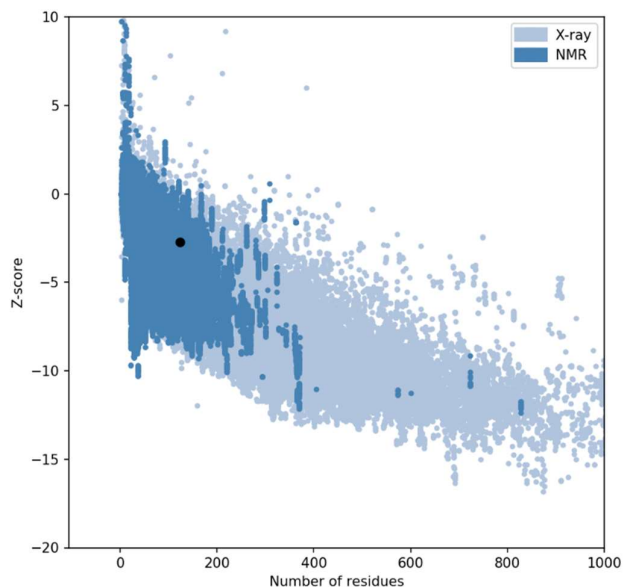


## PcLys1

A



B

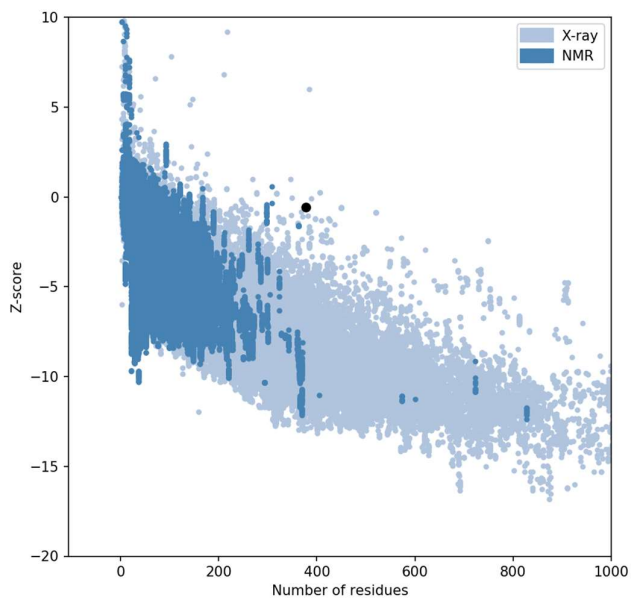
```

Residue [ 11 :ALA] ( -60.38, 175.72) in Allowed region
Residue [ 65 :GLY] (-110.59,  92.99) in Allowed region
Residue [ 71 :ASN] (-118.10,  63.84) in Allowed region
Residue [ 100 :ASN] ( -98.11,  83.29) in Allowed region
Residue [ 104 :GLY] (-176.69,-109.17) in Allowed region
Residue [ 110 :LEU] ( -38.59, 130.51) in Allowed region
Residue [ 12 :SER] ( -38.00, -23.47) in Outlier region
Residue [ 14 :LEU] ( 110.82,  86.34) in Outlier region
Residue [ 55 :PRO] ( -22.00,  87.32) in Outlier region
Residue [ 115 :TYR] (  69.42, 123.35) in Outlier region
Residue [ 119 :GLY] (  45.88, -97.56) in Outlier region
Number of residues in favoured region (~98.0% expected) : 110 ( 90.9%)
Number of residues in allowed region (~2.0% expected)   :  6 (  5.0%)
Number of residues in outlier region                      :  5 (  4.1%)

```

## PcLys2

C



D

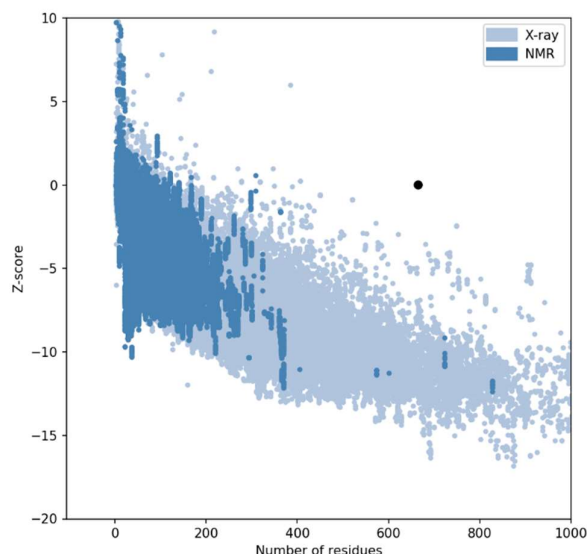
```

Residue [ 53 :ASP] (-110.30,  44.38) in Allowed region
Residue [ 71 :ASP] (-149.91,  -6.62) in Allowed region
Residue [ 139 :VAL] ( -57.78, -71.83) in Allowed region
Residue [ 140 :GLN] (-164.62, 116.85) in Allowed region
Residue [ 147 :LYS] (  67.48, -28.71) in Allowed region
Residue [ 177 :GLY] ( 147.05, -28.93) in Allowed region
Residue [ 178 :TYR] (-116.33,  71.68) in Allowed region
Residue [ 202 :PRO] (-109.87, 169.12) in Allowed region
Residue [ 207 :LYS] ( 175.56,-170.53) in Allowed region
Residue [ 235 :ASN] (-109.79,  51.38) in Allowed region
Residue [ 277 :THR] (-131.76,-159.85) in Allowed region
Residue [ 284 :ASP] (  42.58,  67.41) in Allowed region
Residue [ 290 :THR] (-144.32,-163.99) in Allowed region
Residue [ 337 :LYS] (-137.38,-157.61) in Allowed region
Residue [ 339 :TRP] ( -39.41, 118.78) in Allowed region
Residue [ 342 :GLY] (-179.33, 109.59) in Allowed region
Residue [ 349 :HIS] (-122.73,-143.65) in Allowed region
Residue [ 358 :ASP] (  45.16,  68.87) in Allowed region
Residue [ 18 :SER] ( 108.89, 168.47) in Outlier region
Residue [ 124 :PRO] ( -27.00, 110.28) in Outlier region
Residue [ 190 :LYS] (  64.88,  11.41) in Outlier region
Residue [ 200 :GLY] (-148.21,  87.16) in Outlier region
Residue [ 237 :SER] ( 150.36,-152.55) in Outlier region
Residue [ 247 :GLN] (  97.11, 152.65) in Outlier region
Residue [ 260 :GLU] ( 163.66, 177.38) in Outlier region
Residue [ 269 :CYS] (-161.21,-136.67) in Outlier region
Residue [ 270 :THR] ( -59.59,-130.64) in Outlier region
Residue [ 357 :ASP] ( 160.57,-115.48) in Outlier region
Residue [ 372 :SER] ( 162.19, 168.78) in Outlier region
Number of residues in favoured region (~98.0% expected) : 346 ( 92.3%)
Number of residues in allowed region (~2.0% expected)   : 18 (  4.8%)
Number of residues in outlier region                      : 11 (  2.9%)

```

PcLys3

E



F

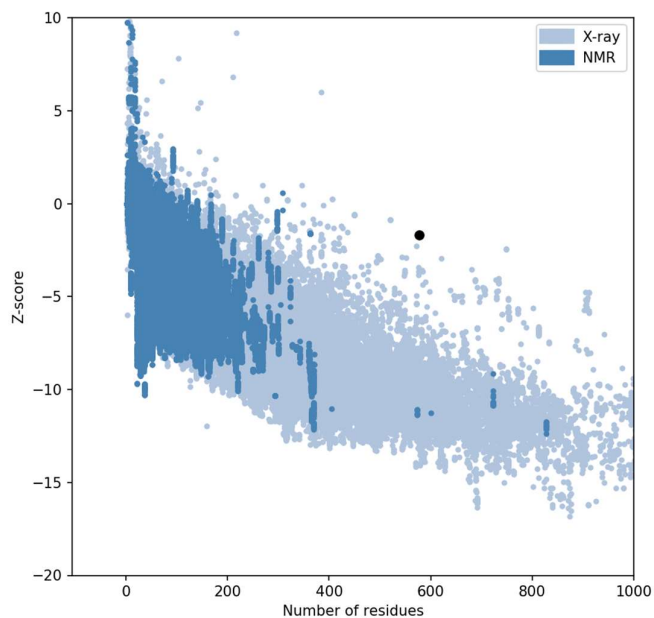
```
Residue [ 82 :ASP] (-133.73, 71.42) in Allowed region
Residue [ 98 :ASP] (-140.58, 40.35) in Allowed region
Residue [ 167 :THR] (-104.66, -74.88) in Allowed region
Residue [ 168 :TYR] (-176.16, 106.49) in Allowed region
Residue [ 176 :CYS] (-134.81, -160.82) in Allowed region
Residue [ 213 :GLU] (-136.42, -161.27) in Allowed region
Residue [ 215 :CYS] (-117.40, -113.05) in Allowed region
Residue [ 235 :THR] (-138.33, -158.82) in Allowed region
Residue [ 236 :THR] (-76.10, -166.84) in Allowed region
Residue [ 256 :ASP] (-85.19, 39.87) in Allowed region
Residue [ 259 :GLY] (-122.96, 65.10) in Allowed region
Residue [ 263 :CYS] ( 74.30, -166.61) in Allowed region
Residue [ 276 :LYS] (-167.19, -170.10) in Allowed region
Residue [ 296 :GLU] (-135.55, -111.32) in Allowed region
Residue [ 323 :THR] ( 45.81, 27.40) in Allowed region
Residue [ 335 :ASN] ( 60.57, -10.16) in Allowed region
Residue [ 347 :TYR] (-154.13, -166.35) in Allowed region
Residue [ 348 :CYS] (-59.10, 105.85) in Allowed region
Residue [ 356 :GLN] (-110.76, 70.73) in Allowed region
Residue [ 360 :GLY] (-162.24, 108.62) in Allowed region
Residue [ 379 :THR] (-81.34, -168.08) in Allowed region
Residue [ 380 :SER] (-57.26, 106.69) in Allowed region
Residue [ 393 :PRO] (-68.11, -173.47) in Allowed region
Residue [ 394 :GLY] (-135.76, -110.61) in Allowed region
Residue [ 398 :ASN] ( 71.35, 146.85) in Allowed region
Residue [ 399 :CYS] (-179.92, -164.35) in Allowed region
Residue [ 419 :CYS] (-121.00, -123.44) in Allowed region
Residue [ 426 :ASN] (-155.98, -138.48) in Allowed region
Residue [ 428 :VAL] (-139.21, -141.10) in Allowed region
Residue [ 433 :LEU] (-173.80, 116.84) in Allowed region
Residue [ 434 :LEU] (-172.11, 96.50) in Allowed region
Residue [ 435 :GLN] (-31.63, 134.82) in Allowed region
Residue [ 436 :TRP] (-172.74, -170.89) in Allowed region
Residue [ 441 :SER] (-148.07, -151.15) in Allowed region
Residue [ 444 :SER] (-70.84, -69.97) in Allowed region
Residue [ 448 :SER] (-52.57, -70.60) in Allowed region
Residue [ 451 :LEU] (-77.29, 12.30) in Allowed region
Residue [ 468 :ASP] (-121.61, -69.09) in Allowed region
Residue [ 487 :SER] (-81.95, -169.34) in Allowed region
Residue [ 492 :PHE] (-179.69, -171.85) in Allowed region
Residue [ 496 :SER] ( 73.28, -22.69) in Allowed region
Residue [ 529 :LYS] (174.34, 151.79) in Allowed region
Residue [ 532 :CYS] (-64.84, 103.56) in Allowed region
Residue [ 533 :THR] (-137.11, -35.29) in Allowed region
Residue [ 539 :ASP] ( 58.16, 0.63) in Allowed region
Residue [ 547 :ARG] (-49.26, 166.76) in Allowed region
Residue [ 564 :LYS] (167.41, 169.07) in Allowed region
Residue [ 565 :SER] (-60.13, -65.16) in Allowed region
Residue [ 614 :ASN] (-141.64, -152.56) in Allowed region
Residue [ 615 :CYS] (-67.25, 61.98) in Allowed region
Residue [ 625 :ASP] (-66.25, 175.82) in Allowed region
Residue [ 663 :VAL] (-155.80, 80.67) in Allowed region
Residue [ 164 :CYS] ( 59.56, 157.26) in Outlier region
Residue [ 165 :GLN] (158.75, 176.96) in Outlier region
Residue [ 252 :SER] ( 99.36, 161.95) in Outlier region
Residue [ 288 :PRO] (-117.35, -176.34) in Outlier region
Residue [ 294 :ASN] (-173.56, -67.45) in Outlier region
Residue [ 303 :LYS] (136.01, 99.13) in Outlier region
Residue [ 336 :ARG] (156.72, -161.33) in Outlier region
Residue [ 372 :ARG] (-170.20, -161.71) in Outlier region
Residue [ 381 :THR] (163.31, 146.42) in Outlier region
Residue [ 387 :PRO] (-55.48, 97.50) in Outlier region
Residue [ 391 :TYR] (-167.46, -122.36) in Outlier region
Residue [ 395 :THR] (-33.26, -167.26) in Outlier region
Residue [ 400 :SER] (166.58, -158.69) in Outlier region
Residue [ 430 :VAL] (170.81, 131.56) in Outlier region
Residue [ 432 :GLN] (126.08, -124.92) in Outlier region
Residue [ 497 :GLY] (-176.98, 42.56) in Outlier region
Residue [ 498 :GLY] (-150.02, 90.40) in Outlier region
Residue [ 502 :LEU] ( 83.27, 117.84) in Outlier region
Residue [ 504 :THR] (-176.03, -78.03) in Outlier region
```

```
Residue [ 504 :THR] (-176.03, -78.03) in Outlier region
Residue [ 509 :ILE] (102.68, 124.64) in Outlier region
Residue [ 598 :THR] ( 72.24, 133.99) in Outlier region
Residue [ 646 :THR] (-27.91, 137.76) in Outlier region
Residue [ 649 :SER] (-163.46, -113.21) in Outlier region
Number of residues in favoured region (~98.0% expected) : 588 ( 88.7%)
Number of residues in allowed region (~2.0% expected) : 52 ( 7.8%)
Number of residues in outlier region : 23 ( 3.5%)
```



PcLys4

G



H

Residue [ 118 :SER] ( -59.71, 168.45) in Allowed region	Residue [ 558 :VAL] ( -32.97, 104.42) in Allowed region
Residue [ 182 :TYR] ( -37.22, 122.87) in Allowed region	Residue [ 113 :SER] ( -50.10, -88.94) in Outlier region
Residue [ 200 :ALA] ( 76.37, -33.40) in Allowed region	Residue [ 121 :LYS] ( 82.64, -7.04) in Outlier region
Residue [ 216 :ASN] ( -114.51, 79.89) in Allowed region	Residue [ 228 :PRO] ( -38.36, 84.55) in Outlier region
Residue [ 226 :THR] ( -74.25, -64.50) in Allowed region	Residue [ 264 :ILE] ( 39.00, 82.76) in Outlier region
Residue [ 227 :PRO] ( -96.70, 101.53) in Allowed region	Residue [ 274 :GLU] ( 148.38, -127.89) in Outlier region
Residue [ 229 :VAL] ( 45.66, 28.85) in Allowed region	Residue [ 278 :SER] ( 136.25, -173.76) in Outlier region
Residue [ 249 :CYS] ( -145.87, -166.83) in Allowed region	Residue [ 283 :LEU] ( 80.11, -158.36) in Outlier region
Residue [ 256 :GLN] ( -165.86, 71.00) in Allowed region	Residue [ 292 :VAL] ( -7.81, 153.58) in Outlier region
Residue [ 276 :PHE] ( -173.20, -165.98) in Allowed region	Residue [ 295 :TYR] ( 62.56, 149.01) in Outlier region
Residue [ 277 :PHE] ( -154.55, -82.33) in Allowed region	Residue [ 300 :ASN] ( 174.43, -102.68) in Outlier region
Residue [ 290 :LEU] ( -145.52, -156.21) in Allowed region	Residue [ 302 :ALA] ( 149.86, -153.92) in Outlier region
Residue [ 296 :TYR] ( -132.51, -166.80) in Allowed region	Residue [ 306 :ILE] ( 172.47, -37.99) in Outlier region
Residue [ 318 :GLY] ( -65.55, -76.38) in Allowed region	Residue [ 308 :MET] ( -164.42, -24.82) in Outlier region
Residue [ 320 :PRO] ( -100.87, 143.80) in Allowed region	Residue [ 319 :ALA] ( -83.04, -103.49) in Outlier region
Residue [ 339 :ASP] ( -98.04, 44.45) in Allowed region	Residue [ 353 :PHE] ( 46.16, -166.87) in Outlier region
Residue [ 346 :GLY] ( -131.87, 63.26) in Allowed region	Residue [ 354 :ILE] ( -32.39, 145.79) in Outlier region
Residue [ 364 :CYS] ( 58.35, -104.34) in Allowed region	Residue [ 357 :ASN] ( 82.88, -10.30) in Outlier region
Residue [ 368 :LYS] ( -151.68, -113.64) in Allowed region	Residue [ 362 :GLN] ( -38.38, 72.46) in Outlier region
Residue [ 370 :ASP] ( -107.60, 58.11) in Allowed region	Residue [ 365 :SER] ( -24.28, 133.36) in Outlier region
Residue [ 375 :VAL] ( -152.89, -160.10) in Allowed region	Residue [ 366 :GLY] ( 175.83, 45.32) in Outlier region
Residue [ 381 :PRO] ( -71.71, 100.19) in Allowed region	Residue [ 439 :LEU] ( -157.93, -122.31) in Outlier region
Residue [ 388 :LEU] ( 69.44, -18.70) in Allowed region	Residue [ 459 :ALA] ( 169.65, -167.48) in Outlier region
Residue [ 407 :LYS] ( -143.46, -143.25) in Allowed region	Residue [ 463 :ASP] ( -70.90, -141.48) in Outlier region
Residue [ 415 :SER] ( 174.90, 159.30) in Allowed region	Residue [ 480 :PRO] ( -55.43, -73.48) in Outlier region
Residue [ 416 :ASP] ( -125.69, 59.91) in Allowed region	Residue [ 497 :SER] ( 159.63, -170.06) in Outlier region
Residue [ 450 :ASN] ( -90.73, -165.70) in Allowed region	Residue [ 505 :GLY] ( 164.09, 95.17) in Outlier region
Residue [ 462 :THR] ( -92.93, -151.07) in Allowed region	Residue [ 509 :ARG] ( 101.87, 110.89) in Outlier region
Residue [ 479 :ASN] ( -110.92, 62.93) in Allowed region	Residue [ 510 :PHE] ( -172.33, -129.04) in Outlier region
Residue [ 491 :GLY] ( 178.56, 116.37) in Allowed region	Residue [ 513 :ARG] ( 129.69, -132.73) in Outlier region
Residue [ 504 :TLE] ( -140.52, -140.74) in Allowed region	Residue [ 524 :ASP] ( -47.76, -109.66) in Outlier region
Residue [ 507 :CYS] ( -139.66, -68.83) in Allowed region	Residue [ 549 :SER] ( -175.30, -118.53) in Outlier region
Residue [ 517 :GLY] ( -38.76, 149.10) in Allowed region	
Residue [ 519 :SER] ( -142.79, -130.95) in Allowed region	Number of residues in favoured region (~98.0% expected) : 507 ( 88.2%)
Residue [ 520 :LEU] ( -53.74, 174.40) in Allowed region	Number of residues in allowed region (~2.0% expected) : 37 ( 6.4%)
Residue [ 557 :CYS] ( -105.72, 71.67) in Allowed region	Number of residues in outlier region : 31 ( 5.4%)