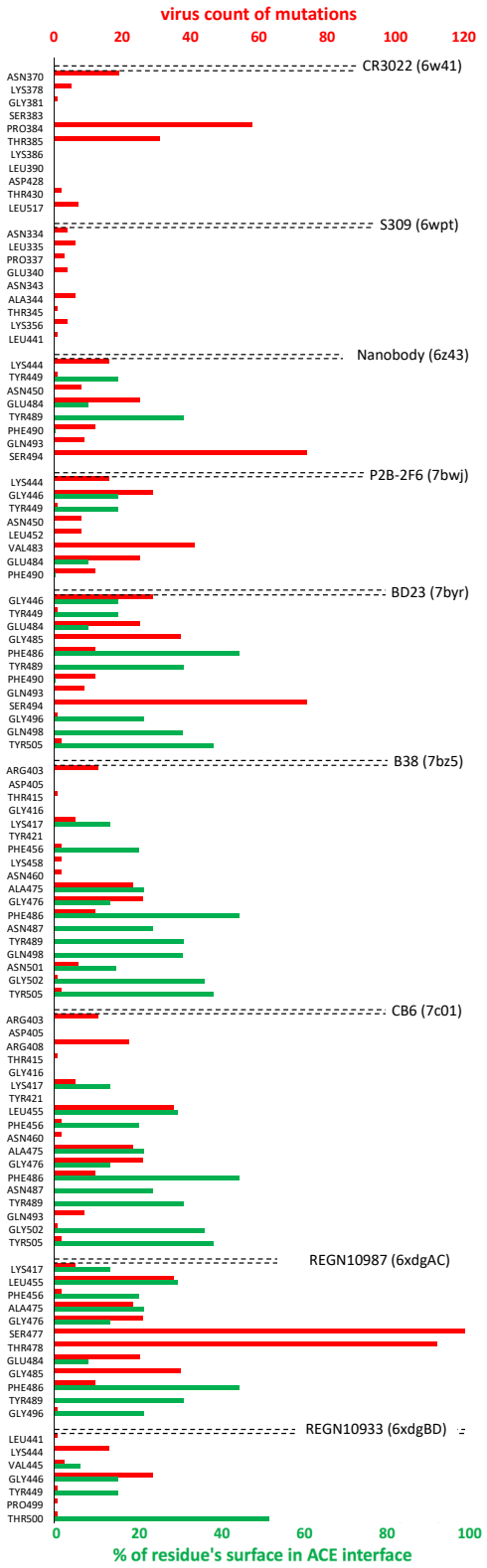
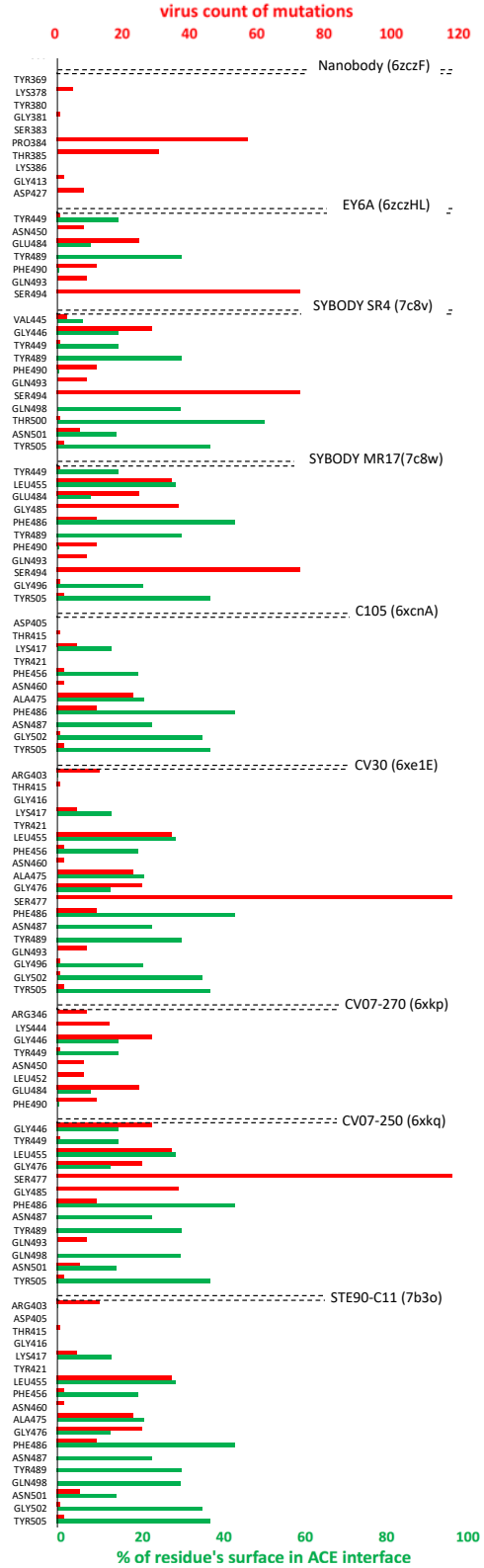
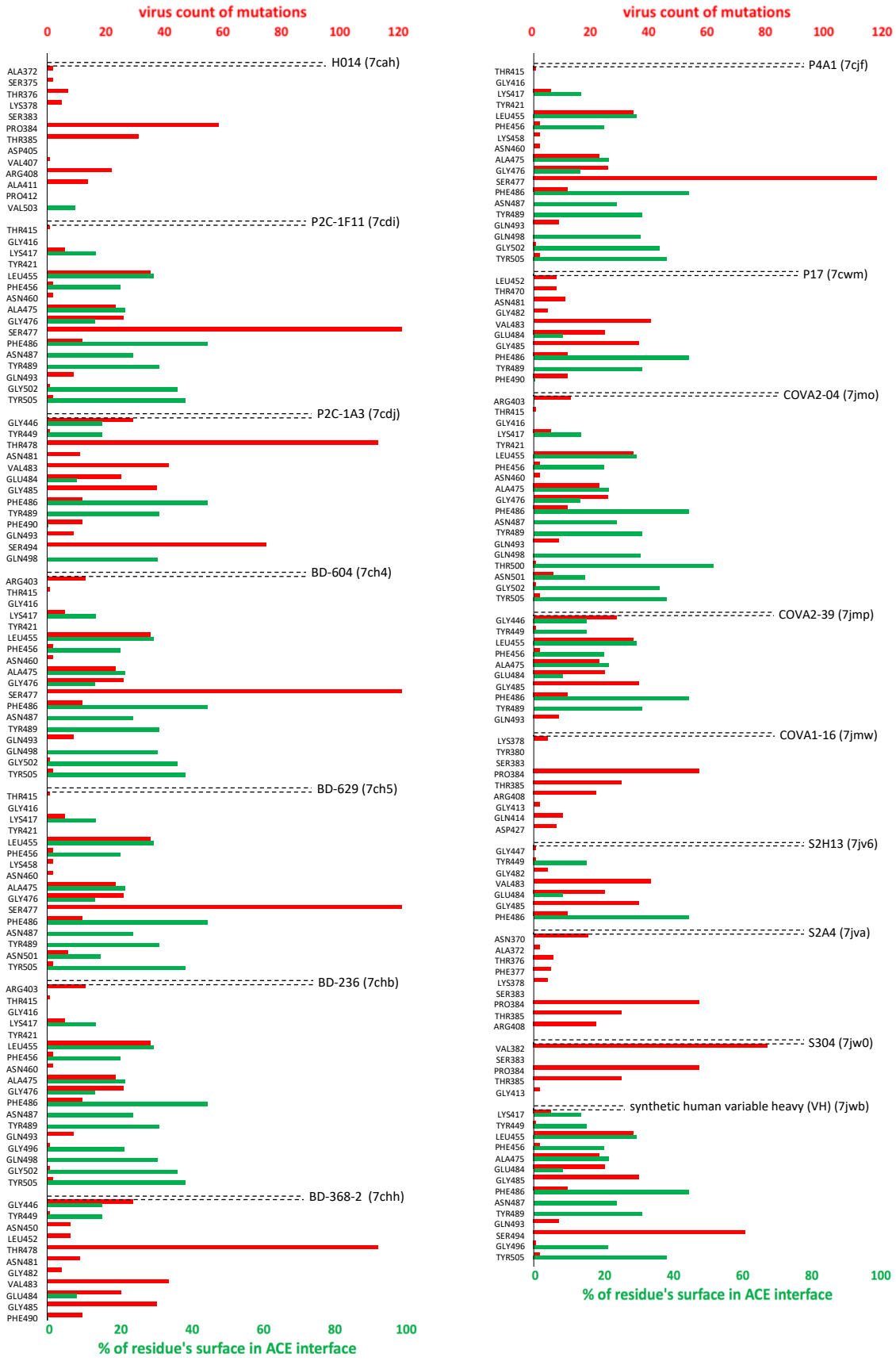
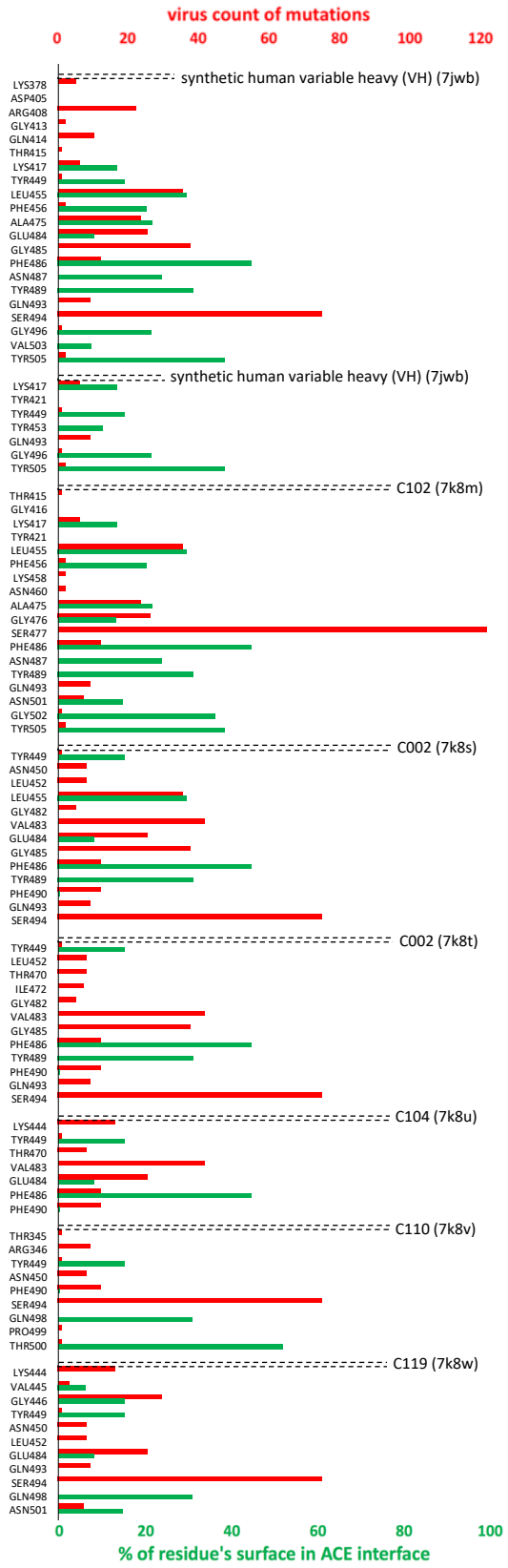
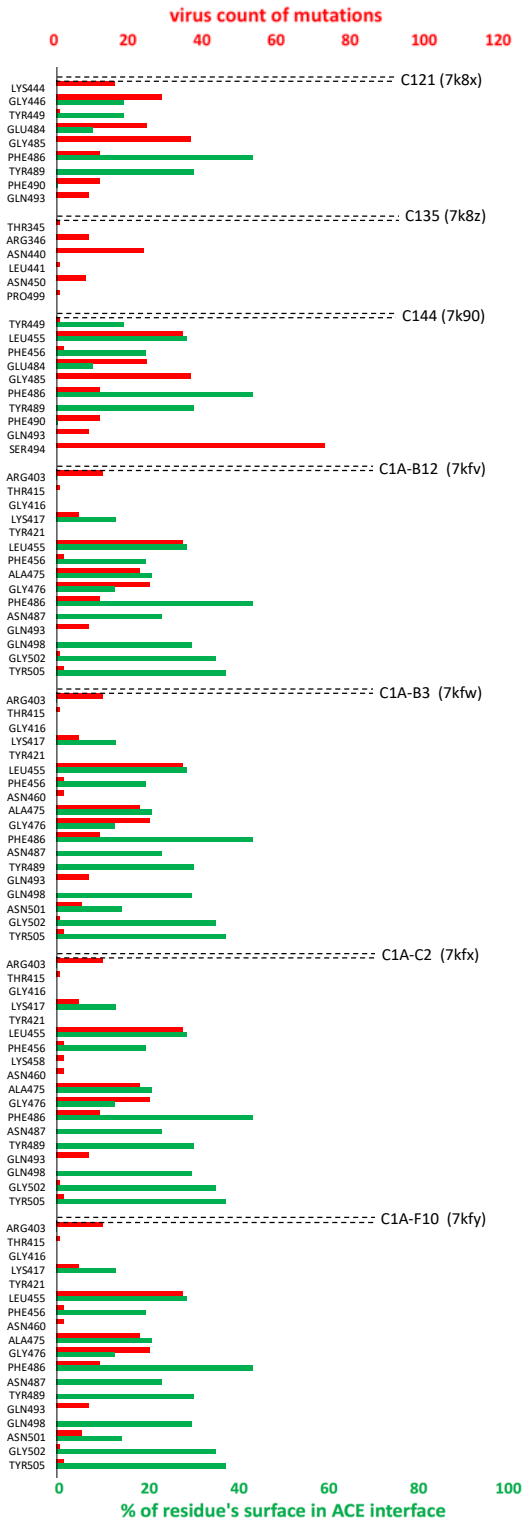

virus count of mutations
0
20
40
60
80
100
120
CR3022 (6w41)
ASN370
LYS378
GLY381
SER383
PRO384
THR385
LYS386
LEU390
ASP428
THR430
LEU517
S309 (6wpt)
ASN334
LEU335
PRO337
GLU340
ASN343
ALA344
THR345
LYS356
LEU441
Nanobody (6z43)
LYS444
TYR449
ASN450
GLU484
TYR489
PHE490
GLN493
SER494
P2B-2F6 (7bwj)
LYS444
GLY446
TYR449
ASN450
LEU452
VAL483
GLU484
PHE490
BD23 (7byr)
GLY446
TYR449
GLU484
GLY485
PHE486
TYR489
PHE490
GLN493
SER494
GLY496
GLN498
TYR505
B38 (7bz5)
ARG403
ASP405
THR415
GLY416
LYS417
TYR421
PHE456
LYS458
ASN460
ALA475
GLY476
PHE486
ASN487
TYR489
GLN498
ASN501
GLY502
TYR505
CB6 (7c01)
ARG403
ASP405
ARG408
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
ASN460
ALA475
GLY476
PHE486
ASN487
TYR489
GLN493
GLY502
TYR505
REGN10987 (6xdgAC)
LYS417
LEU455
PHE456
ALA475
GLY476
SER477
THR478
GLU484
GLY485
PHE486
TYR489
GLY496
REGN10933 (6xdgBD)
LEU441
LYS444
VAL445
GLY446
TYR449
PRO499
THR500
0
20
40
60
80
100
% of residue's surface in ACE interface


virus count of mutations
0
20
40
60
80
100
120
Nanobody (6zczF)
TYR369
LYS378
TYR380
GLY381
SER383
PRO384
THR385
LYS386
GLY413
ASP427
EY6A (6zczHL)
TYR449
ASN450
GLU484
TYR489
PHE490
GLN493
SER494
SYBODY SR4 (7c8v)
VAL445
GLY446
TYR449
TYR489
PHE490
GLN493
SER494
GLN498
THR500
ASN501
TYR505
SYBODY MR17(7c8w)
TYR449
LEU455
GLU484
GLY485
PHE486
TYR489
PHE490
GLN493
SER494
GLY496
TYR505
C105 (6xcnA)
ASP405
THR415
LYS417
TYR421
PHE456
ASN460
ALA475
PHE486
ASN487
GLY502
TYR505
CV30 (6xe1E)
ARG403
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
ASN460
ALA475
GLY476
SER477
PHE486
ASN487
TYR489
GLN493
GLY496
GLY502
TYR505
CV07-270 (6xkp)
ARG346
LYS444
GLY446
TYR449
ASN450
LEU452
GLU484
PHE490
CV07-250 (6xkq)
GLY446
TYR449
LEU455
GLY476
SER477
GLY485
PHE486
ASN487
TYR489
GLN493
GLN498
ASN501
TYR505
STE90-C11 (7b3o)
ARG403
ASP405
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
ASN460
ALA475
GLY476
PHE486
ASN487
TYR489
GLN498
ASN501
GLY502
TYR505
0
20
40
60
80
100
% of residue's surface in ACE interface


virus count of mutations
0 20 40 60 80 100 120
H014 (7cah)
ALA372
SER375
THR376
LYS378
SER383
PRO384
THR385
ASP405
VAL407
ARG408
ALA411
PRO412
VAL503
P2C-1F11 (7cdi)
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
ASN460
ALA475
GLY476
SER477
PHE486
ASN487
TYR489
GLN493
GLY502
TYR505
P2C-1A3 (7cdj)
GLY446
TYR449
THR478
ASN481
VAL483
GLU484
GLY485
PHE486
TYR489
PHE490
GLN493
SER494
GLN498
BD-604 (7ch4)
ARG403
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
ASN460
ALA475
GLY476
SER477
PHE486
ASN487
TYR489
GLN493
GLN498
GLY502
TYR505
BD-629 (7ch5)
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
LYS458
ASN460
ALA475
GLY476
SER477
PHE486
ASN487
TYR489
ASN501
TYR505
BD-236 (7chb)
ARG403
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
ASN460
ALA475
GLY476
PHE486
ASN487
TYR489
GLN493
GLY496
GLN498
GLY502
TYR505
BD-368-2 (7chh)
GLY446
TYR449
ASN450
LEU452
THR478
ASN481
GLY482
VAL483
GLU484
GLY485
PHE490
0 20 40 60 80 100
% of residue's surface in ACE interface
virus count of mutations
0 20 40 60 80 100 120
P4A1 (7cjf)
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
LYS458
ASN460
ALA475
GLY476
SER477
PHE486
ASN487
TYR489
GLN493
GLN498
GLY502
TYR505
P17 (7cwm)
LEU452
THR470
ASN481
GLY482
VAL483
GLU484
GLY485
PHE486
TYR489
PHE490
COVA2-04 (7jmo)
ARG403
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
ASN460
ALA475
GLY476
PHE486
ASN487
TYR489
GLN493
GLN498
THR500
ASN501
GLY502
TYR505
COVA2-39 (7jmp)
GLY446
TYR449
LEU455
PHE456
ALA475
GLU484
GLY485
PHE486
TYR489
GLN493
COVA1-16 (7jmw)
LYS378
TYR380
SER383
PRO384
THR385
ARG408
GLY413
GLN414
ASP427
S2H13 (7jv6)
GLY447
TYR449
GLY482
VAL483
GLU484
GLY485
PHE486
S2A4 (7jva)
ASN370
ALA372
THR376
PHE377
LYS378
SER383
PRO384
THR385
ARG408
S304 (7jw0)
VAL382
SER383
PRO384
THR385
GLY413
synthetic human variable heavy (VH) (7jwb)
LYS417
TYR449
LEU455
PHE456
ALA475
GLU484
GLY485
PHE486
ASN487
TYR489
GLN493
SER494
GLY496
TYR505
0 20 40 60 80 100
% of residue's surface in ACE interface


virus count of mutations
0 20 40 60 80 100 120
synthetic human variable heavy (VH) (7jwb)
LYS378
ASP405
ARG408
GLY413
GLN414
THR415
LYS417
TYR449
LEU455
PHE456
ALA475
GLU484
GLY485
PHE486
ASN487
TYR489
GLN493
SER494
GLY496
VAL503
TYR505
synthetic human variable heavy (VH) (7jwb)
LYS417
TYR421
TYR449
TYR453
GLN493
GLY496
TYR505
C102 (7k8m)
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
LYS458
ASN460
ALA475
GLY476
SER477
PHE486
ASN487
TYR489
GLN493
ASN501
GLY502
TYR505
C002 (7k8s)
TYR449
ASN450
LEU452
LEU455
GLY482
VAL483
GLU484
GLY485
PHE486
TYR489
PHE490
GLN493
SER494
C002 (7k8t)
TYR449
LEU452
THR470
ILE472
GLY482
VAL483
GLY485
PHE486
TYR489
PHE490
GLN493
SER494
C104 (7k8u)
LYS444
TYR449
THR470
VAL483
GLU484
PHE486
PHE490
C110 (7k8v)
THR345
ARG346
TYR449
ASN450
PHE490
SER494
GLN498
PRO499
THR500
C119 (7k8w)
LYS444
VAL445
GLY446
TYR449
ASN450
LEU452
GLU484
GLN493
SER494
GLN498
ASN501
0 20 40 60 80 100
% of residue's surface in ACE interface


virus count of mutations
0 20 40 60 80 100 120
C121 (7k8x)
LYS444
GLY446
TYR449
GLU484
GLY485
PHE486
TYR489
PHE490
GLN493
C135 (7k8z)
THR345
ARG346
ASN440
LEU441
ASN450
PRO499
C144 (7k90)
TYR449
LEU455
PHE456
GLU484
GLY485
PHE486
TYR489
PHE490
GLN493
SER494
C1A-B12 (7kfv)
ARG403
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
ALA475
GLY476
PHE486
ASN487
GLN493
GLN498
GLY502
TYR505
C1A-B3 (7kfw)
ARG403
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
ASN460
ALA475
GLY476
PHE486
ASN487
TYR489
GLN493
GLN498
ASN501
GLY502
TYR505
C1A-C2 (7kfx)
ARG403
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
LYS458
ASN460
ALA475
GLY476
PHE486
ASN487
TYR489
GLN493
GLN498
GLY502
TYR505
C1A-F10 (7kfy)
ARG403
THR415
GLY416
LYS417
TYR421
LEU455
PHE456
ASN460
ALA475
GLY476
PHE486
ASN487
TYR489
GLN493
GLN498
ASN501
GLY502
TYR505
0 20 40 60 80 100
% of residue's surface in ACE interface