

Scored residue / atom

CRAMP1 (310-440)

CRAMP1 (660-760)

GON4L (1590-1810)

120 / 0

100 / 0

100

200

220

0

100

200

CRAMP1 (310-440)

100

120 / 0

CRAMP1 (660-760)

100 / 0

GON4L (1590-1810)

100

200

220

Aligned residue / atom

