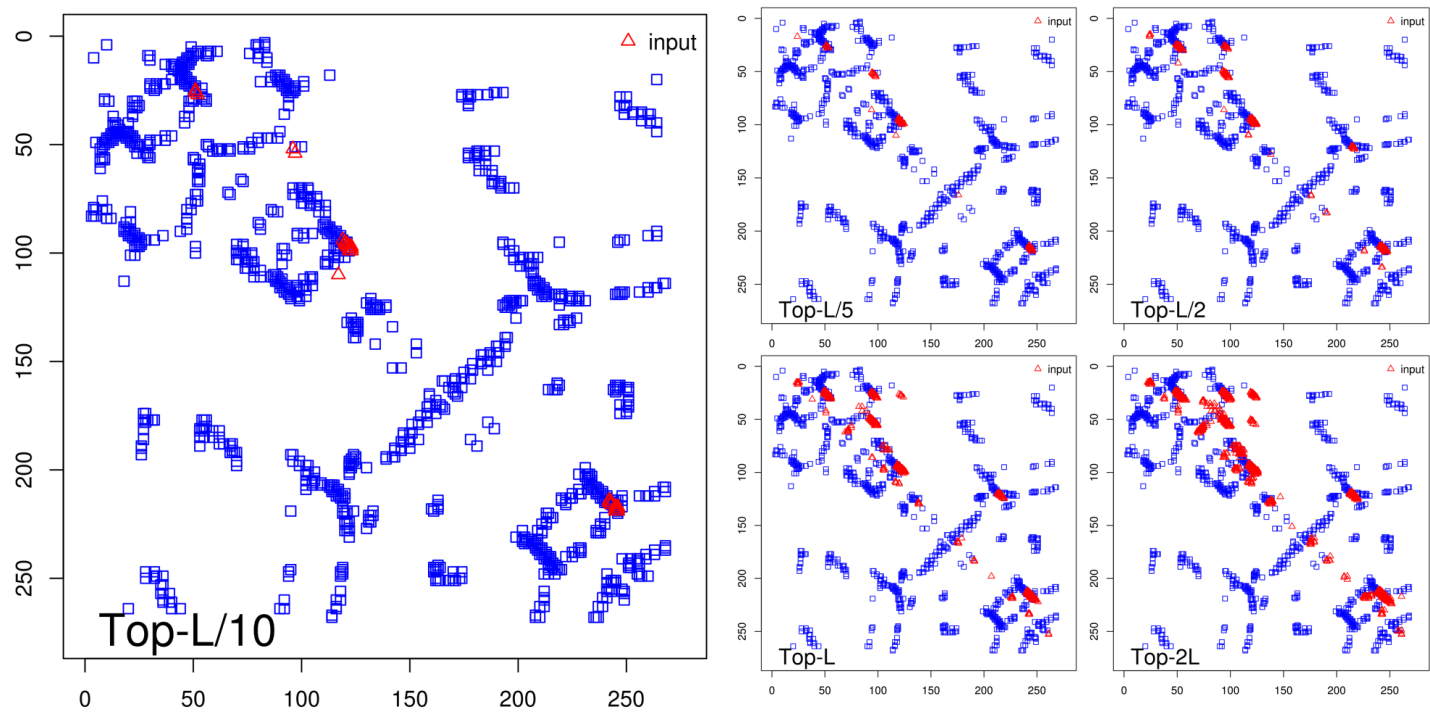
RR-File	Total	Not in Native	Remaining Total	ALL Contacts			L (= 268) from Native PDB (ignoring gaps)					
				Short-Range	Medium-Range	Long-Range	5	L/10	L/5	L/2	L	2L
all	27600	1306	26294	966 (4%)	2314 (9%)	23014 (88%)	5	27	54	134	268	536

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

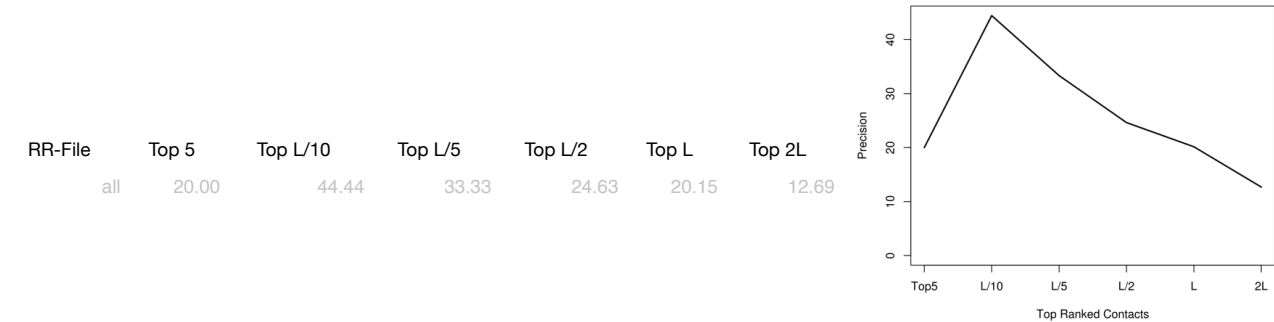
Section III Chord Diagrams [see description](#)



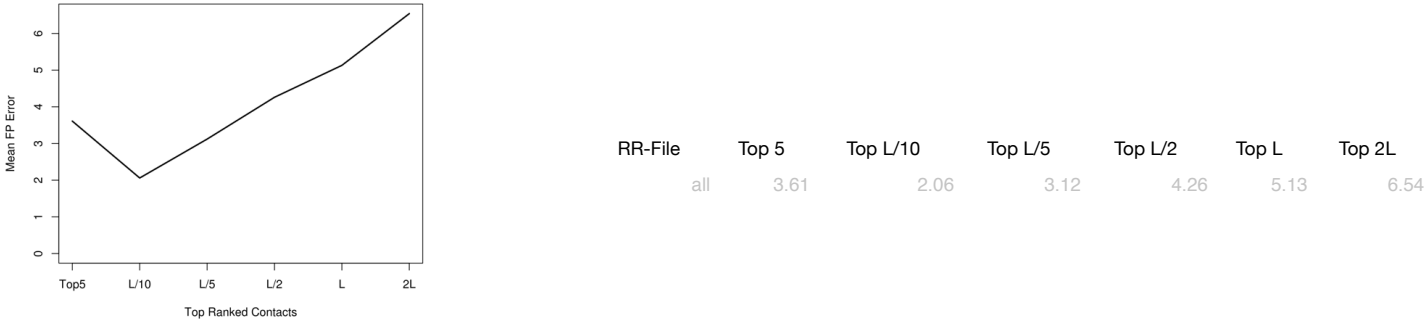
Section IV Contact Maps (with native in blue background)



Section V Precision [see description](#)

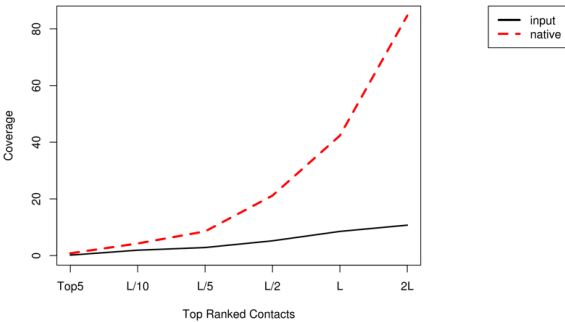


Section VI Mean False Positive Error [see description](#)

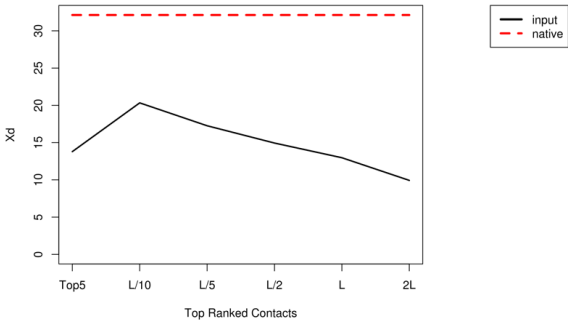


Section VII Coverage [see description](#)

RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
input	0.16	1.90	2.84	5.21	8.53	10.74
native	0.79	4.27	8.53	21.17	42.34	84.68



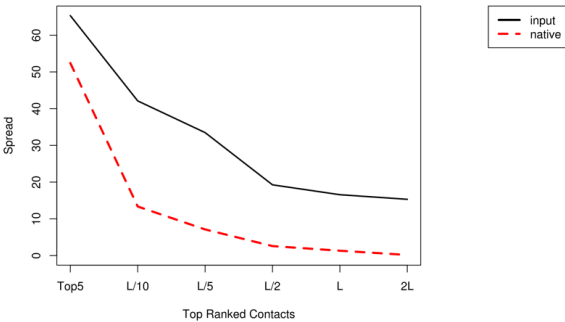
Section VIII X_d (Distance distribution) [see description](#)



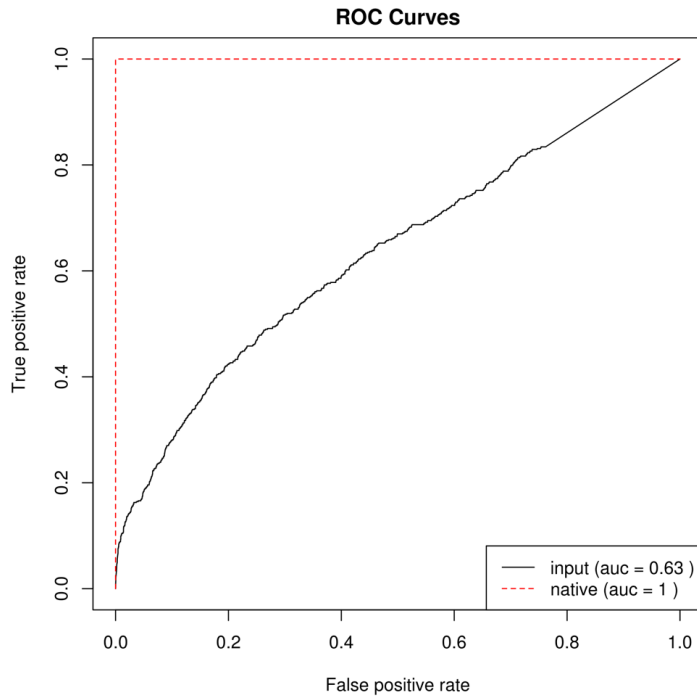
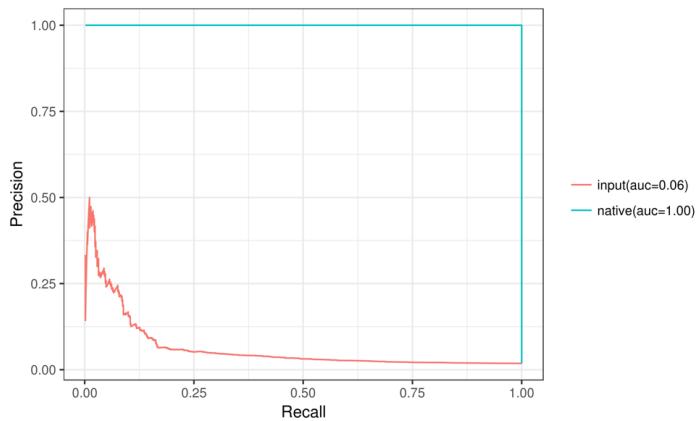
RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
input	13.79	20.33	17.26	14.94	12.97	9.93
native	32.12	32.12	32.12	32.12	32.12	32.12

Section IX Spread [see description](#)

RR-File	Top 5	Top L/10	Top L/5	Top L/2	Top L	Top 2L
input	65.33	42.11	33.48	19.26	16.57	15.32
native	52.42	13.36	7.12	2.58	1.32	0.17



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	86	677	33143	547	0.11
native	633	0	33820	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
 GPLGSMSSIGLAHNVTILGSGETTIVVLGHGYGTDQSVKLLVLPYLVDDYKVLVLDHMGAGTTNPDPYDFDRYSLLEGYSYDLIAILEEFQVSKCIYVGHGS [sequence]
 -----2543-----18*****9213-19-----16-131-59*****9554541-----234558*-5*-2*7-47--4-69***** [input: 536 pairs 162 residues]
 --143-4766457633167***9766769175-274-26311899***7998666513-3511-2631722652344175-33-53599***9*965777 [native: 633 pairs 235 residues]

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      110      120      130      140      150      160      170      180      190      200
      |      |      |      |      |      |      |      |      |
MSSMAAAVASIFRPDLFHKLVMI SPTPR LINT EY YGGFEQKVMD ETL RSLDENFKSLSLGTAPLLLACDLESAA MQEY CRTLFNMRPDIACCITRMICG [sequence]
83149934*6423--175*****83643---123552-----1---1-----1---21-3322-----46--4---41-----12-12---21- [input: 536 pairs 162 residues]
89567332228768**8***8*7995---3375422--4--33--43--42-231--431598422-2-561162-85225431443444344546364- [native: 633 pairs 235 residues]

      210      220      230      240      250      260      270
      |      |      |      |      |      |      |
LDLRPYLGHVTVPCHI IQSSNDIMVPVAVGEYLRKNLGGPSVVEVMPTEGHLP HLSMPEVTIPVVL RHIRQDITDH [sequence]
1-----2--2378*****95422234-17--52--2-455996755565521----2--4----- [input: 536 pairs 162 residues]
46426488*99***656576341661284-44563766659277**9886942-464-363-56--26----- [native: 633 pairs 235 residues]
```