wwPDB EM Validation Summary Report (i)

Mar 29, 2026 – 05:11 PM UTC

PDB ID	:	6XR4 / pdb_00006xr4
EMDB ID	:	EMD-20825
Title	:	Integrative in situ structure of Parkinsons disease-linked human LRRK2
Authors	:	Villa, E.; Lasker, K.; Audagnotto, M.
Deposited on	:	2020-07-10
Resolution	:	14.00 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

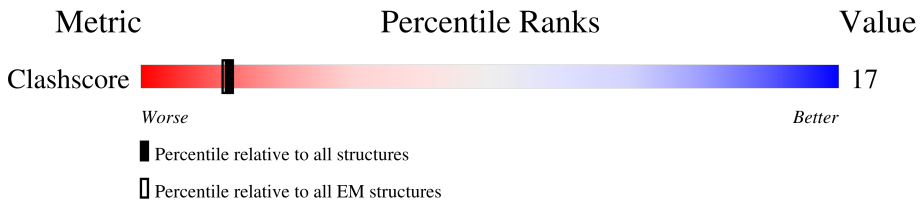
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

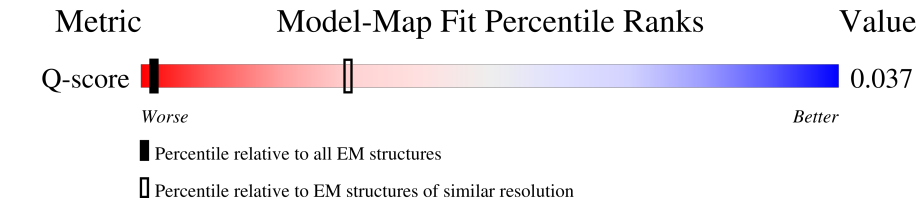
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 14.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	61 (13.50 - 14.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1-A	2527	10% 41% 59%
1	1-B	2527	14% 41% 59%
1	10-A	2527	40% • 59%
1	10-B	2527	40% • 59%
1	11-A	2527	41% 59%
1	11-B	2527	41% 59%

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Mol	Chain	Length	Quality of chain
1	12-A	2527	40% · 59%
1	12-B	2527	40% · 59%
1	13-A	2527	40% · 59%
1	13-B	2527	40% · 59%
1	14-A	2527	39% · 59%
1	14-B	2527	39% · 59%
1	15-A	2527	40% · 59%
1	15-B	2527	40% · 59%
1	16-A	2527	39% · 59%
1	16-B	2527	39% · 59%
1	17-A	2527	41% 59%
1	17-B	2527	41% 59%
1	18-A	2527	40% · 59%
1	18-B	2527	40% · 59%
1	19-A	2527	40% · 59%
1	19-B	2527	40% · 59%
1	2-A	2527	41% 59%
1	2-B	2527	41% 59%
1	20-A	2527	40% · 59%
1	20-B	2527	40% · 59%
1	21-A	2527	40% · 59%
1	21-B	2527	40% · 59%
1	22-A	2527	40% · 59%
1	22-B	2527	40% · 59%
1	23-A	2527	41% 59%

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Mol	Chain	Length	Quality of chain
1	23-B	2527	41% 59%
1	24-A	2527	39% 59%
1	24-B	2527	39% 59%
1	25-A	2527	39% 59%
1	25-B	2527	39% 59%
1	26-A	2527	41% 59%
1	26-B	2527	41% 59%
1	27-A	2527	40% 59%
1	27-B	2527	40% 59%
1	28-A	2527	40% 59%
1	28-B	2527	40% 59%
1	29-A	2527	40% 59%
1	29-B	2527	40% 59%
1	3-A	2527	41% 59%
1	3-B	2527	41% 59%
1	30-A	2527	40% 59%
1	30-B	2527	40% 59%
1	31-A	2527	41% 59%
1	31-B	2527	41% 59%
1	32-A	2527	40% 59%
1	32-B	2527	40% 59%
1	33-A	2527	40% 59%
1	33-B	2527	40% 59%
1	34-A	2527	40% 59%
1	34-B	2527	40% 59%

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Mol	Chain	Length	Quality of chain
1	35-A	2527	40% · 59%
1	35-B	2527	40% · 59%
1	36-A	2527	40% · 59%
1	36-B	2527	40% · 59%
1	37-A	2527	41% · 59%
1	37-B	2527	40% · 59%
1	38-A	2527	39% · 59%
1	38-B	2527	39% · 59%
1	39-A	2527	40% · 59%
1	39-B	2527	40% · 59%
1	4-A	2527	40% · 59%
1	4-B	2527	41% 59%
1	40-A	2527	40% · 59%
1	40-B	2527	40% · 59%
1	41-A	2527	39% · 59%
1	41-B	2527	38% · 59%
1	42-A	2527	40% · 59%
1	42-B	2527	40% · 59%
1	43-A	2527	40% · 59%
1	43-B	2527	40% · 59%
1	44-A	2527	41% 59%
1	44-B	2527	41% 59%
1	45-A	2527	40% · 59%
1	45-B	2527	40% · 59%
1	46-A	2527	39% · 59%

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Mol	Chain	Length	Quality of chain
1	46-B	2527	40% · 59%
1	47-A	2527	40% · 59%
1	47-B	2527	40% · 59%
1	48-A	2527	40% · 59%
1	48-B	2527	40% · 59%
1	49-A	2527	40% · 59%
1	49-B	2527	40% · 59%
1	5-A	2527	40% · 59%
1	5-B	2527	40% · 59%
1	50-A	2527	39% · 59%
1	50-B	2527	39% · 59%
1	51-A	2527	39% · 59%
1	51-B	2527	39% · 59%
1	52-A	2527	39% · 59%
1	52-B	2527	39% · 59%
1	53-A	2527	39% · 59%
1	53-B	2527	39% · 59%
1	6-A	2527	41% 59%
1	6-B	2527	41% 59%
1	7-A	2527	39% · 59%
1	7-B	2527	39% · 59%
1	8-A	2527	40% · 59%
1	8-B	2527	40% · 59%
1	9-A	2527	41% 59%
1	9-B	2527	40% · 59%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 110240 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Leucine-rich repeat serine/threonine-protein kinase 2.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
1	1-A	1040	1040	1040	0	1040
1	2-A	1040	1040	1040	0	1040
1	3-A	1040	1040	1040	0	1040
1	4-A	1040	1040	1040	0	1040
1	5-A	1040	1040	1040	0	1040
1	6-A	1040	1040	1040	0	1040
1	7-A	1040	1040	1040	0	1040
1	8-A	1040	1040	1040	0	1040
1	9-A	1040	1040	1040	0	1040
1	10-A	1040	1040	1040	0	1040
1	11-A	1040	1040	1040	0	1040
1	12-A	1040	1040	1040	0	1040
1	13-A	1040	1040	1040	0	1040
1	14-A	1040	1040	1040	0	1040
1	15-A	1040	1040	1040	0	1040
1	16-A	1040	1040	1040	0	1040
1	17-A	1040	1040	1040	0	1040

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Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
1	18-A	1040	1040	1040	0	1040
1	19-A	1040	1040	1040	0	1040
1	20-A	1040	1040	1040	0	1040
1	21-A	1040	1040	1040	0	1040
1	22-A	1040	1040	1040	0	1040
1	23-A	1040	1040	1040	0	1040
1	24-A	1040	1040	1040	0	1040
1	25-A	1040	1040	1040	0	1040
1	26-A	1040	1040	1040	0	1040
1	27-A	1040	1040	1040	0	1040
1	28-A	1040	1040	1040	0	1040
1	29-A	1040	1040	1040	0	1040
1	30-A	1040	1040	1040	0	1040
1	31-A	1040	1040	1040	0	1040
1	32-A	1040	1040	1040	0	1040
1	33-A	1040	1040	1040	0	1040
1	34-A	1040	1040	1040	0	1040
1	35-A	1040	1040	1040	0	1040
1	36-A	1040	1040	1040	0	1040
1	37-A	1040	1040	1040	0	1040
1	38-A	1040	1040	1040	0	1040

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Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
1	39-A	1040	1040	1040	0	1040
			Total	C		
1	40-A	1040	1040	1040	0	1040
			Total	C		
1	41-A	1040	1040	1040	0	1040
			Total	C		
1	42-A	1040	1040	1040	0	1040
			Total	C		
1	43-A	1040	1040	1040	0	1040
			Total	C		
1	44-A	1040	1040	1040	0	1040
			Total	C		
1	45-A	1040	1040	1040	0	1040
			Total	C		
1	46-A	1040	1040	1040	0	1040
			Total	C		
1	47-A	1040	1040	1040	0	1040
			Total	C		
1	48-A	1040	1040	1040	0	1040
			Total	C		
1	49-A	1040	1040	1040	0	1040
			Total	C		
1	50-A	1040	1040	1040	0	1040
			Total	C		
1	51-A	1040	1040	1040	0	1040
			Total	C		
1	52-A	1040	1040	1040	0	1040
			Total	C		
1	53-A	1040	1040	1040	0	1040
			Total	C		
1	1-B	1040	1040	1040	0	1040
			Total	C		
1	2-B	1040	1040	1040	0	1040
			Total	C		
1	3-B	1040	1040	1040	0	1040
			Total	C		
1	4-B	1040	1040	1040	0	1040
			Total	C		
1	5-B	1040	1040	1040	0	1040
			Total	C		
1	6-B	1040	1040	1040	0	1040

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Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
1	7-B	1040	1040	1040	0	1040
			Total	C		
1	8-B	1040	1040	1040	0	1040
			Total	C		
1	9-B	1040	1040	1040	0	1040
			Total	C		
1	10-B	1040	1040	1040	0	1040
			Total	C		
1	11-B	1040	1040	1040	0	1040
			Total	C		
1	12-B	1040	1040	1040	0	1040
			Total	C		
1	13-B	1040	1040	1040	0	1040
			Total	C		
1	14-B	1040	1040	1040	0	1040
			Total	C		
1	15-B	1040	1040	1040	0	1040
			Total	C		
1	16-B	1040	1040	1040	0	1040
			Total	C		
1	17-B	1040	1040	1040	0	1040
			Total	C		
1	18-B	1040	1040	1040	0	1040
			Total	C		
1	19-B	1040	1040	1040	0	1040
			Total	C		
1	20-B	1040	1040	1040	0	1040
			Total	C		
1	21-B	1040	1040	1040	0	1040
			Total	C		
1	22-B	1040	1040	1040	0	1040
			Total	C		
1	23-B	1040	1040	1040	0	1040
			Total	C		
1	24-B	1040	1040	1040	0	1040
			Total	C		
1	25-B	1040	1040	1040	0	1040
			Total	C		
1	26-B	1040	1040	1040	0	1040
			Total	C		
1	27-B	1040	1040	1040	0	1040

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Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
1	28-B	1040	1040	1040	0	1040
1	29-B	1040	1040	1040	0	1040
1	30-B	1040	1040	1040	0	1040
1	31-B	1040	1040	1040	0	1040
1	32-B	1040	1040	1040	0	1040
1	33-B	1040	1040	1040	0	1040
1	34-B	1040	1040	1040	0	1040
1	35-B	1040	1040	1040	0	1040
1	36-B	1040	1040	1040	0	1040
1	37-B	1040	1040	1040	0	1040
1	38-B	1040	1040	1040	0	1040
1	39-B	1040	1040	1040	0	1040
1	40-B	1040	1040	1040	0	1040
1	41-B	1040	1040	1040	0	1040
1	42-B	1040	1040	1040	0	1040
1	43-B	1040	1040	1040	0	1040
1	44-B	1040	1040	1040	0	1040
1	45-B	1040	1040	1040	0	1040
1	46-B	1040	1040	1040	0	1040
1	47-B	1040	1040	1040	0	1040
1	48-B	1040	1040	1040	0	1040

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Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
1	49-B	1040	1040	1040	0	1040
			Total	C		
1	50-B	1040	1040	1040	0	1040
			Total	C		
1	51-B	1040	1040	1040	0	1040
			Total	C		
1	52-B	1040	1040	1040	0	1040
			Total	C		
1	53-B	1040	1040	1040	0	1040

There are 2 discrepancies between the modelled and reference sequences:

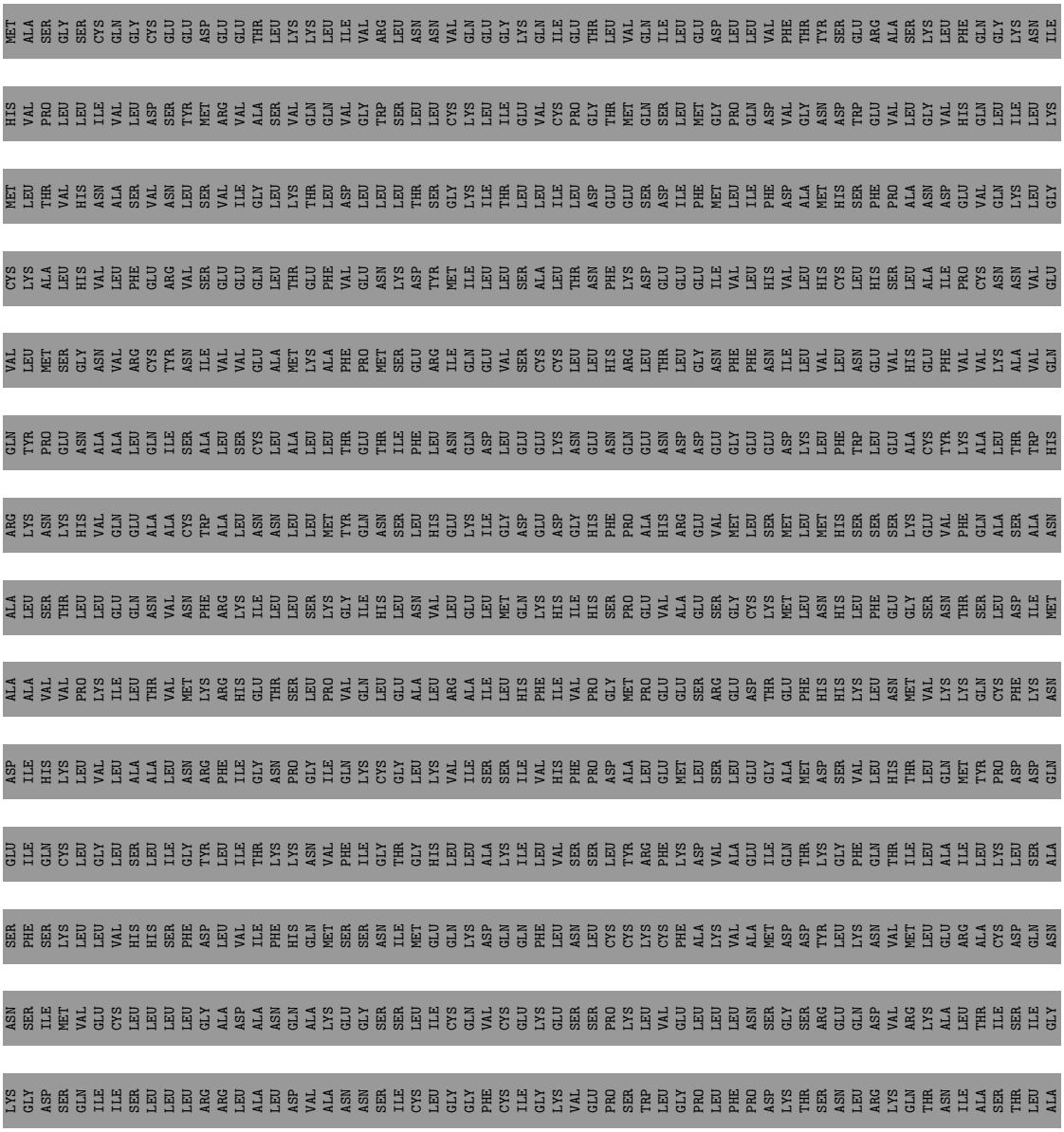
Chain	Residue	Modelled	Actual	Comment	Reference
A	2020	THR	ILE	variant	UNP Q5S007
B	2020	THR	ILE	variant	UNP Q5S007

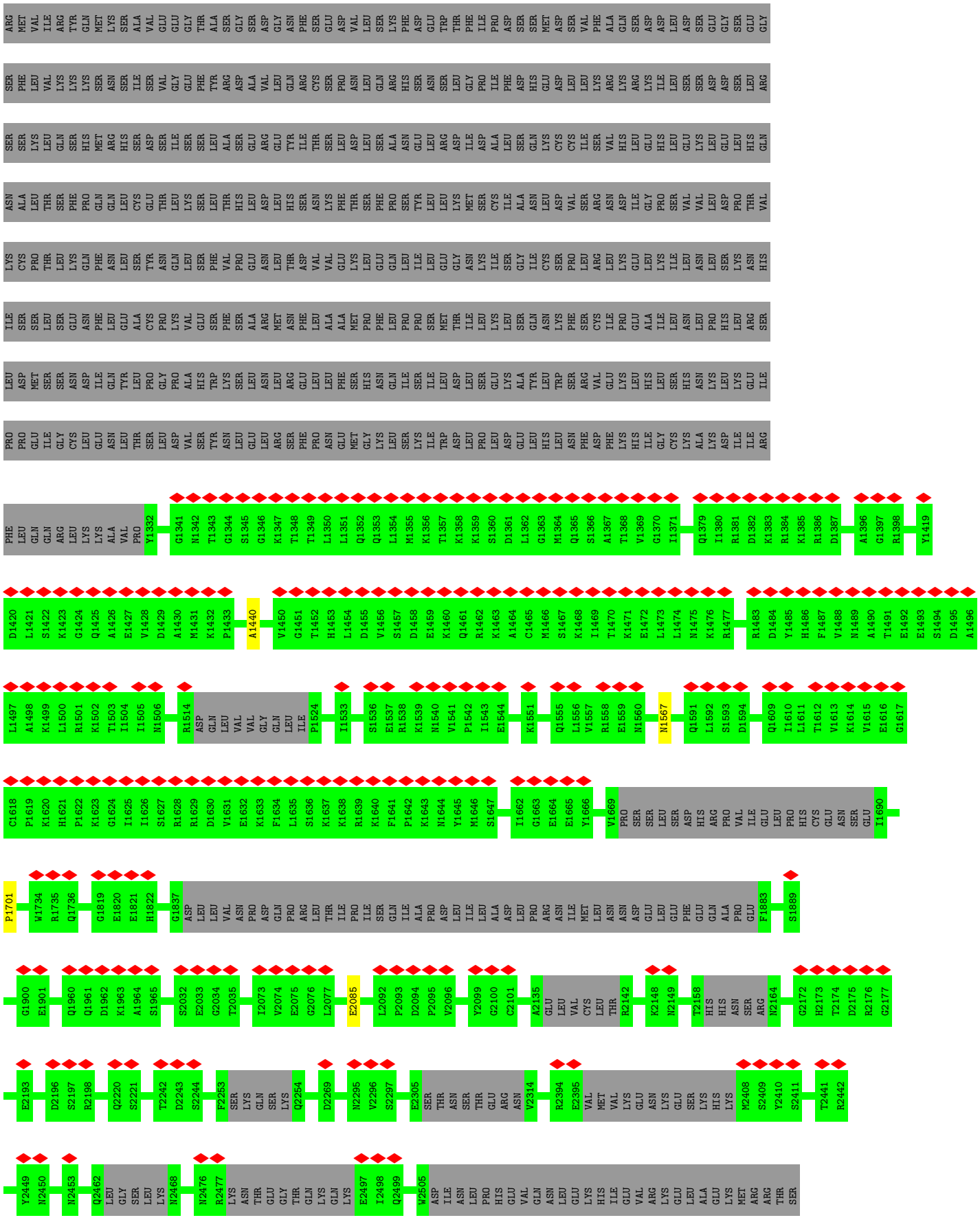
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 1-A:




ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP SER GLU GLY SER GLU GLY
SER PHE LEU VAL LYS LYS LYS SER ASN SER SER ILE SER VAL GLY GLU PHE PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG HIS SER ILE LEU SER SER ASP LEU LEU SER ARG
SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU GLU LYS LYS GLU LEU
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LYS GLU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS ILE LEU LEU ASN LEU SER LYS LYS ASN HIS
ILE SER SER LEU GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER LEU LEU LYS LEU SER GLN ASN PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER
LEU ASP MET SER SER ASN ASP ILE GLN TYR LEU PRO GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG GLU LEU PHE SER HIS ASN GLN GLU GLU LEU SER GLU LYS ALA TYR LEU TRP SER ARG VAL GLU LYS LEU HIS LEU LEU SER HIS ASN LYS LEU LYS GLU ILE
PRO PRO GLU ILE GLY CYS LEU GLU ASN LEU THR SER LEU ASP VAL SER TYR ASN LEU GLU LEU PHE PRO ASN GLU MET GLY LYS LEU SER LYS ILE TRP ASP LEU PRO LEU ASP GLU LEU HIS LEU ASN PHE ASP PHE LYS HIS ILE GLY CYS LYS ALA LYS ASP ILE ILE ARG
PHE LEU GLN GLN ARG LEU LYS LYS ALA VAL PRO Y1332 G1341 N1342 T1343 G1344 S1345 G1346 K1347 T1348 T1349 L1350 L1351 Q1352 Q1353 L1354 M1355 K1356 T1357 K1358 K1359 S1360 D1361 L1362 G1363 M1364 Q1365 S1366 A1367 T1368 V1369 G1370 I1371 Q1379 I1380 R1381 D1382 K1383 R1384 K1385 R1386 D1387 A1396 G1397 R1398 Y1419
D1420 L1421 S1422 K1423 G1424 Q1425 A1426 E1427 V1428 D1429 A1430 M1431 K1432 P1433 A1440 V1450 G1451 T1452 H1453 L1454 D1455 V1456 S1457 D1458 E1459 K1460 Q1461 R1462 K1463 A1464 C1465 M1466 S1467 K1468 I1469 T1470 K1471 E1472 L1473 L1474 N1475 K1476 R1477 R1483 D1484 Y1485 H1486 F1487 V1488 N1489 A1490 T1491 E1492 E1493 S1494 D1495 A1496
L1497 A1498 K1499 L1500 R1501 K1502 T1503 I1504 I1505 N1506 R1514 ASP GLN LEU VAL VAL GLY GLN LEU ILE P1524 I1533 S1536 E1537 R1538 K1539 N1540 V1541 P1542 I1543 E1544 K1551 Q1555 L1556 V1557 R1558 E1559 N1560 N1567 Q1591 L1592 S1593 D1594 Q1609 I1610 L1611 T1612 V1613 K1614 V1615 E1616 G1617
C1618 P1619 K1620 H1621 P1622 K1623 G1624 I1625 I1626 S1627 R1628 R1629 D1630 V1631 E1632 K1633 F1634 L1635 S1636 K1637 K1638 R1639 K1640 F1641 P1642 K1643 N1644 Y1645 M1646 S1647 I1662 G1663 E1664 E1665 Y1666 V1669 PRO SER SER LEU SER ASP HIS ARG PRO VAL ILE GLU LEU PRO HIS CYS GLU ASN SER GLU I1690
P1701 W1734 R1735 Q1736 G1819 E1820 E1821 H1822 G1837 ASP LEU LEU VAL ASN PRO ASP GLN PRO ARG LEU THR ILE PRO ILE SER GLN ILE ALA PRO ASP LEU ILE LEU ALA ASP LEU PRO ARG ASN ILE MET LEU ASN ASN ASP GLU LEU GLU PHE GLU GLN ALA PRO GLU F1883 S1889
G1900 E1901 Q1960 Q1961 D1962 K1963 A1964 S1965 S2032 E2033 G2034 T2035 I2073 V2074 E2075 G2076 L2077 E2085 L2092 P2093 D2094 P2095 V2096 Y2099 G2100 C2101 A2135 GLU LEU VAL CYS LEU THR R2142 K2148 N2149 T2158 HIS HIS ASN SER ARG W2164 G2172 H2173 T2174 D2175 R2176 G2177
E2193 D2196 S2197 R2198 Q2220 S2221 T2242 D2243 S2244 F2253 SER LYS GLN SER LYS Q2254 D2269 N2295 V2296 S2297 E2305 SER THR ASN SER THR GLU ARG ASN V2314 R2394 E2395 VAL MET VAL LYS GLU ASN LYS GLU SER LYS HIS LYS M2408 S2409 Y2410 S2411 T2441 R2442
Y2449 N2450 N2453 Q2462 LEU GLY SER LEU LYS N2468 N2476 R2477 LYS ASN THR GLU GLY THR GLN LYS GLN LYS E2497 I2498 Q2499 W2505 ASP ILE ASN LEU PRO HIS GLU VAL GLN ASN LEU GLU LYS HIS ILE GLU VAL ARG LYS GLU LEU ALA GLU LYS MET ARG ARG THR SER

VAL
GLU

- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 1-B:

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU GLU ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR THR SER LEU PRO VAL GLN LEU GLU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO GLY MET PRO GLU MET LEU SER LEU GLU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU LEU ALA LYS ILE LEU VAL SER SER LEU VAL ALA GLU ILE GLN THR THR LYS GLY PHE GLN THR HIS LEU ILE LEU LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS LYS PHE ALA ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU LEU GLU ARG ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS ALA GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER CYS CYS PRO LYS LEU GLU GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

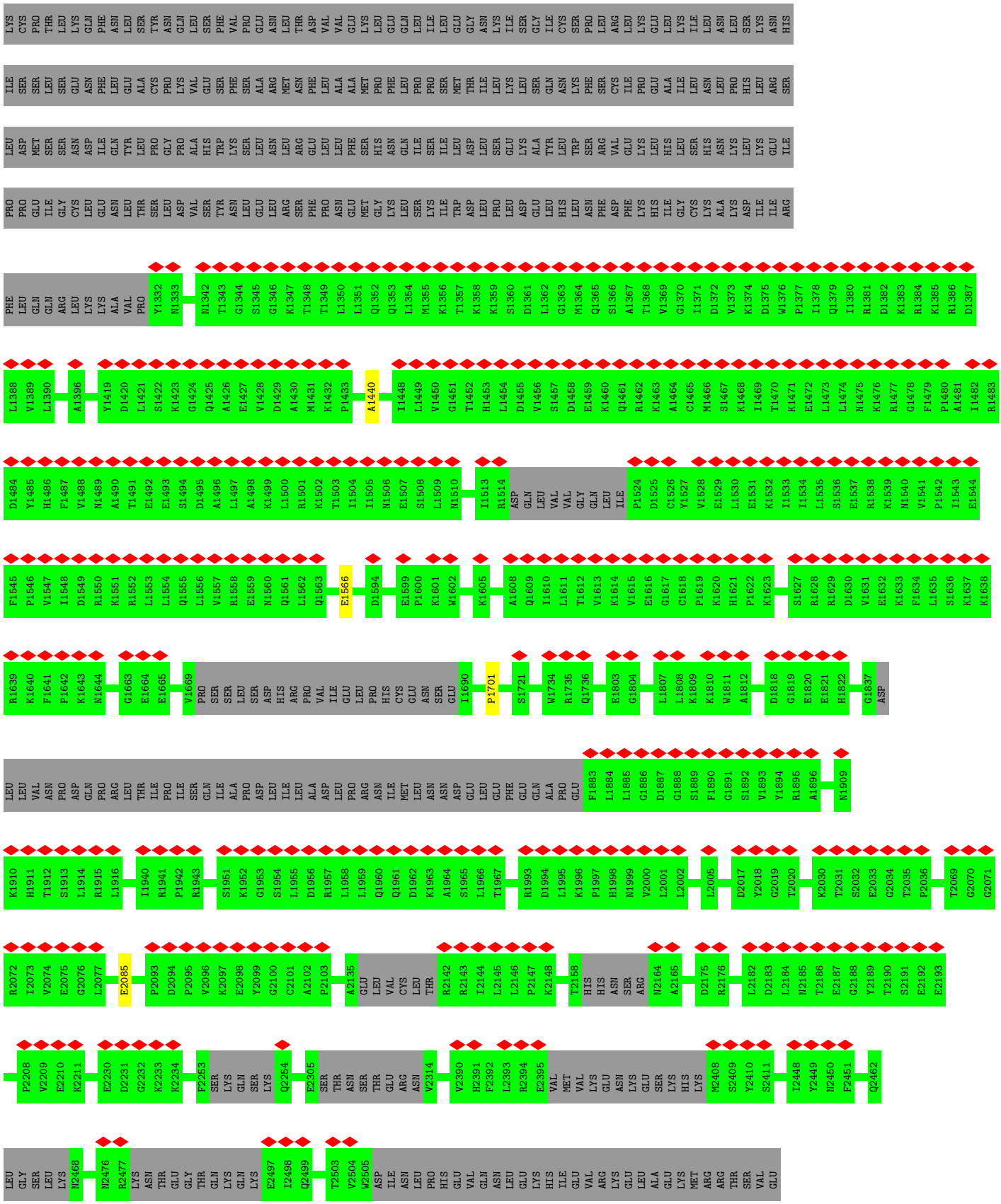
LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ASP GLN GLN ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS SER ASN SER ILE SER VAL LYS LYS VAL ASN ASN ALA ARG ASP VAL LEU GLN ARG CYS SER PRO ASN SER LEU LEU GLN ARG HIS SER ASN LEU LEU ASP GLU PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

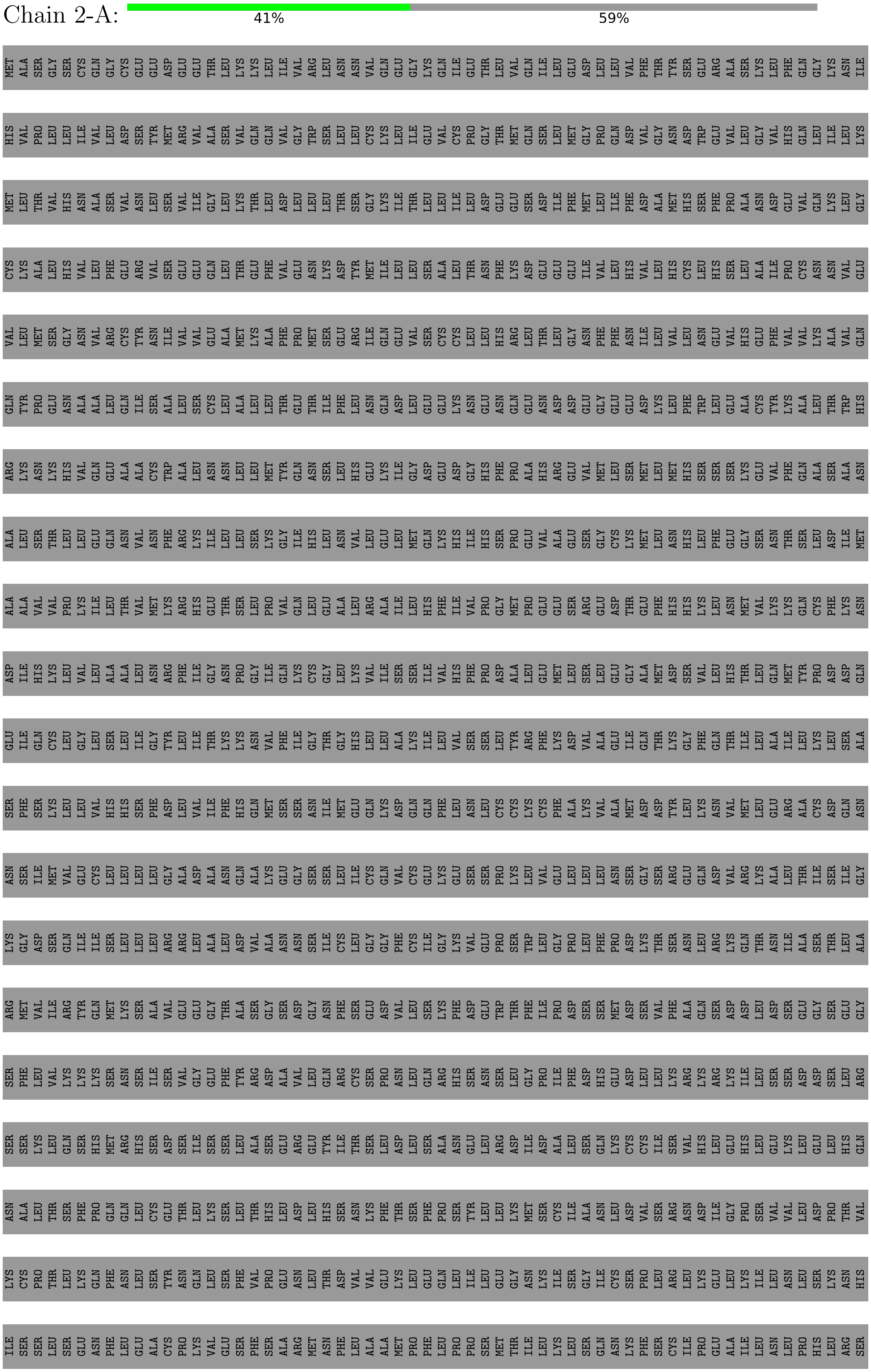
SER SER LYS LEU GLN SER HIS MET ARG HIS SER SER ASP SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER SER LEU ALA ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU GLU LYS LEU LEU GLY HIS GLN

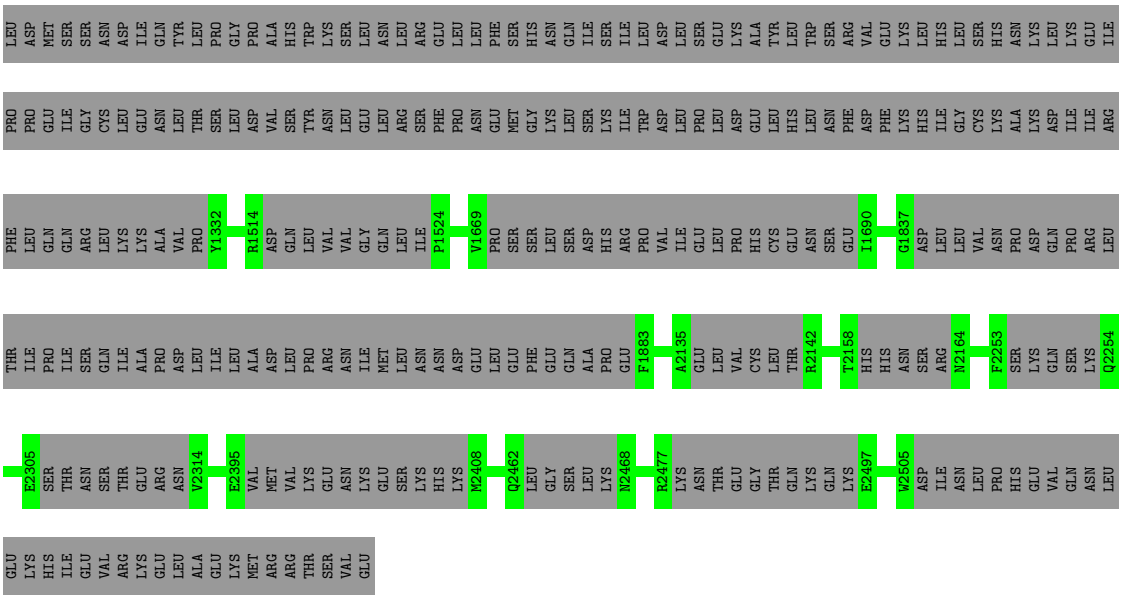
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

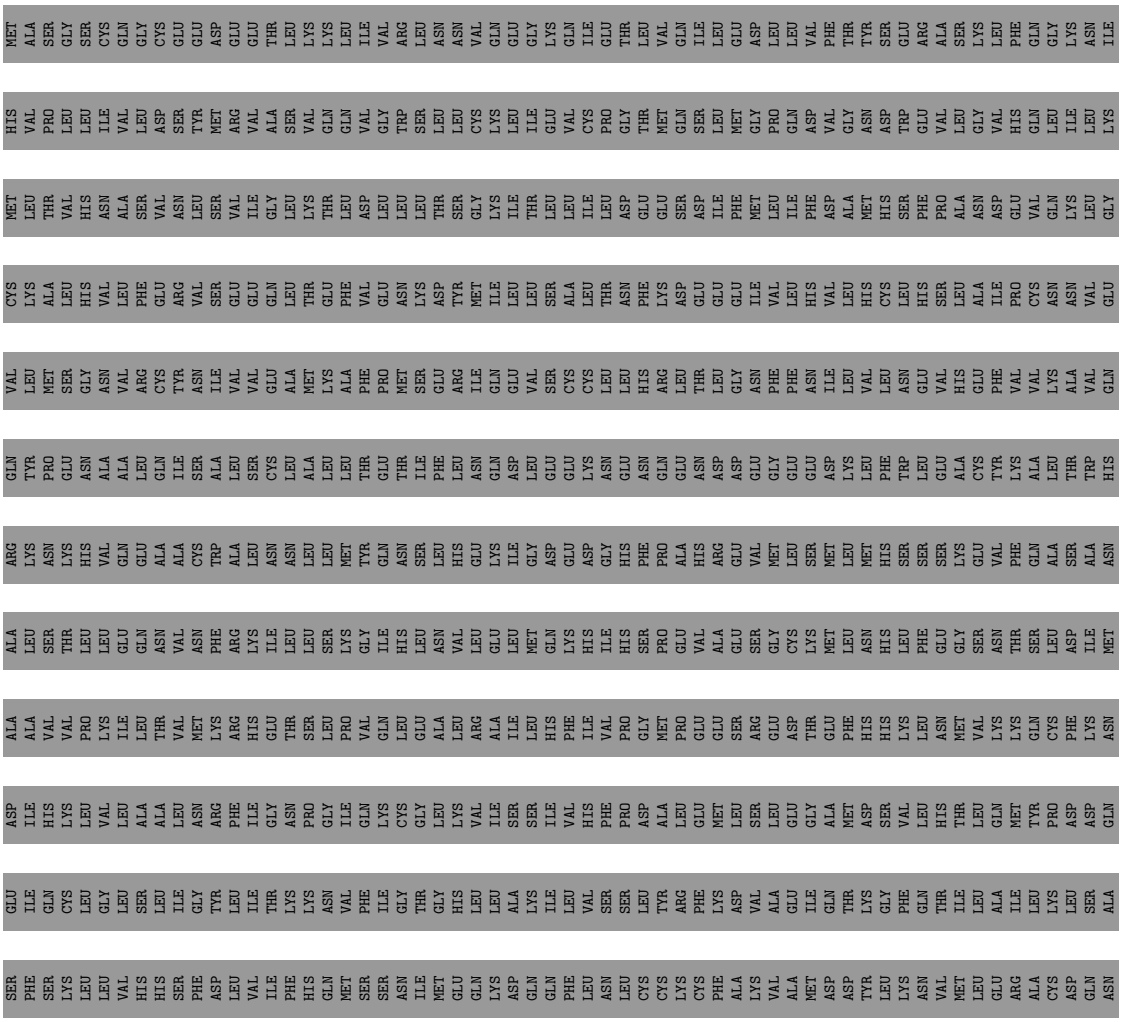
Chain 2-A:

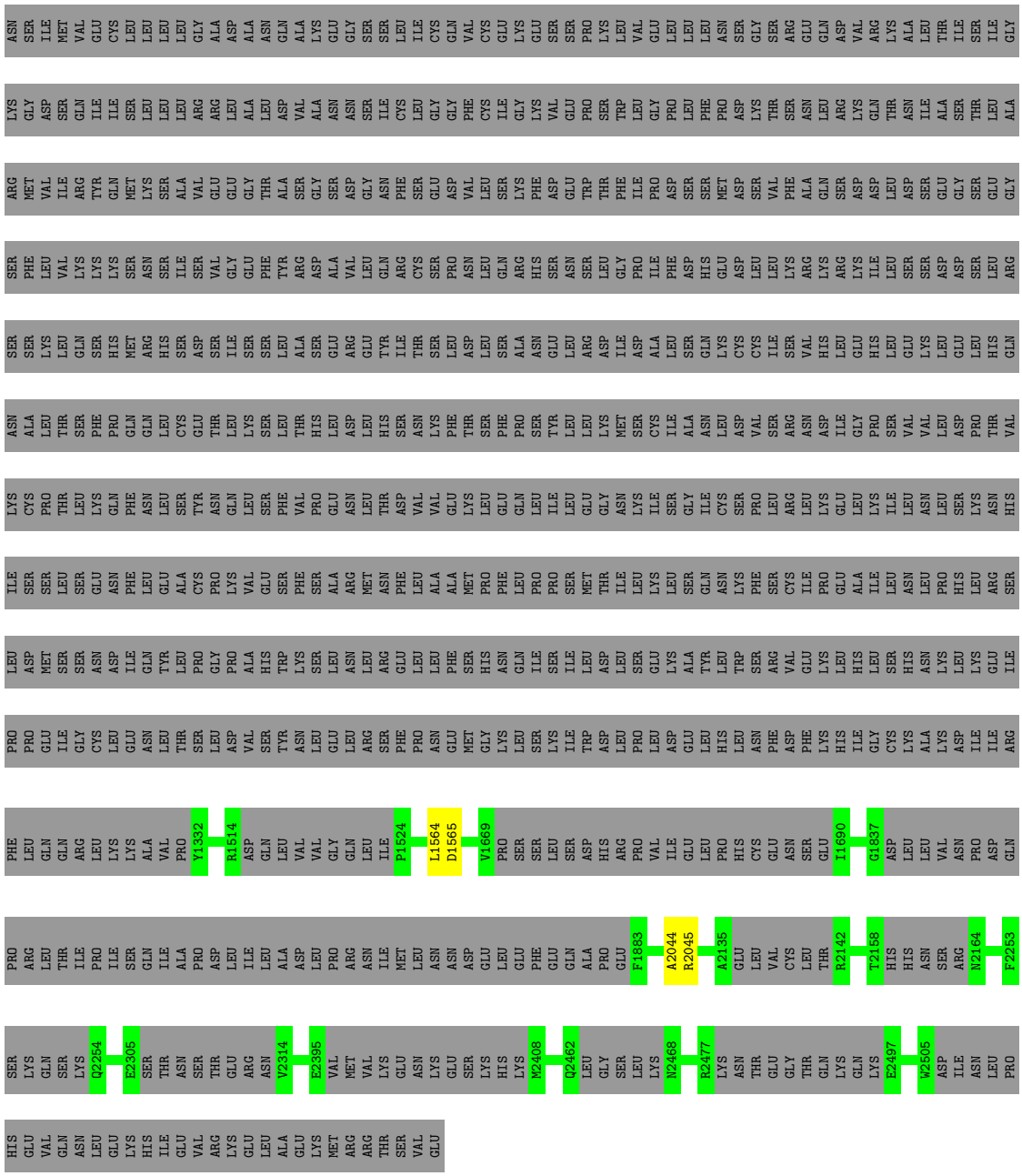




• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

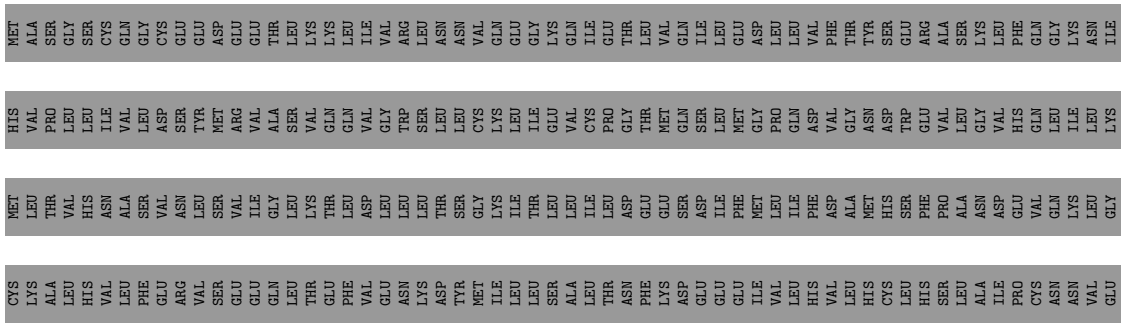
Chain 2-B: 41% 59%



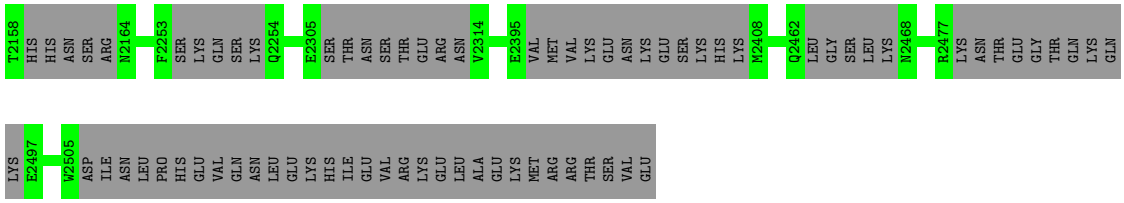


• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 3-A: 41% 59%

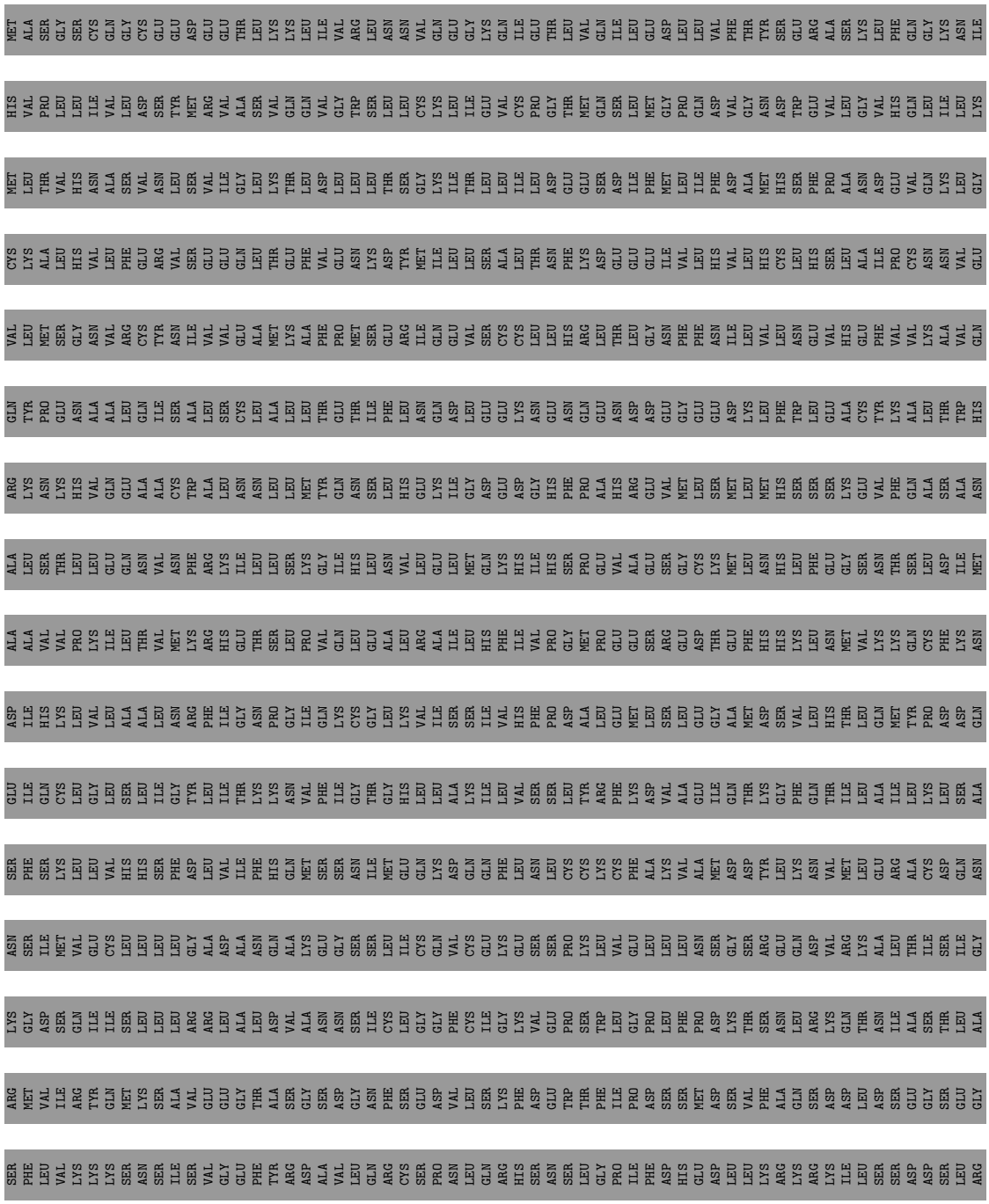


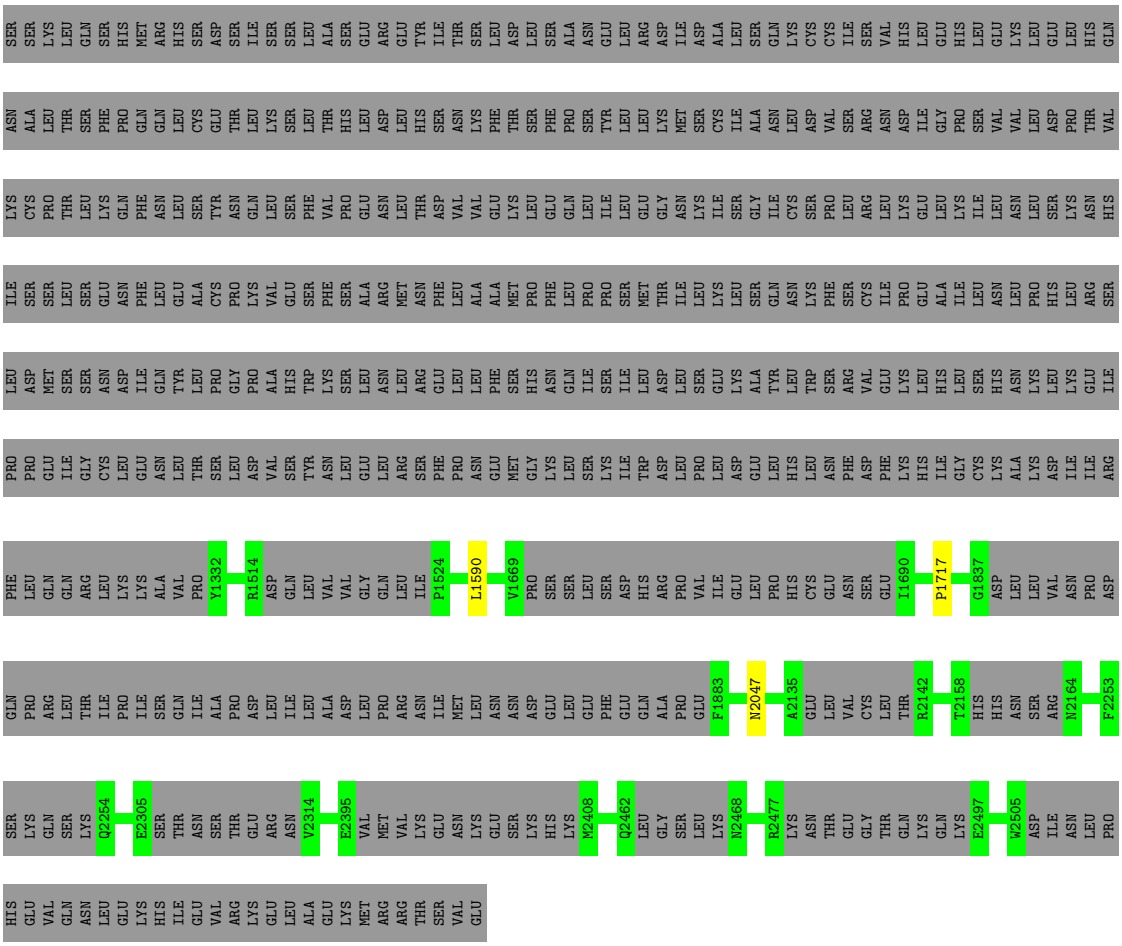
VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS ALA ALA VAL ALA ARG LEU LYS ALA LEU THR TRP HIS
GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LYS LEU PHE TRP LEU GLU GLU LYS ASN GLU ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE LYS ALA LEU THR TRP HIS
ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN LYS ALA LEU LEU ASN
ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY LYS LEU ASP
ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN LEU ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU VAL GLU GLU ASP ASP ILE HIS HIS LYS LEU THR THR ASP PHE LYS
ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ARG ALA ILE LEU LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO GLY ASP ALA LEU GLU GLU MET LEU SER LEU GLU THR ASP ASP GLN
GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU LEU ALA LYS ILE LEU VAL SER SER LYS ILE LEU TYR ARG PHE LYS ASP VAL ALA LYS VAL GLU GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA
SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN SER LEU LEU LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU ARG CYS GLN GLN ASP SER VAL LEU HIS THR ILE LEU GLU ARG ARG ALA CYS ASP GLN ASN
ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA ALA LEU THR ILE SER ILE GLY
LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA
ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN GLN ASP VAL ARG LYS ASP ASP SER GLU GLY SER GLU GLY
SER PHE LEU VAL LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU LYS PHE ILE PHE ASP HIS ASP LEU LEU LYS ARG LYS ARG ILE LEU SER LEU ARG
SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU GLU HIS LEU GLU HIS GLN
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LYS ALA ASN ASP SER ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO LEU VAL HIS THR
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU VAL PRO GLU VAL GLU LYS GLU GLN LEU ILE LEU LEU GLU GLY ILE CYS SER PRO LEU ARG LEU LYS LYS ILE LYS ILE SER GLY ILE CYS SER LYS ASN HIS
ILE SER SER LEU SER GLU ALA ALA PHE SER ALA ALA ALA MET PRO PHE LEU ALA ALA ARG MET ASN PHE LEU PRO LEU LEU MET PRO SER GLU MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER LEU ASP ILE ILE LEU ARG SER
LEU ASP MET SER SER ASN ILE GLN TYR LEU PRO GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG GLU LEU LEU ASP LEU SER GLU LYS ALA TYR LEU TRP SER ARG VAL GLU LYS LEU LEU HIS LYS LEU LEU SER HIS LYS LEU LYS GLU ILE
PRO PRO GLU ILE GLY CYS LEU GLU ASN LEU THR SER LEU ASP VAL SER TYR ASN LEU GLU SER PHE PRO ASN GLU MET GLY LYS LEU GLN ILE LYS ILE LEU TRP ASP LEU PRO LEU ASP GLU LEU HIS LEU ASN PHE ASP PHE LYS HIS LYS ASP ILE PRO ARG
PHE LEU GLN GLN ARG LEU LYS ALA VAL PRO Y1332 R1514 ASP GLN LEU VAL VAL GLY GLN LEU ILE P1524 Q1563 L1564 D1565 E1566 N1567 V1669 PRO SER SER LEU SER ASP HIS ARG PRO VAL ILE GLU LEU PRO HIS CYS GLU ASN SER GLU I1690 R1731 G1837 ASP LEU LEU
VAL ASN PRO ASP GLN PRO ARG LEU THR ILE PRO ILE SER GLN ILE ALA PRO ASP LEU ILE LEU ALA ASP LEU PRO ASN ILE MET LEU ASN ASP GLU LEU GLU PHE GLU GLN ALA PRO GLU F1883 A2044 F2079 P2080 N2081 E2082 A2135 GLU LEU VAL CYS LEU THR R2142



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

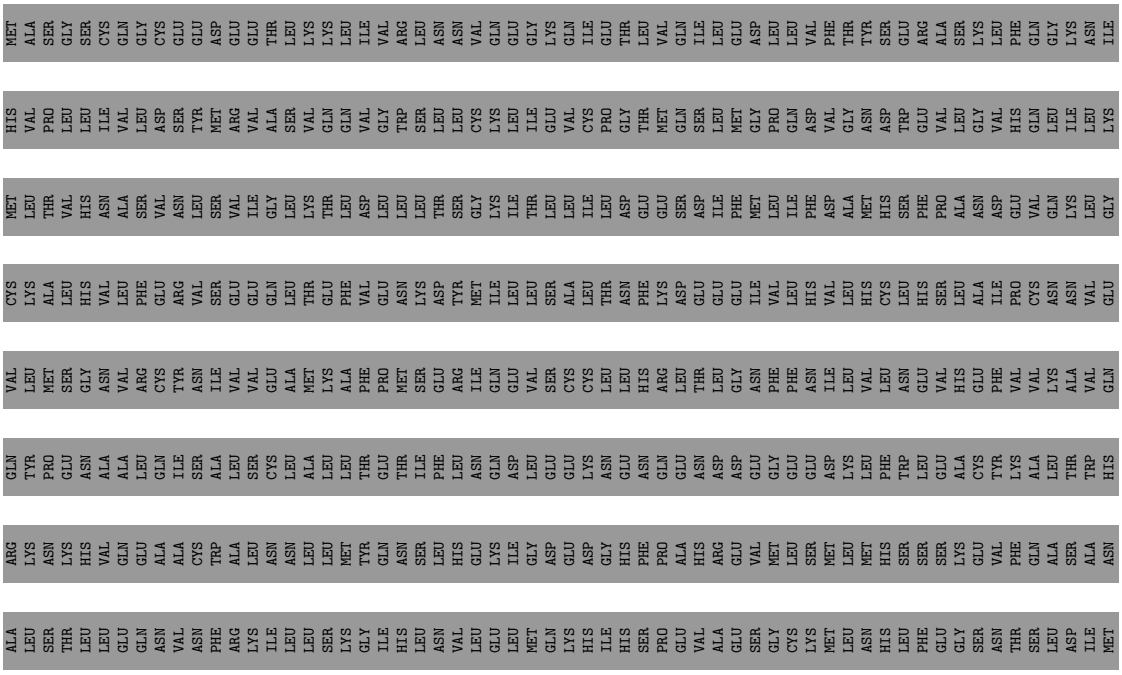
Chain 3-B:

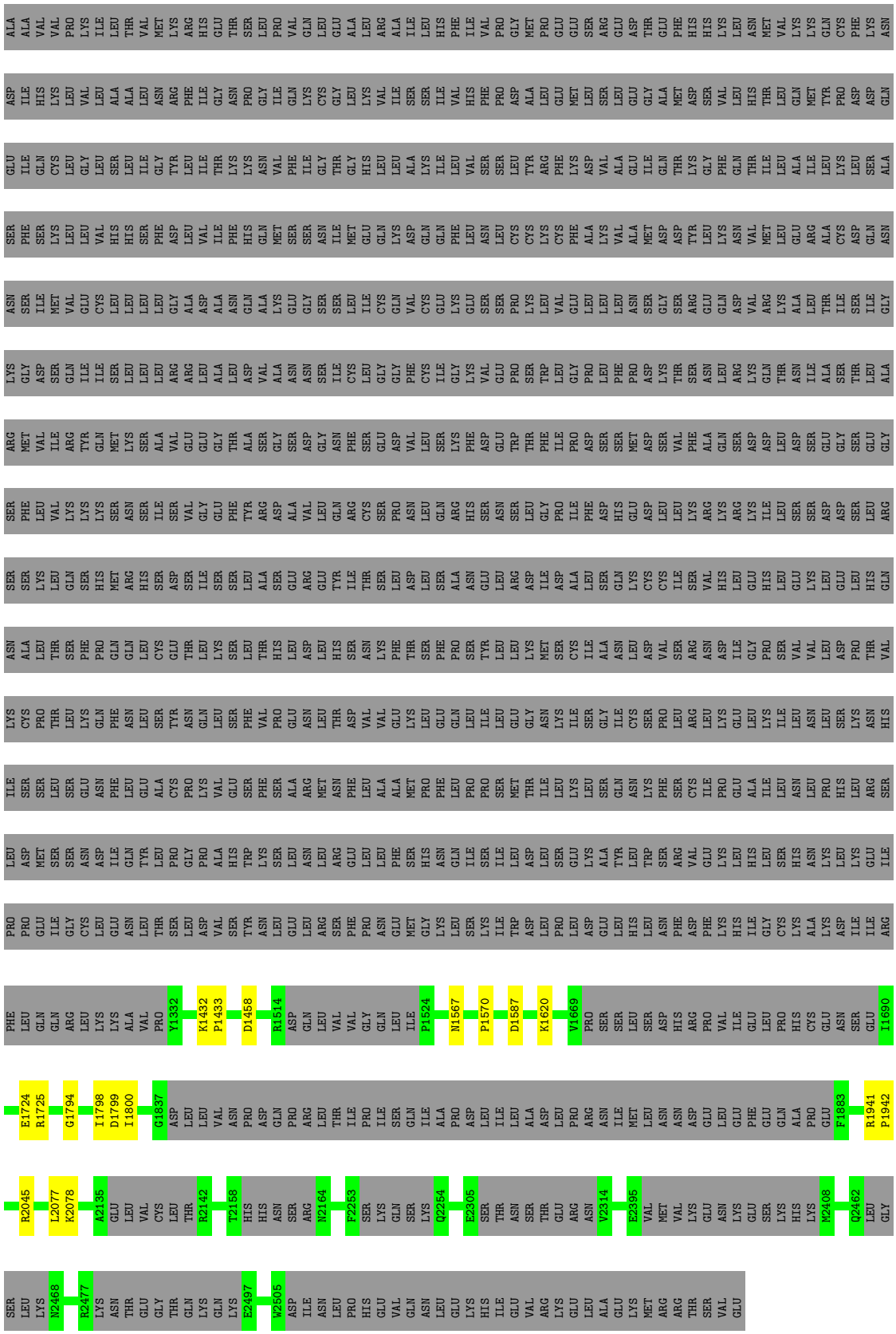




- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 4-A:





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 4-B: 41% 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLN GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

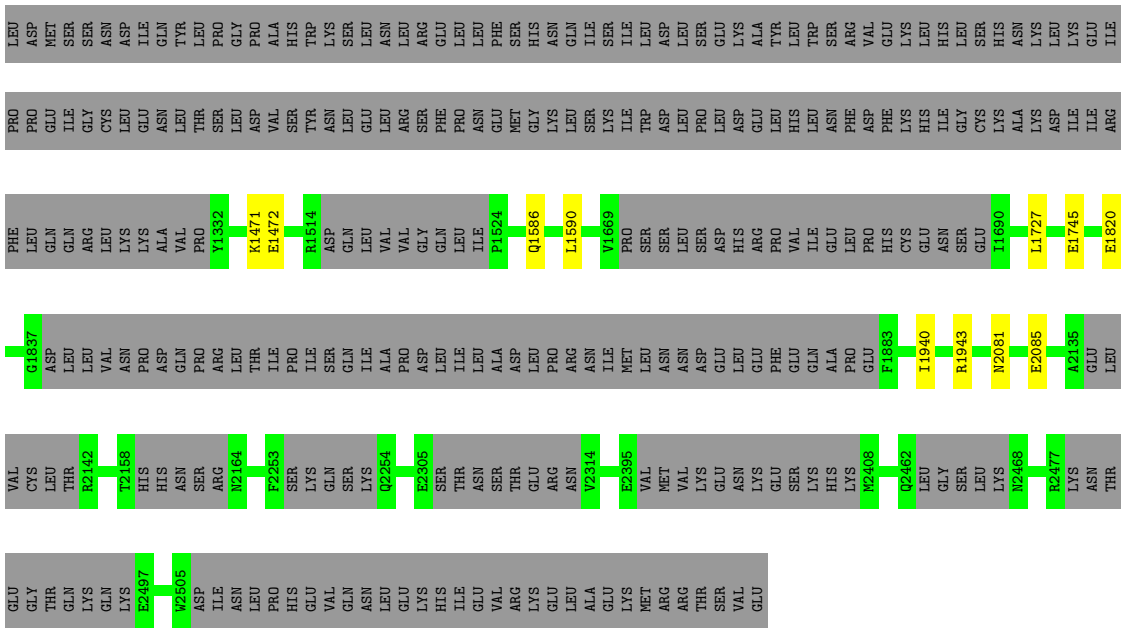
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

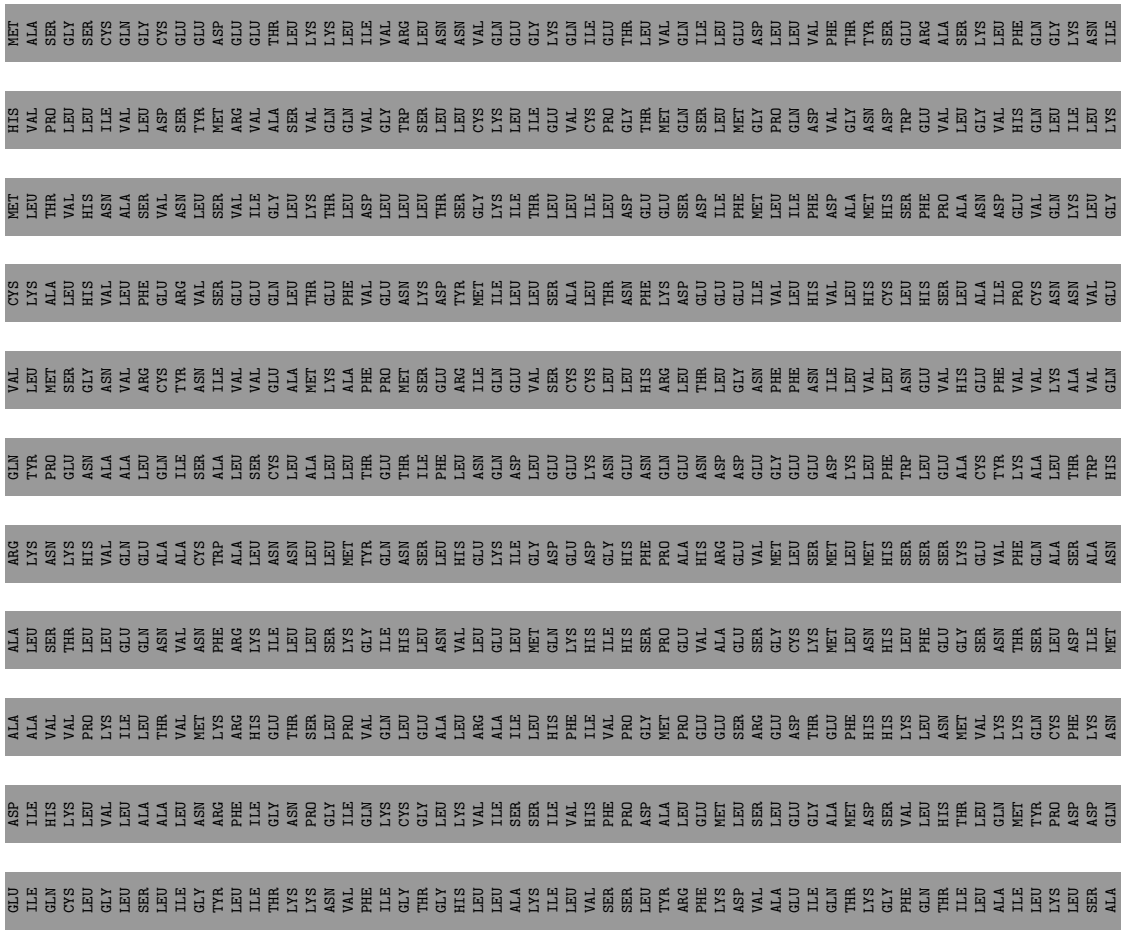
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

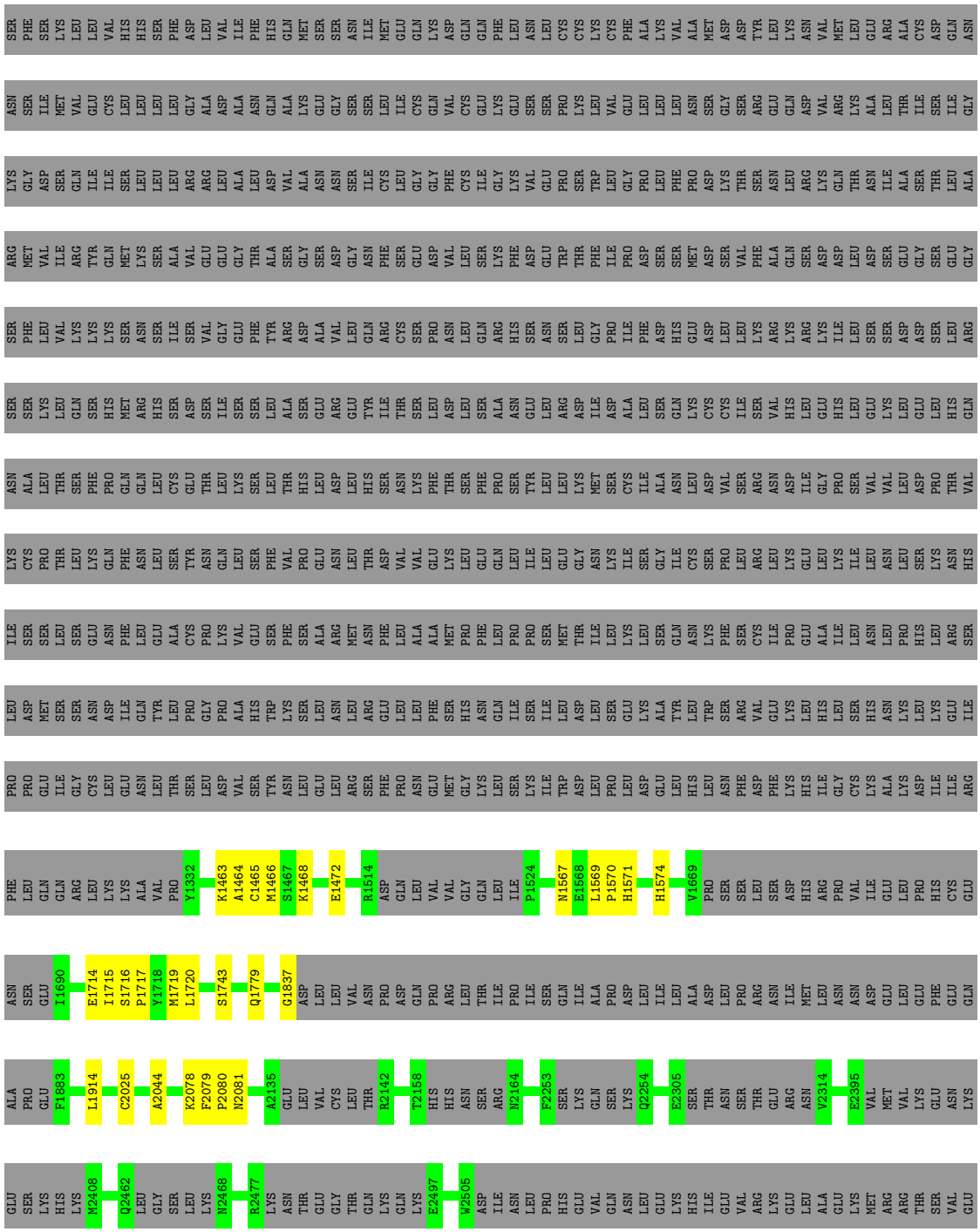
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

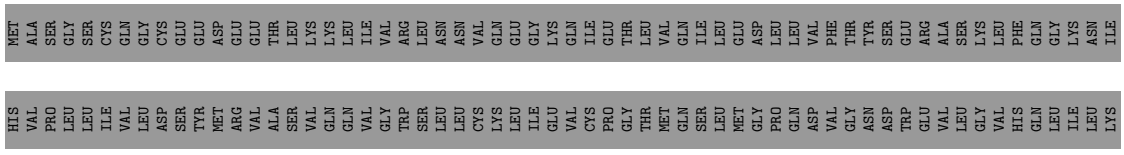
Chain 5-A: 40% • 59%





• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 5-B:



MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

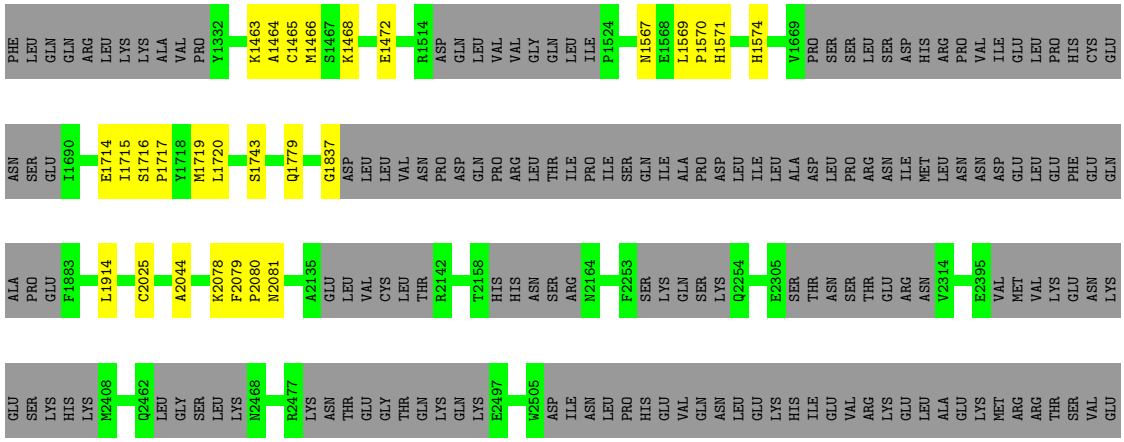
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER

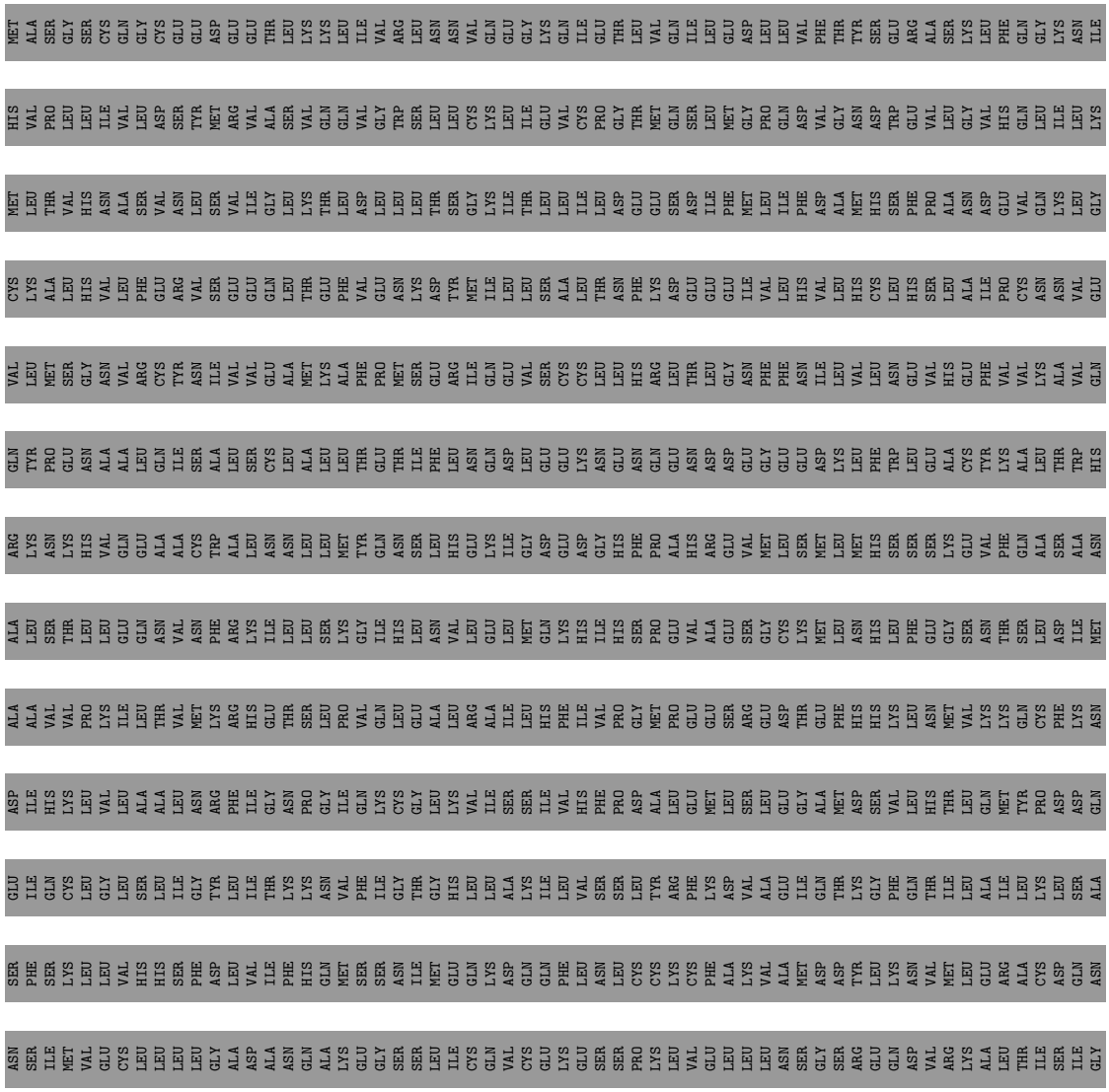
LEU ASP MET SER SER ASN ASP ILE GLN TYR LEU PRO GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG GLU LEU LEU PHE SER HIS ASN GLN ILE SER ILE LEU ASP LEU SER GLU LYS ALA TYR LEU TRP SER ARG VAL GLU LYS LEU HIS LEU SER HIS ASN LYS LEU LYS GLU ILE

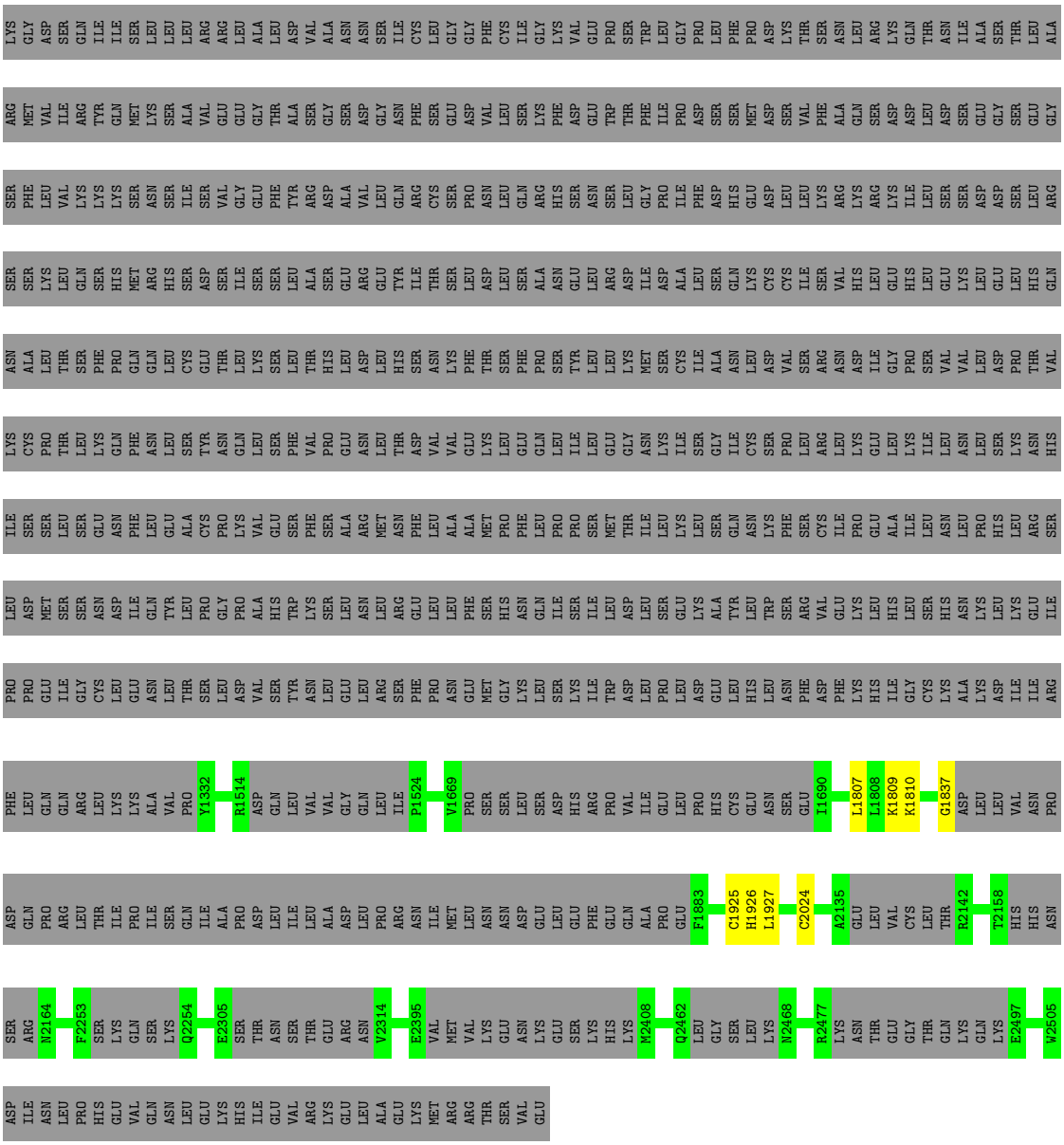
PRO PRO GLU ILE GLY CYS LEU GLU ASN LEU THR SER LEU ASP VAL SER TYR ASN LEU GLU LEU ARG SER PHE PRO ASN GLU MET GLY LYS LEU SER LYS ILE TRP ASP LEU PRO LEU ASP GLU LEU HIS LEU ASN PHE ASP PHE LYS HIS ILE GLY CYS LYS ALA LYS ASP ILE ILE ARG



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 6-A: 41% 59%





• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

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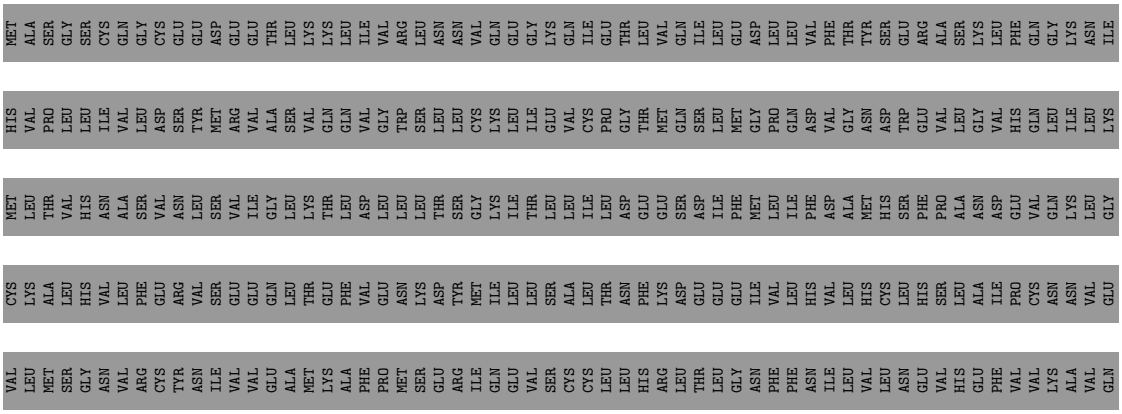

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LYS LEU LEU GLU GLU LYS ASN GLU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS
ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS HIS PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER LYS GLU VAL GLN ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLN ALA SER ASN ALA
ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS GLU LEU ASN VAL LEU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER LYS THR GLY ASN ALA
ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN
ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU GLY ALA MET MET ASP SER LEU GLU GLY ALA MET ASP TYR LEU LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU ASN
GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY GLN LEU LEU ALA LYS LYS LEU TYR ARG PHE LYS ASP VAL GLU ILE GLN THR ILE LEU ALA ILE LEU LYS LEU ASN
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ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP SER GLU GLY GLU GLU GLY
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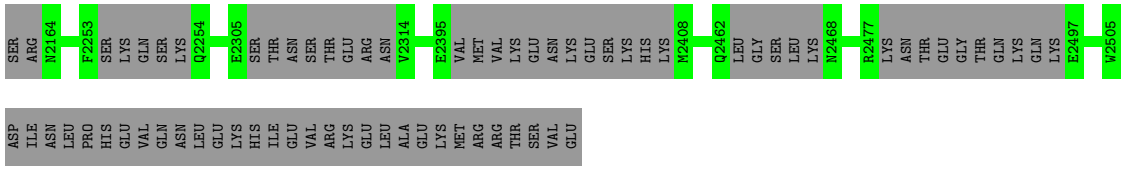
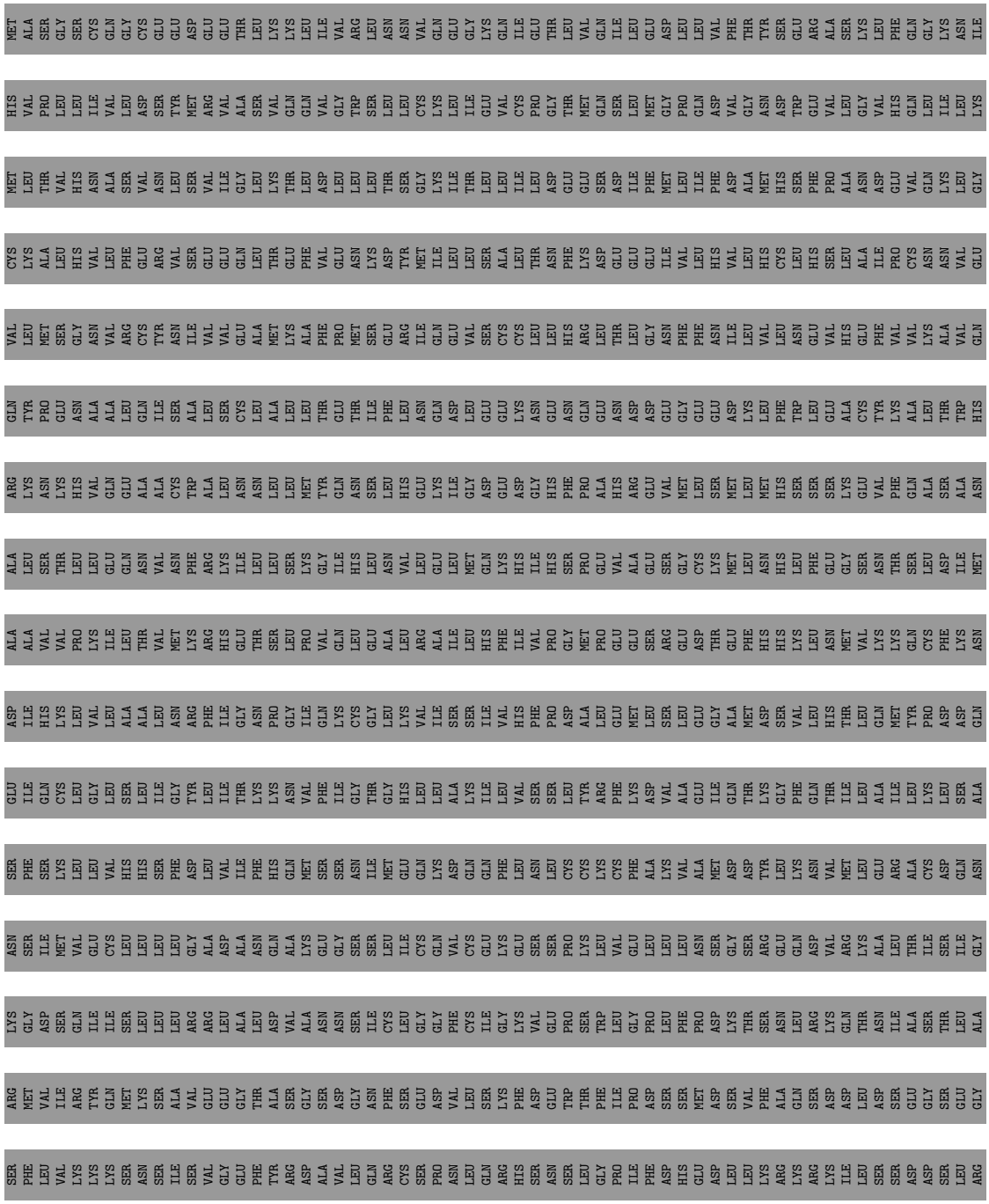
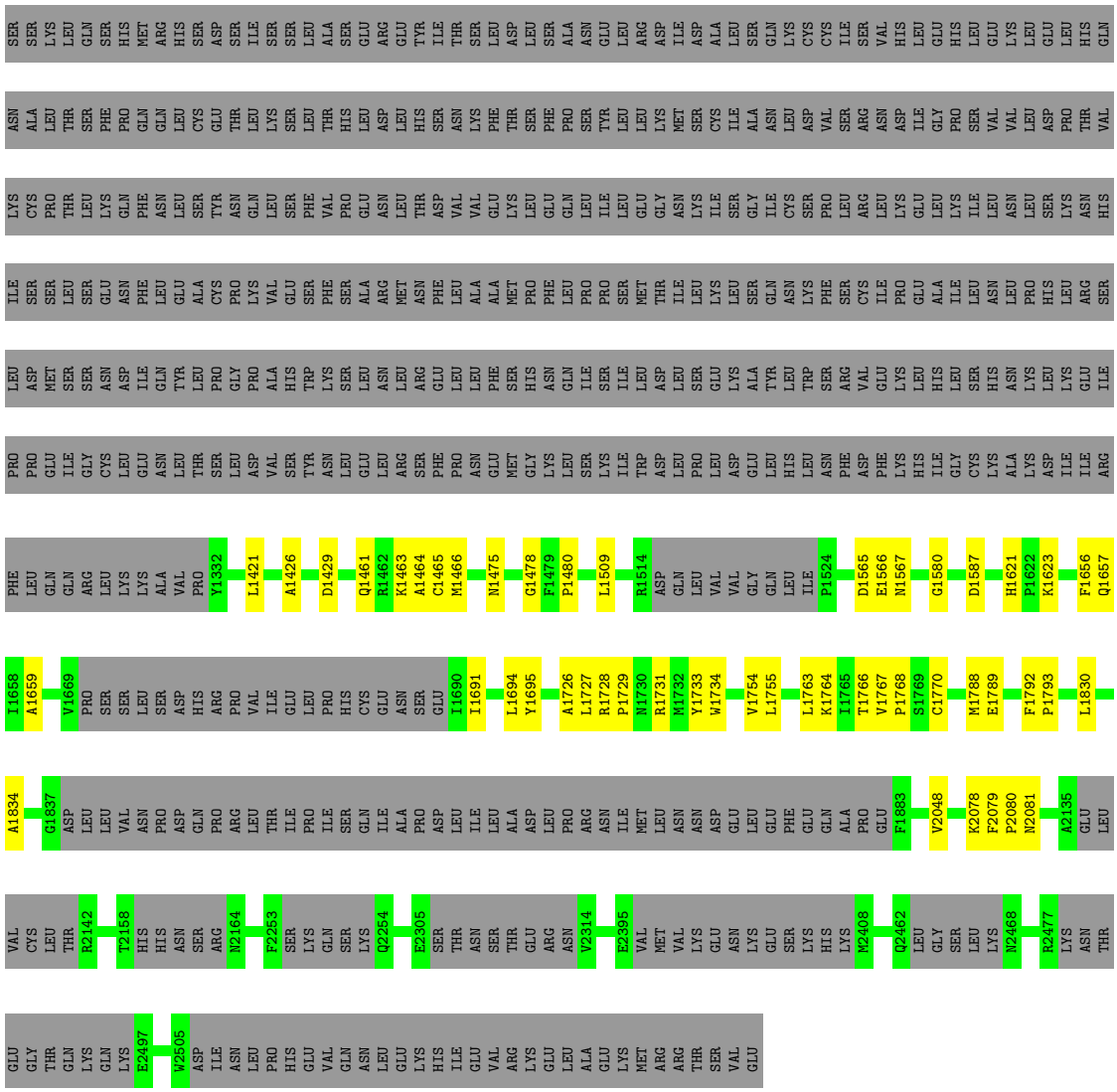
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER LEU LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE SER VAL HIS LEU ASP LEU ILE LEU ASP ASN LEU ILE LYS LEU ILE LEU ILE LEU ASN ILE GLU PRO GLU ALA ILE LEU GLY PRO SER VAL VAL LEU ASP PRO HIS LEU ARG SER
LEU ASP MET SER SER ASN ASP ILE GLN TYR LEU PRO GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG GLU LYS SER GLU ILE LEU SER LYS ALA TYR LEU TRP SER GLU LYS LEU SER GLN ASN LYS PHE SER ARG VAL GLU LYS LEU HIS LEU LEU ILE SER ILE LEU ILE LEU ASN LYS LEU LYS GLU ILE
PRO PRO GLU ILE GLY CYS LEU GLU ASN LEU THR SER LEU ASP VAL SER TYR ASN LEU GLU ARG SER PHE PRO ASN GLU MET GLY LYS LEU GLU GLN ILE SER LYS ILE TRP ASP LEU PRO LEU ASP GLU LEU HIS LEU ASN PHE ASP PHE LYS HIS ILE GLY LYS HIS LEU ASP ILE ILE ARG
PHE LEU GLN GLN ARG LEU THR ILE LYS LYS ALA VAL PRO Y1332 R1514 ASP GLN LEU VAL VAL GLY GLN LEU ILE P1524 D1565 E1566 V1669 PRO SER SER LEU SER ASP HIS ARG PRO VAL ILE GLU LEU PRO HIS CYS GLU ASN SER GLU I1690 Q1779 G1837 ASP LEU LEU VAL ASN PRO
ASP GLN PRO ARG LEU THR ILE PRO ILE SER GLN ILE ALA PRO ASP LEU ILE LEU ALA ASP LEU PRO ARG ASN ILE MET LEU ASN ASP GLU LEU GLU PHE GLU GLN ALA PRO GLU F1883 S1913 K2078 N2081 A2135 GLU LEU VAL CYS LEU THR R2142 T2158 HIS HIS ASN



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 7-A: 39% • 59%





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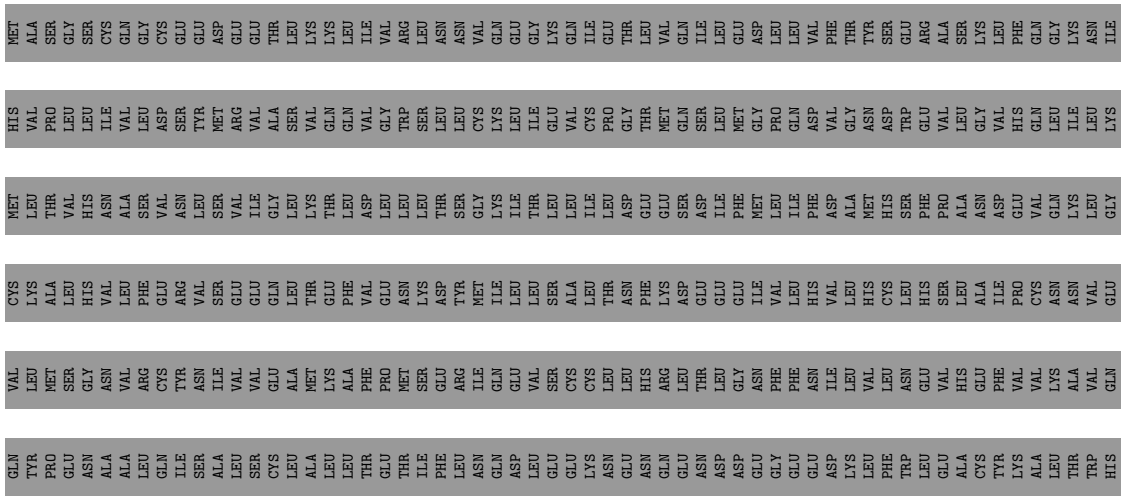

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ASP	SER	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN
LEU	LEU	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS
LEU	SER	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS
VAL	ASP	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL
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PRO	ARG	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU
ASP	PRO	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA
GLN	VAL	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA
PRO	ILE	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS
ARG	GLU	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP
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THR	PRO	L1421	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU
ILE	HIS		VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN
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GLU	P1793	VAL	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG
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ALA	D1799	P1524	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET
PRO			PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU
GLU	F1816	D1565	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET
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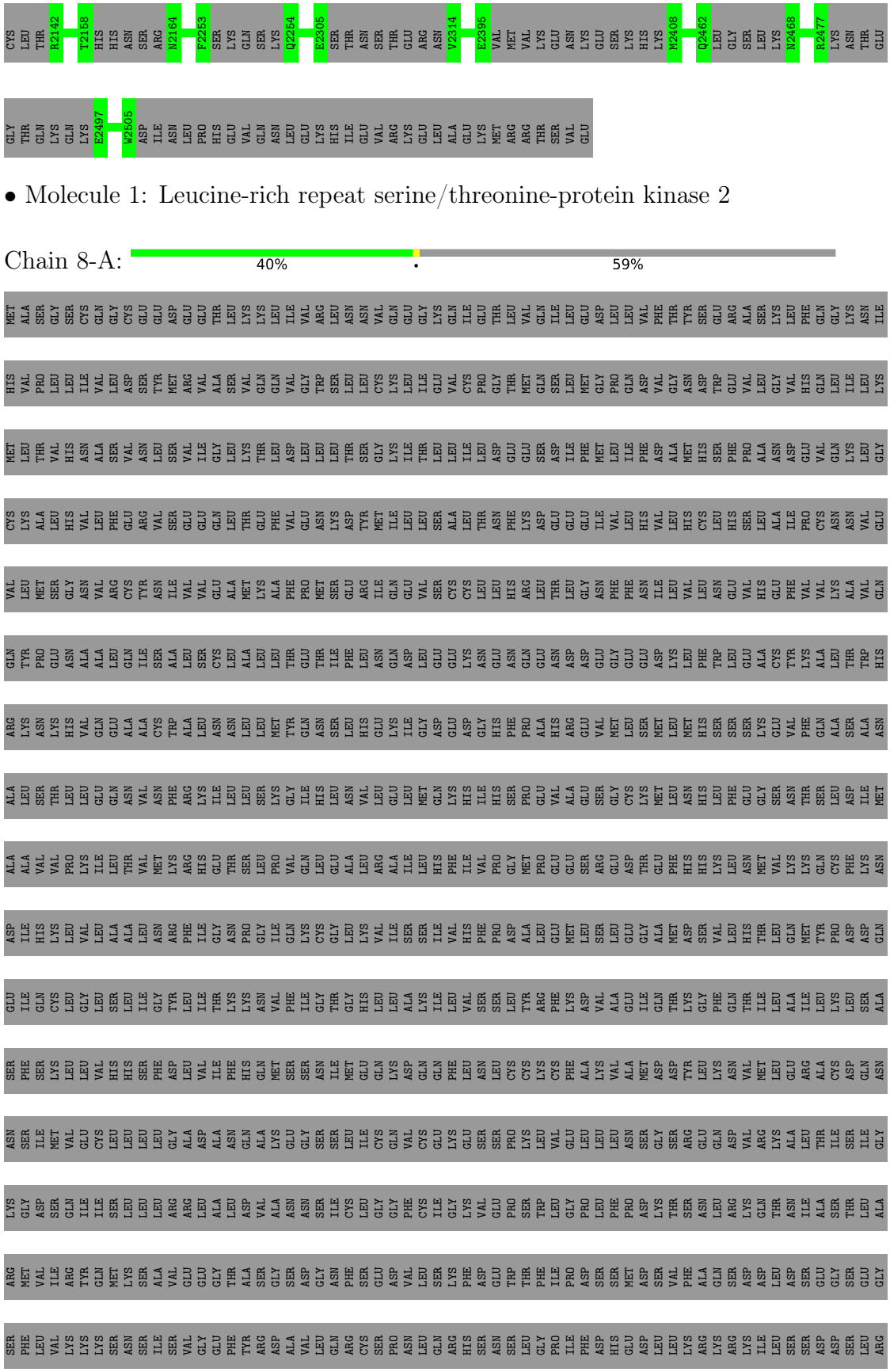
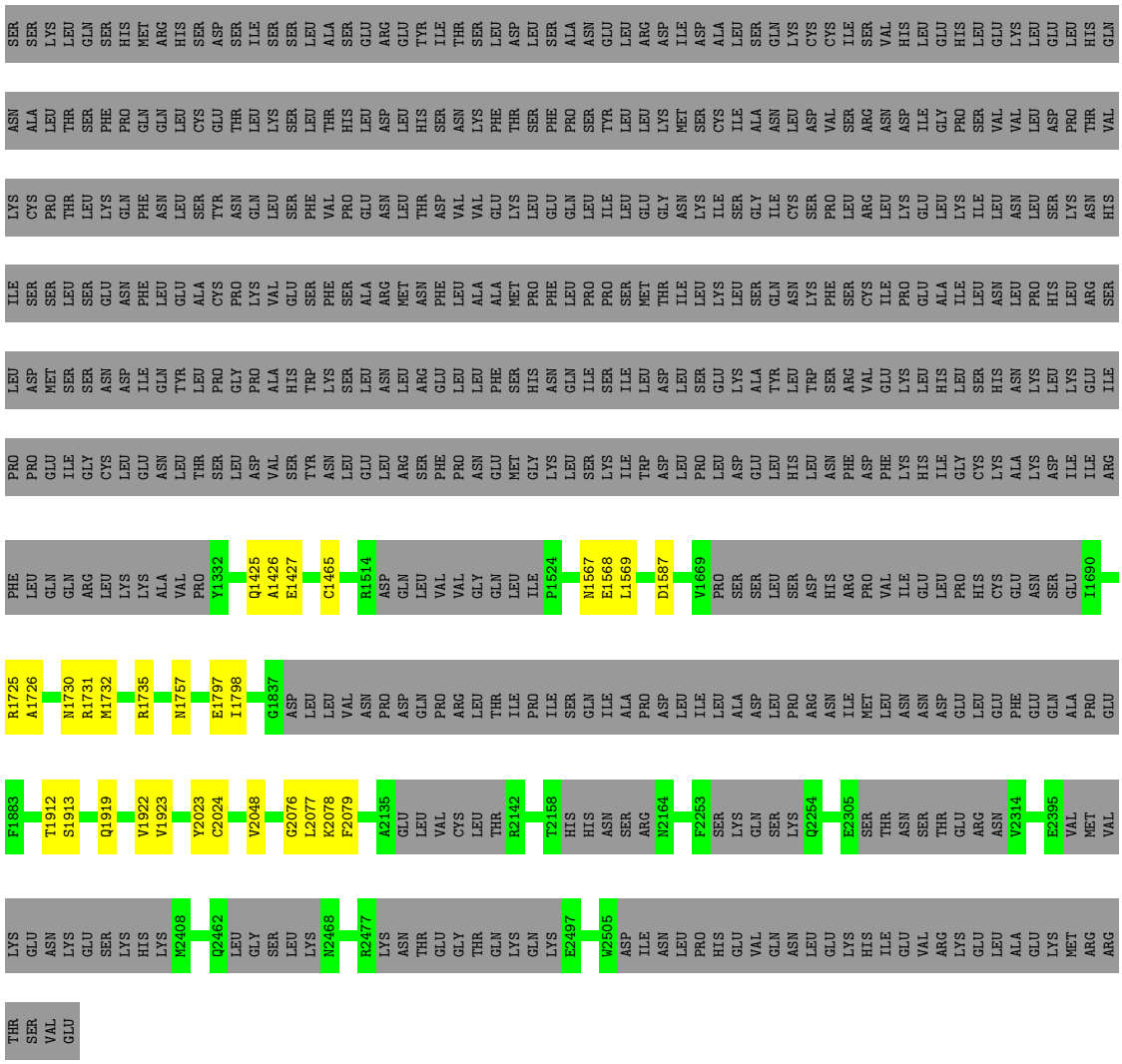
	D1818	N1567	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER
V2048	G1819		HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER
	E1820	G1580	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER
K2078	E1821		GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS
F2079	H1822	D1587	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU
P2080	Q1823		LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL
N2081	K1824	F1656	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE
	I1825	Q1657	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN
A2135	L1826	I1658	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA
GLU		A1659	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER
LEU	L1830		ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA
VAL	M1831	V1669	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN



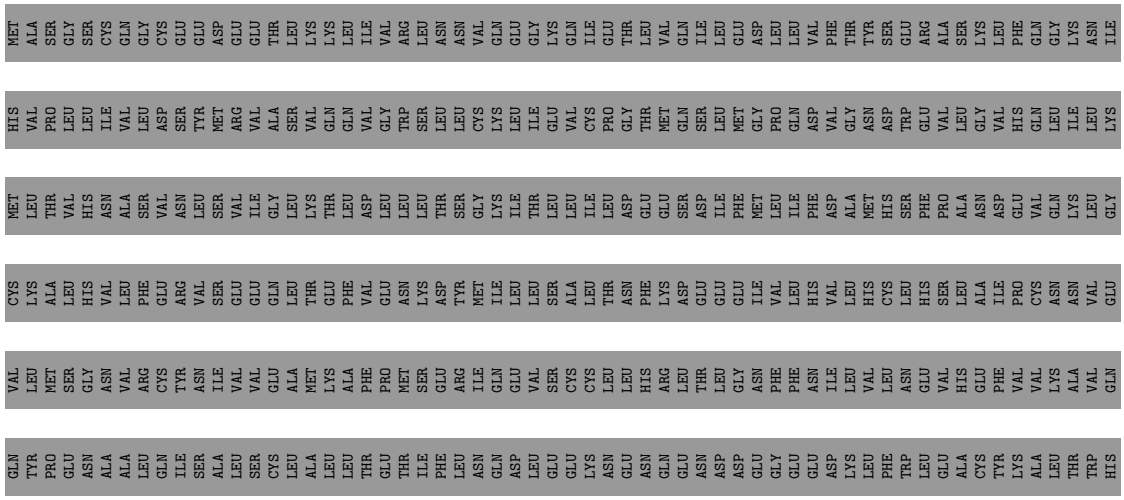
• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 8-A: 40% • 59%



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 8-B:



F1883	R1725	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA	ARG
	A1726	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS
T1912		GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN
S1913	N1730	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS
	R1731	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS
Q1919	M1732	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL
		LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN
V1922	R1735	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU
V1923		ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA
	N1757	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA
Y2023		PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS
C2024	E1797	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP
	I1798		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA
V2048		Q1425	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU
	G1837	A1426	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN
G2076	ASP	E1427	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN
L2077	LEU		TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU
K2078	LEU	C1465	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU
F2079	VAL		LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET
	ASN	R1514	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR
A2135	PRO	ASP	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN
GLU	ASP	GLN	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN
LEU	GLN	LEU	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER
VAL	PRO	VAL	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU
CYS	ARG	VAL	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS
LEU	LEU	GLY	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU
THR	THR	GLN	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS
R2142	ILE	LEU	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE
	PRO	ILE	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY
T2158	ILE	P1524	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP
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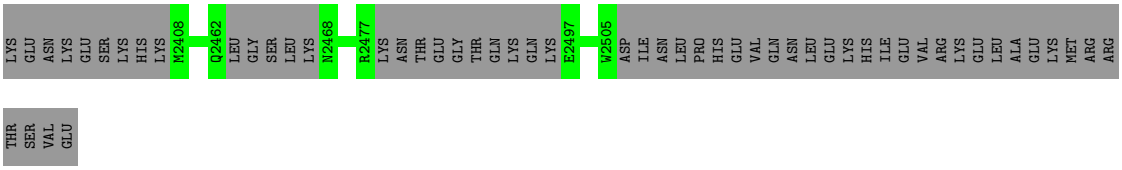
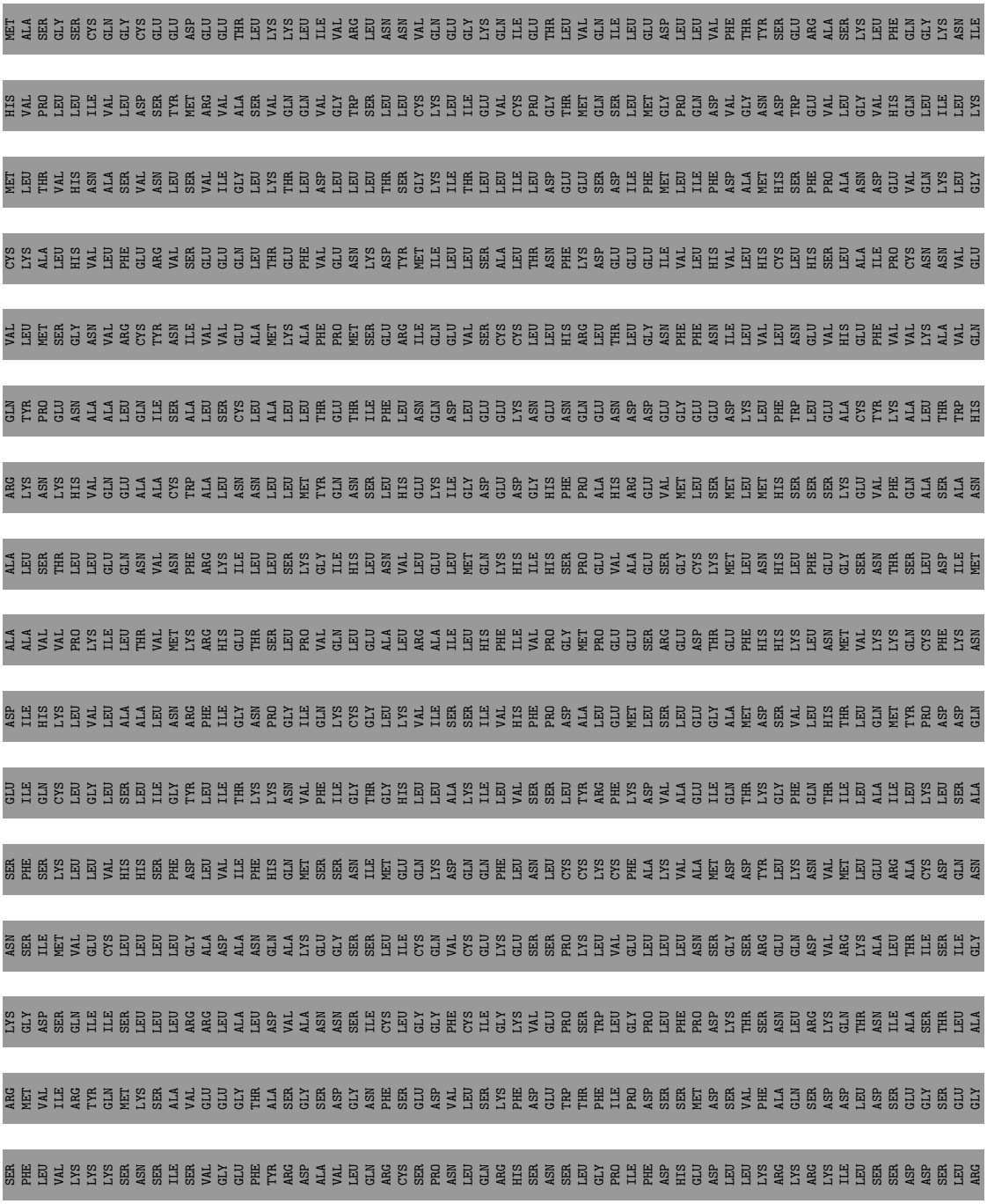
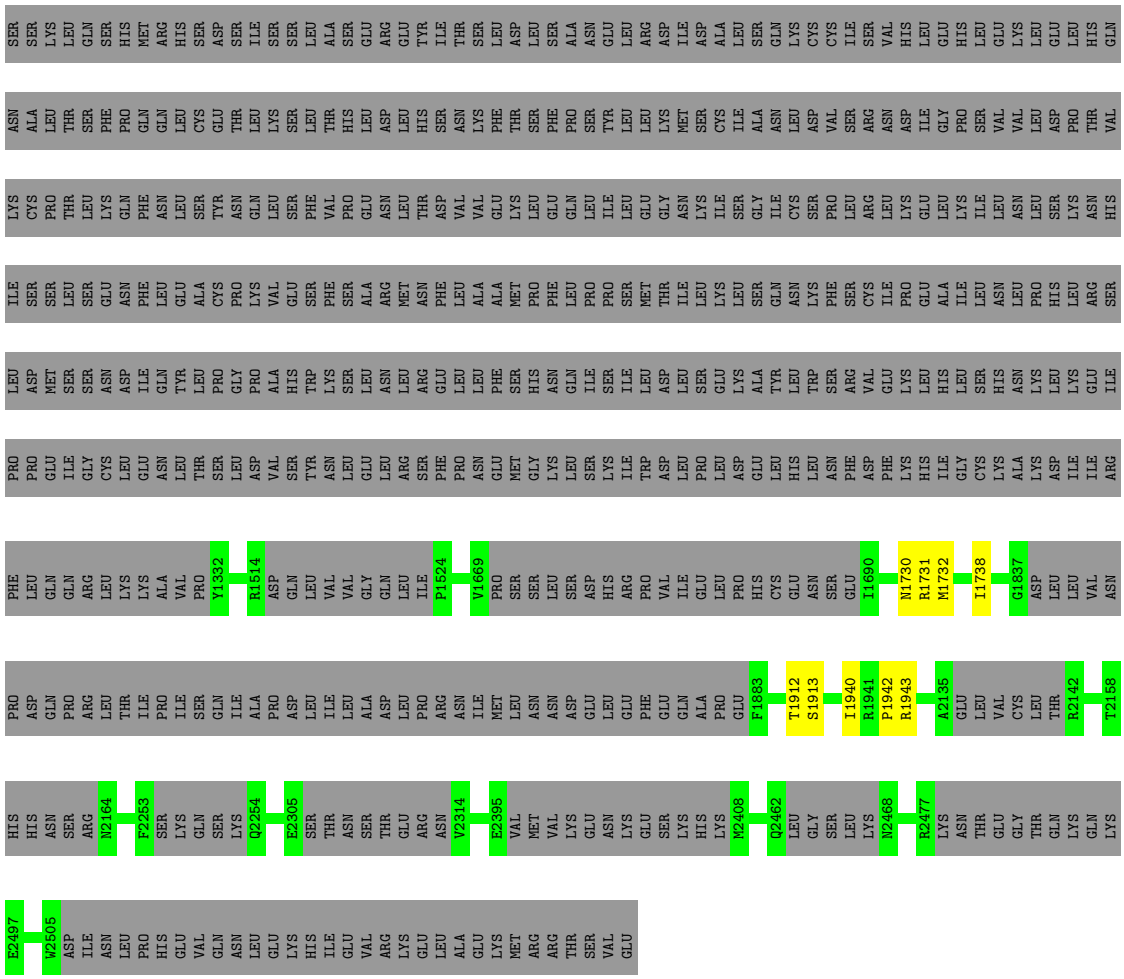
HIS	GLN	N1567	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP
ASN	ILE	E1568	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY
SER	ALA	L1569	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS
ARG	PRO		TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE
N2164	ASP	D1587	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO
	LEU		LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA
F2253	ILE	V1669	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS
SER	LEU	PRO	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG
LYS	ALA	SER	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU
GLN	ASP	SER	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL
SER	LEU	LEU	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET
LYS	PRO	SER	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU
Q2254	ARG	ASP	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER
	ASN	HIS	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET
E2305	ILE	ARG	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU
SER	MET	PRO	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET
THR	LEU	VAL	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS
ASN	ASN	ILE	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER
SER	ASN	GLU	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER
THR	ASP	LEU	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER
GLU	GLU	PRO	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS
ARG	LEU	HIS	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU
ASN	GLU	CYS	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL
V2314	PHE	GLU	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE
	GLU	ASN	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN
E2395	GLN	SER	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA
VAL	ALA	GLU	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER
MET	PRO	I1690	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA
VAL	GLU		ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

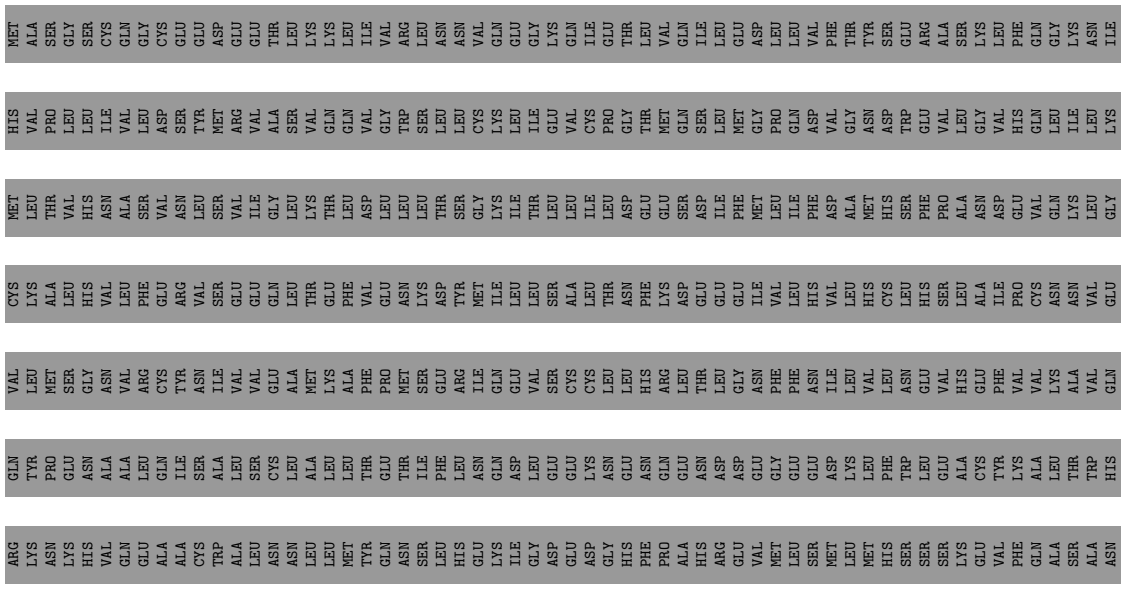
Chain 9-A: 41% 59%





• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 9-B:



VAL	PRO	SER	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA
LYS	GLU	GLU	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU
GLU	F1883	I1690	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER
ASN			GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR
LYS	K1910	R1728	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU
GLU		P1729	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU
SER	S1913		LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU
LYS		Y1733	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN
HIS	G1939	W1734	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN
LYS	I1940		VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL
M2408	R1941	S1752	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN
	P1942		Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE
Q2462		I1798		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG
LEU	V2043		G1478	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS
GLY	A2044	E1820		VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE
SER			R1514	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU
LEU	N2047	G1837	ASP	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU
LYS		ASP	GLN	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER
N2468	N2081	LEU	LEU	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS
	E2082	LEU	VAL	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY
R2477		VAL	VAL	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE
LYS	A2135	ASN	GLY	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS
ASN	GLU	PRO	GLN	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU
THR	LEU	ASP	LEU	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN
GLU	VAL	GLN	ILE	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL
GLY	CYS	PRO	P1524	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU
THR	LEU	ARG		GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU
GLN	THR	LEU	K1551	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU
LYS	R2142	THR		GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET
GLN		ILE	Q1591	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN
LYS	T2158	PRO	L1592	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS
E2497	HIS	ILE	S1593	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS
	HIS	SER		LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE
W2505	ASN	GLN	Q1648	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS
ASP	SER	ILE		TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER
ILE	ARG	ALA	F1656	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO
ASN	N2164	PRO		LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU
LEU		ASP	G1663	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL
PRO	F2253	LEU		LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA
HIS	SER	ILE	Y1666	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU
GLU	LYS	LEU		GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER
VAL	GLN	ALA	V1669	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY
GLN	SER	ASP	PRO	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS
ASN	LYS	LEU	SER	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS
LEU	Q2254	PRO	SER	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET
GLU		ARG	LEU	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU
LYS	E2305	ASN	SER	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN
HIS	SER	ILE	ASP	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS
ILE	THR	MET	HIS	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU
GLU	ASN	LEU	ARG	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE
VAL	SER	ASN	PRO	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU
ARG	THR	ASN	VAL	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY
LYS	GLU	ASP	ILE	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER
GLU	ARG	GLU	GLU	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN
LEU	ASN	LEU	LEU	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR
ALA	V2314	GLU	PRO	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER
GLU		PHE	HIS	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU
LYS	E2395	GLU	CYS	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP
MET	VAL	GLN	GLU	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE
ARG	MET	ALA	ASN	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET

ARG THR SER VAL GLU

- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 10-A: 40% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER SER TYR MET ARG VAL ALA ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU LEU GLY VAL HIS GLN ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS VAL LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU LEU SER LEU GLU GLU GLY MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS GLU GLN LEU LEU ALA LYS ILE LEU VAL SER SER LEU ALA ALA LYS LYS VAL ALA GLU ILE GLN THR THR LYS GLY PHE GLN THR LEU LYS LEU ALA ILE LEU LYS ARG PHE LYS ASP VAL ALA GLU SER LEU GLU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU LEU GLN ILE ALA ILE LEU ARG CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

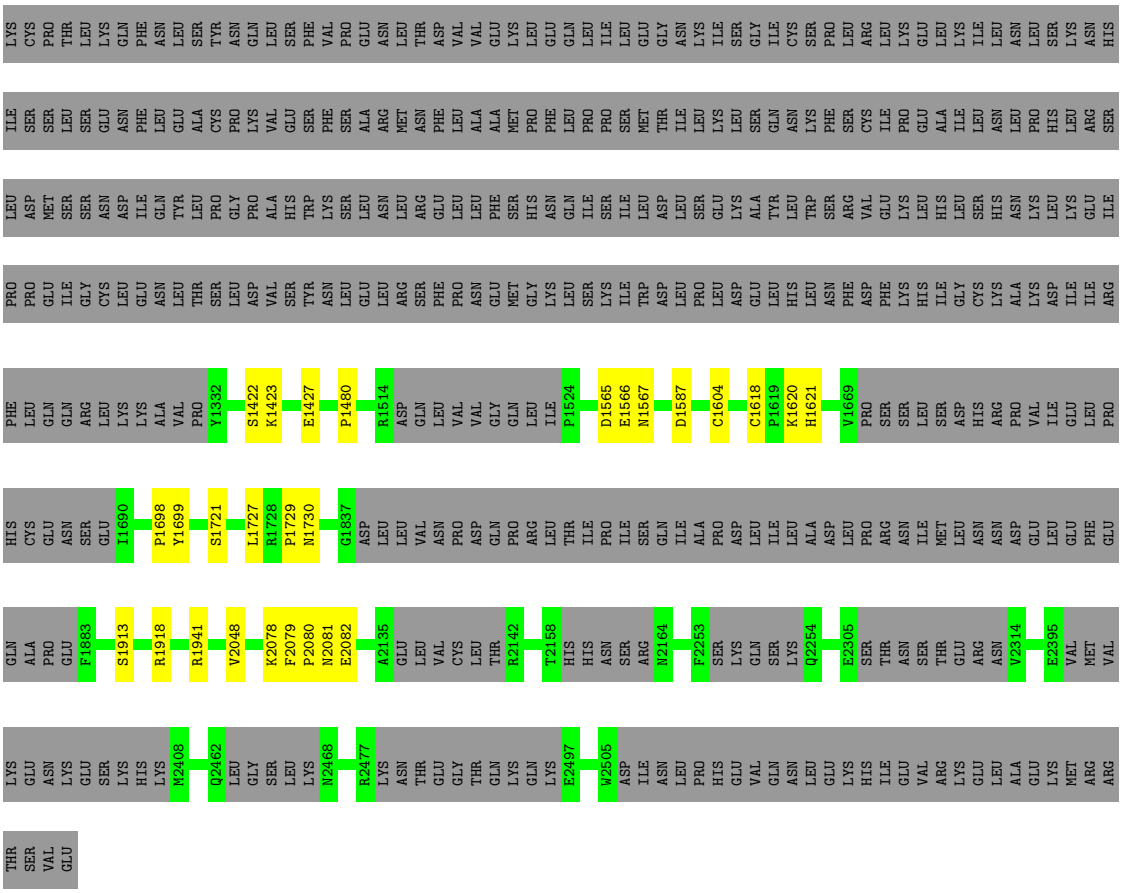
LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA ALA LEU ASP VAL ALA ASN ASN SER SER ILE CYS LEU GLU GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU GLN LYS LEU ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN GLU SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PHE ASP ALA ASN SER LEU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

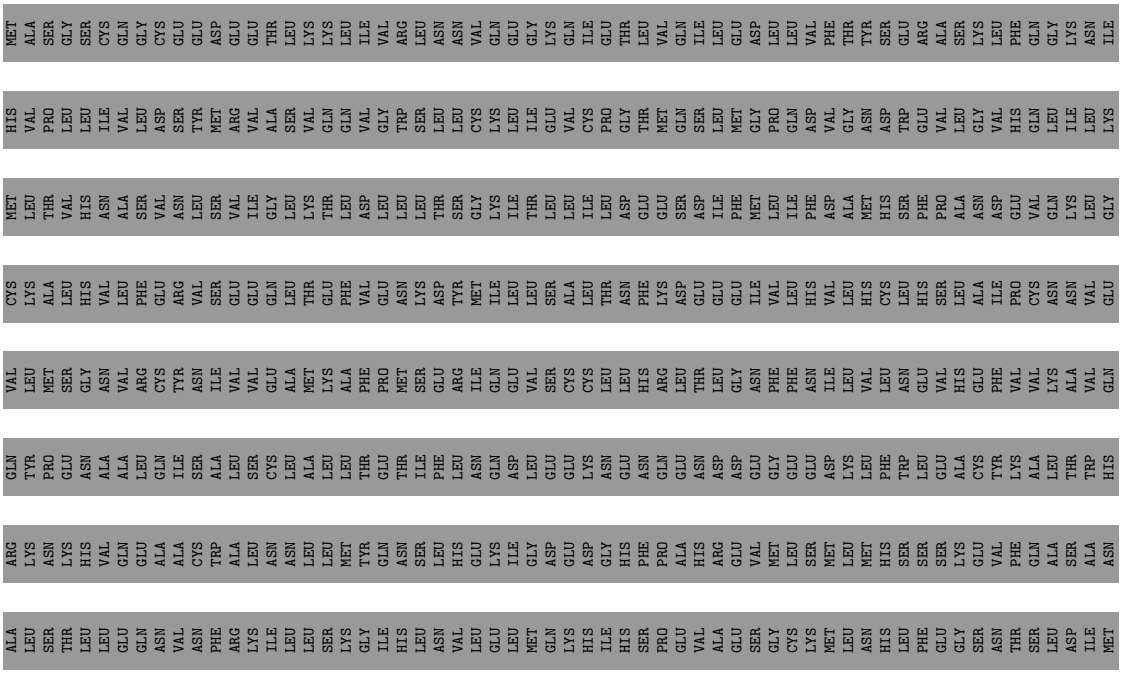
SER SER LYS LEU GLN SER HIS MET ARG HIS SER SER ASP SER ILE SER SER LEU ALA ALA SER GLU GLU ARG GLU TYR ILE THR SER LEU SER SER LEU ASP HIS GLU ALA ASN SER LEU ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU LEU GLU GLU LYS LEU LEU GLU GLU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 10-B:



THR	LYS	GLN	GLU	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA
SER	GLU	ALA	I1690	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA
VAL	ASN	PRO		GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL
GLU	LYS	GLU	P1698	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL
	GLU	F1883	Y1699	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO
	SER			LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS
	LYS	S1913	S1721	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE
	HIS			LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU
	LYS	R1918	L1727	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR
	M2408		R1728	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL
		R1941	P1729	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET
	Q2462		N1730	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS
	LEU	V2048			LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG
	GLY		G1804	S1422	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS
	SER	K2078		K1423	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU
	LEU	F2079	L1807		SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR
	LYS	P2080	L1808	E1427	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER
	N2468	N2081			ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU
		E2082	G1837	P1480	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO
	R2477		ASP		GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL
	LYS	A2135	LEU	R1514	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN
	ASN	GLU	LEU	ASP	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU
	THR	LEU	VAL	GLN	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU
	GLU	VAL	ASN	LEU	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA
	GLY	CYS	PRO	VAL	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU
	THR	LEU	ASP	VAL	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG
	GLN	THR	GLN	GLY	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA
	LYS	R2142	PRO	GLN	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE
	GLN		ARG	LEU	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU
	LYS	T2158	LEU	ILE	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS
	E2497	HIS	THR	P1524	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE
		HIS	ILE		SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE
	W2505	ASN	PRO	D1565	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL
	ASP	SER	ILE	E1566	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO
	ILE	ARG	SER	N1567	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY
	ASN	N2164	GLN		ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET
	LEU		ILE	D1587	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO
	PRO	F2253	ALA		PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU
	HIS	SER	PRO	C1604	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU
	GLU	LYS	ASP		ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER
	VAL	GLN	LEU	V1669	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG
	GLN	SER	ILE	PRO	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU
	ASN	LYS	LEU	SER	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP
	LEU	Q2254	ALA	SER	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR
	GLU		ASP	LEU	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU
	LYS	E2305	LEU	SER	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE
	HIS	SER	PRO	ASP	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS
	ILE	THR	ARG	HIS	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS
	GLU	ASN	ASN	ARG	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS
	VAL	SER	ILE	PRO	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU
	ARG	THR	MET	VAL	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN
	LYS	GLU	LEU	ILE	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET
	GLU	ARG	ASN	GLU	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL
	LEU	ASN	ASN	LEU	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS
	ALA	V2314	ASP	PRO	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS
	GLU		GLU	HIS	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN
	LYS	E2395	LEU	CYS	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS
	MET	VAL	GLU	GLU	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE
	ARG	MET	PHE	ASN	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS
	ARG	VAL	GLU	SER	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN

• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 11-A: 41% 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

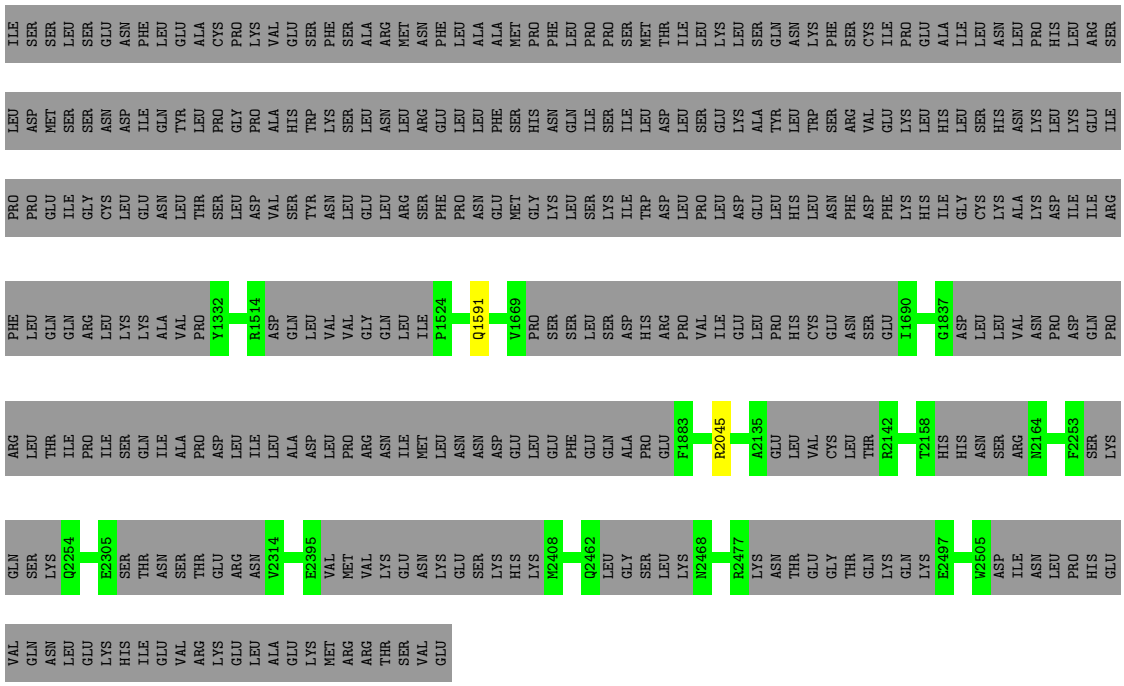
ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLY GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

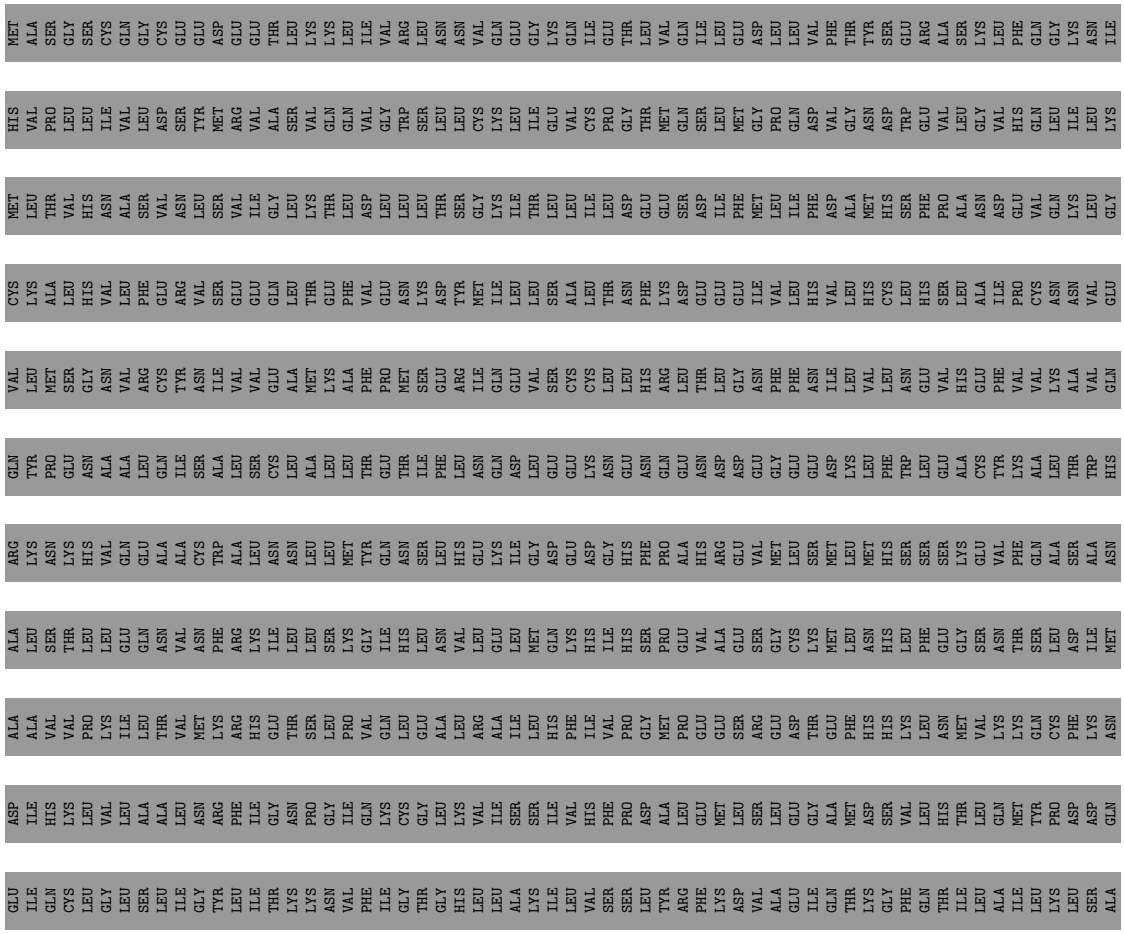
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

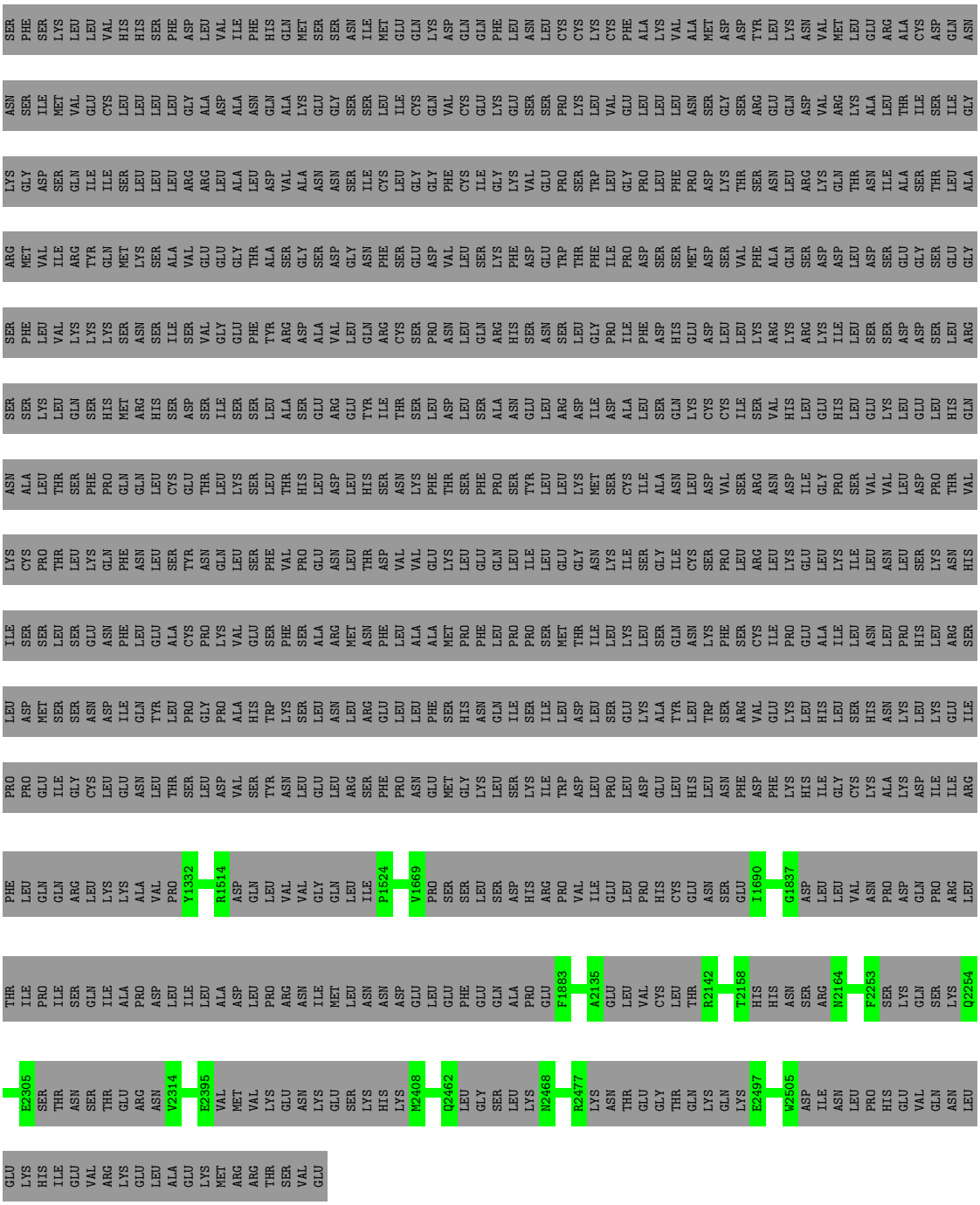
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

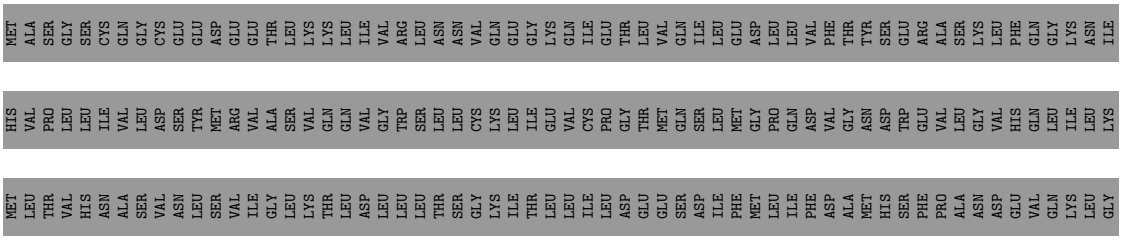
Chain 11-B:



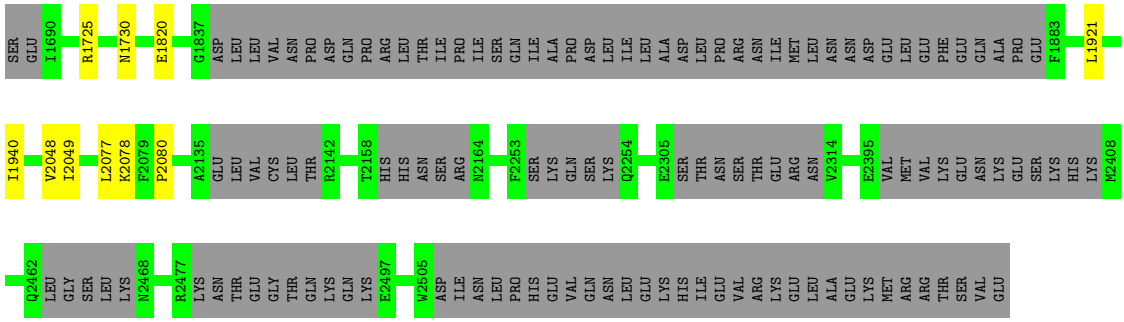


• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 12-A: 40% • 59%

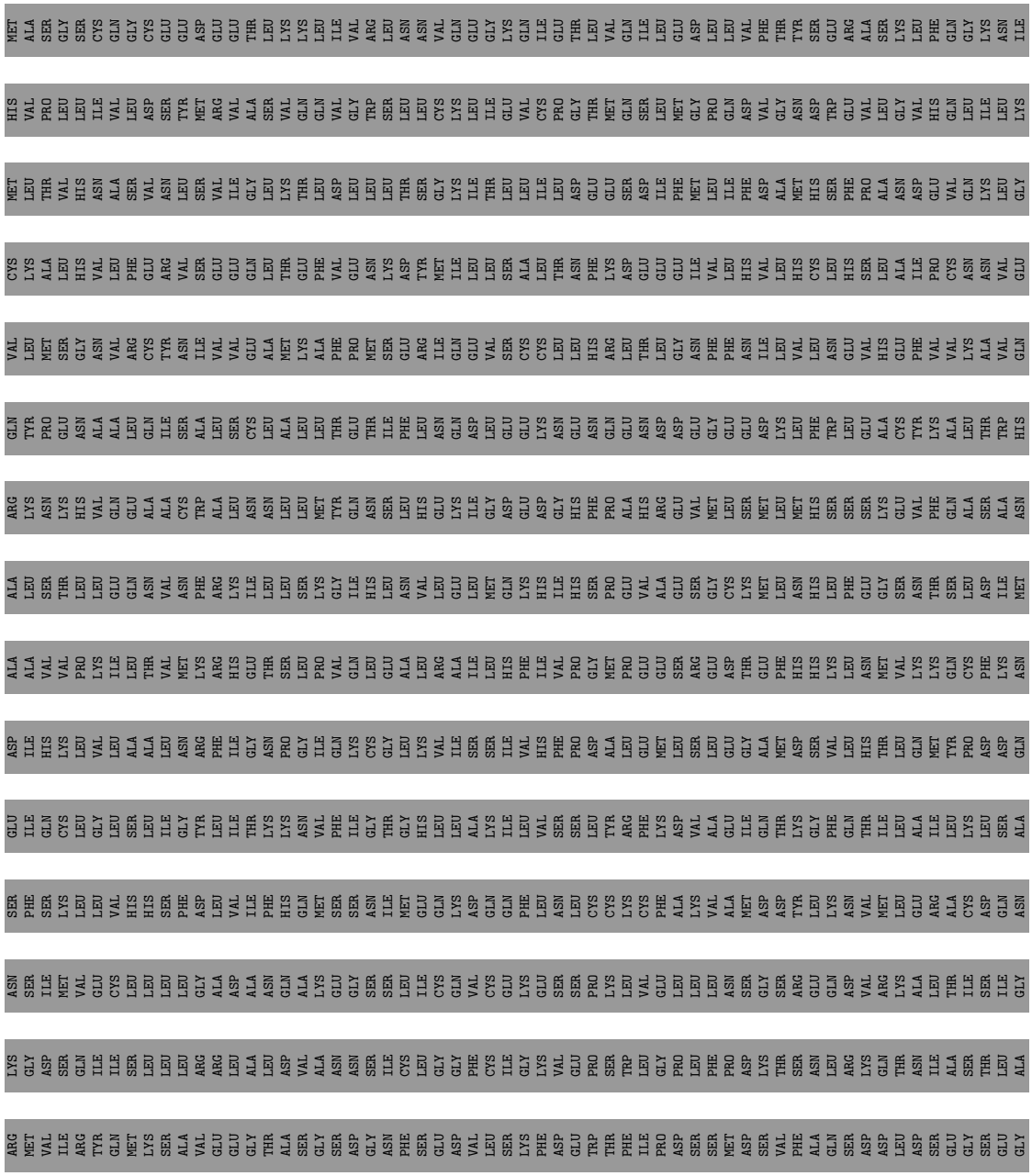


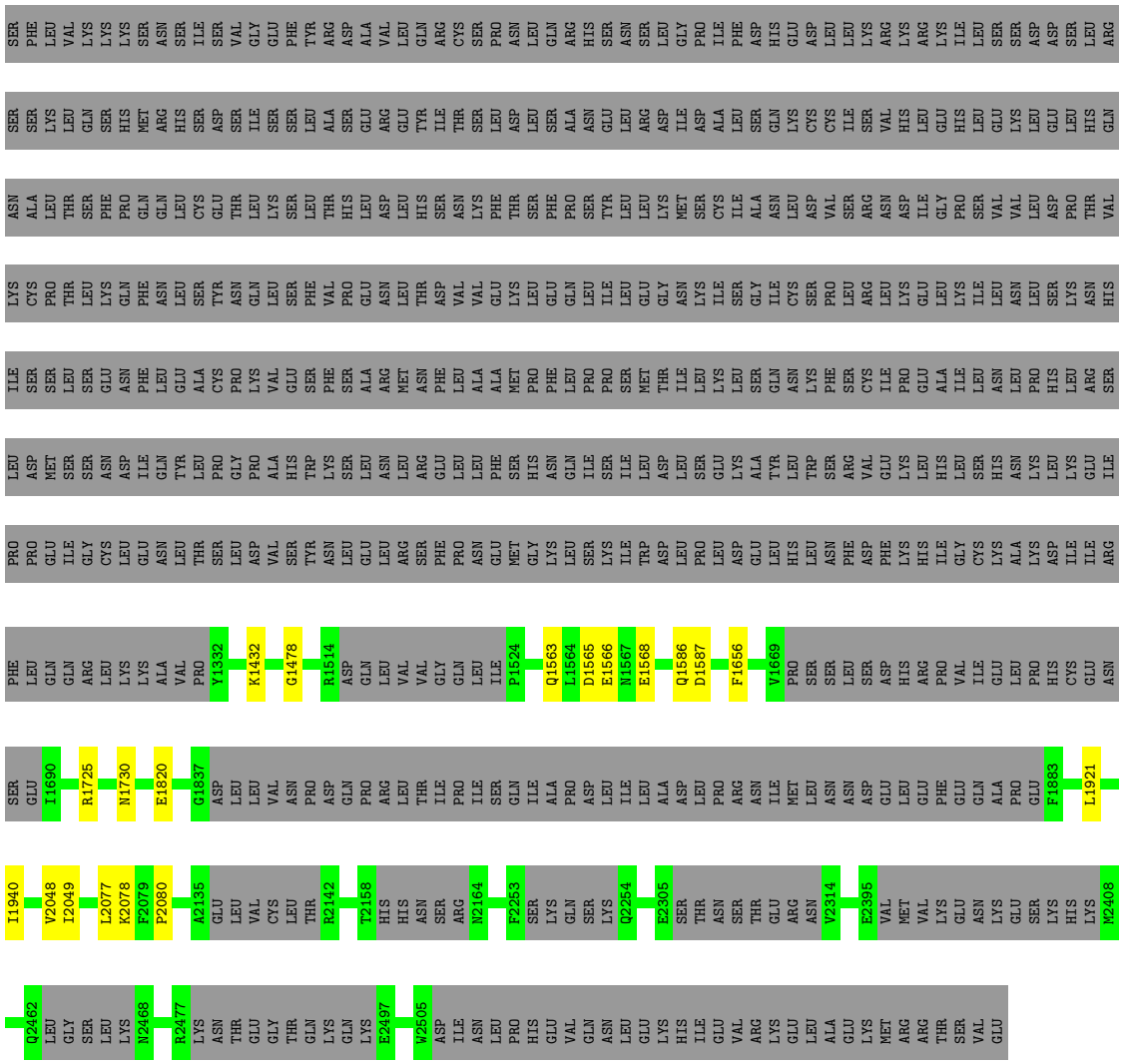
PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA	ARG	GLN	VAL	CYS
LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS	TYR	LEU	LYS
GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN	PRO	MET	ALA
GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS	GLU	SER	LEU
ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS	ASN	GLY	HIS
LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL	ALA	ASN	VAL
LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN	ALA	VAL	LEU
LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU	LEU	ARG	PHE
ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA	GLN	CYS	GLU
VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA	ILE	TYR	ARG
PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS	SER	ASN	VAL
Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP	ALA	ILE	SER
	LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA	LEU	VAL	GLU
K1432	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU	SER	VAL	GLU
	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN	CYS	GLU	GLN
G1478	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN	LEU	ALA	LEU
	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU	ALA	MET	THR
R1514	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU	LEU	LYS	GLU
ASP	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET	LEU	ALA	PHE
GLN	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR	THR	PHE	VAL
LEU	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN	GLU	PRO	GLU
VAL	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN	THR	MET	ASN
VAL	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER	ILE	SER	LYS
GLY	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU	PHE	GLU	ASP
GLN	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS	LEU	ARG	TYR
LEU	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU	ASN	ILE	MET
ILE	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS	GLN	GLN	ILE
P1524	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE	ASP	GLU	LEU
	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY	LEU	VAL	LEU
Q1563	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP	GLU	SER	SER
L1564	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU	GLU	CYS	ALA
D1565	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP	LYS	CYS	LEU
E1566	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY	ASN	LEU	THR
N1567	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS	GLU	LEU	ASN
E1568	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE	ASN	HIS	PHE
	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO	GLN	ARG	LYS
Q1586	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA	GLU	LEU	ASP
D1587	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS	ASN	THR	GLU
	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG	ASP	LEU	GLU
F1656	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU	ASP	GLY	GLU
	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL	GLU	ASN	ILE
V1669	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET	GLY	PHE	VAL
PRO	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU	GLU	PHE	LEU
SER	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER	GLU	ASN	HIS
SER	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET	ASP	ILE	VAL
LEU	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU	LYS	LEU	LEU
SER	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET	LEU	VAL	HIS
ASP	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS	PHE	LEU	CYS
HIS	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER	TRP	ASN	LEU
ARG	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER	LEU	GLU	HIS
PRO	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER	GLU	VAL	SER
VAL	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS	ALA	HIS	LEU
ILE	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU	CYS	GLU	ALA
GLU	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL	TYR	PHE	ILE
LEU	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE	LYS	VAL	PRO
PRO	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN	ALA	VAL	CYS
HIS	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA	LEU	LYS	ASN
CYS	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER	THR	ALA	ASN
GLU	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA	TRP	VAL	VAL
ASN	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN	HIS	GLN	GLU



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

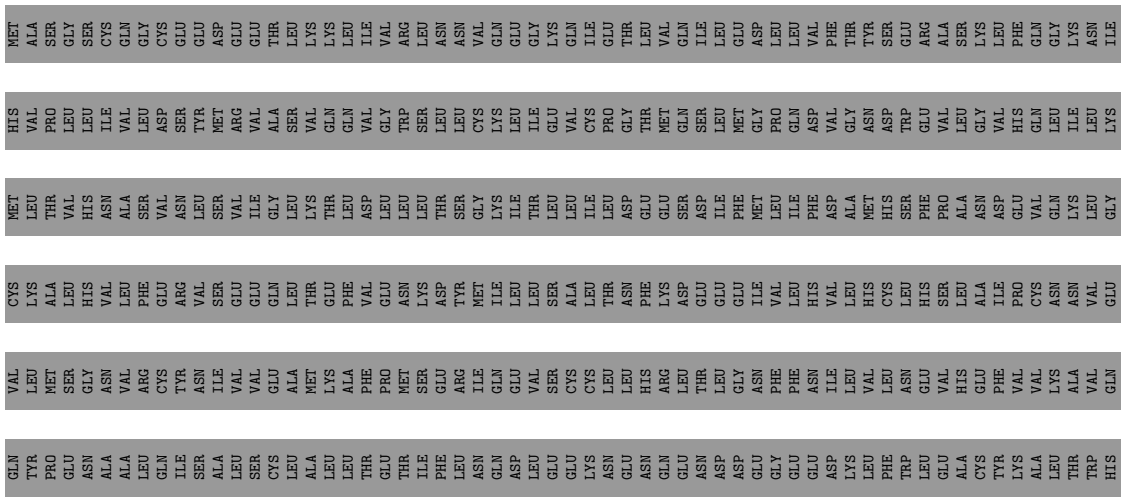
Chain 12-B: 40% 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 13-A: 40% 59%



GLU	HIS	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA	ARG
PHE	CYS	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS
GLU	GLU	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN
GLN	ASN	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS
ALA	SER	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS
PRO	GLU	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL
GLU	I1690	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN
F1883		LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU
	P1717	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA
R1915		VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA
	R1723	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS
L1921		Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP
	L1727		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA
A2044	R1728	T1343	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	HIS	LEU
	P1729	G1344	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN
L2077	N1730		SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN
K2078	R1731	T1348	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU
F2079	M1732		ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU
P2080		A1367	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET
	I1765	T1368	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR
N2118			LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN
	G1837	I1371	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN
A2135	ASP		SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER
GLU	LEU	R1514	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU
LEU	LEU	ASP	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS
VAL	VAL	GLN	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU
CYS	ASN	LEU	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS
LEU	PRO	VAL	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE
THR	ASP	VAL	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY
R2142	GLN	GLY	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP
	PRO	GLN	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU
T2158	ARG	LEU	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP
HIS	LEU	ILE	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY
HIS	THR	P1524	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS
ASN	ILE		TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE
SER	PRO	D1565	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO
ARG	ILE	E1566	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA
N2164	SER	N1567	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS
	GLN	E1568	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG
F2253	ILE	L1569	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU
SER	ALA	P1570	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL
LYS	PRO		LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET
GLN	ASP	L1590	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU
SER	LEU	Q1591	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER
LYS	ILE		ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET
Q2254	LEU	V1669	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU
	ALA	PRO	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET
E2305	ASP	SER	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS
SER	LEU	SER	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER
THR	PRO	LEU	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER
ASN	ARG	SER	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER
SER	ASN	ASP	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS
THR	ILE	HIS	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU
GLU	MET	ARG	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL
ARG	LEU	PRO	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE
ASN	ASN	VAL	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN
V2314	ASN	ILE	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA
	ASP	GLU	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER
E2395	GLU	LEU	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA
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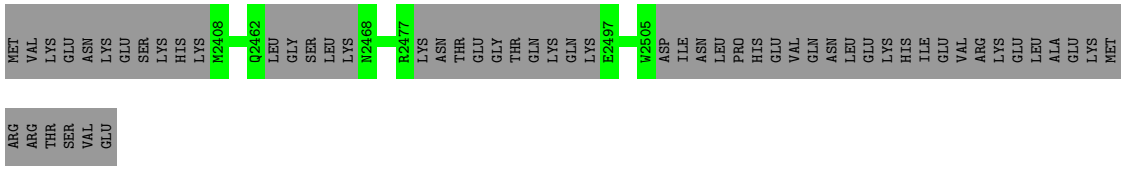
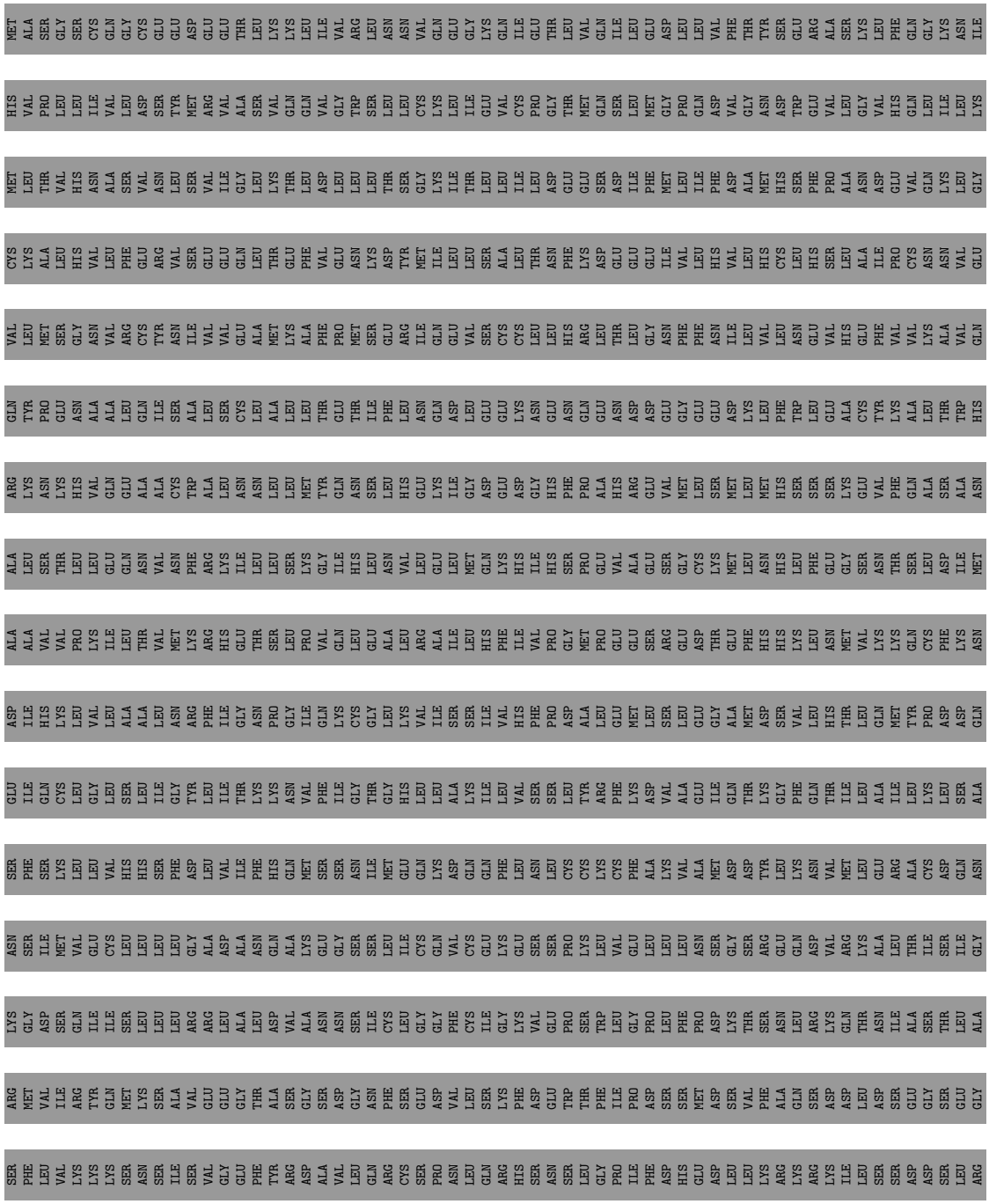
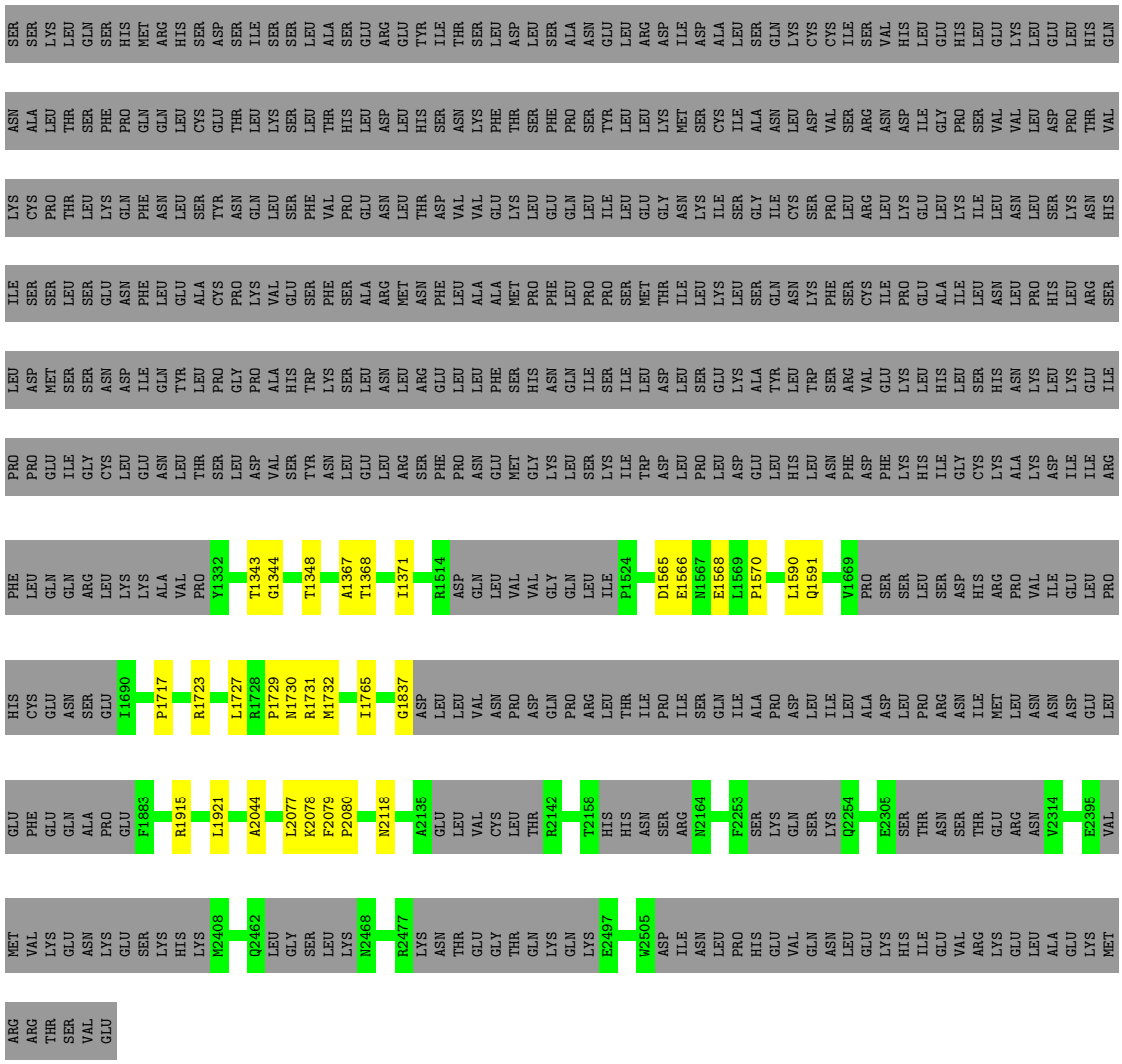


• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

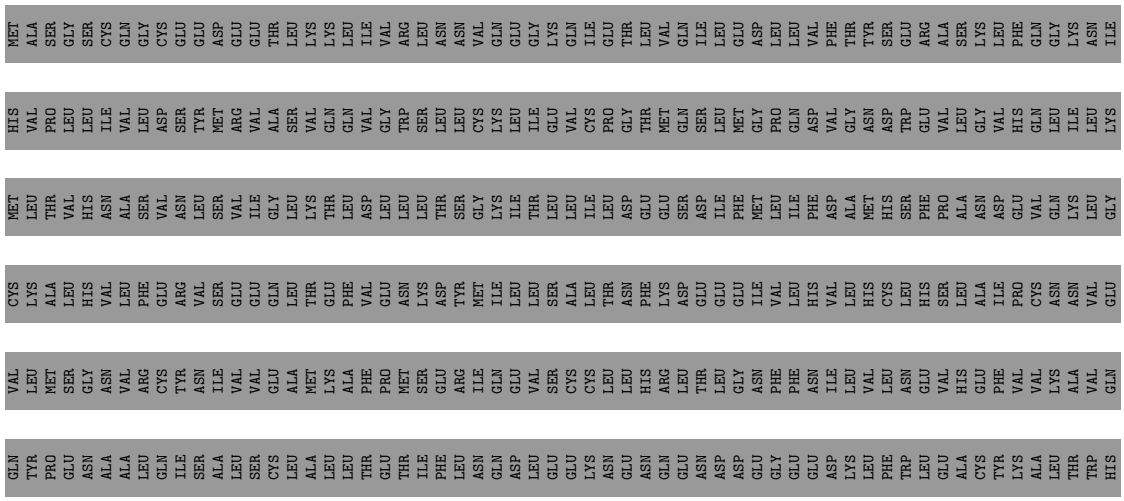
Chain 13-B:





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 14-A: 39% • 59%



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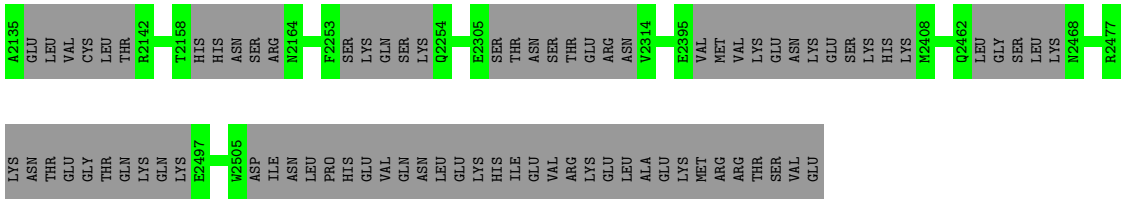
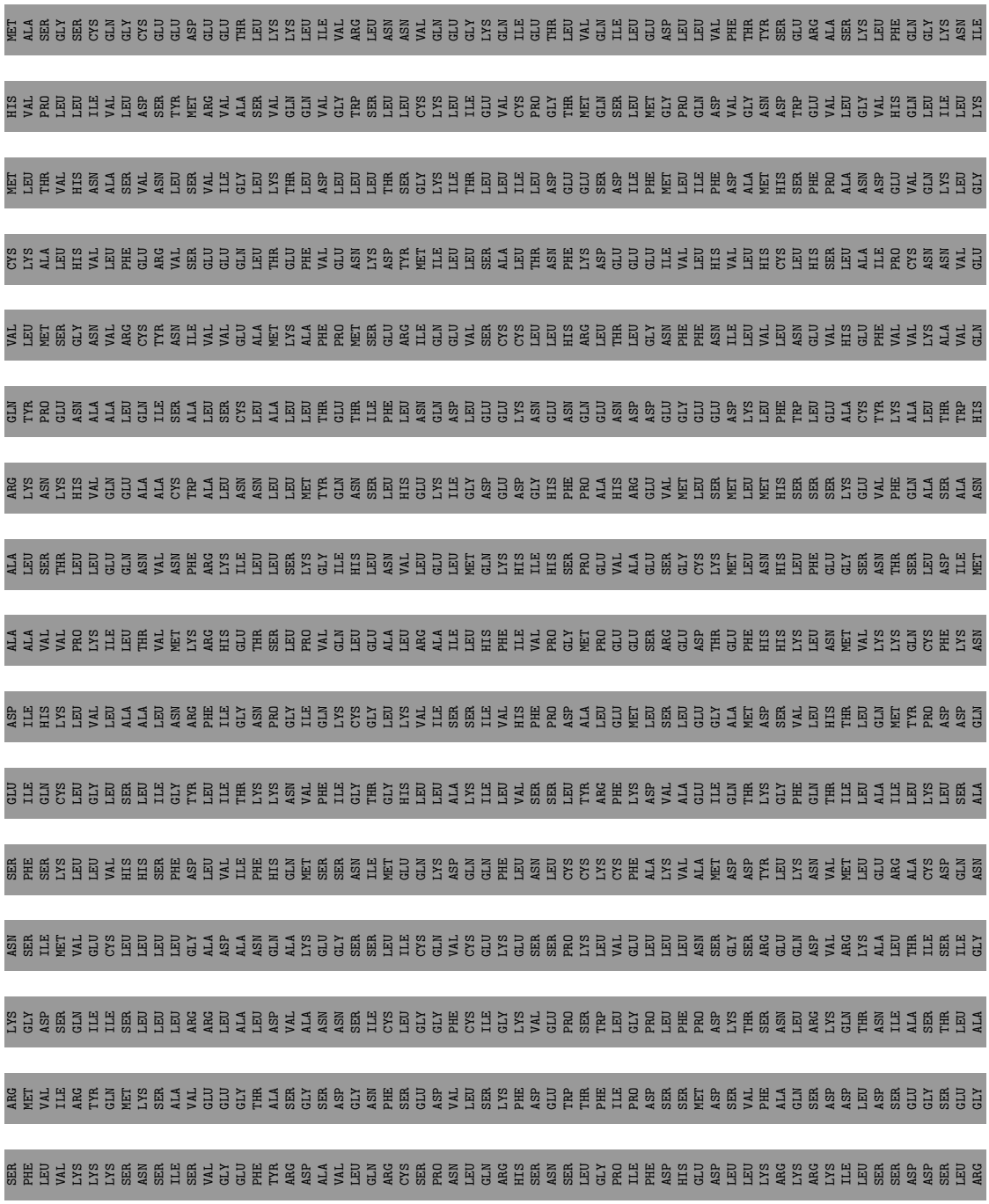
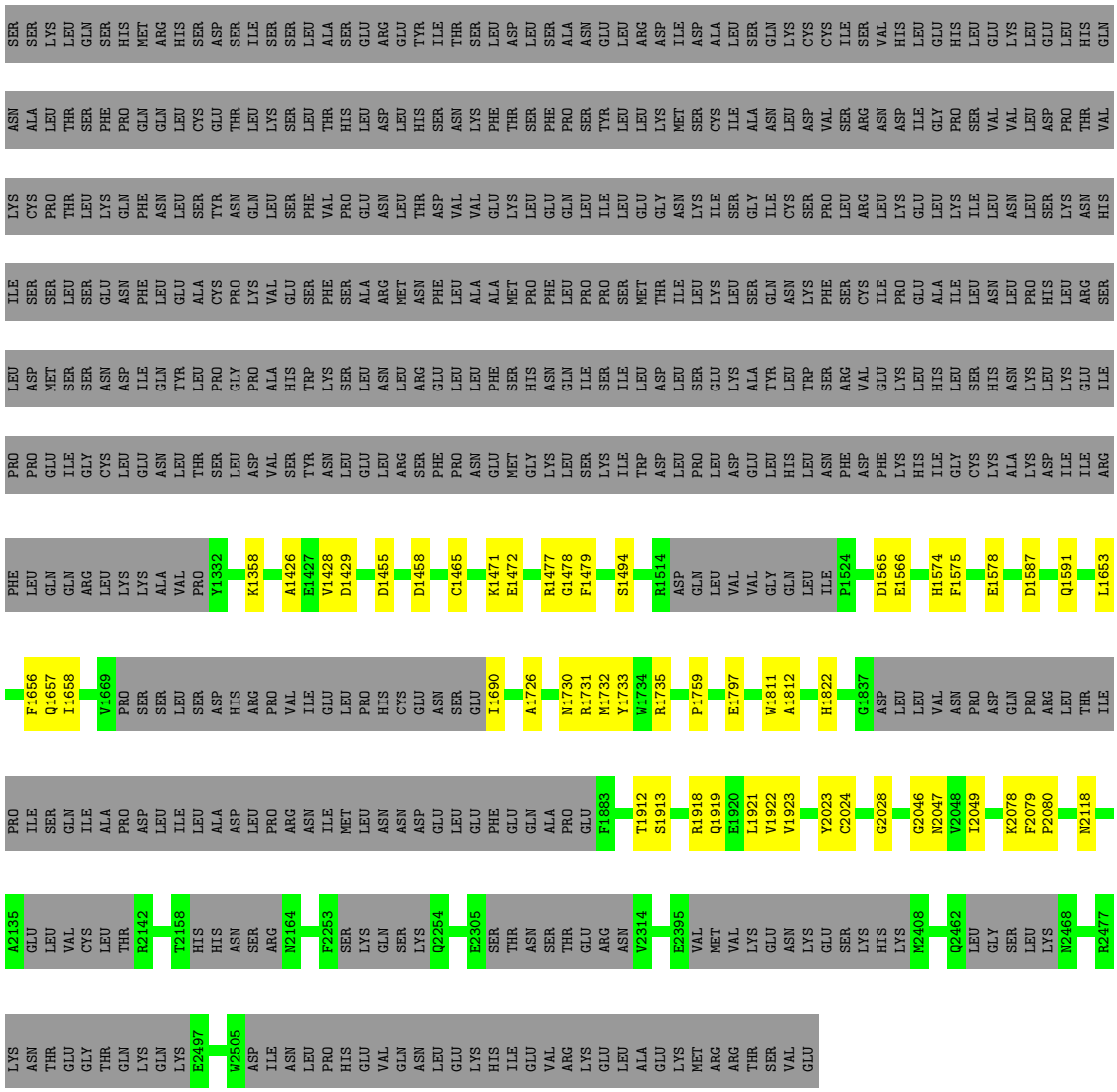
SER	L1653	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN
GLN		GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS
ILE	F1656	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS
ALA	Q1657	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL
PRO	I1658	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN
ASP		LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU
LEU	V1669	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA
ILE	PRO	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA
LEU	SER	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS
ALA	SER	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP
ASP	LEU		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA
LEU	SER	K1358	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU
PRO	ASP		VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN
ARG	HIS	A1426	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN
ASN	ARG	E1427	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU
ILE	PRO	V1428	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU
MET	VAL	D1429	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET
LEU	ILE		GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR
ASN	GLU	D1455	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN
ASN	LEU		ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN
ASP	PRO	D1458	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER
GLU	HIS		PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU
LEU	CYS	C1465	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS
GLU	GLU		ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU
PHE	ASN	K1471	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS
GLU	SER	E1472	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE
GLN	GLU		GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY
ALA	I1690	R1477	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP
PRO		G1478	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU
GLU	A1726	F1479	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP
F1883			LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY
	N1730	S1494	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS
T1912	R1731		TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE
S1913	M1732	R1514	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO
	Y1733	ASP	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA
R1918	W1734	GLN	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS
Q1919	R1735	LEU	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG
E1920		VAL	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU
L1921	P1759	VAL	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL
V1922		GLY	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET
V1923	E1797	GLN	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU
		LEU	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER
Y2023	H1822	ILE	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET
C2024		P1524	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU
	G1837		ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET
G2028	ASP	D1565	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS
	LEU	E1566	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER
G2046	LEU		HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER
N2047	VAL	H1574	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER
V2048	ASN	F1575	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS
I2049	PRO		CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU
	ASP	E1578	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL
K2078	GLN		ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE
F2079	PRO	D1587	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN
P2080	ARG		ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA
	LEU	Q1591	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER
N2118	THR		ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA
	ILE	K1623	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

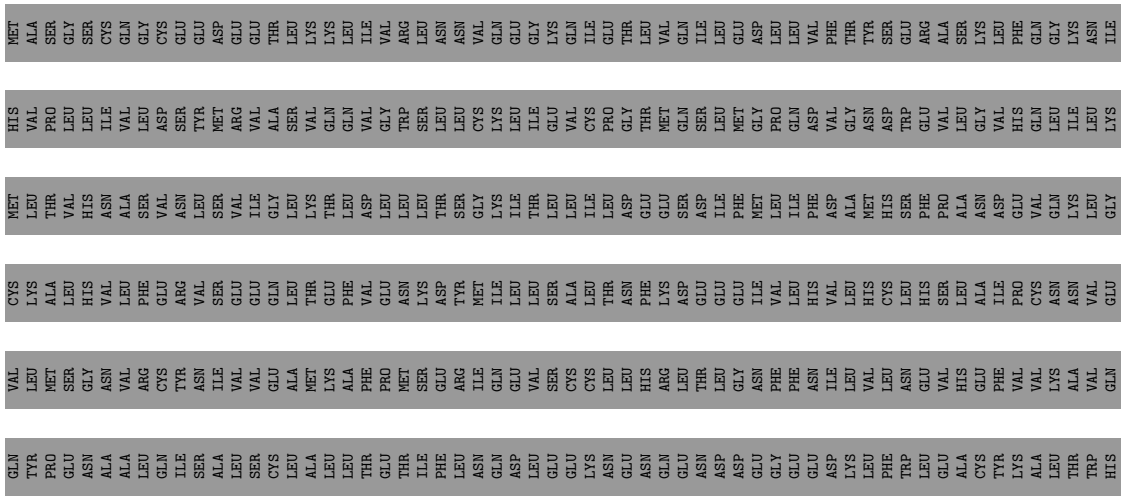
Chain 14-B:



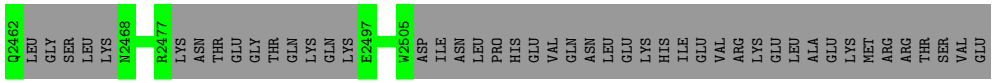


- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 15-A: 40% 59%

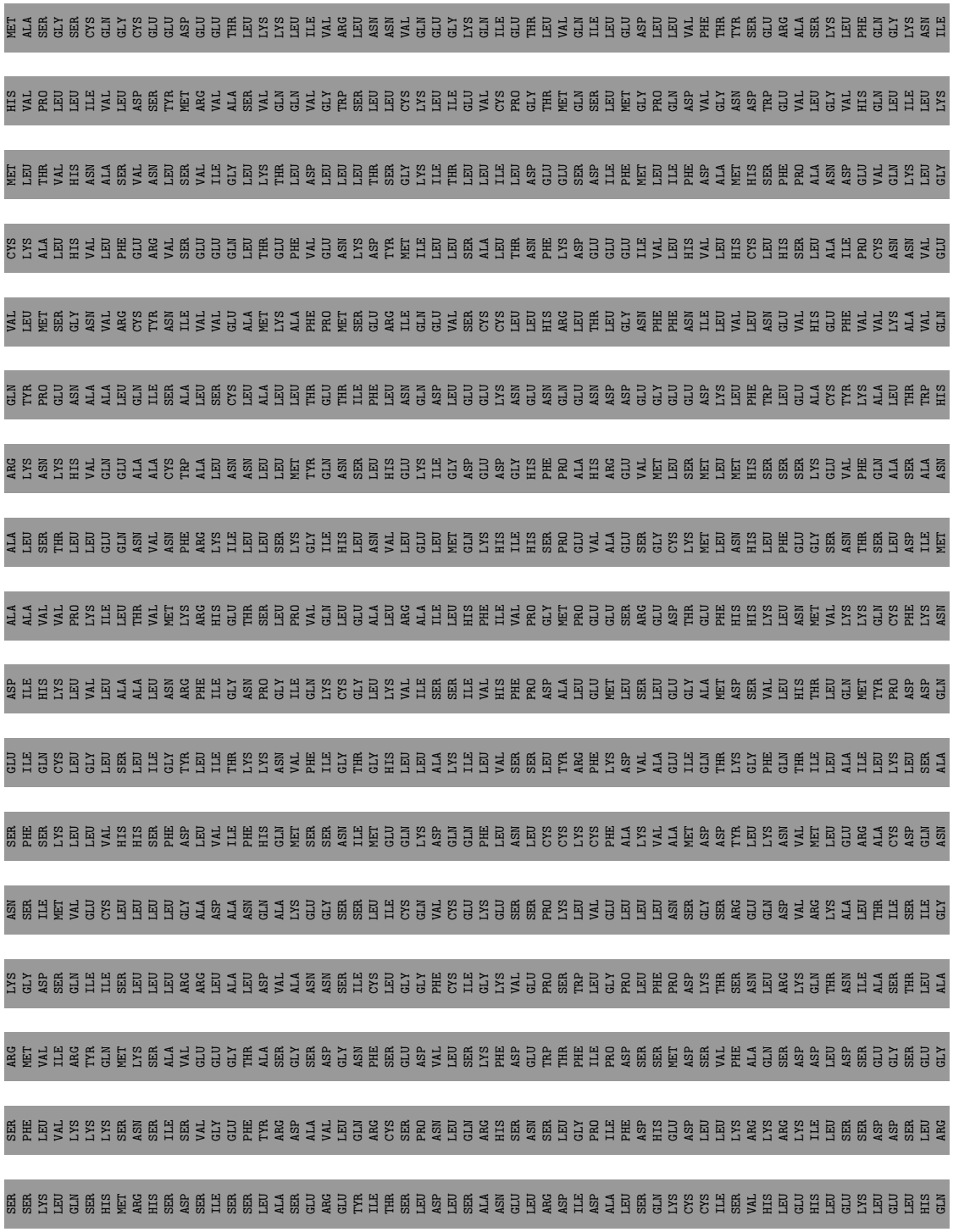


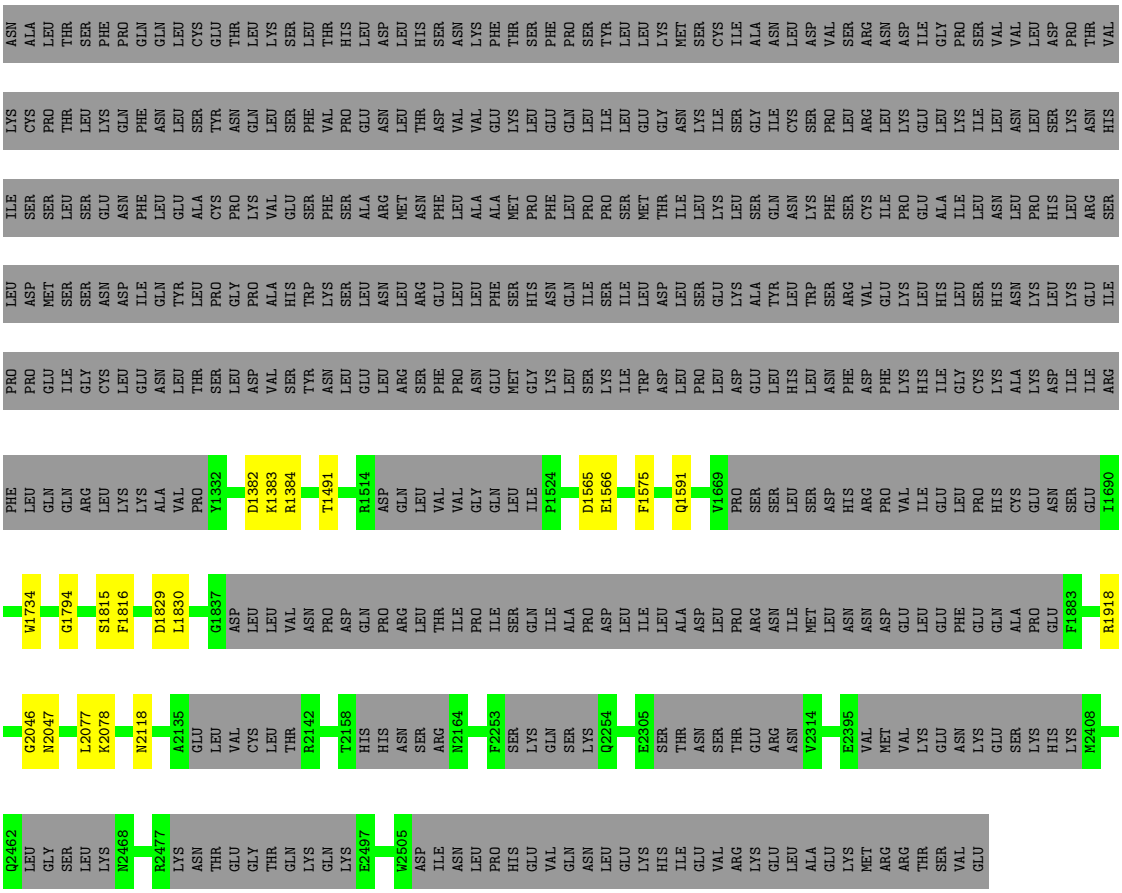
	CYS	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA	ARG
G2046	GLU	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS
N2047	ASN	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN
	SER	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS
L2077	GLU	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS
K2078	I1690	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL
		LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN
N2118	W1734	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU
		ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA
A2135	G1794	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA
GLU		PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS
LEU	G1837	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP
VAL	ASP		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA
CYS	LEU	D1382	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU
LEU	LEU	K1383	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN
THR	VAL	R1384	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN
R2142	ASN		TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU
	PRO	D1458	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU
T2158	ASP	E1459	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET
HIS	GLN		GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR
HIS	PRO	R1462	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN
ASN	ARG	K1463	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN
SER	LEU		SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER
ARG	THR	T1491	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU
N2164	ILE		PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS
	PRO	R1514	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU
F2253	ILE	ASP	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS
SER	SER	GLN	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE
LYS	GLN	LEU	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY
GLN	ILE	VAL	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP
SER	ALA	VAL	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU
LYS	PRO	GLY	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP
Q2254	ASP	GLN	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY
	LEU	LEU	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS
E2305	ILE	ILE	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE
SER	LEU	P1524	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO
THR	ALA		LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA
ASN	ASP	D1565	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS
SER	LEU	E1566	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG
THR	PRO		ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU
GLU	ARG	F1575	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL
ARG	ASN		LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET
ASN	ILE	Q1591	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU
V2314	MET		LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER
	LEU	V1669	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET
E2395	ASN	PRO	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU
VAL	ASN	SER	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET
MET	ASP	SER	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS
VAL	GLU	LEU	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER
LYS	LEU	SER	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER
GLU	GLU	ASP	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER
ASN	PHE	HIS	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS
LYS	GLU	ARG	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU
GLU	GLN	PRO	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL
SER	ALA	VAL	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE
LYS	PRO	ILE	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN
HIS	GLU	GLU	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA
LYS	F1883	LEU	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER
M2408		PRO	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA
	R1918	HIS	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

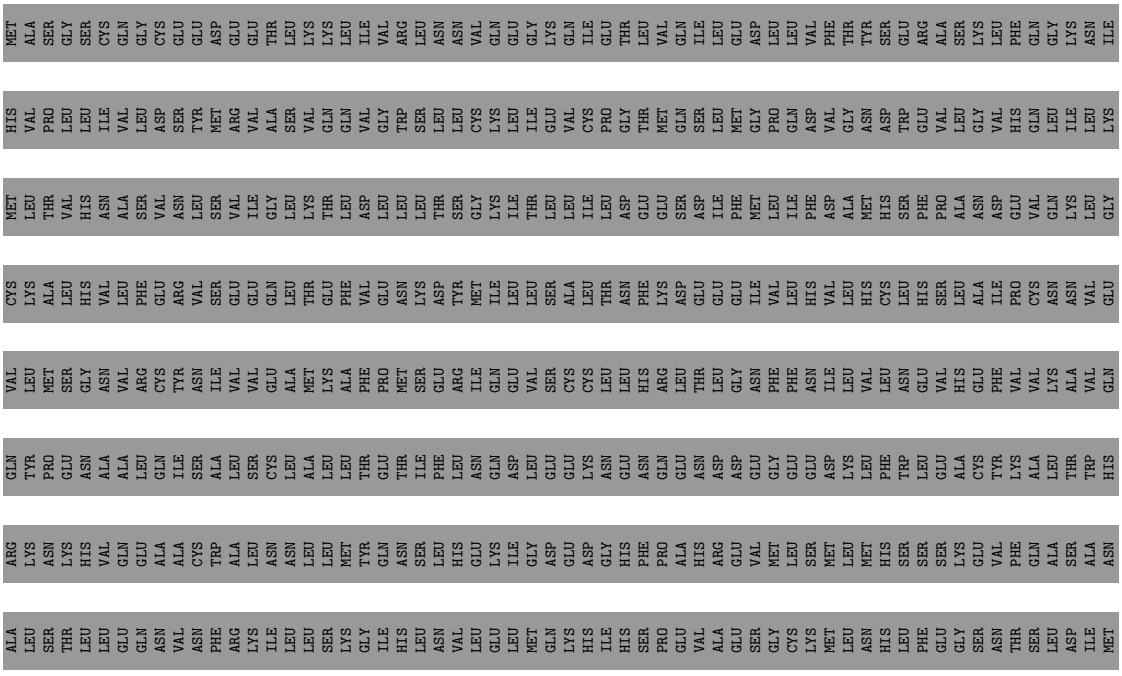
Chain 15-B:





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 16-A:



LYS	T2158	ASP	L1590	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA
E2497	HIS	LEU		LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA
	HIS	PRO	V1669	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL
W2505	ASN	ARG	PRO	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL
ASP	SER	ASN	SER	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO
ILE	ARG	ILE	SER	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS
ASN	N2164	MET	LEU	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE
LEU		LEU	SER	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU
PRO	F2253	ASN	ASP	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR
HIS	SER	ASN	HIS	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL
GLU	LYS	ASP	ARG	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET
VAL	GLN	GLU	PRO	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS
GLN	SER	LEU	VAL		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG
ASN	LYS	GLU	ILE	S1366	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS
LEU	Q2254	PHE	GLU	A1367	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU
GLU		GLU	LEU	T1368	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR
LYS	E2305	GLN	PRO	V1369	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER
HIS	SER	ALA	HIS	G1370	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU
ILE	THR	PRO	CYS		LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO
GLU	ASN	GLU	GLU	F1395	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL
VAL	SER	F1883	ASN	A1396	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN
ARG	THR		SER	G1397	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU
LYS	GLU	T1912	GLU	R1398	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU
GLU	ARG	S1913	I1690	E1399	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA
LEU	ASN			E1400	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU
ALA	V2314	R1918	A1726		ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG
GLU		Q1919		T1404	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA
LYS	E2395	E1920	N1730		MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE
MET	VAL	L1921	R1731	R1514	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU
ARG	MET	V1922	M1732	ASP	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS
ARG	VAL	V1923	Y1733	GLN	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE
THR	LYS		W1734	LEU	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE
SER	GLU	Y2023	R1735	VAL	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL
VAL	ASN	C2024		VAL	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO
GLU	LYS		G1837	GLY	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY
	GLU	I2029	ASP	GLN	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET
	SER		LEU	LEU	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO
	LYS	A2044	LEU	ILE	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU
	HIS	R2045	VAL	P1524	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU
	LYS	G2046	ASN		ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER
	M2408	N2047	PRO	Y1527	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG
		V2048	ASP		LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU
	Q2462		GLN	E1531	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP
	LEU	L2077	PRO		LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR
	GLY	K2078	ARG	D1565	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU
	SER	F2079	LEU	E1566	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE
	LEU	P2080	THR	N1567	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS
	LYS	N2081	ILE	E1568	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS
	N2468		PRO	L1569	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS
		N2118	ILE	P1570	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU
	R2477		SER	H1571	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN
	LYS	A2135	GLN	A1572	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET
	ASN	GLU	ILE		CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL
	THR	LEU	ALA	F1575	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS
	GLU	VAL	PRO	L1576	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS
	GLY	CYS	ASP	N1577	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN
	THR	LEU	LEU	E1578	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS
	GLN	THR	ILE	S1579	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE
	LYS	R2142	LEU	G1580	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS
	GLN		ALA		ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN

• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 16-B: 39% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU THR SER GLY LYS ILE THR LEU LEU LEU THR ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN LEU HIS GLU GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ILE ASP LEU GLU GLU LYS ASN GLU ASP ASP GLU GLY GLU GLU ASP LYS LEU TYR ALA ALA GLU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS LYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ALA ASN GLN LYS GLU ALA ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS LEU THR ILE ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU GLN THR LYS ARG LYS ALA LEU THR ASN ILE ALA

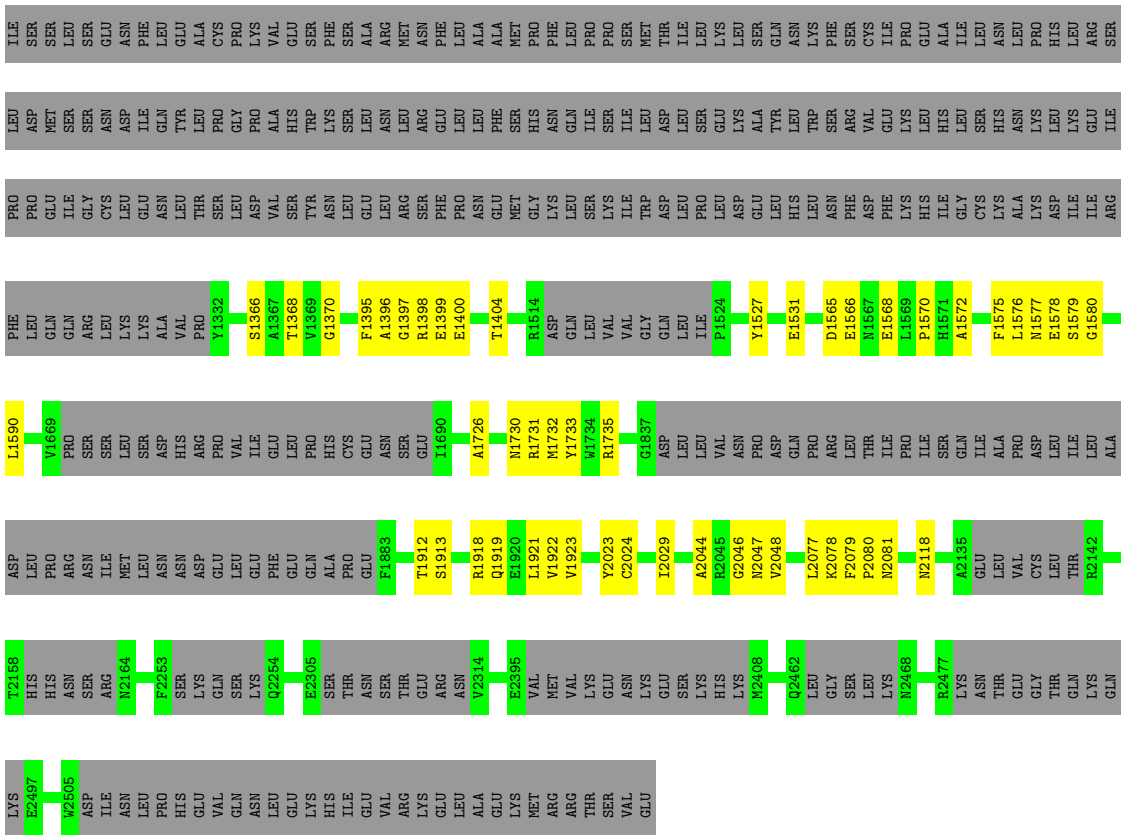
ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP LEU LEU SER SER MET ASP SER VAL PHE SER ALA GLN ASP VAL ARG LYS ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS SER ASN SER ILE SER VAL GLU GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN LEU GLY PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA GLN LYS CYS CYS ILE SER VAL HIS LEU GLU GLU GLU HIS LEU GLU

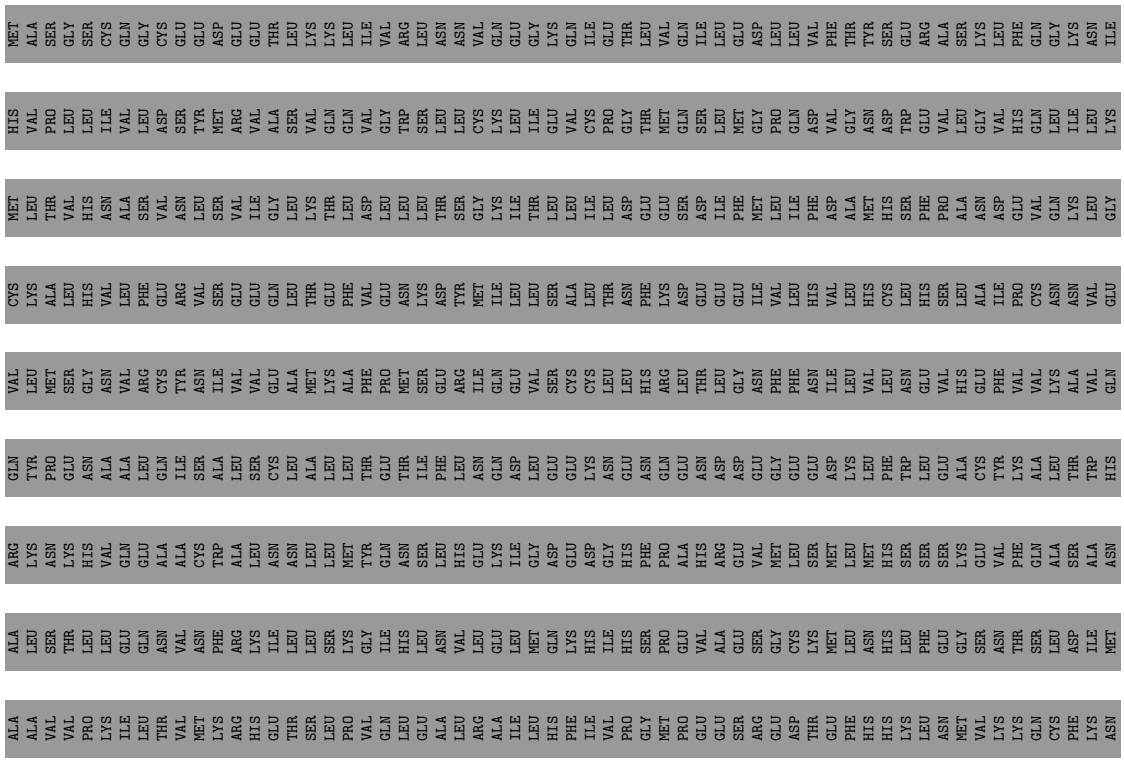
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU HIS LEU ASP HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU ARG LYS LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO ILE LEU VAL VAL LEU ASP

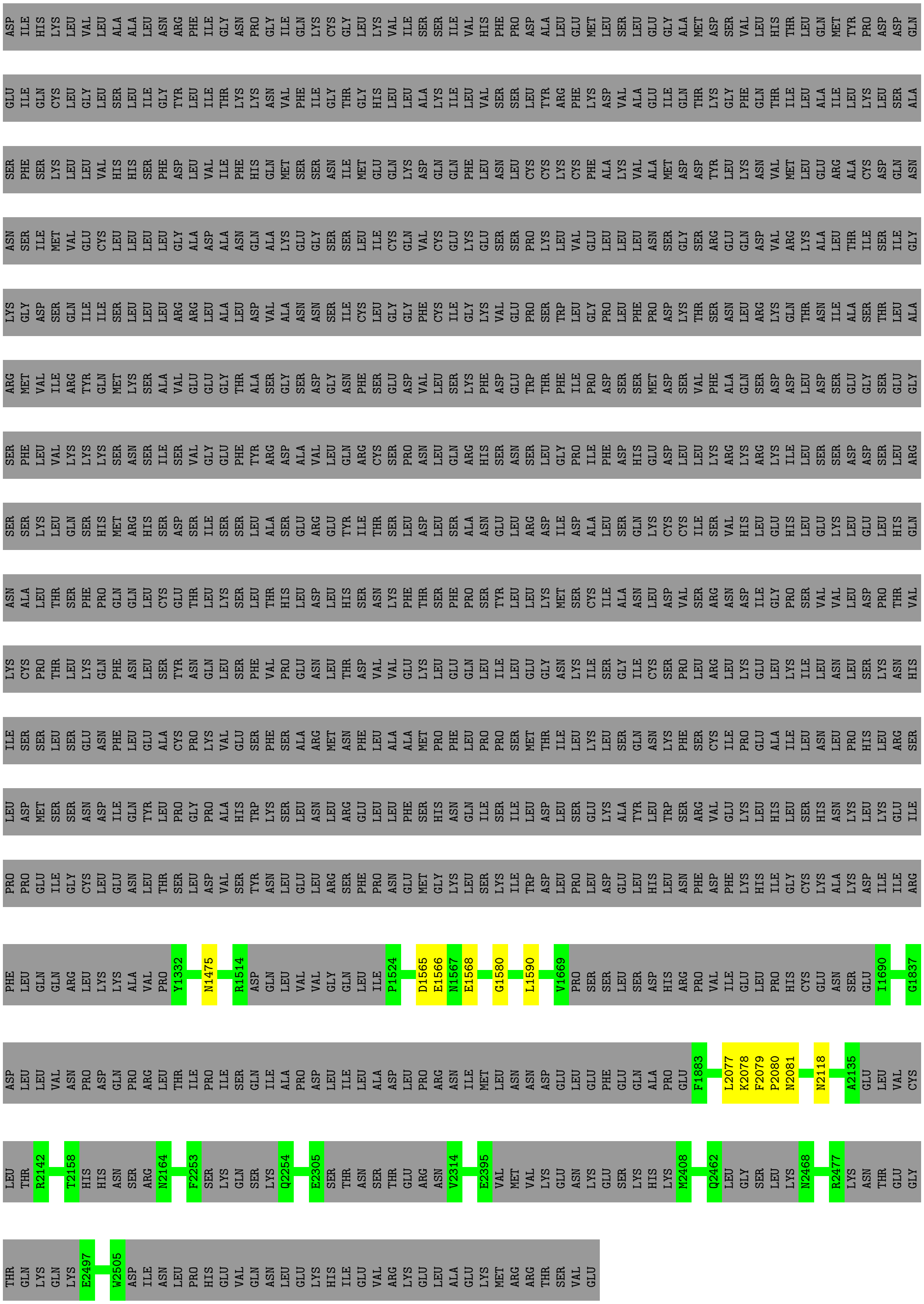
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 17-A:





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 17-B:

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

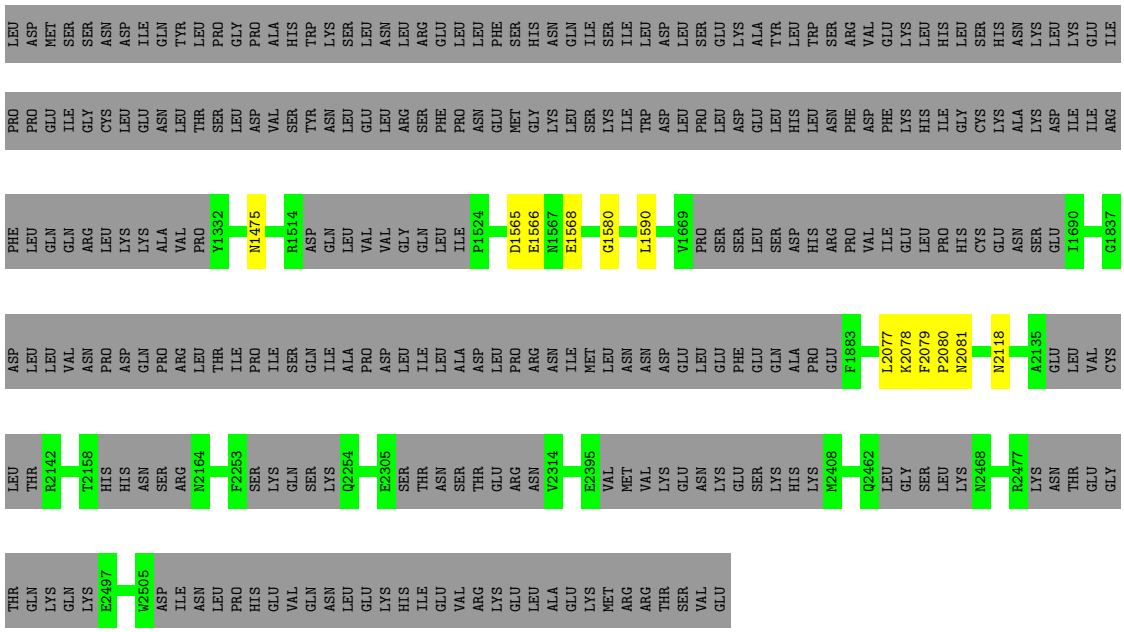
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

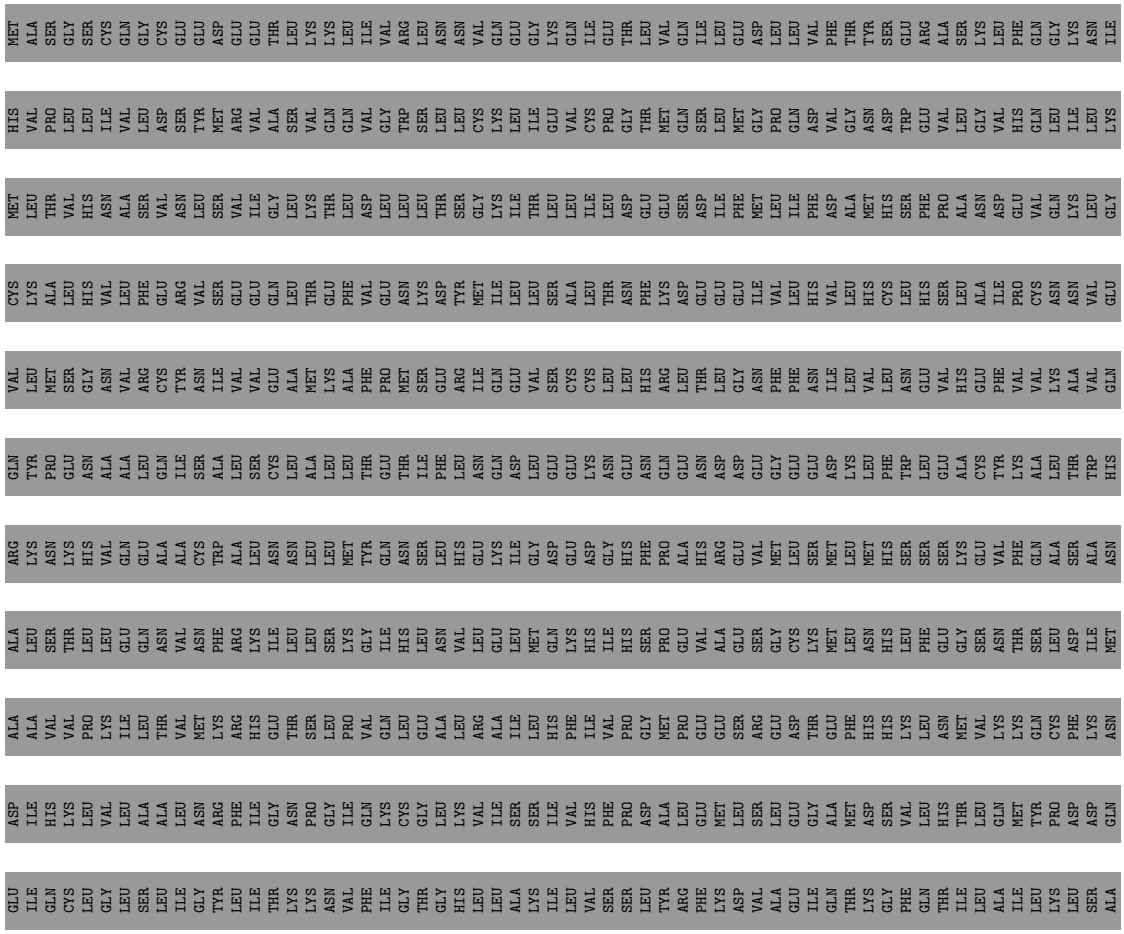
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

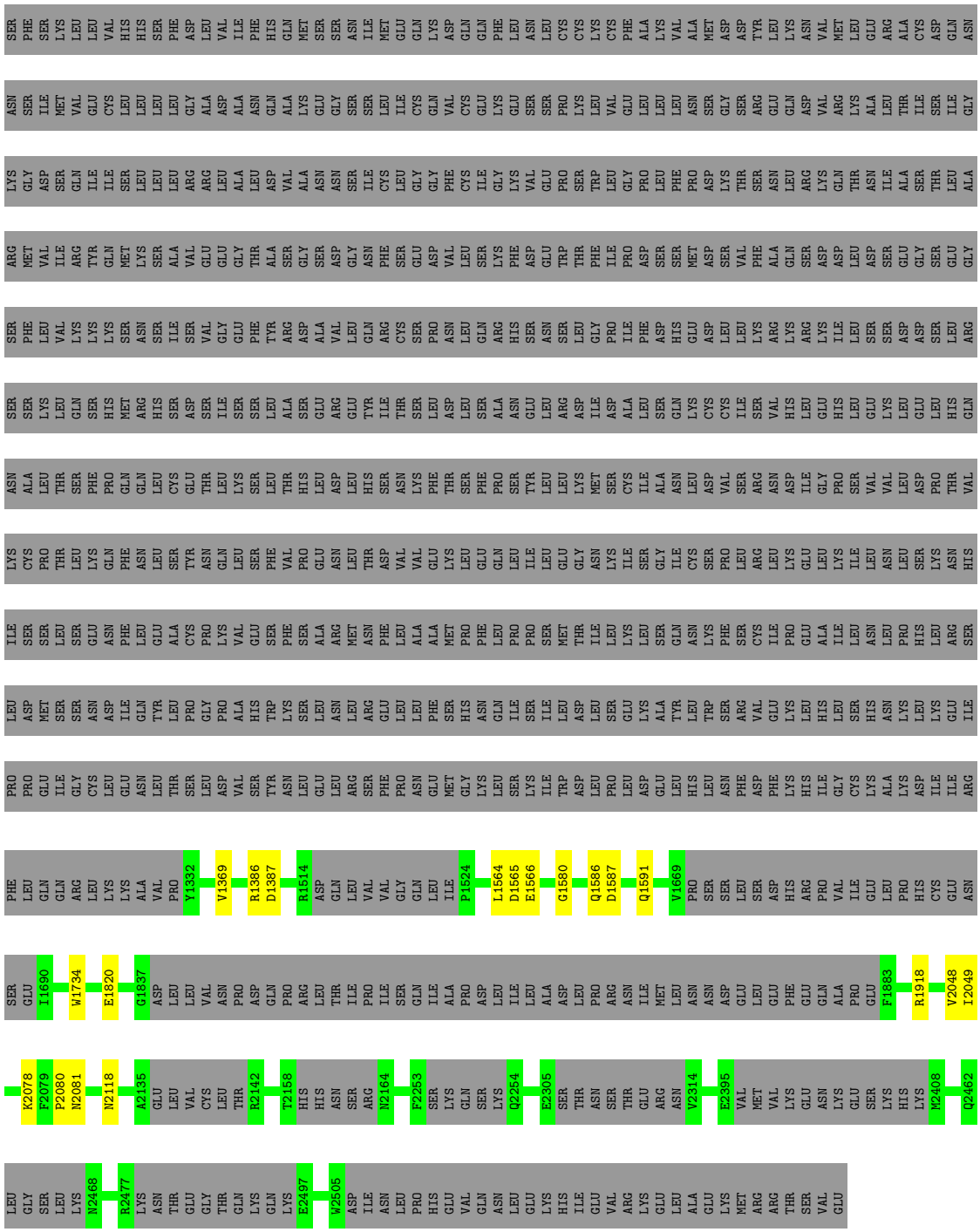
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

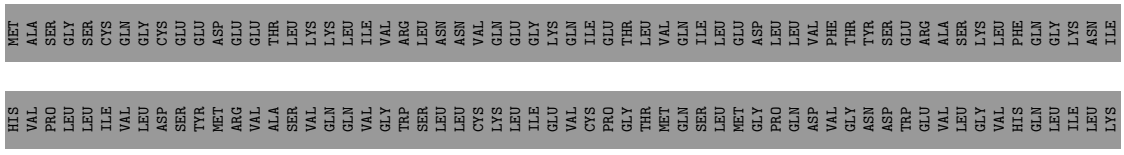
Chain 18-A: 40% • 59%





• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 18-B:



MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

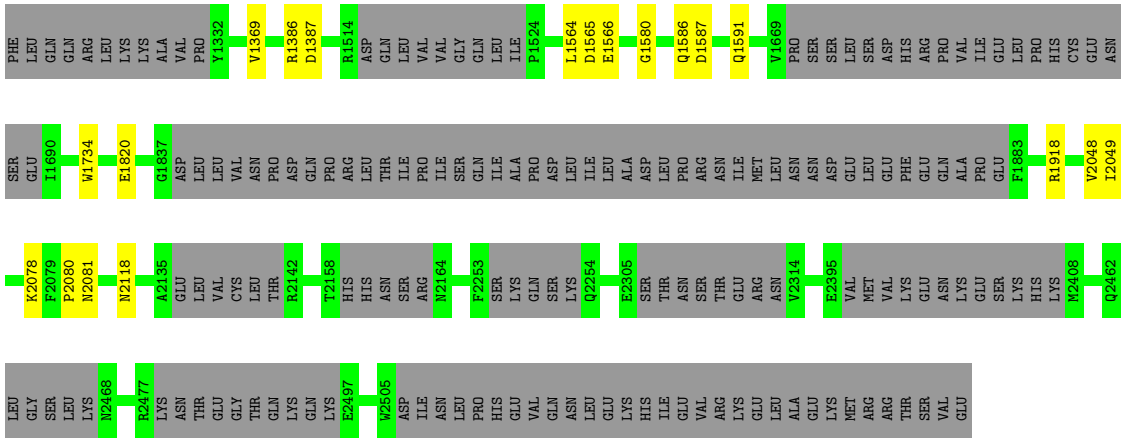
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER

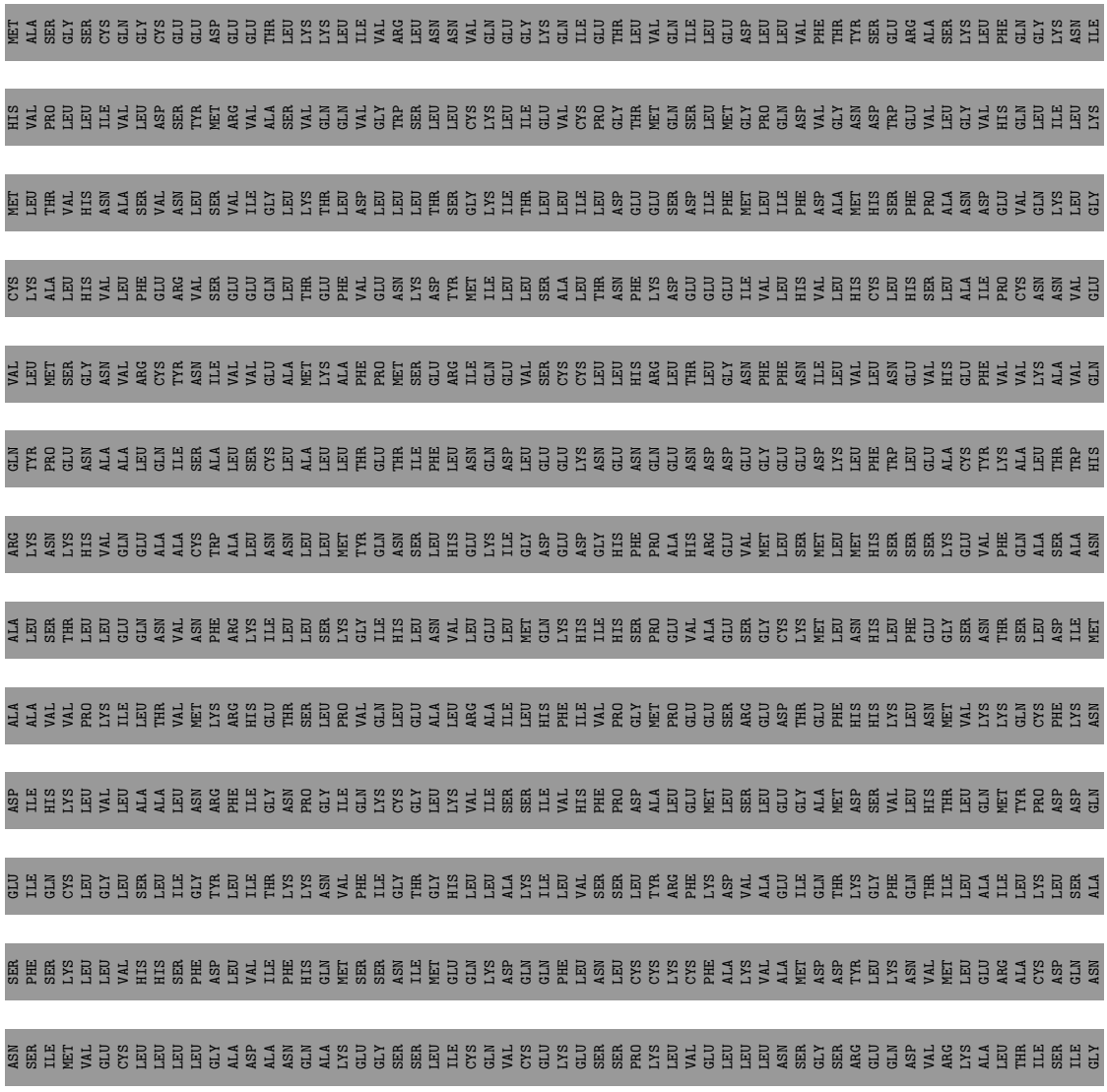
LEU ASP MET SER SER ASN ASP ILE GLN TYR LEU PRO GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG GLU LEU LEU PHE SER HIS ASN GLN ILE SER ILE LEU ASP LEU SER GLU LYS ALA TYR LEU TRP SER ARG VAL GLU LYS LEU HIS LEU SER HIS ASN LYS LEU LYS GLU ILE

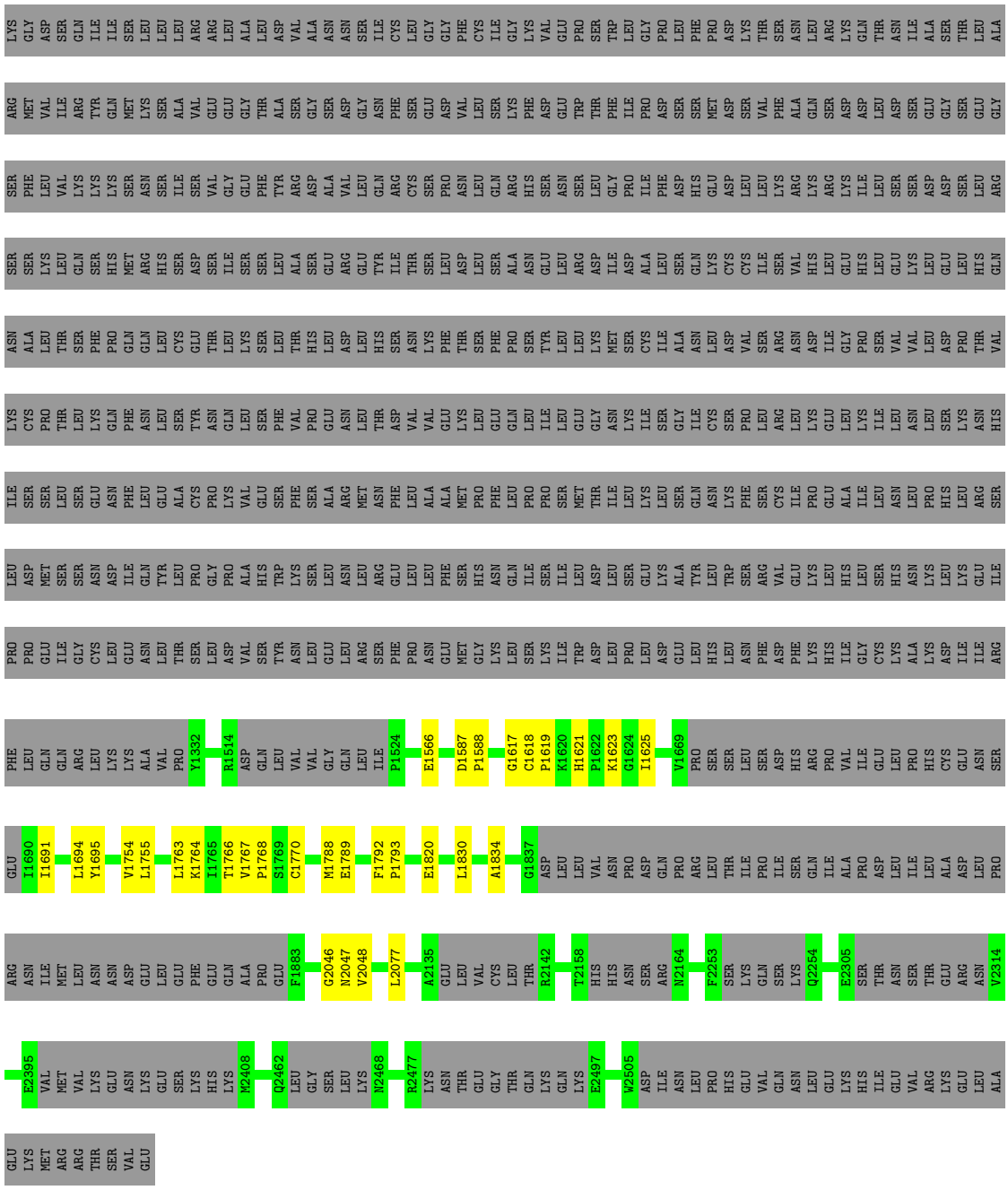
PRO PRO GLU ILE GLY CYS LEU GLU ASN LEU THR SER LEU ASP VAL SER TYR ASN LEU GLU LEU ARG SER PHE PRO ASN GLU MET GLY LYS LEU SER LYS ILE TRP ASP LEU PRO LEU ASP GLU LEU HIS LEU ASN PHE ASP PHE LYS HIS ILE GLY CYS LYS ALA LYS ASP ILE ILE ARG



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 19-A:

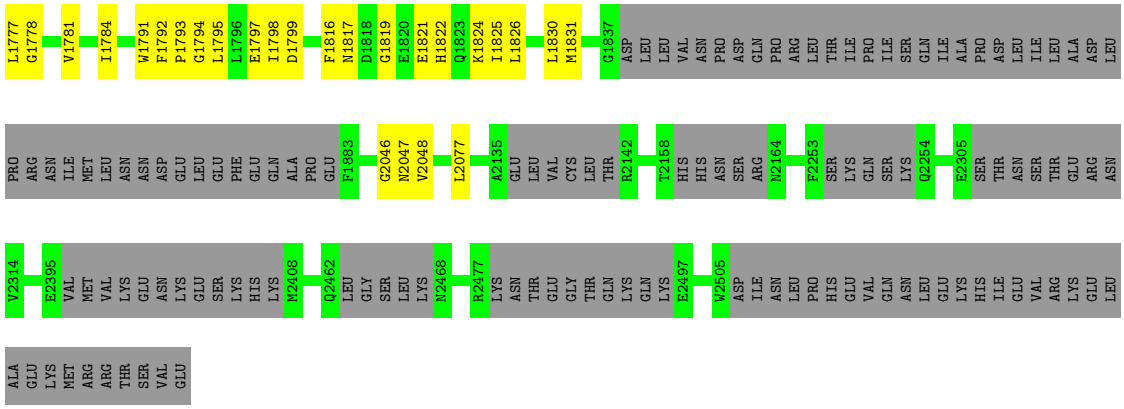




- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

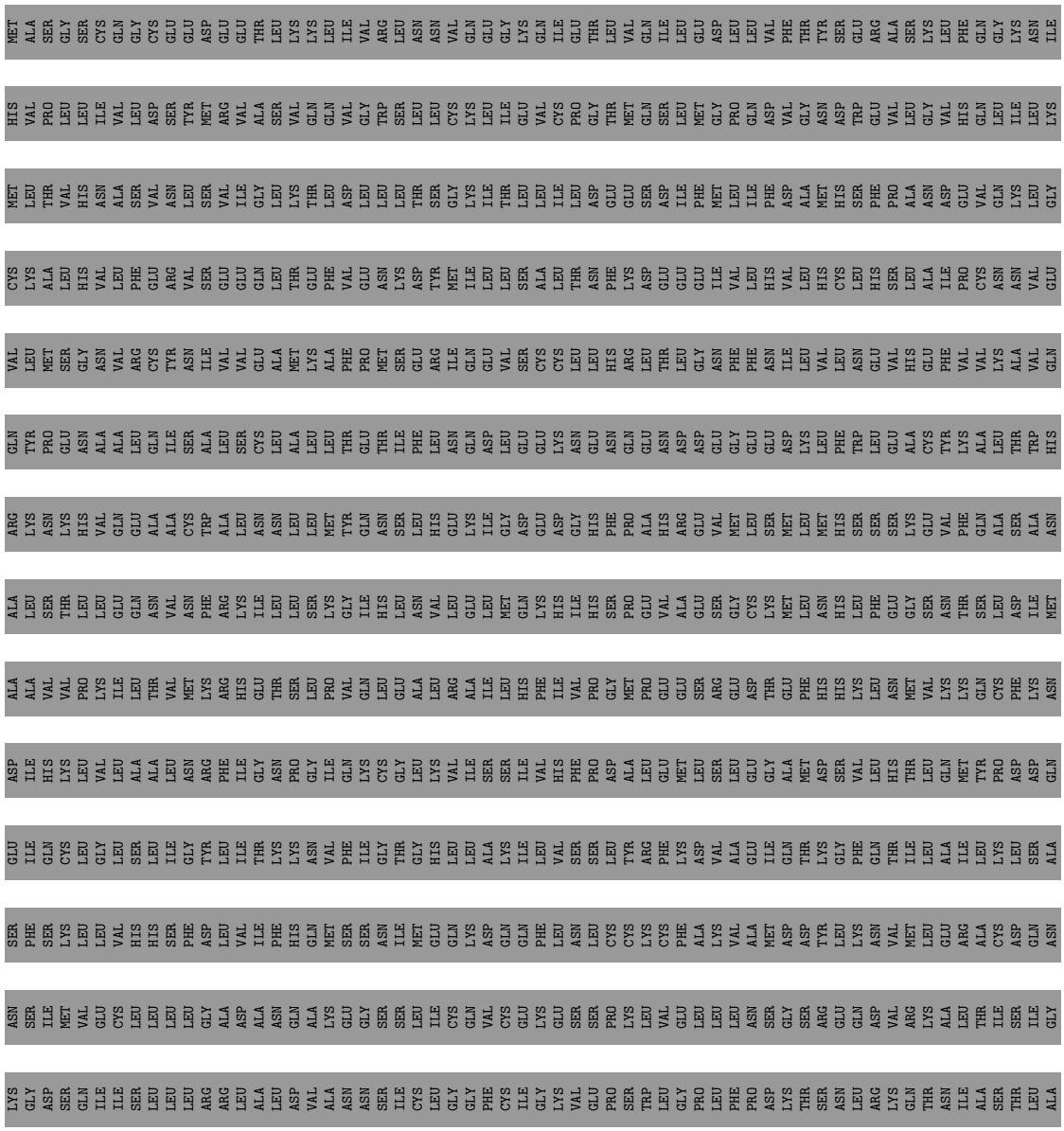
Chain 19-B:

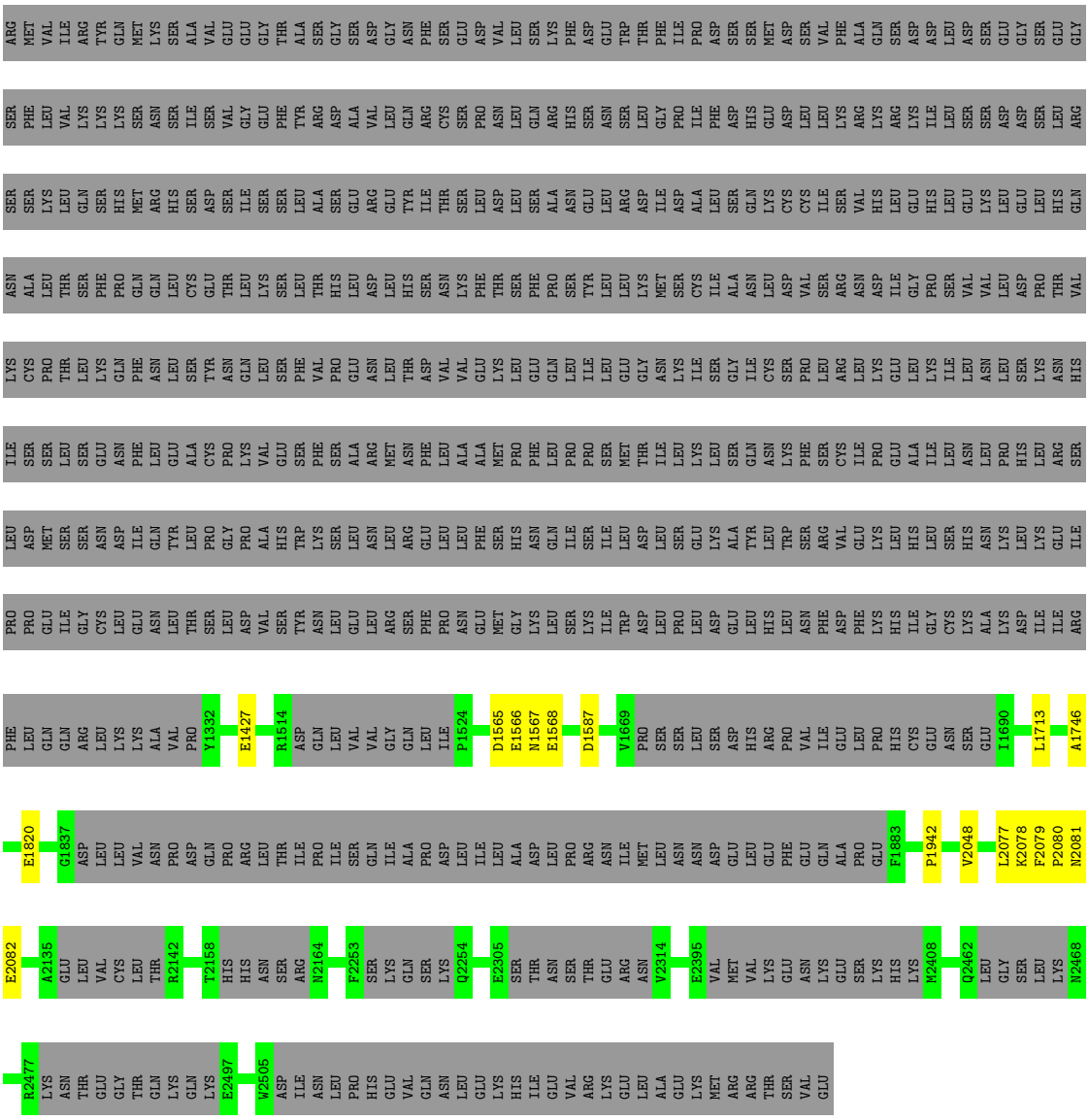
Y1332
R1514
P1524
E1566
D1587
P1588
V1669
I1690
F1700
P1701
F1704
I1765



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

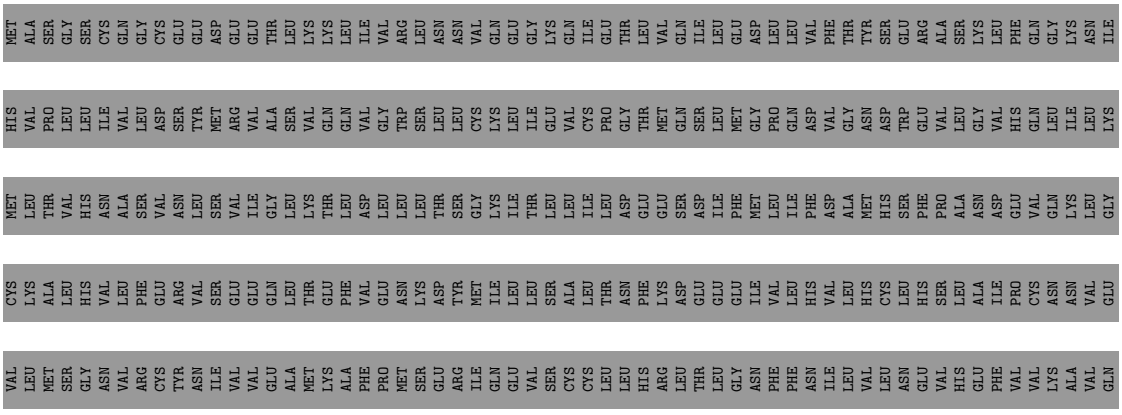
Chain 20-A: 40% 59%



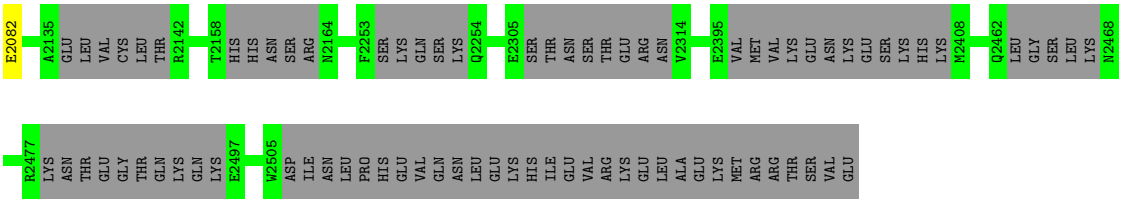


• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 20-B:

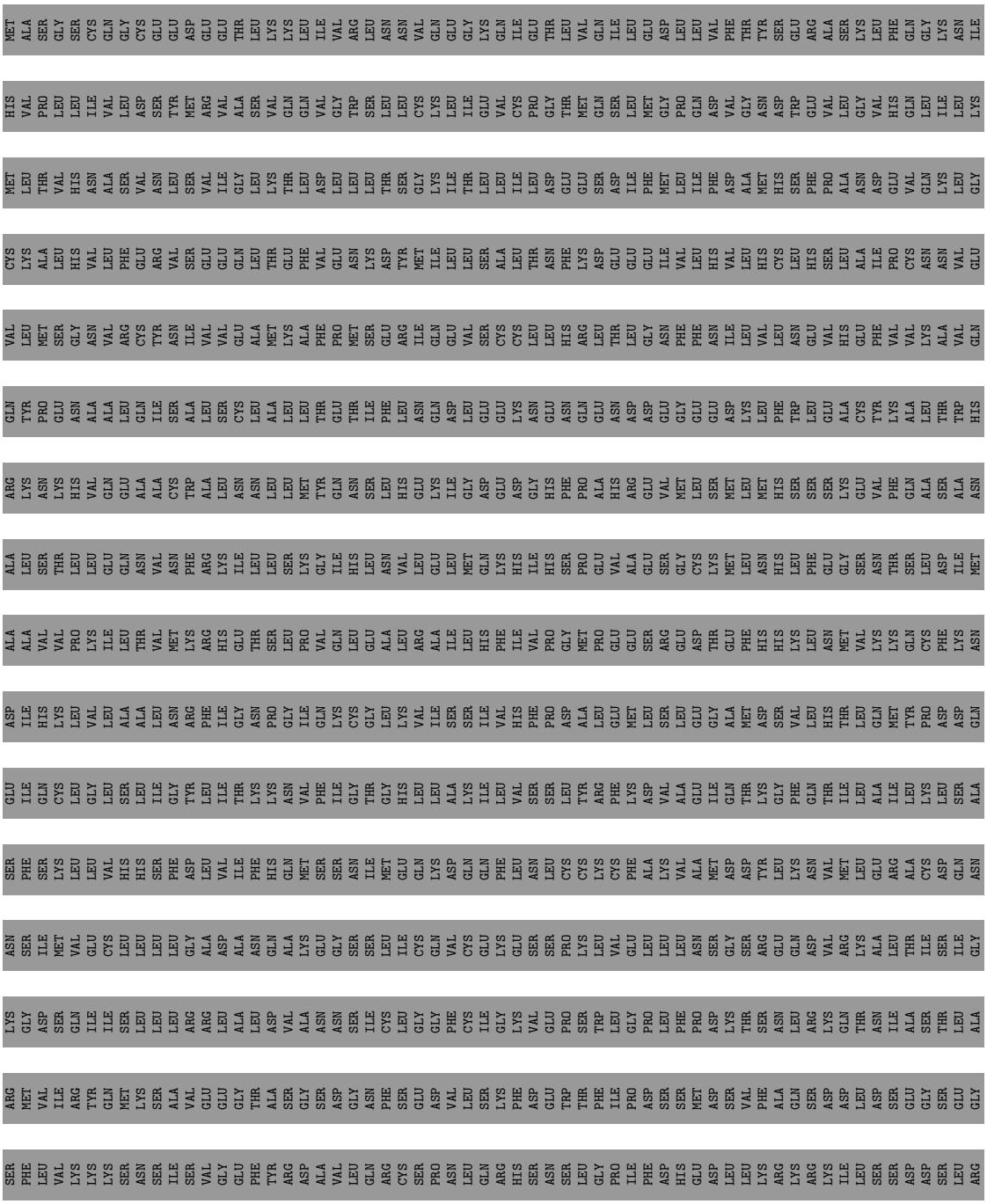


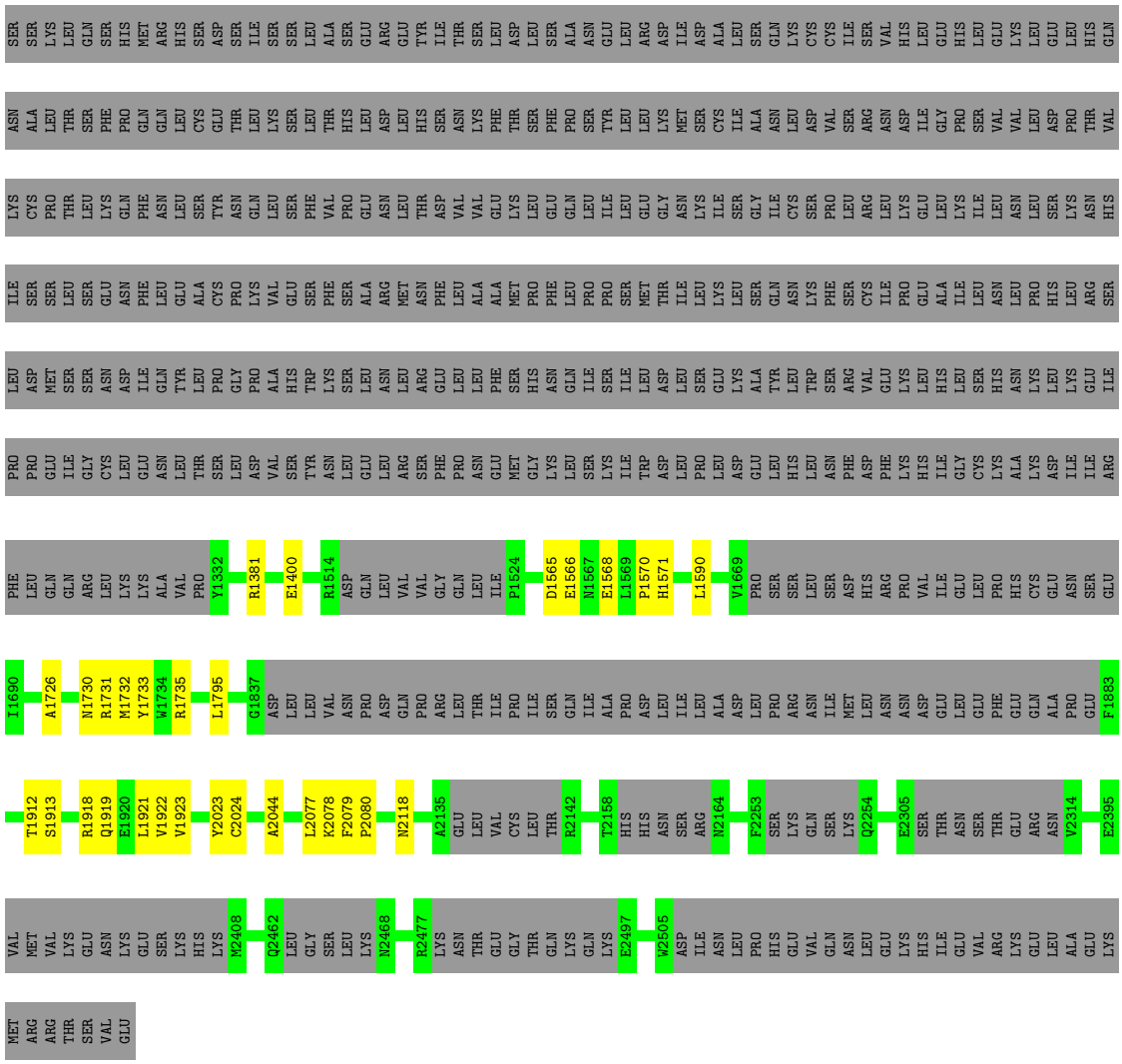
	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA	ARG	GLN
E1820	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS	TYR
	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN	PRO
G1837	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS	GLU
ASP	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS	ASN
LEU	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL	ALA
LEU	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN	ALA
VAL	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU	LEU
ASN	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA	GLN
PRO	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA	ILE
ASP	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS	SER
GLN	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP	ALA
PRO		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA	LEU
ARG	E1427	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU	SER
LEU		VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN	CYS
THR	R1514	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN	LEU
ILE	ASP	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU	ALA
PRO	GLN	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU	LEU
ILE	LEU	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET	LEU
SER	VAL	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR	THR
GLN	VAL	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN	GLU
ILE	GLY	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN	THR
ALA	GLN	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER	ILE
PRO	LEU	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU	PHE
ASP	ILE	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS	LEU
LEU	P1524	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU	ASN
ILE		GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS	GLN
LEU	D1565	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE	ASP
ALA	E1566	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY	LEU
ASP	N1567	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP	GLU
LEU	E1568	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU	GLU
PRO		SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP	LYS
ARG	D1587	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY	ASN
ASN		ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS	GLU
ILE	V1669	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE	ASN
MET	PRO	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO	GLN
LEU	SER	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA	GLU
ASN	SER	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS	ASN
ASN	LEU	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG	ASP
ASP	SER	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU	ASP
GLU	ASP	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL	GLU
LEU	HIS	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET	GLY
GLU	ARG	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU	GLU
PHE	PRO	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER	GLU
GLU	VAL	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET	ASP
GLN	ILE	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU	LYS
ALA	GLU	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET	LEU
PRO	LEU	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS	PHE
GLU	PRO	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER	TRP
F1883	HIS	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER	LEU
	CYS	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER	GLU
P1942	GLU	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS	ALA
	ASN	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU	CYS
V2048	SER	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL	TYR
	GLU	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE	LYS
L2077	I1690	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN	ALA
K2078		ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA	LEU
F2079	N1710	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER	THR
P2080		ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA	TRP
N2081	A1746	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN	HIS



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

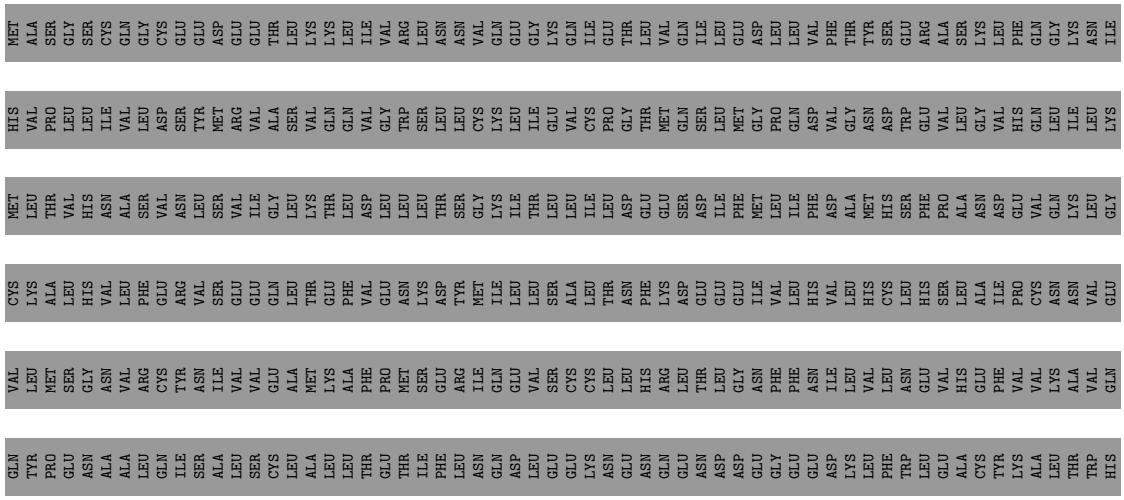
Chain 21-A: 40% 59%





• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 21-B:



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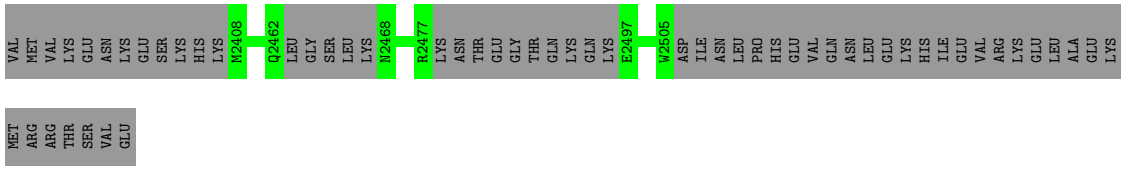
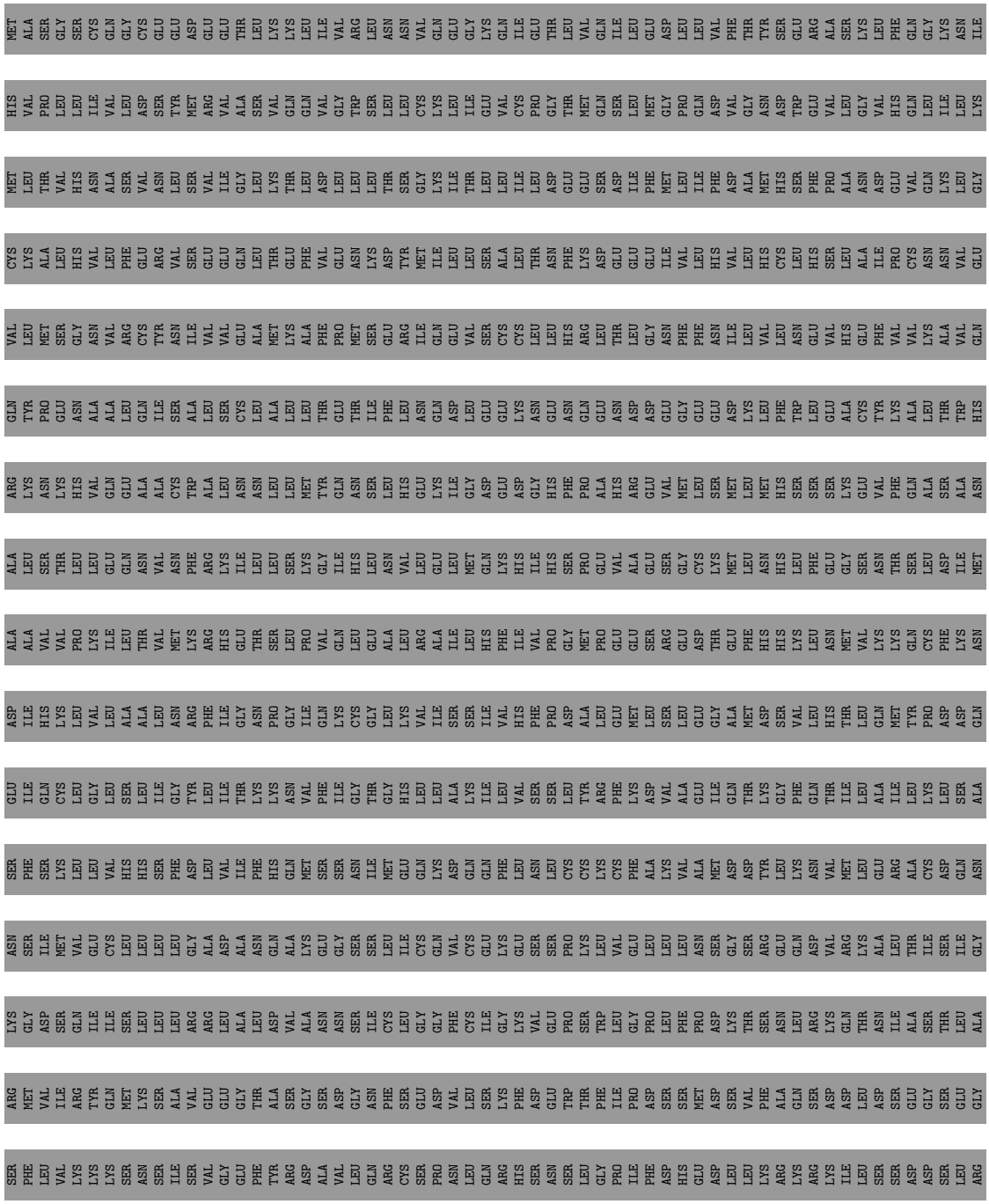
T1912		LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS
S1913	A1726	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN
		GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS
R1918	N1730	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS
Q1919	R1731	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL
E1920	M1732	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN
L1921	Y1733	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU
V1922	W1734	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA
V1923	R1735	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA
		PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS
Y2023	L1795	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP
C2024			LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA
	G1837	R1381	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU
A2044	ASP		VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN
	LEU	E1400	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN
L2077	LEU		TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU
K2078	VAL	R1514	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU
F2079	ASN	ASP	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET
P2080	PRO	GLN	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR
	ASP	LEU	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN
N2118	GLN	VAL	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN
	PRO	VAL	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER
A2135	ARG	GLY	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU
GLU	LEU	GLN	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS
LEU	THR	LEU	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU
VAL	ILE	ILE	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS
CYS	PRO	P1524	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE
LEU	ILE		GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY
THR	SER	D1565	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP
R2142	GLN	E1566	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU
	ILE	N1567	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP
T2158	ALA	E1568	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY
HIS	PRO	L1569	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS
HIS	ASP	P1570	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE
ASN	LEU	H1571	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO
SER	ILE		LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA
ARG	LEU	L1590	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS
N2164	ALA		LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG
	ASP	V1669	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU
F2253	LEU	PRO	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL
SER	PRO	SER	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET
LYS	ARG	SER	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU
GLN	ASN	LEU	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER
SER	ILE	SER	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET
LYS	MET	ASP	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU
Q2254	LEU	HIS	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET
	ASN	ARG	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS
E2305	ASN	PRO	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER
SER	ASP	VAL	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER
THR	GLU	ILE	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER
ASN	LEU	GLU	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS
SER	GLU	LEU	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU
THR	PHE	PRO	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL
GLU	GLU	HIS	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE
ARG	GLN	CYS	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN
ASN	ALA	GLU	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA
V2314	PRO	ASN	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER
	GLU	SER	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA
E2395	F1883	GLU	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 22-A: 40% • 59%



SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER

LEU ASP MET SER SER ASN ASP ILE GLN TYR LEU PRO GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG GLU LEU LEU PHE SER HIS ASN GLN ILE SER ILE LEU ASP LEU SER GLU LYS ALA TYR LEU TRP SER ARG VAL GLU LYS LEU HIS LEU SER HIS ASN LYS LEU LYS GLU ILE

PRO PRO GLU ILE GLY CYS LEU GLU ASN LEU THR SER LEU ASP VAL SER TYR ASN LEU GLU LEU ARG SER PHE PRO ASN GLU MET GLY LYS LEU SER LYS ILE TRP ASP LEU PRO LEU ASP GLU LEU HIS LEU ASN PHE ASP PHE LYS HIS ILE GLY CYS LYS ALA LYS ASP ILE ILE ARG

PHE LEU GLN GLN ARG LEU LYS LYS ALA VAL PRO Y1332 T1343 T1368 V1369 G1370 R1514 ASP GLN LEU VAL VAL GLY GLN LEU ILE P1524 L1564 D1565 E1566 P1570 Q1586 D1587 Q1591 V1669 PRO SER SER LEU SER ASP HIS ARG PRO VAL ILE GLU LEU PRO HIS CYS GLU

ASN SER GLU I1690 I1825 L1826 L1827 D1828 D1829 G1837 ASP LEU LEU VAL ASN PRO ASP GLN PRO ARG LEU THR ILE PRO ILE SER GLN ILE ALA PRO ASP LEU ILE LEU ALA ASP LEU PRO ARG ASN ILE MET LEU ASN ASN ASP GLU LEU GLU PHE GLU GLN ALA PRO GLU F1883 A2044

V2048 I2049 L2077 K2078 F2079 P2080 N2118 A2135 GLU LEU VAL CYS LEU THR R2142 T2158 HIS HIS ASN SER ARG N2164 F2253 SER LYS GLN SER LYS Q2254 E2305 SER THR ASN SER THR GLU ARG ASN V2314 E2395 VAL MET VAL LYS GLU ASN LYS GLU SER LYS HIS LYS

M2408 Q2462 LEU GLY SER LEU LYS N2468 R2477 LYS ASN THR GLU GLY THR GLN LYS GLN LYS E2497 W2505 ASP ILE ASN LEU PRO HIS GLU VAL GLN ASN LEU GLU LYS HIS ILE GLU VAL ARG LYS GLU LEU ALA GLU LYS MET ARG ARG THR SER VAL GLU

• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 22-B: 40% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

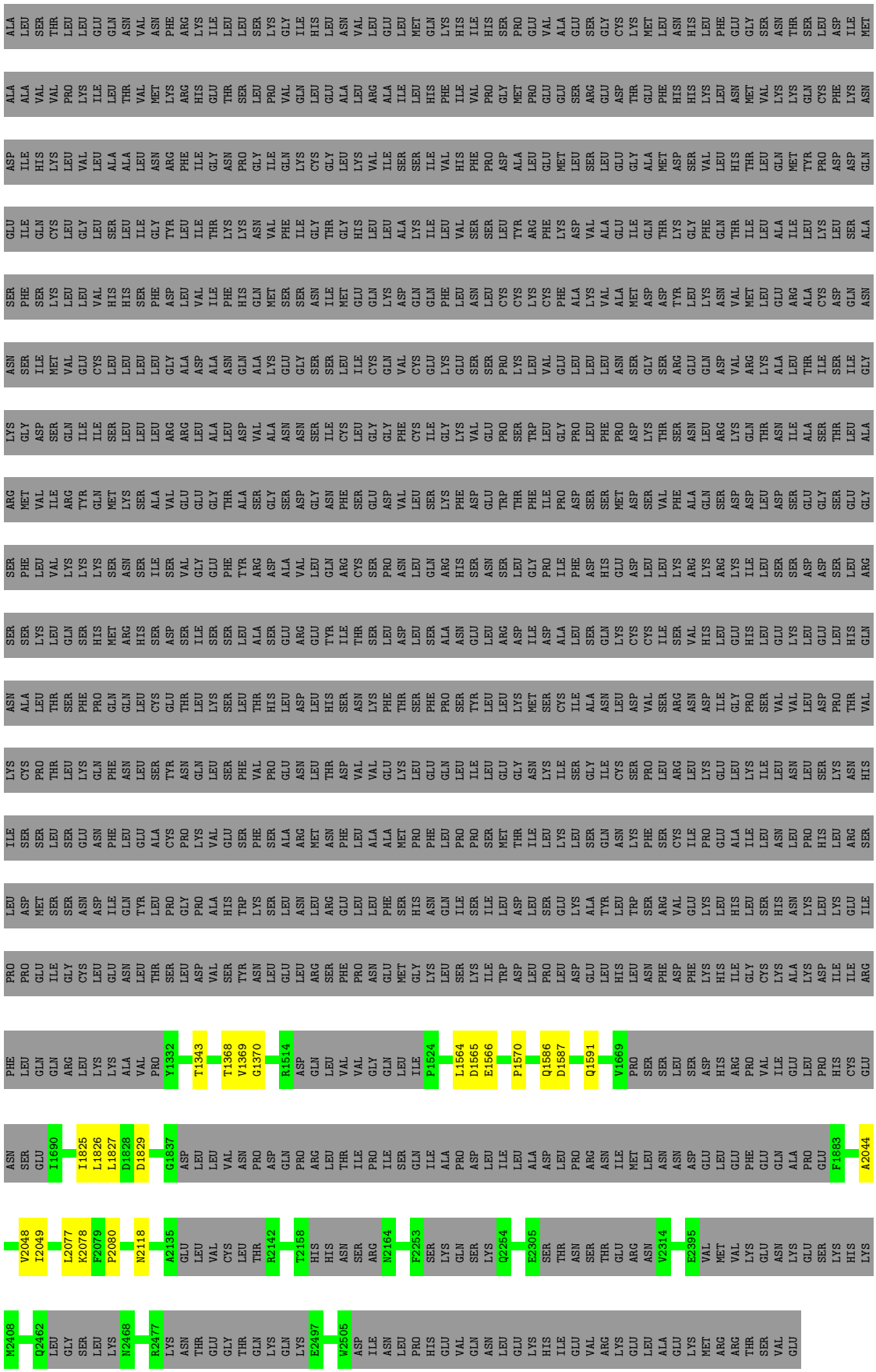
MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN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N2468
R2477
W2505
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T2158
R2142
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V2048
I2049
L2077
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F2079
P2080
N2118
I1690
I1825
L1826
L1827
D1828
D1829
G1837
Y1332
T1343
T1368
V1369
G1370
R1514
P1524
L1564
D1565
E1566
P1570
Q1586
D1587
Q1591
V1669
V2314
E2395
Q2254
E2305
F1863
A2044

• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 23-A: 41% 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN ILE LEU

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN LYS VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU TRP GLU ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA ALA GLU ILE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS LYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU GLN ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS GLN THR ILE LEU ALA ILE LEU THR ILE SER GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU LYS ARG LYS GLN THR ASN ILE SER THR LEU ALA

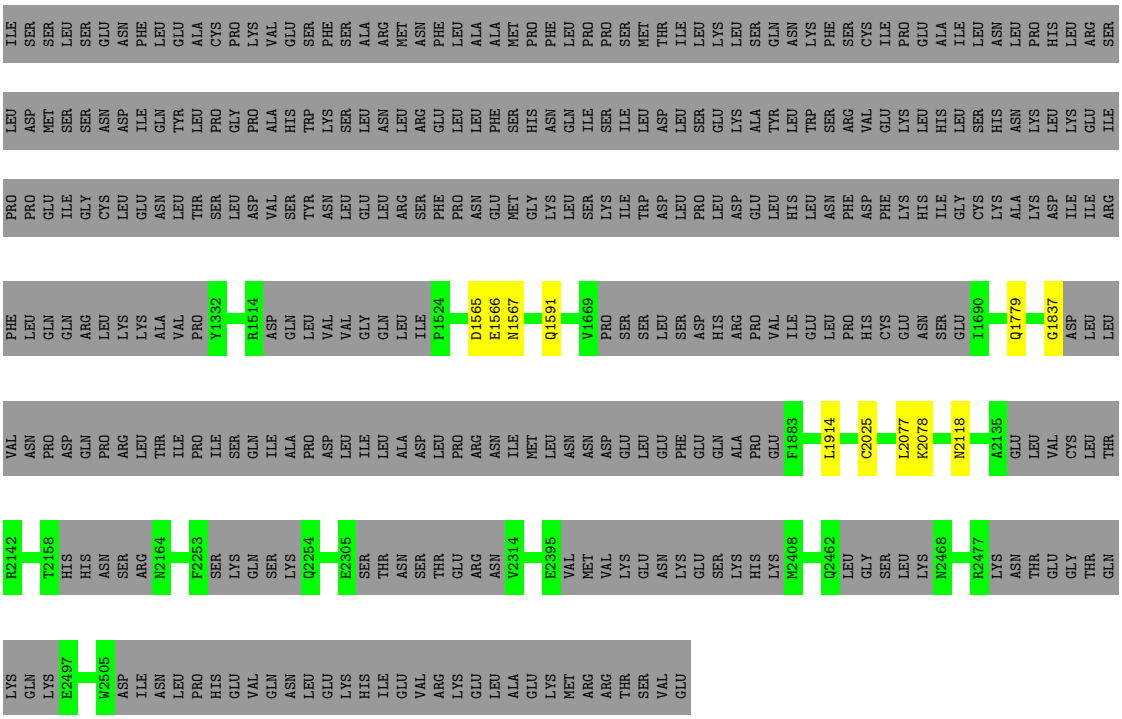
ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE GLU GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ARG ALA GLN ASP SER ASP ASP LYS GLN THR ASP SER GLU GLY

SER PHE LEU VAL LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN LEU GLY PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP LEU GLU

SER SER LYS LEU GLN HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU SER ALA LEU ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU GLU HIS LEU GLU ASP SER

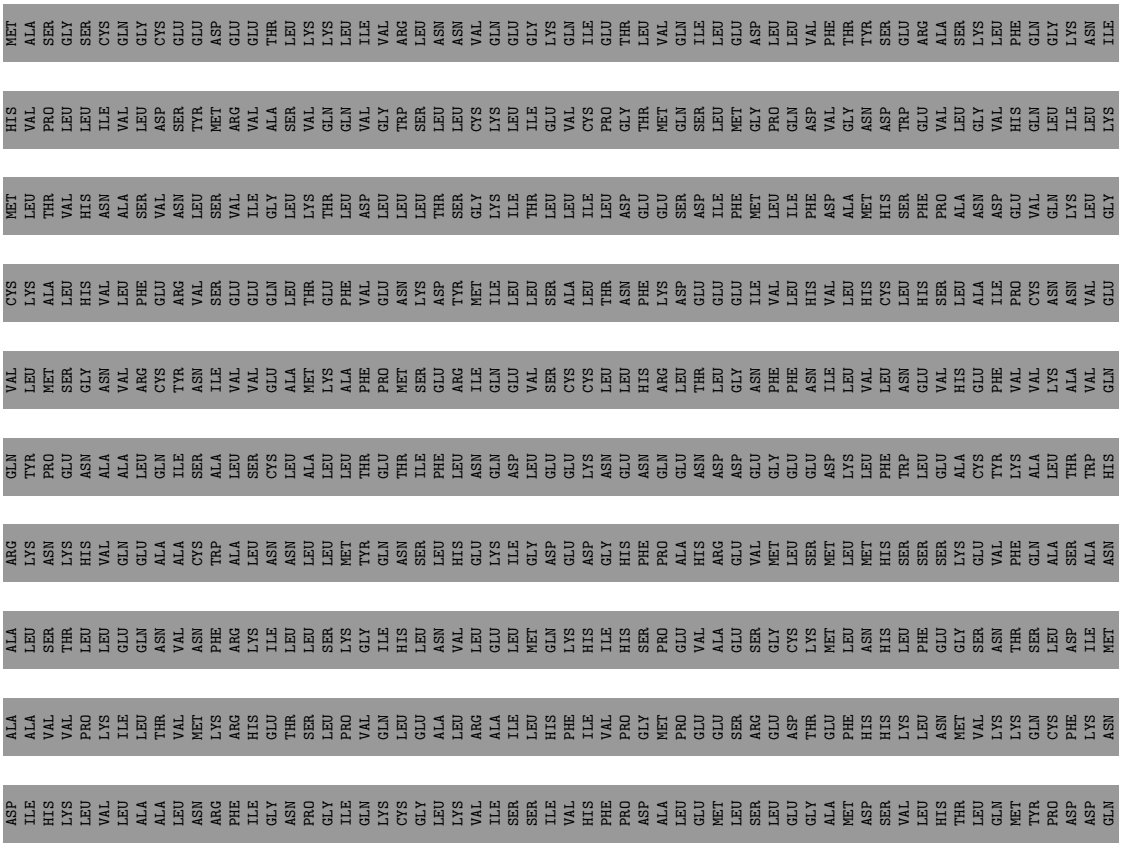
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR HIS LEU ASN LYS PHE THR SER PHE PRO SER TYR SER LEU LYS GLU GLN GLN LEU ASP LEU HIS SER ASN LEU LYS LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO LEU ILE ASP VAL LEU VAL ASP SER

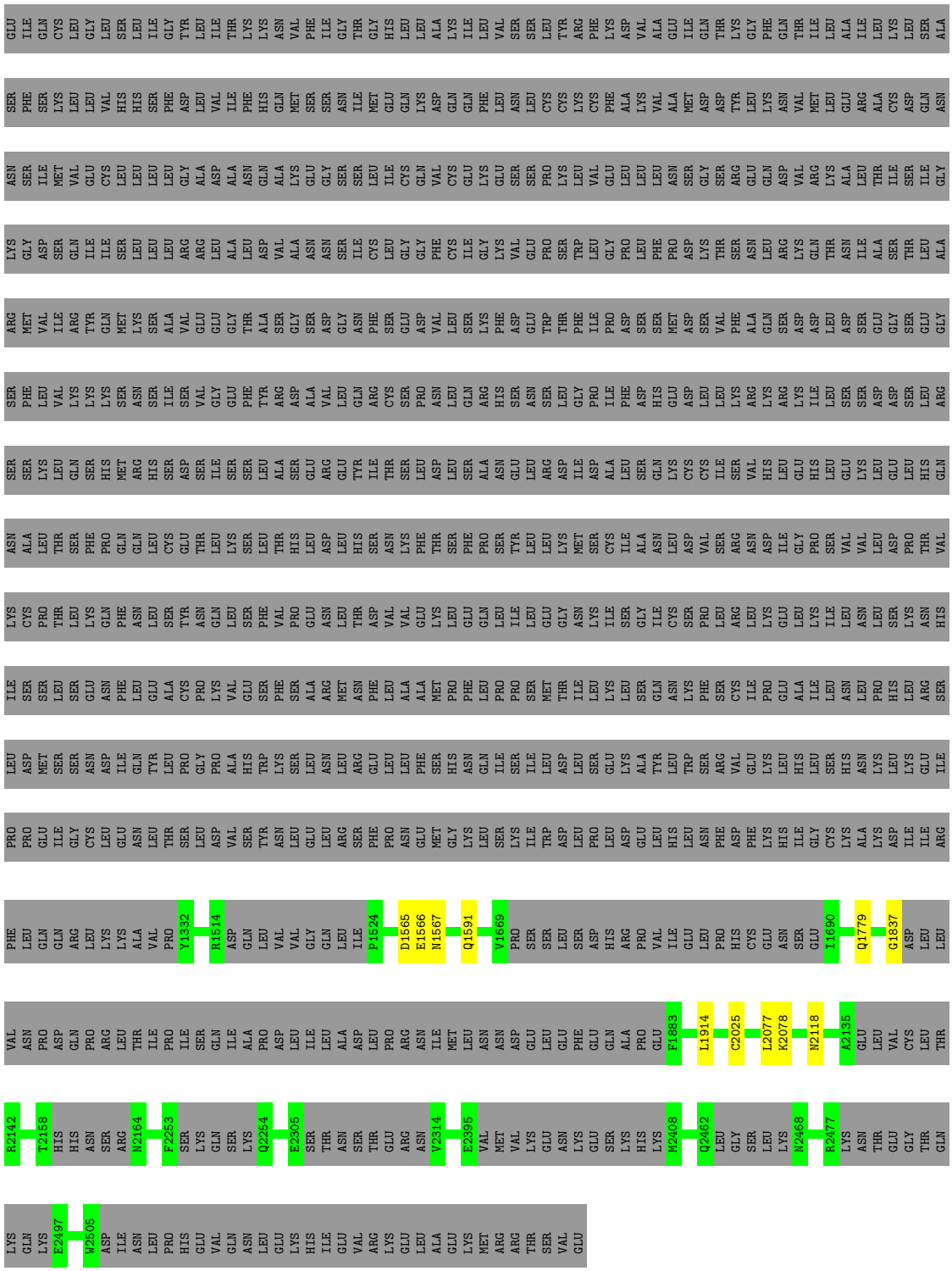
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU ASP PRO LYS ASN HIS



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 23-B: 41% 59%

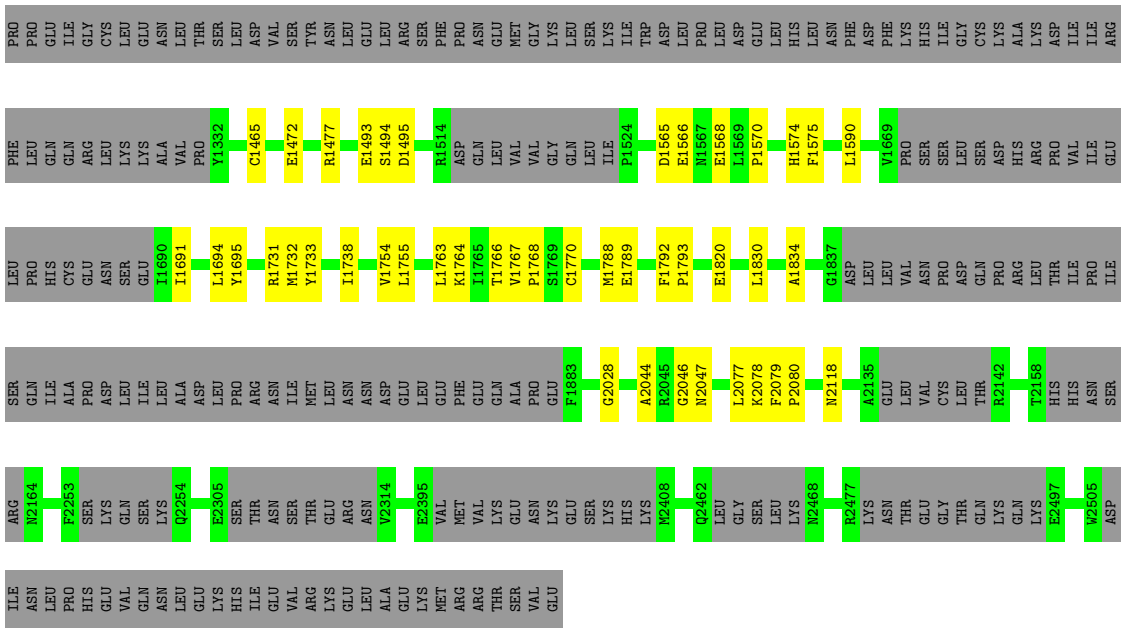




- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

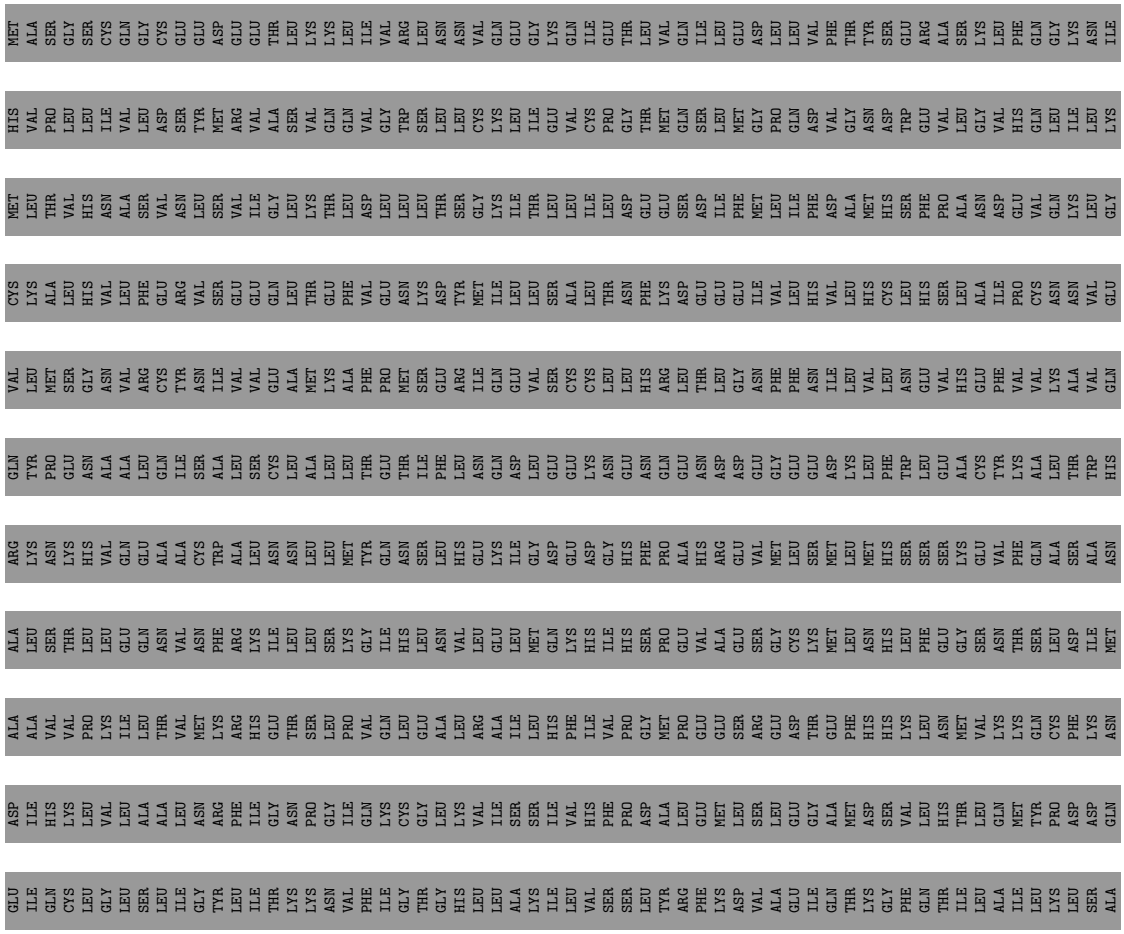
Chain 24-A:

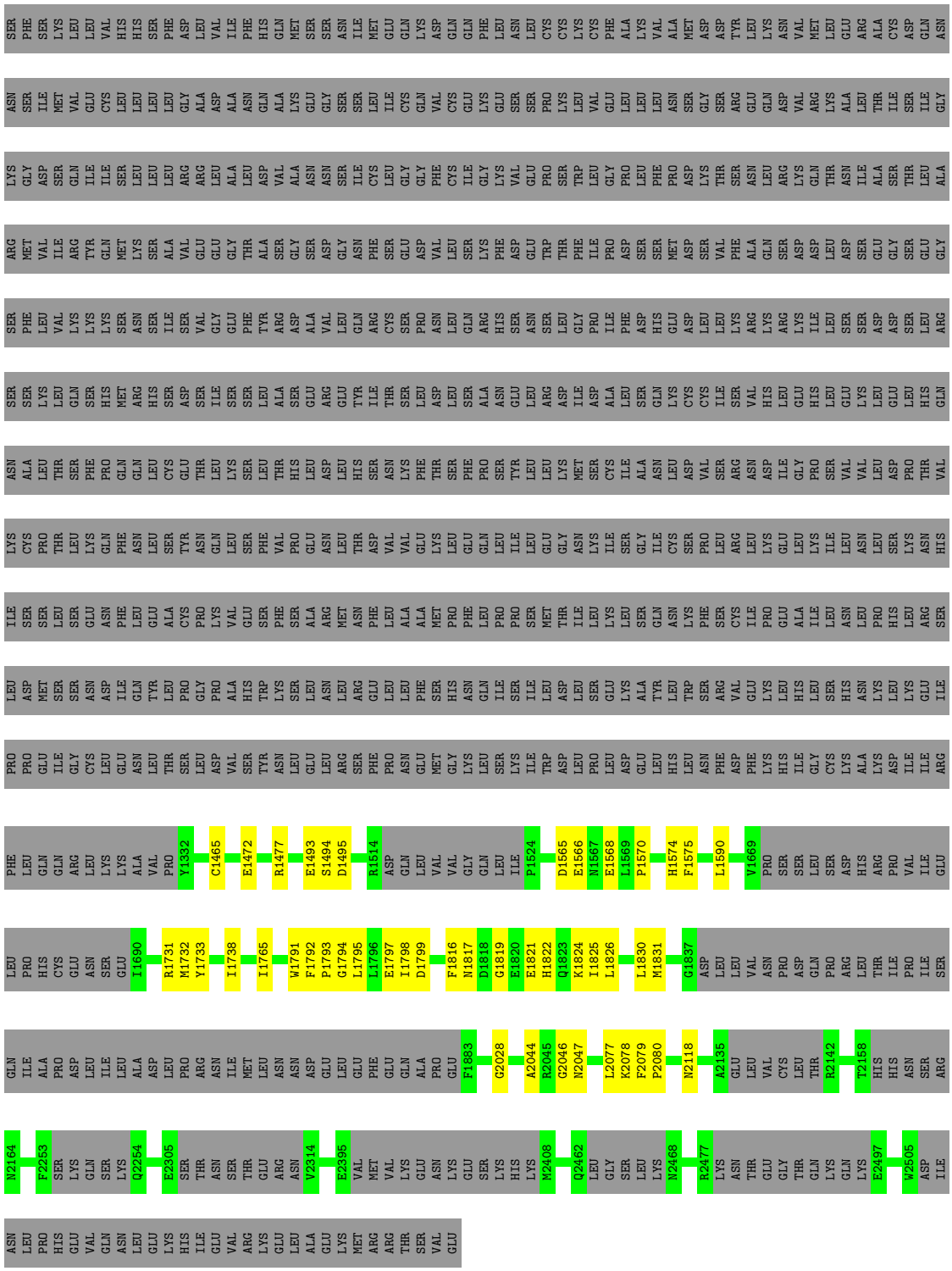
HIS VAL PRO LEU LEU ILE VAL LEU ASP SER SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLN LEU ILE LEU GLY LYS
MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL LEU GLY
CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU
VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS ILE GLU ALA ASN ILE LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN HIS GLU PHE VAL VAL LYS ALA VAL GLN
GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LYS LEU GLU LYS ASN GLN GLU LYS ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU ALA CYS TYR LYS ALA LEU THR TRP HIS
ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU GLY ILE ILE GLY ASP GLU GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA
ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU GLU SER ARG GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER SER ASN THR SER LEU ASP ILE MET
ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN
ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL LEU ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU ASP MET ALA GLU GLY ALA MET ASP SER VAL LEU HIS VAL GLN GLN
GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU LYS THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR ILE LEU GLN LEU LEU ILE LEU LYS LEU SER ALA
SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN SER CYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU LEU GLU ARG ASP GLN ASN
ASN SER ILE MET VAL GLU CYS LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS ALA ASN SER SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER LYS GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS THR ILE SER ILE GLY
LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG ARG LYS GLN THR ASN ALA SER THR LEU ALA
ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN ASP VAL ARG LYS ASP ASP LEU ASP SER GLU GLY GLU GLY
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLU GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY LYS HIS ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ILE LEU LEU SER GLU GLN
SER SER LYS LEU GLN SER HIS MET ARG HIS SER SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS GLN
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR SER LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS LYS THR LYS LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN LEU ASP VAL LEU SER GLU LYS LEU LEU ASP LEU ILE SER
LYS CYS PRO THR LEU LYS GLN PHE ASN GLN LEU SER TYR ASN GLN LEU THR VAL HIS GLN LEU LYS LYS GLU GLN LEU ILE LEU GLU GLY ILE CYS SER PRO LEU ARG ARG LEU LYS GLU LEU ASN LEU LYS ILE LEU LEU ASN ASN HIS
ILE SER SER LEU SER GLU ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN LEU ALA ALA ARG MET ASN PHE LEU ALA ALA CYS ILE PRO PHE LEU ILE LEU LEU ASN LEU PRO HIS LEU ARG SER
LEU ASP MET SER ASN ILE GLN LEU ARG GLU LEU LEU LEU PHE SER HIS ASN GLN ILE SER LYS GLU ASP LEU SER GLU LYS ALA TYR LEU TRP SER ARG VAL GLU LYS LEU SER HIS ASN LYS LEU ARG GLU
WORLDWIDE PDB PROTEIN DATA BANK



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 24-B: 39% • 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 25-A: 39% 59%

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

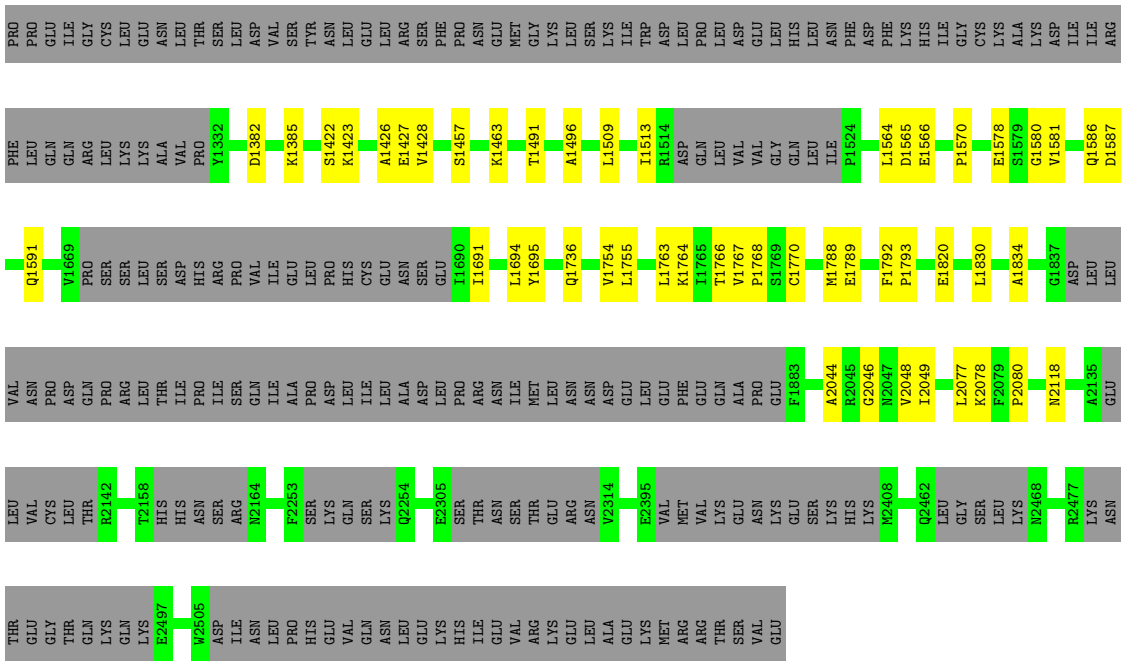
SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

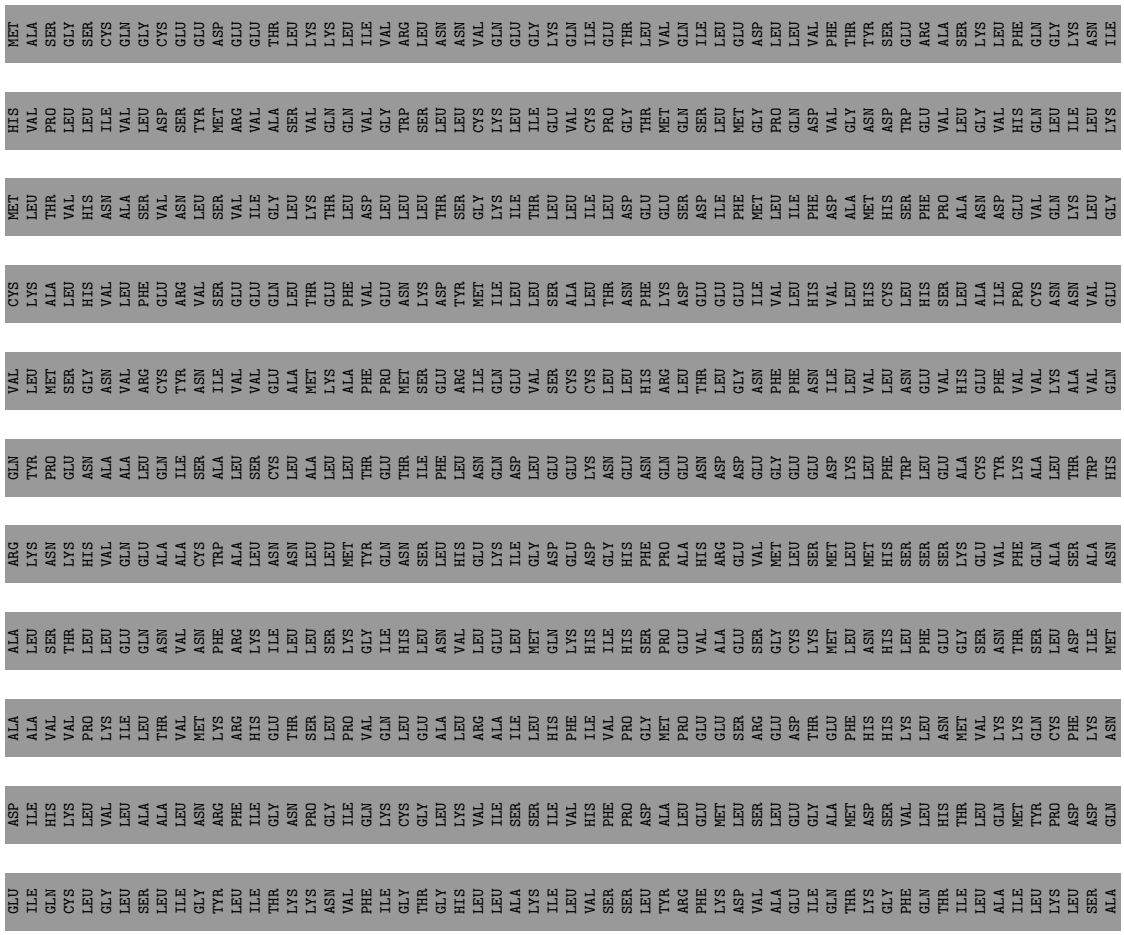
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER

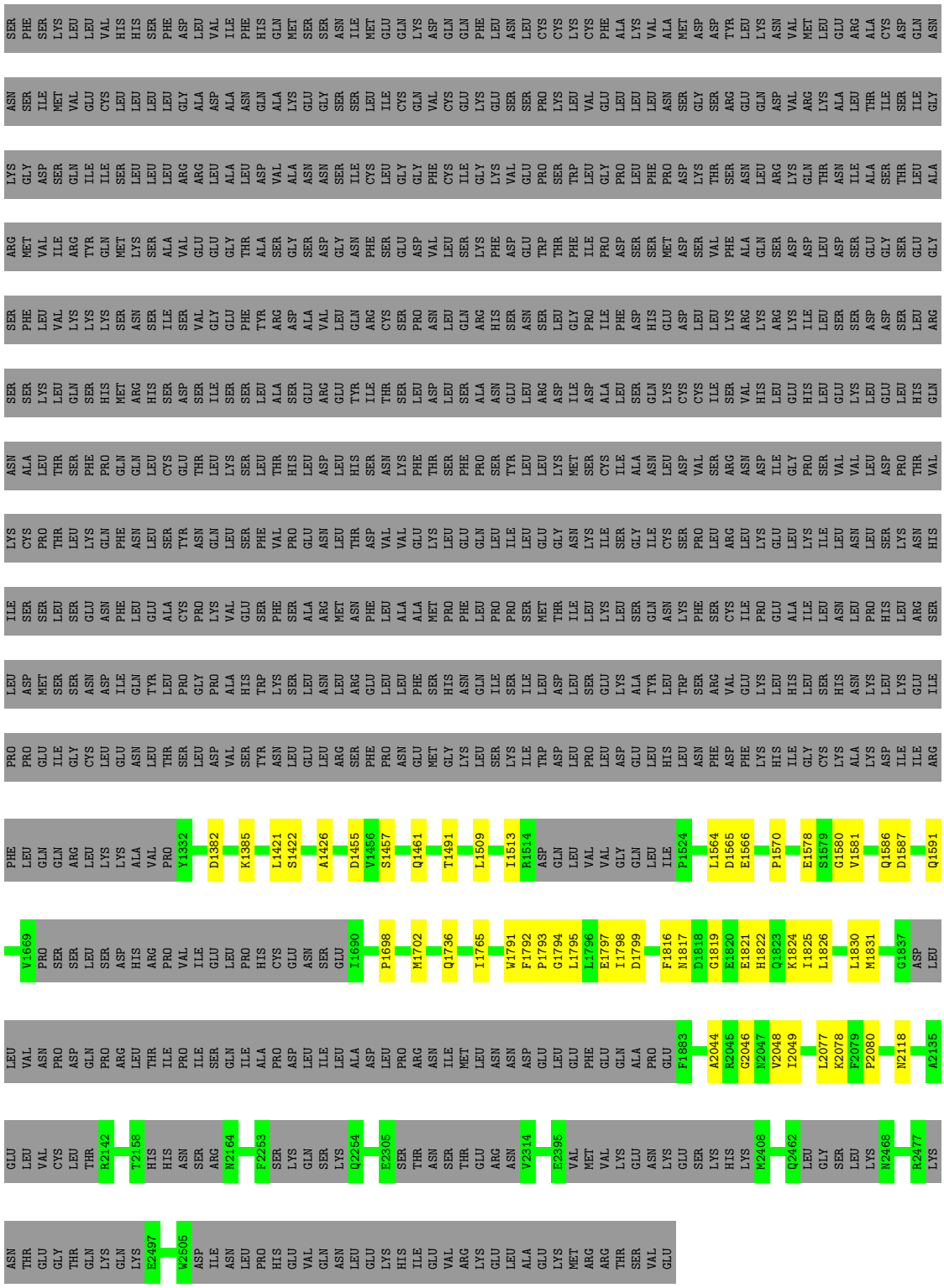
LEU ASP MET SER SER ASN ASP ILE GLN TYR LEU PRO GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG GLU LEU LEU PHE SER HIS ASN GLN ILE SER ILE LEU ASP LEU SER GLU LYS ALA TYR LEU TRP SER ARG VAL GLU LYS LEU HIS LEU SER HIS ASN LYS LEU LYS GLU ILE



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 25-B: 39% • 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 26-A: 41% • 59%

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

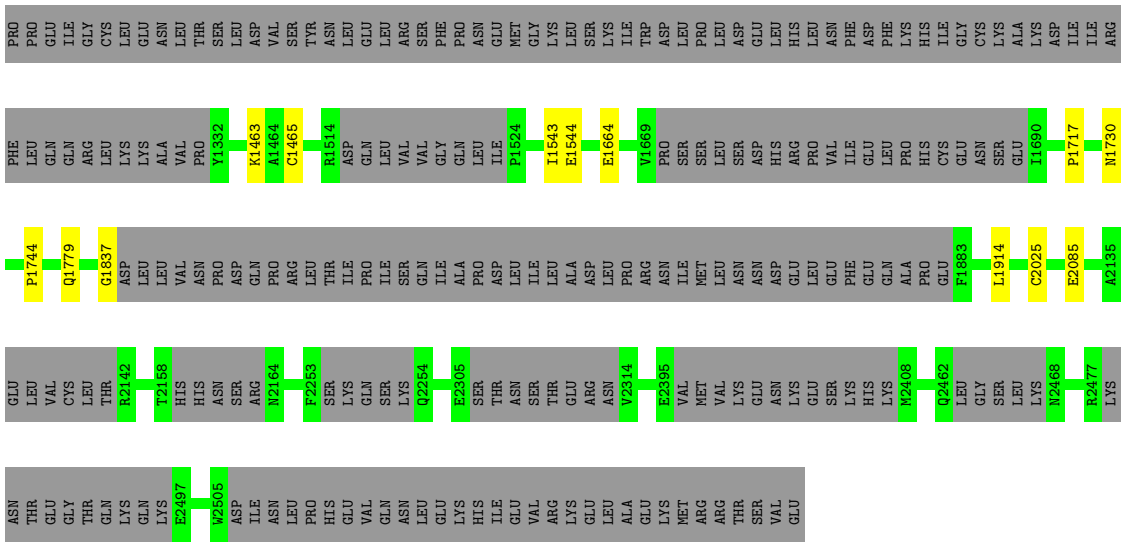
SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

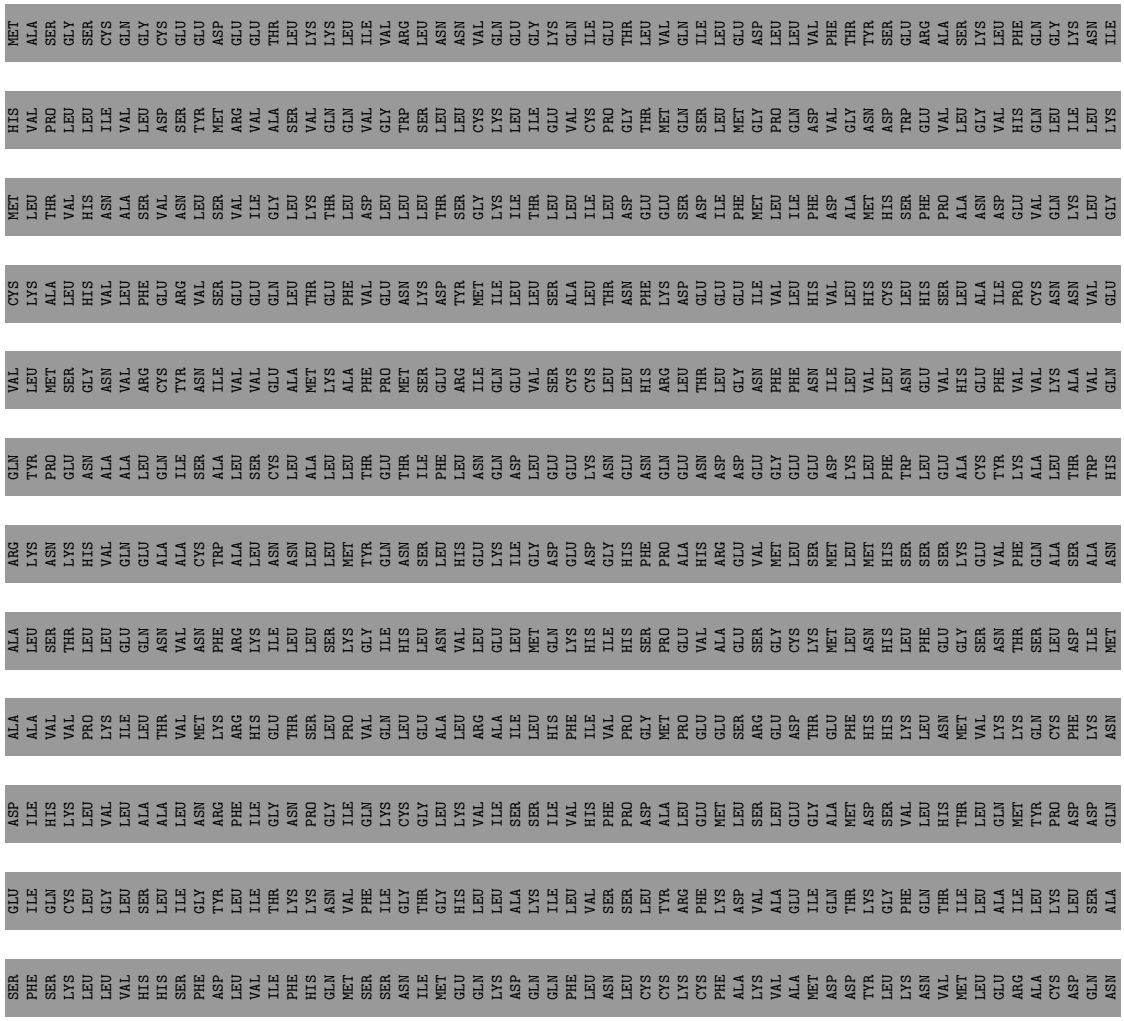
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER

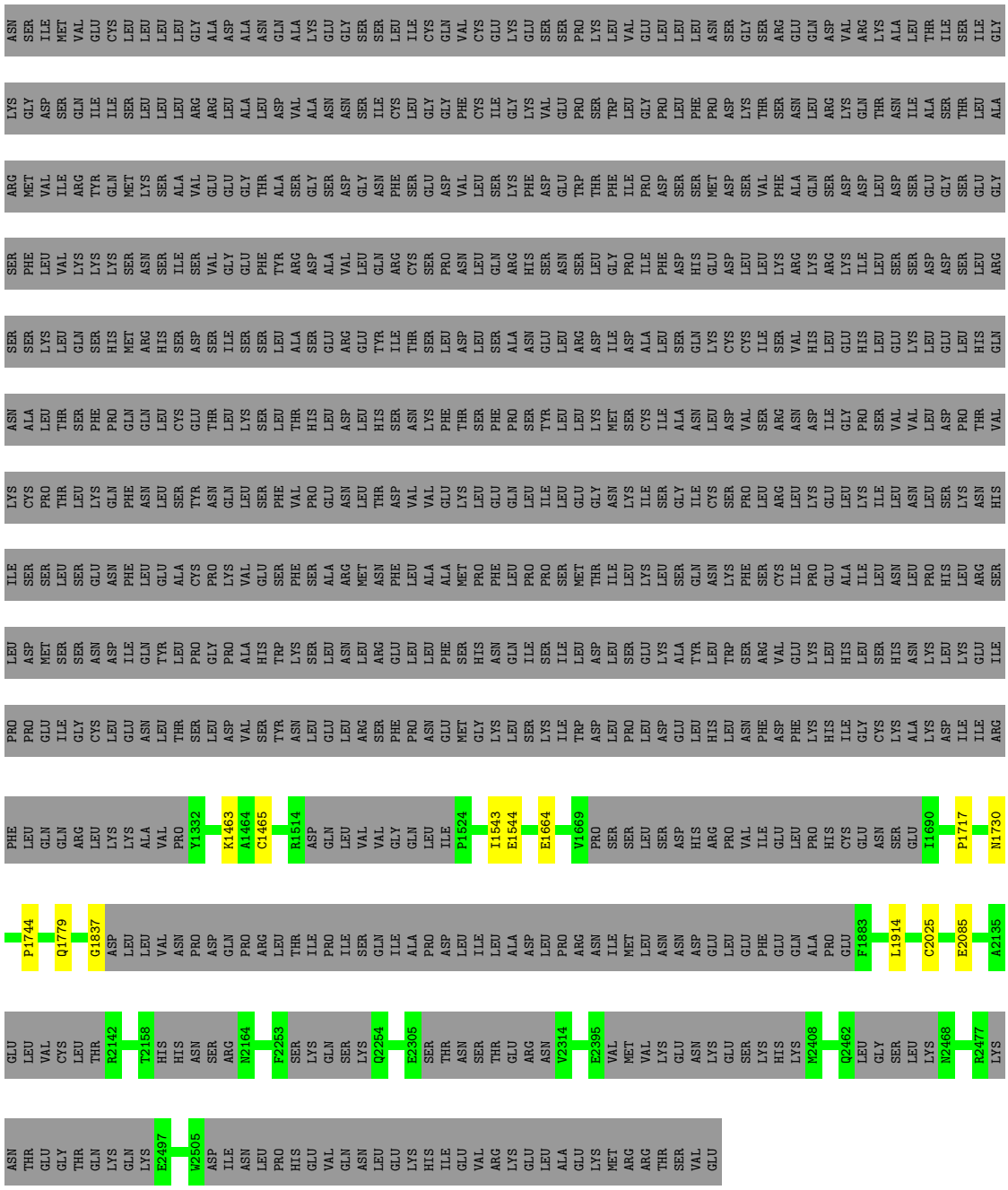
LEU ASP MET SER SER ASN ASP ILE GLN TYR LEU PRO GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG GLU LEU LEU PHE SER HIS ASN GLN ILE SER ILE LEU ASP LEU SER GLU LYS ALA TYR LEU TRP SER ARG VAL GLU LYS LEU HIS LEU SER HIS ASN LYS LEU LYS GLU ILE



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

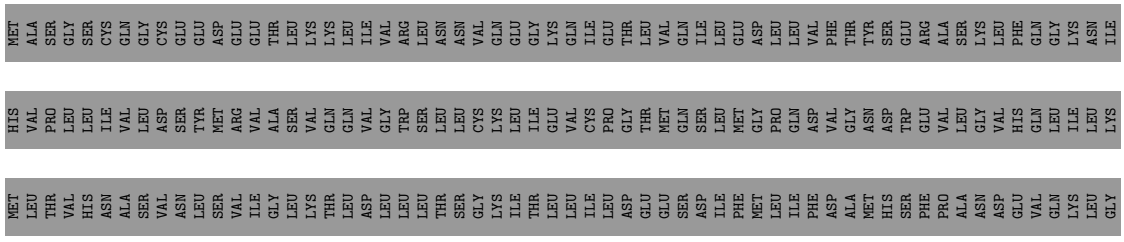
Chain 26-B: 41% • 59%



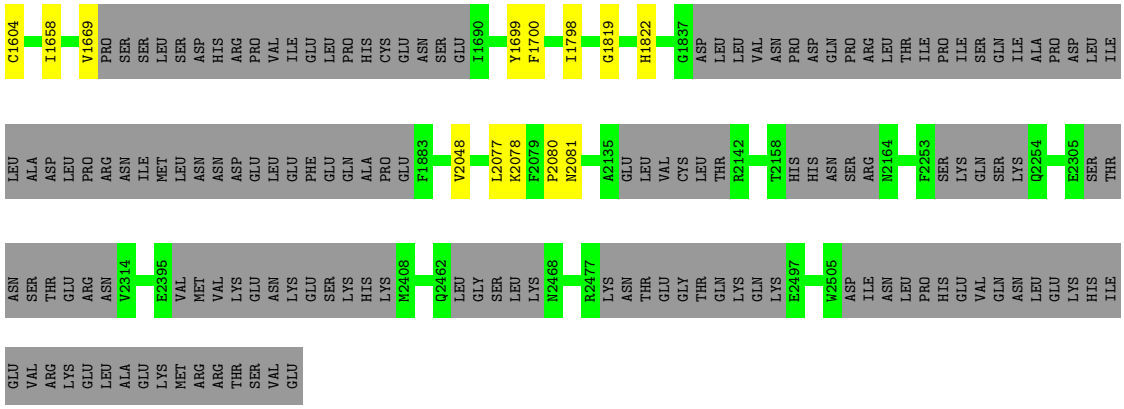


• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 27-A: 40% • 59%

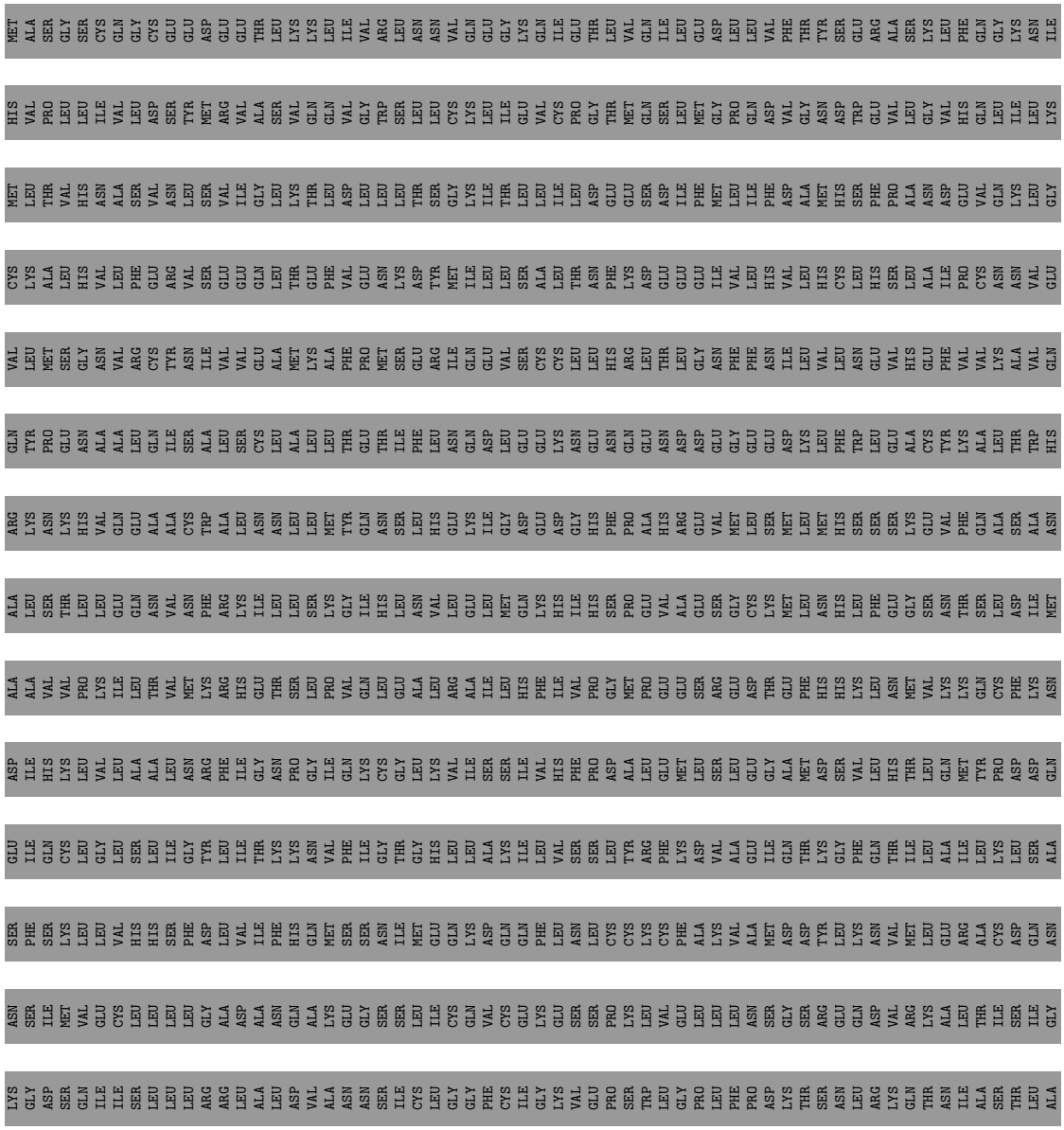


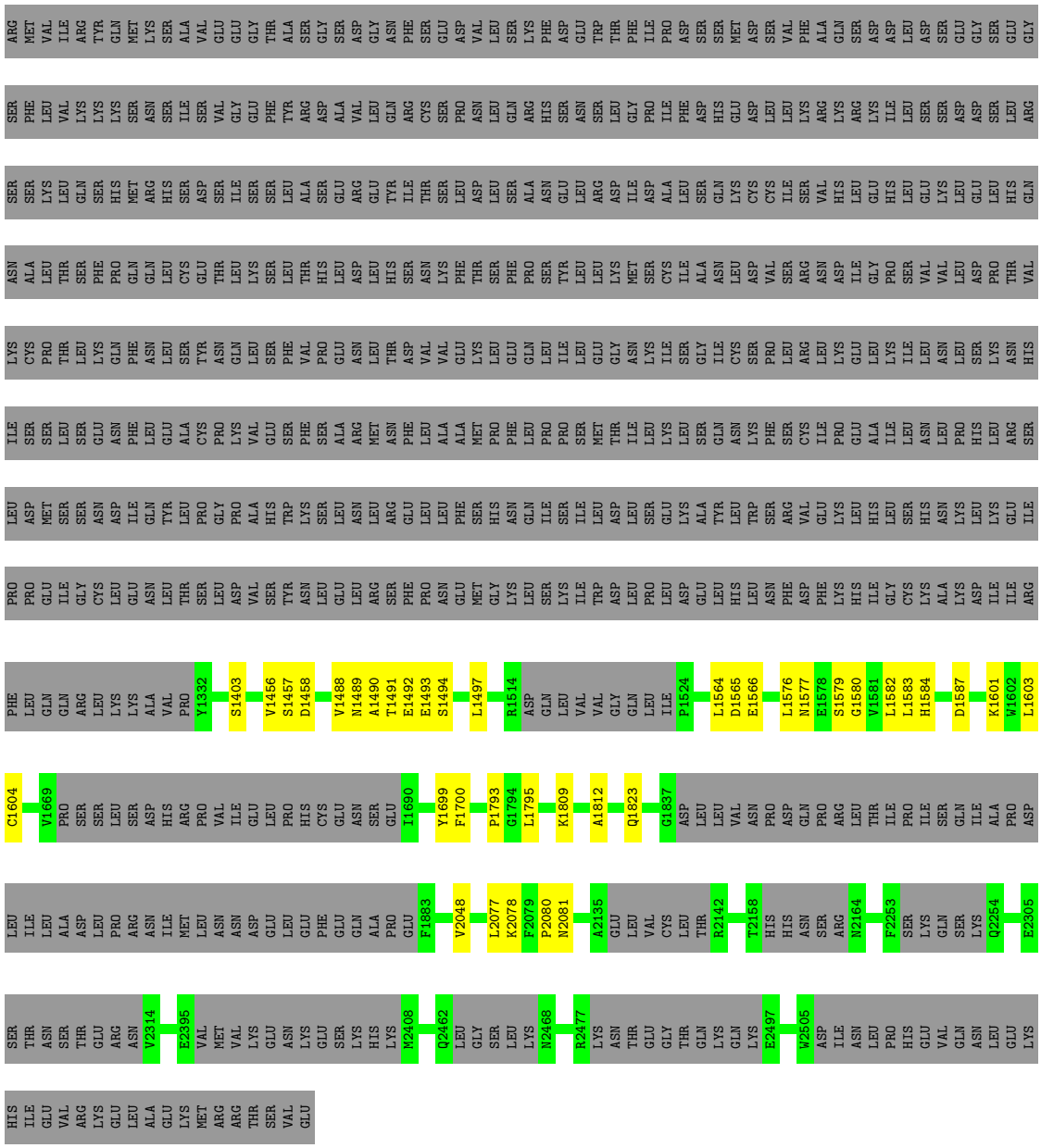
PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA	ARG	GLN	VAL	CYS
LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS	TYR	LEU	LYS
GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN	PRO	MET	ALA
GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS	GLU	SER	LEU
ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS	ASN	GLY	HIS
LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL	ALA	ASN	VAL
LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN	ALA	VAL	LEU
LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU	LEU	ARG	PHE
ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA	GLN	CYS	GLU
VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA	ILE	TYR	ARG
PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS	SER	ASN	VAL
Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP	ALA	ILE	SER
	LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA	LEU	VAL	GLU
S1403	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU	SER	VAL	GLU
	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN	CYS	GLU	GLN
V1456	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN	LEU	ALA	LEU
S1457	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU	ALA	MET	THR
D1458	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU	LEU	LYS	GLU
	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET	LEU	ALA	PHE
V1488	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR	THR	PHE	VAL
N1489	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN	GLU	PRO	GLU
A1490	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN	THR	MET	ASN
T1491	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER	ILE	SER	LYS
E1492	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU	PHE	GLU	ASP
E1493	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS	LEU	ARG	TYR
S1494	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU	ASN	ILE	MET
	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS	GLN	GLN	ILE
L1497	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE	ASP	GLU	LEU
	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY	LEU	VAL	LEU
R1514	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP	GLU	SER	SER
ASP	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU	GLU	CYS	ALA
GLN	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP	LYS	CYS	LEU
LEU	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY	ASN	LEU	THR
VAL	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS	GLU	LEU	ASN
VAL	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE	ASN	HIS	PHE
GLY	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO	GLN	ARG	LYS
GLN	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA	GLU	LEU	ASP
LEU	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS	ASN	THR	GLU
ILE	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG	ASP	LEU	GLU
P1524	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU	ASP	GLY	GLU
	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL	GLU	ASN	ILE
L1564	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET	GLY	PHE	VAL
D1565	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU	GLU	PHE	LEU
E1566	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER	GLU	ASN	HIS
	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET	ASP	ILE	VAL
L1576	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU	LYS	LEU	LEU
N1577	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET	LEU	VAL	HIS
E1578	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS	PHE	LEU	CYS
S1579	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER	TRP	ASN	LEU
G1580	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER	LEU	GLU	HIS
V1581	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER	GLU	VAL	SER
L1582	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS	ALA	HIS	LEU
L1583	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU	CYS	GLU	ALA
H1584	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL	TYR	PHE	ILE
	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE	LYS	VAL	PRO
D1587	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN	ALA	VAL	CYS
	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA	LEU	LYS	ASN
K1601	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER	THR	ALA	ASN
W1602	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA	TRP	VAL	VAL
L1603	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN	HIS	GLN	GLU



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

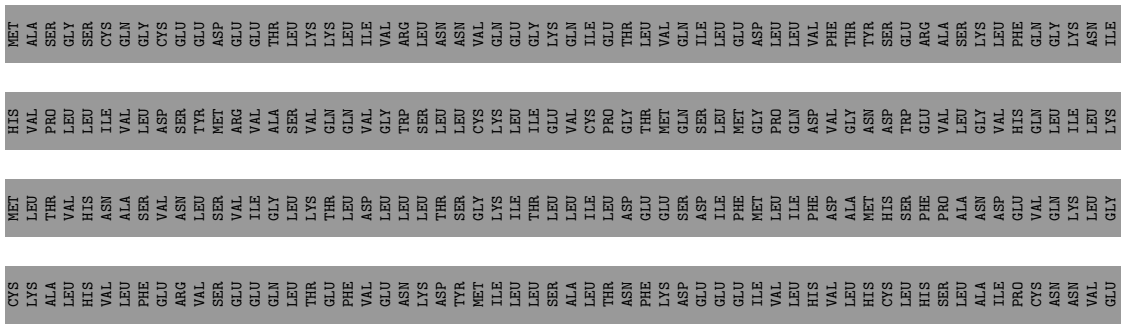
Chain 27-B:





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 28-A: 40% 59%



SER	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA	ARG	GLN	VAL
ASP	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS	TYR	LEU
HIS	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN	PRO	MET
ARG	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS	GLU	SER
PRO	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS	ASN	GLY
VAL	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL	ALA	ASN
ILE	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN	ALA	VAL
GLU	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU	LEU	ARG
LEU	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA	GLN	CYS
PRO	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA	ILE	TYR
HIS	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS	SER	ASN
CYS	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP	ALA	ILE
GLU		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA	LEU	VAL
ASN	Q1353	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU	SER	VAL
SER		VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN	CYS	GLU
GLU	D1455	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN	LEU	ALA
I1690		TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU	ALA	MET
	N1489	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU	LEU	LYS
W1734	A1490	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET	LEU	ALA
	T1491	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR	THR	PHE
G1837	E1492	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN	GLU	PRO
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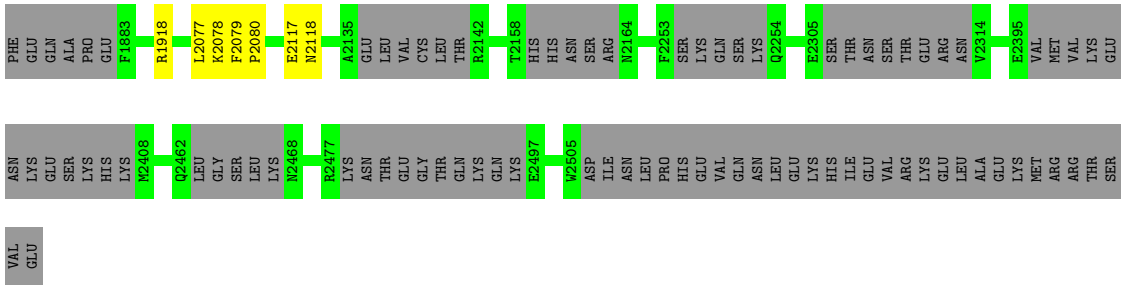
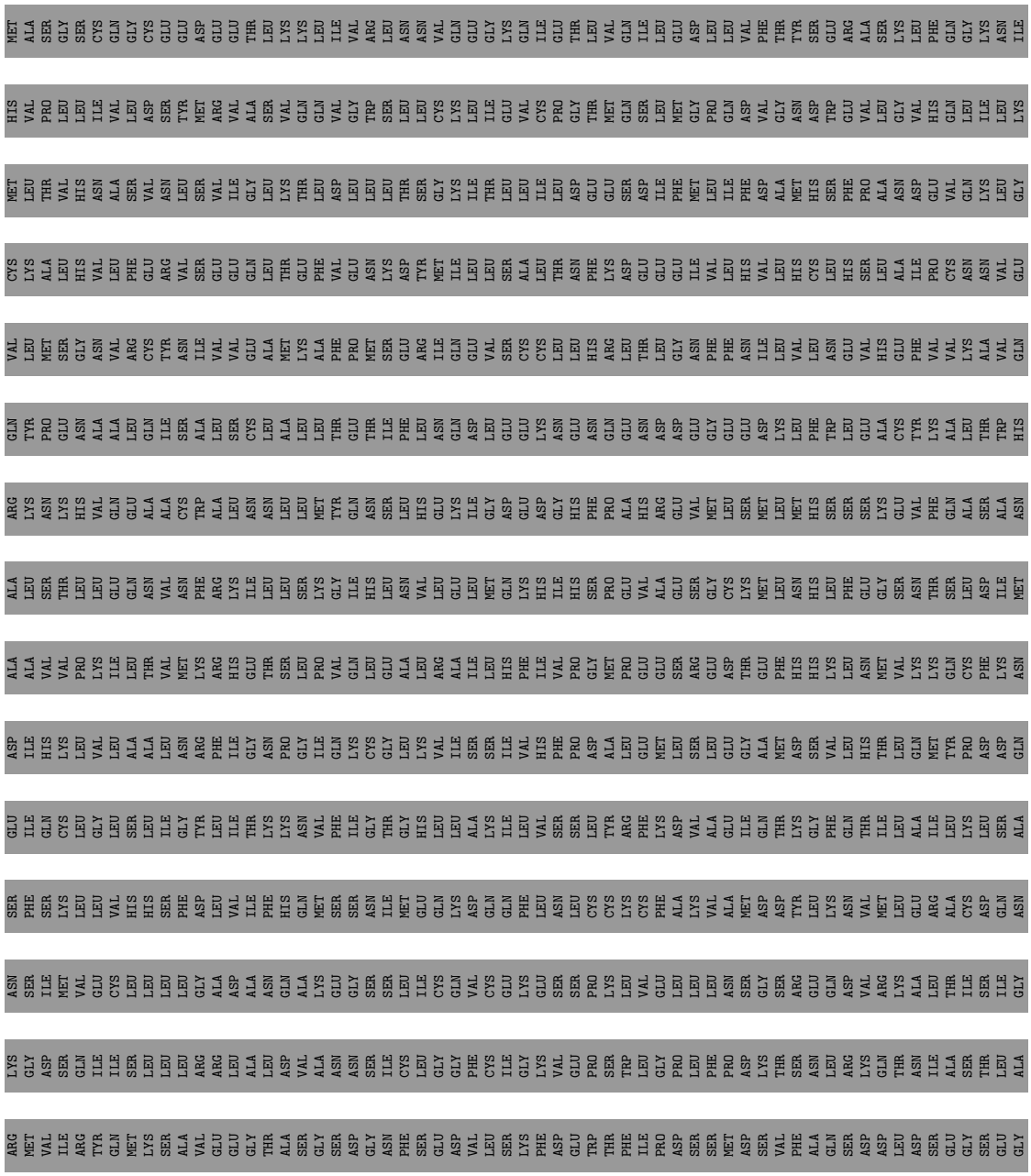
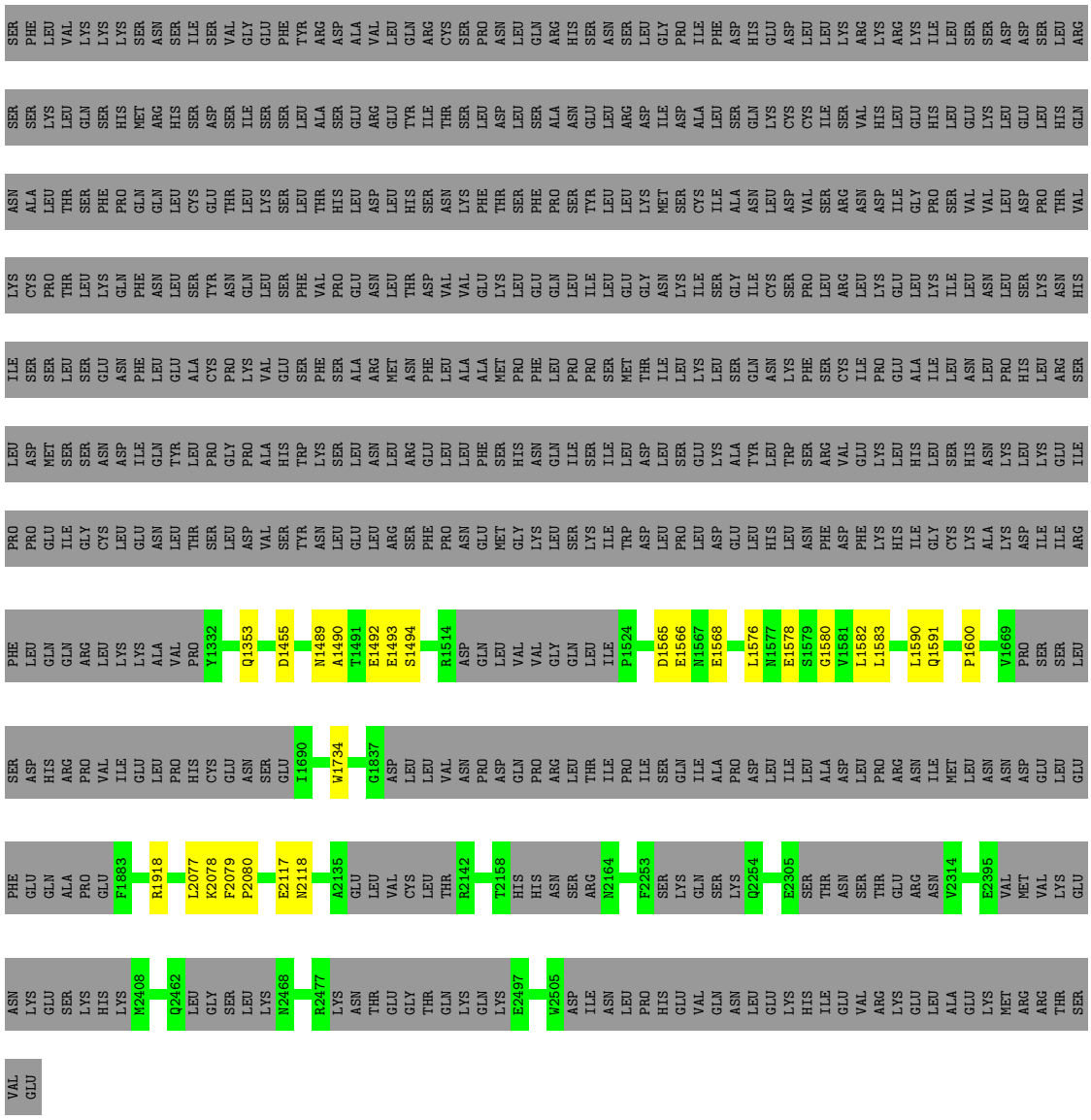
LEU	S1494	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER	ILE	SER
LEU		PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU	PHE	GLU
VAL	R1514	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS	LEU	ARG
ASN	ASP	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU	ASN	ILE
PRO	GLN	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS	GLN	GLN
ASP	LEU	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE	ASP	GLU
GLN	VAL	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY	LEU	VAL
PRO	VAL	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP	GLU	SER
ARG	GLY	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU	GLU	CYS
LEU	GLN	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP	LYS	CYS
THR	LEU	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY	ASN	LEU
ILE	ILE	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS	GLU	LEU
PRO	P1524	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE	ASN	HIS
ILE		ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO	GLN	ARG
SER	D1565	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA	GLU	LEU
GLN	E1566	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS	ASN	THR
ILE	N1567	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG	ASP	LEU
ALA	E1568	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU	ASP	GLY
PRO		GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL	GLU	ASN
ASP	L1576	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET	GLY	PHE
LEU	N1577	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU	GLU	PHE
ILE	E1578	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER	GLU	ASN
LEU	S1579	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET	ASP	ILE
ALA	G1580	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU	LYS	LEU
ASP	V1581	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET	LEU	VAL
LEU	L1582	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS	PHE	LEU
PRO	L1583	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER	TRP	ASN
ARG		HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER	LEU	GLU
ASN	L1590	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER	GLU	VAL
ILE	Q1591	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS	ALA	HIS
MET		CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU	CYS	GLU
LEU	P1600	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL	TYR	PHE
ASN		ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE	LYS	VAL
ASN	V1669	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN	ALA	VAL
ASP	PRO	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA	LEU	LYS
GLU	SER	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER	THR	ALA
LEU	SER	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA	TRP	VAL
GLU	LEU	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN	HIS	GLN



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

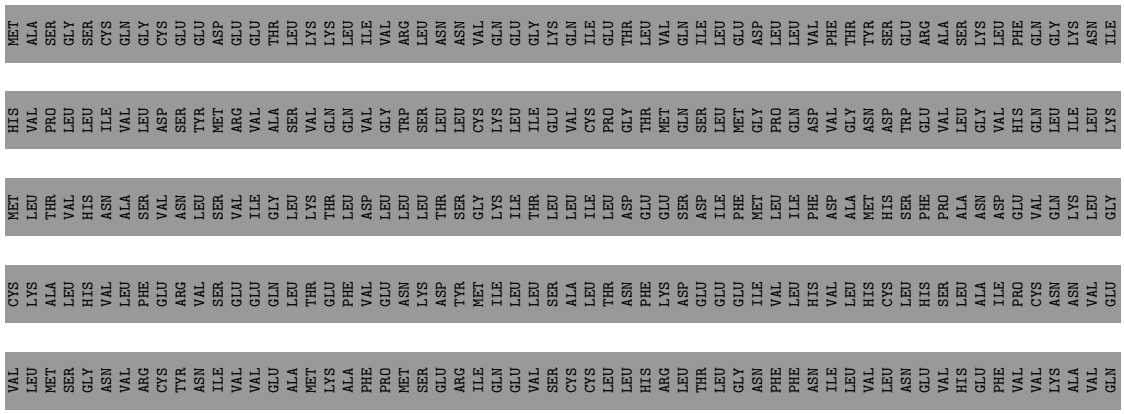
Chain 28-B: 40% • 59%





• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 29-A: 40% • 59%



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ASN	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS	TYR
SER	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN	PRO
GLU	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS	GLU
I1690	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS	ASN
	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL	ALA
R1725	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN	ALA
A1726	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU	LEU
	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA	GLN
N1730	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA	ILE
R1731	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS	SER
M1732	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP	ALA
		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA	LEU
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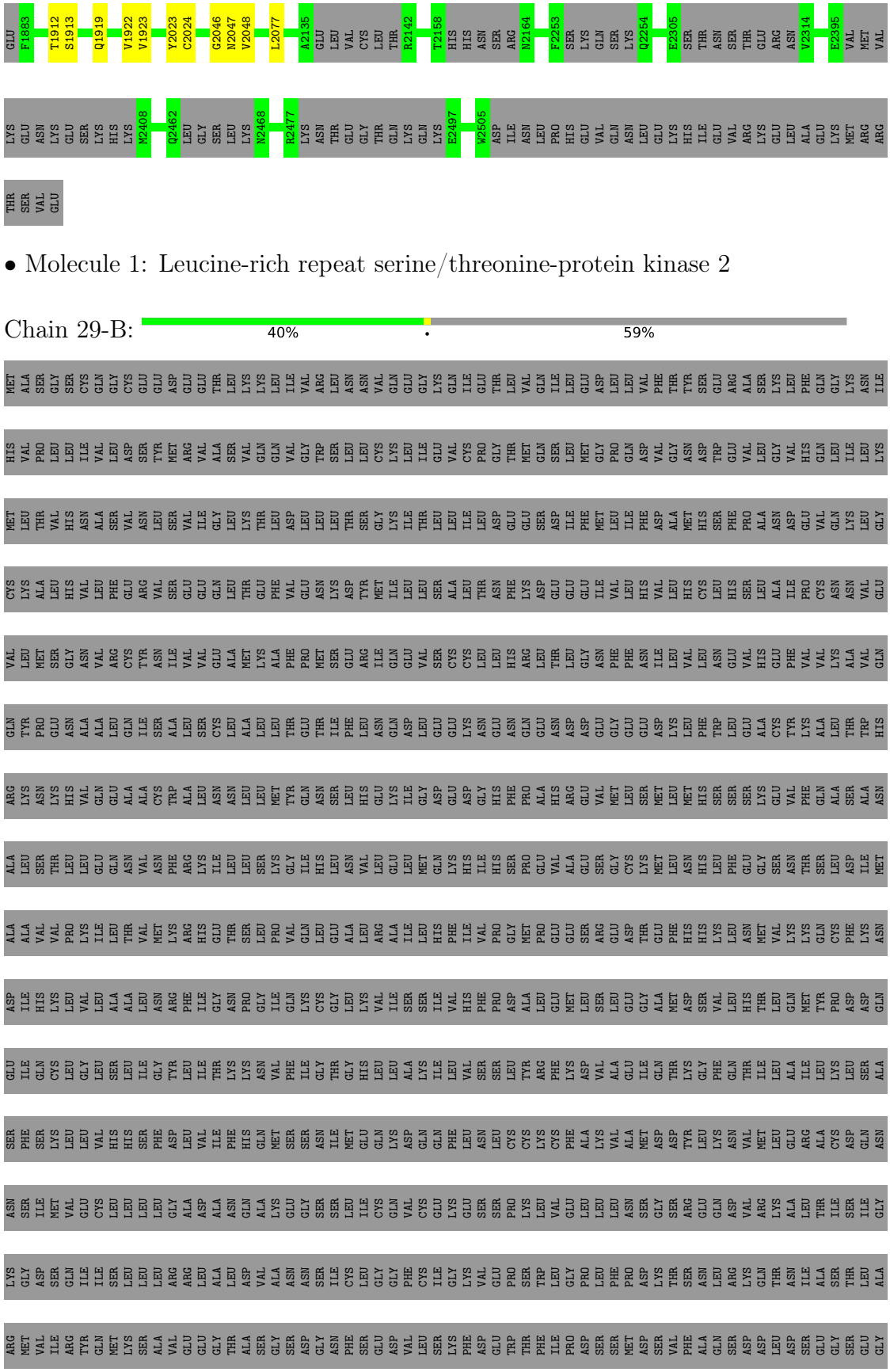
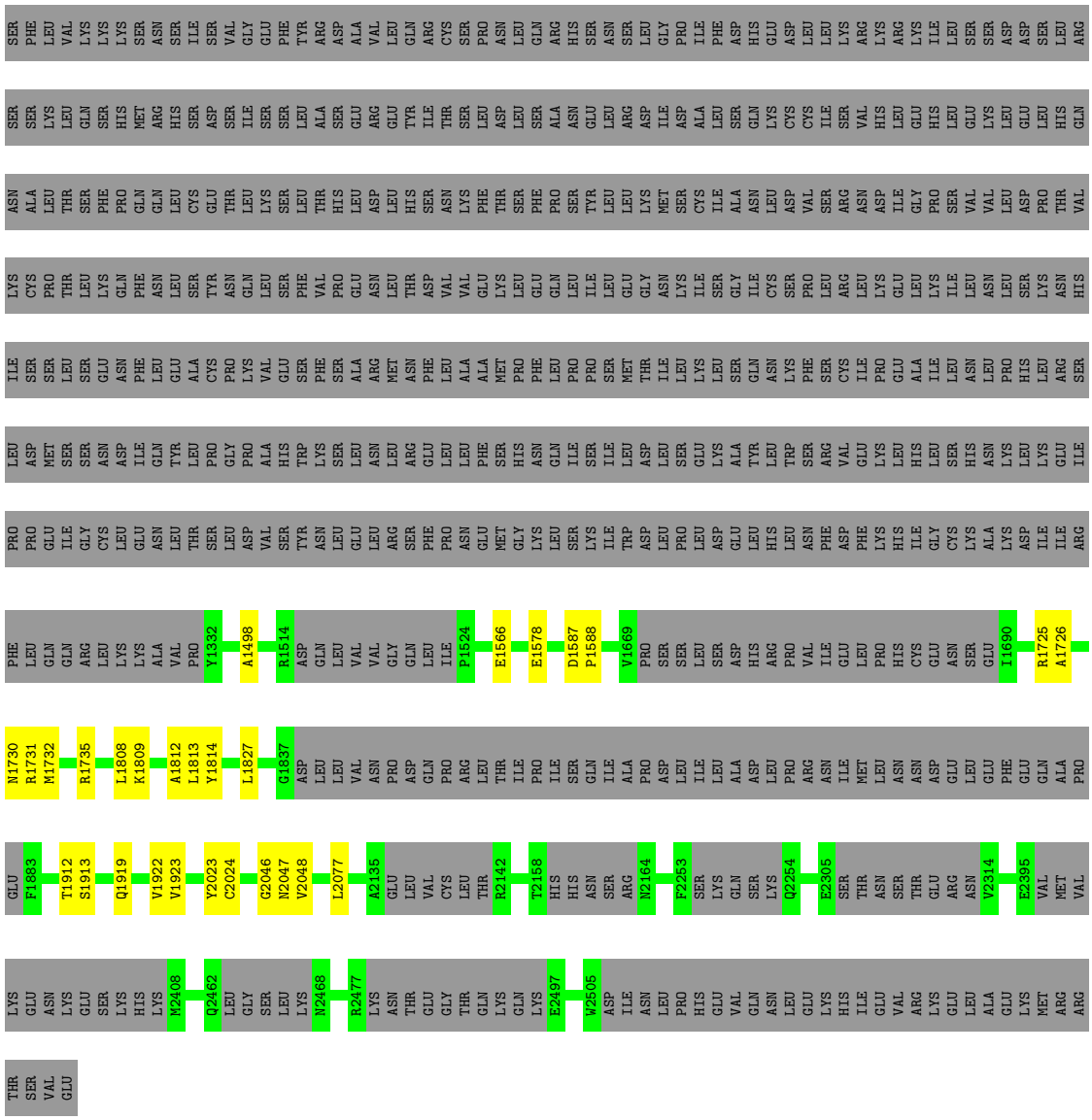
G1837	R1514	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN	LEU
ASP	ASP	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU	ALA
LEU	GLN	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU	LEU
LEU	LEU	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET	LEU
VAL	VAL	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR	THR
ASN	VAL	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN	GLU
PRO	GLY	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN	THR
ASP	GLN	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER	ILE
GLN	LEU	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU	PHE
PRO	ILE	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS	LEU
ARG	P1524	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU	ASN
LEU		GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS	GLN
THR	E1566	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE	ASP
ILE		GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY	LEU
PRO	E1578	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP	GLU
ILE		LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU	GLU
SER	D1587	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP	LYS
GLN	P1588	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY	ASN
ILE		ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS	GLU
ALA	E1616	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE	ASN
PRO	G1617	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO	GLN
ASP	C1618	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA	GLU
LEU	P1619	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS	ASN
ILE	K1620	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG	ASP
LEU	H1621	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU	ASP
ALA	P1622	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL	GLU
ASP	K1623	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET	GLY
LEU		HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU	GLU
PRO	V1669	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER	GLU
ARG	PRO	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET	ASP
ASN	SER	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU	LYS
ILE	SER	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET	LEU
MET	LEU	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS	PHE
LEU	SER	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER	TRP
ASN	ASP	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER	LEU
ASN	HIS	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER	GLU
ASP	ARG	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS	ALA
GLU	PRO	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU	CYS
LEU	VAL	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL	TYR
GLU	ILE	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE	LYS
PHE	GLU	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN	ALA
GLU	LEU	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA	LEU
GLN	PRO	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER	THR
ALA	HIS	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA	TRP
PRO	CYS	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN	HIS

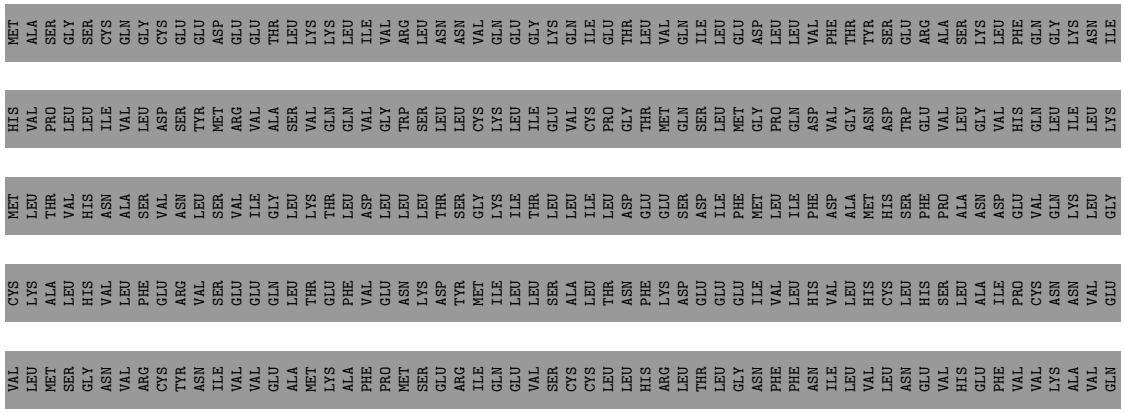


• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 30-A:



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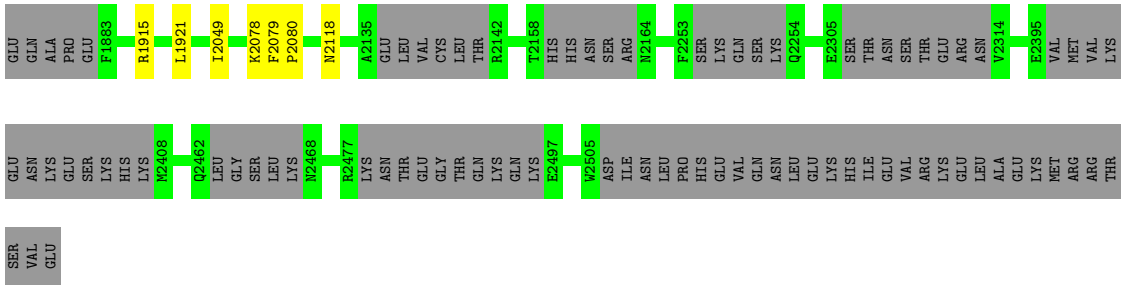
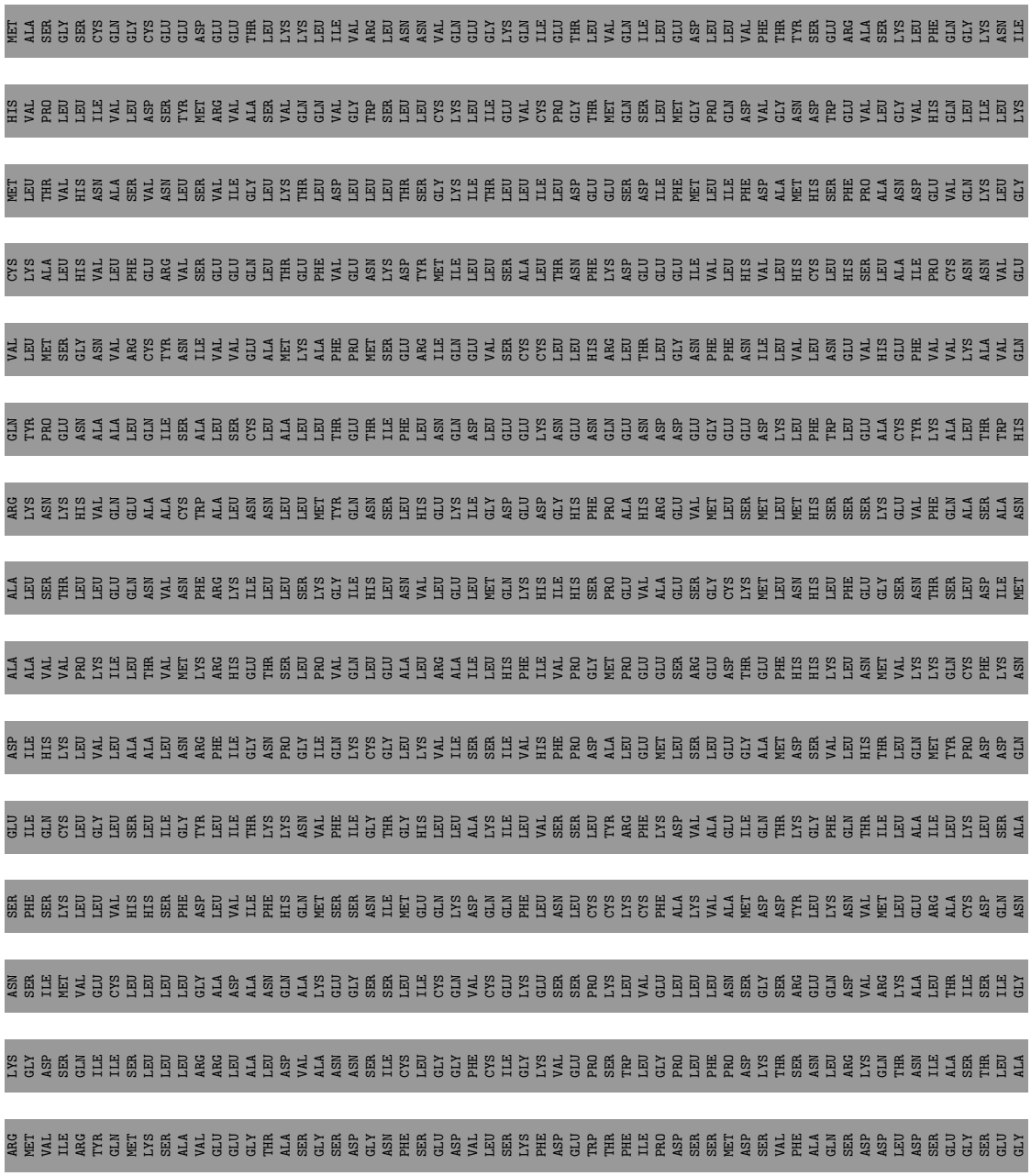
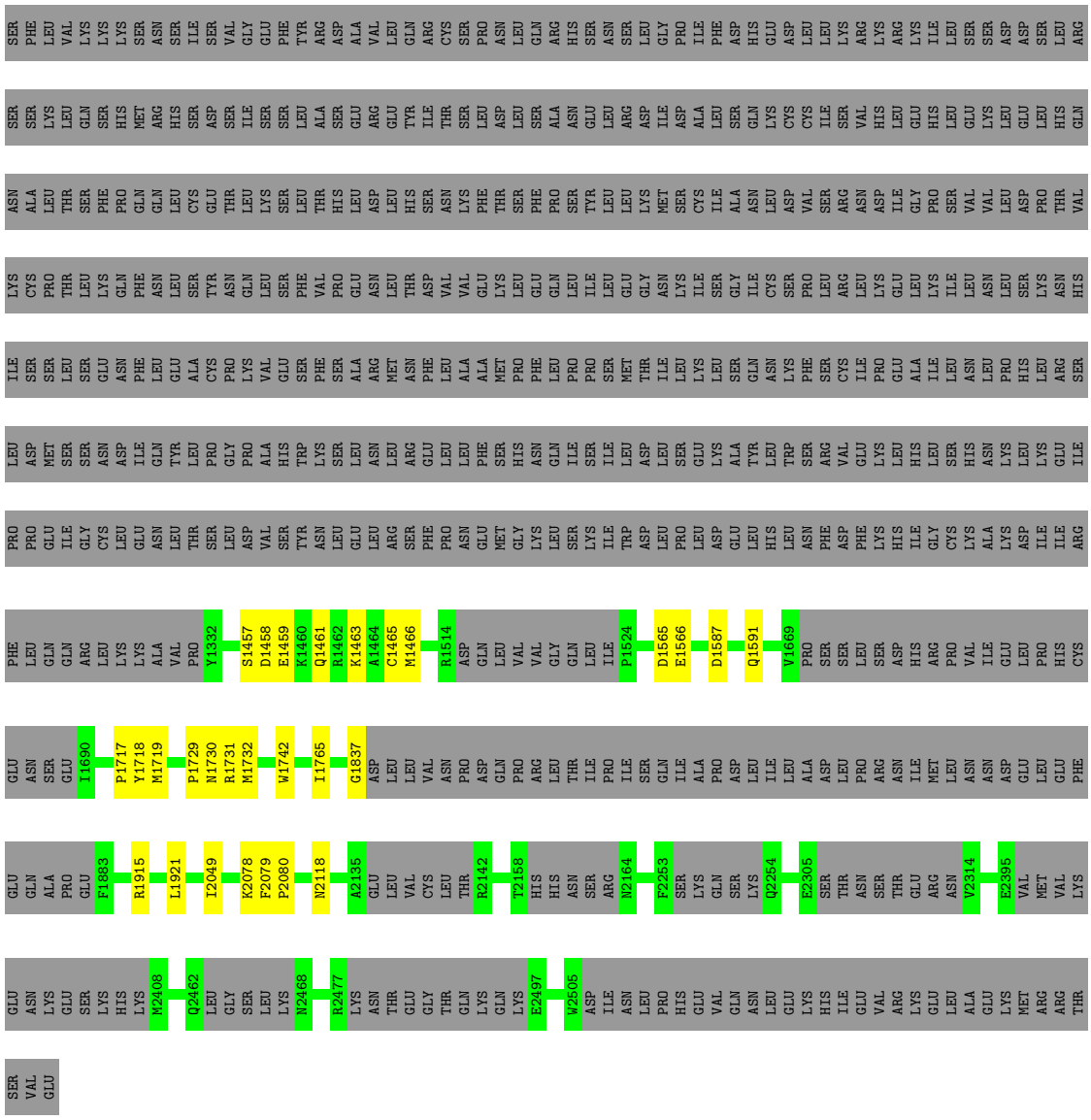
ASN	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS	TYR
SER	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN	PRO
GLU	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS	GLU
I1690	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS	ASN
	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL	ALA
P1717	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN	ALA
Y1718	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU	LEU
M1719	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA	GLN
	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA	ILE
P1729	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS	SER
N1730	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP	ALA
R1731		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA	LEU
M1732	S1457	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU	SER
	D1458	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN	CYS
W1742	E1459	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN	LEU
	K1460	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU	ALA
I1765	Q1461	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU	LEU
	R1462	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET	LEU
G1837	K1463	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR	THR
ASP	A1464	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN	GLU
LEU	C1465	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN	THR
LEU	M1466	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER	ILE
VAL		PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU	PHE
ASN	R1514	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS	LEU
PRO	ASP	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU	ASN
ASP	GLN	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS	GLN
GLN	LEU	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE	ASP
PRO	VAL	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY	LEU
ARG	VAL	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP	GLU
LEU	GLY	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU	GLU
THR	GLN	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP	LYS
ILE	LEU	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY	ASN
PRO	ILE	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS	GLU
ILE	P1524	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE	ASN
SER		ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO	GLN
GLN	D1565	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA	GLU
ILE	E1566	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS	ASN
ALA		LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG	ASP
PRO	D1587	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU	ASP
ASP		GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL	GLU
LEU	Q1591	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET	GLY
ILE		HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU	GLU
LEU	V1669	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER	GLU
ALA	PRO	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET	ASP
ASP	SER	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU	LYS
LEU	SER	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET	LEU
PRO	LEU	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS	PHE
ARG	SER	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER	TRP
ASN	ASP	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER	LEU
ILE	HIS	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER	GLU
MET	ARG	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS	ALA
LEU	PRO	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU	CYS
ASN	VAL	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL	TYR
ASN	ILE	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE	LYS
ASP	GLU	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN	ALA
GLU	LEU	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA	LEU
LEU	PRO	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER	THR
GLU	HIS	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA	TRP
PHE	CYS	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN	HIS



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

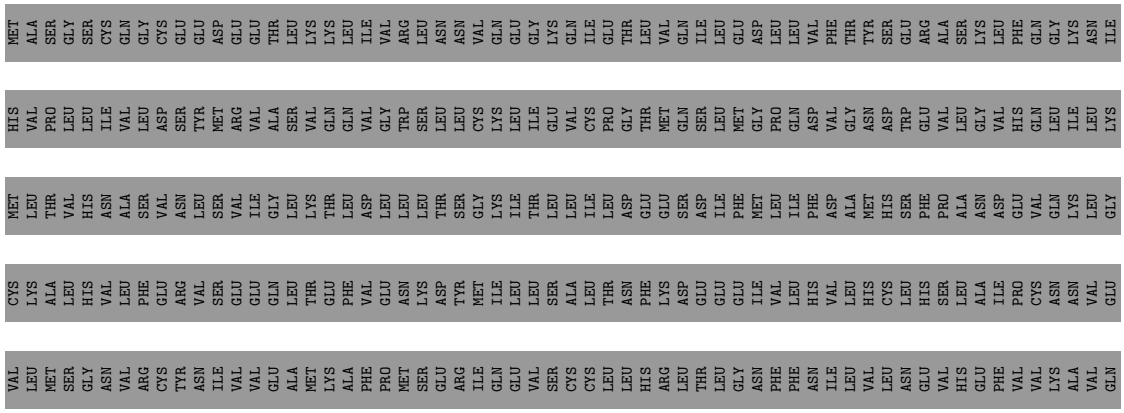
Chain 30-B: 40% 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 31-A: 41% 59%



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LEU	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN	PRO
VAL	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS	GLU
ASN	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS	ASN
PRO	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL	ALA
ASP	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN	ALA
GLN	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU	LEU
PRO	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA	GLN
ARG	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA	ILE
LEU	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS	SER
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PRO	N1475	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU	SER
ILE		VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN	CYS
SER	R1514	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN	LEU
GLN	ASP	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU	ALA
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ALA	LEU	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET	LEU
PRO	VAL	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR	THR
ASP	VAL	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN	GLU
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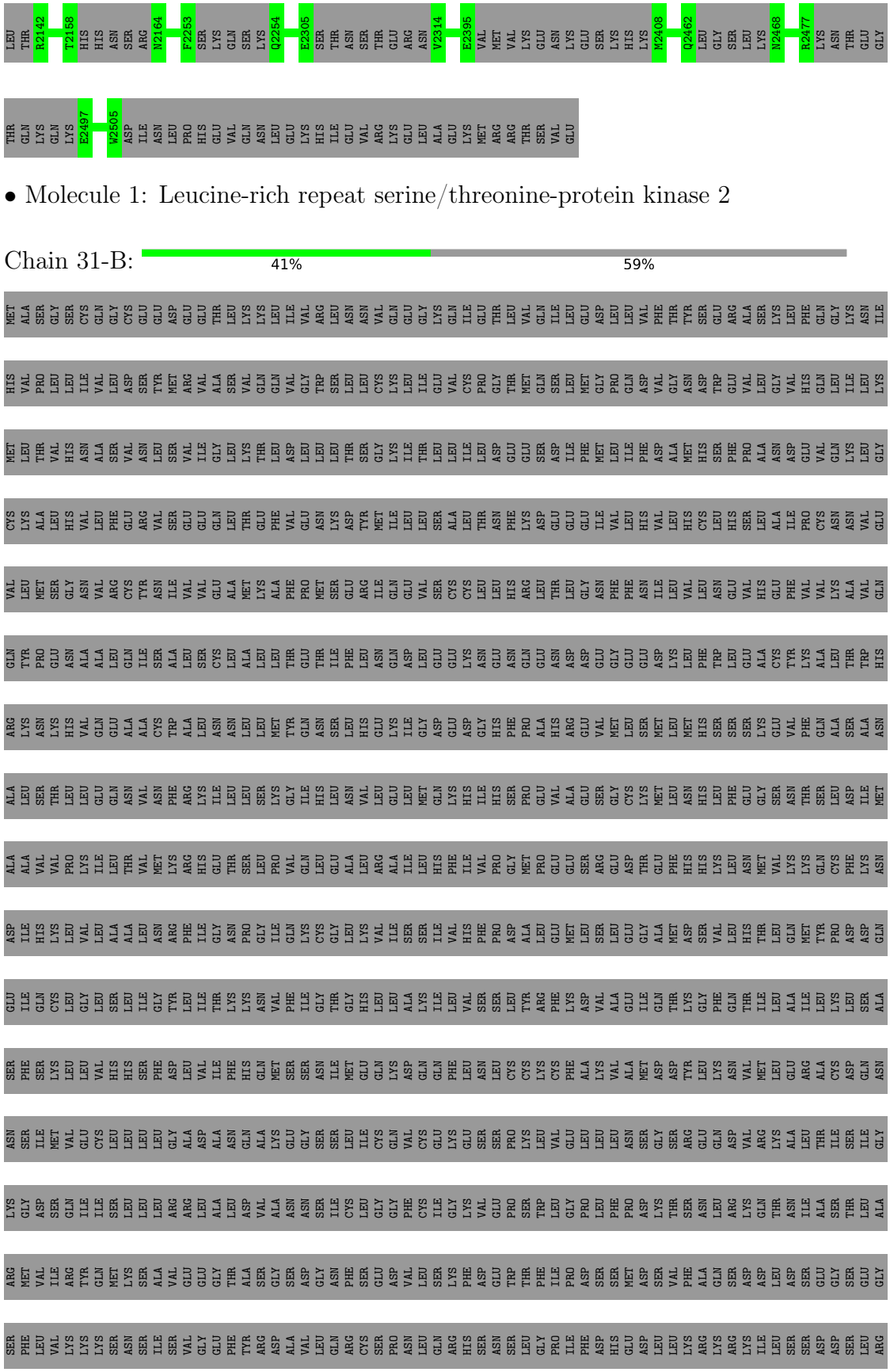
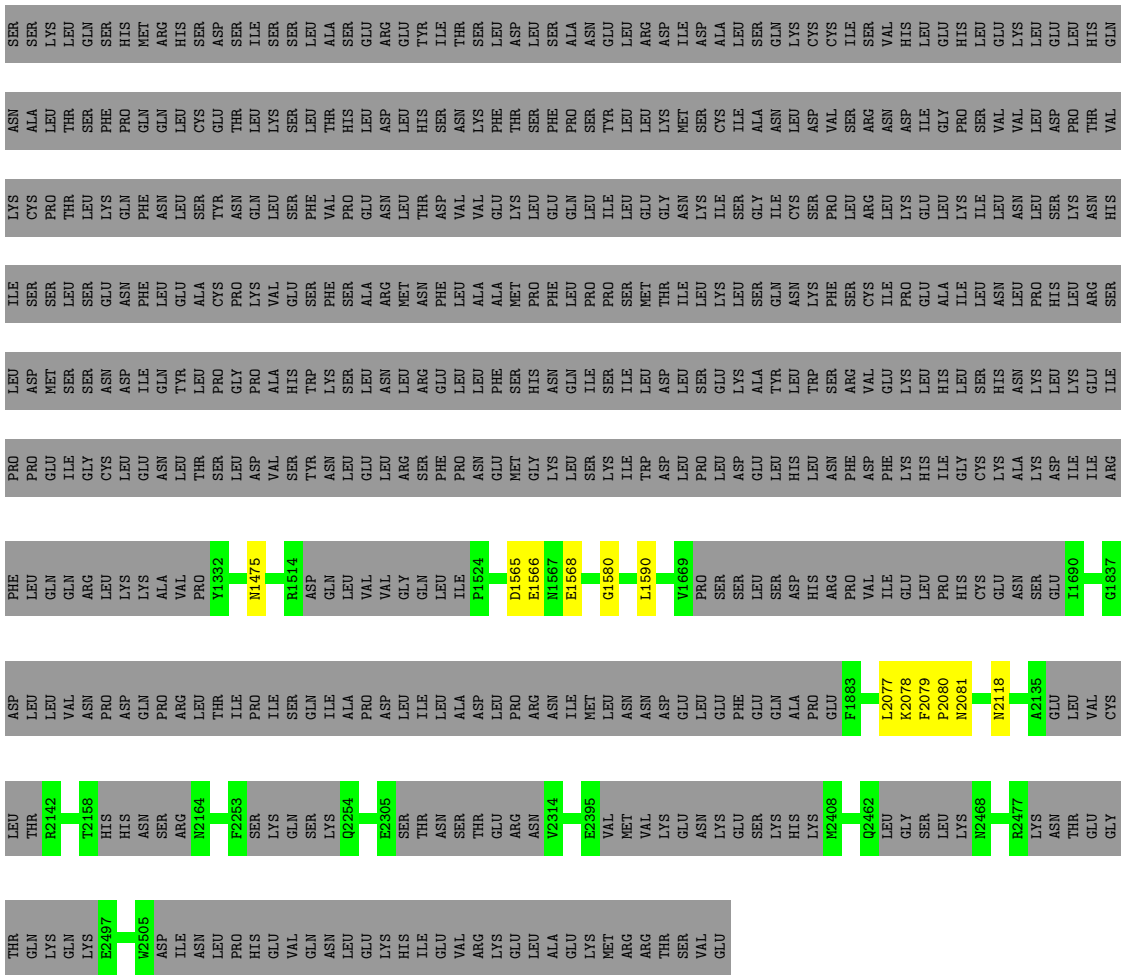
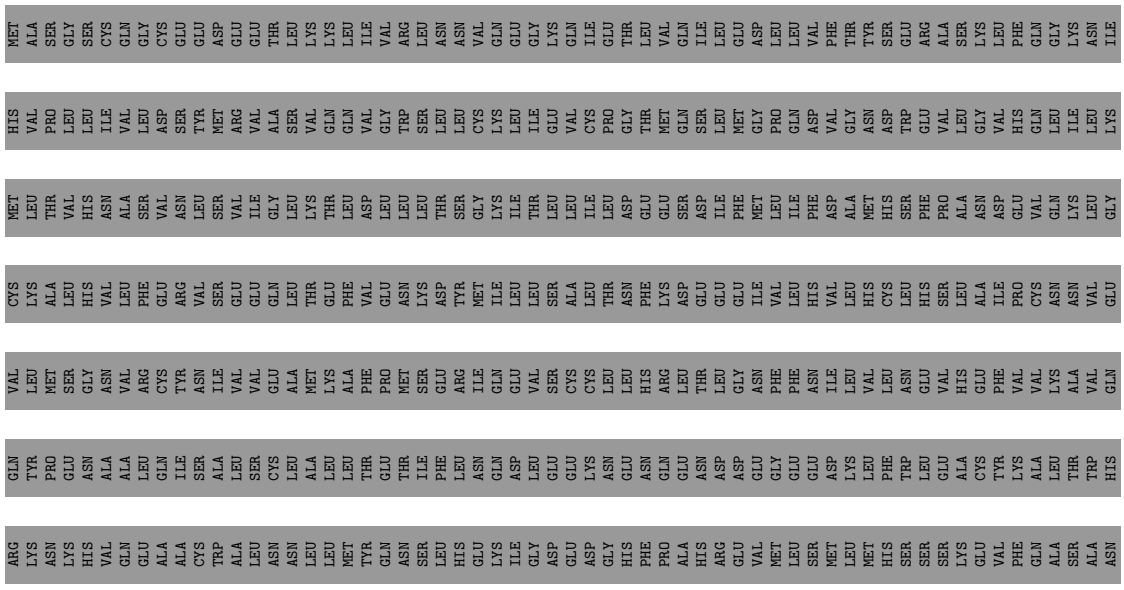
ILE	GLN	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER	ILE
LEU	LEU	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU	PHE
ALA	ILE	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS	LEU
ASP	P1524	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU	ASN
LEU		GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS	GLN
PRO	D1565	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE	ASP
ARG	E1566	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY	LEU
ASN	N1567	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP	GLU
ILE	E1568	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU	GLU
MET		SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP	LYS
LEU	G1580	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY	ASN
ASN		ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS	GLU
ASN	L1590	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE	ASN
ASP		ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO	GLN
GLU	V1669	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA	GLU
LEU	PRO	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS	ASN
GLU	SER	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG	ASP
PHE	SER	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU	ASP
GLU	LEU	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL	GLU
GLN	SER	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET	GLY
ALA	ASP	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU	GLU
PRO	HIS	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER	GLU
GLU	ARG	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET	ASP
F1883	PRO	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU	LYS
	VAL	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET	LEU
L2077	ILE	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS	PHE
K2078	GLU	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER	TRP
F2079	LEU	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER	LEU
P2080	PRO	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER	GLU
N2081	HIS	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS	ALA
	CYS	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU	CYS
N2118	GLU	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL	TYR
	ASN	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE	LYS
A2135	SER	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN	ALA
GLU	GLU	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA	LEU
LEU	I1690	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER	THR
VAL		ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA	TRP
CYS	G1837	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN	HIS


LEU THR R2142 T2158 HIS HIS ASN SER ARG N2164 F2253 SER LYS GLN SER LYS Q2254 E2305 SER THR ASN SER THR GLU ARG ASN V2314 E2395 VAL MET VAL LYS GLU ASN LYS GLU SER LYS HIS LYS M2408 Q2462 LEU GLY SER LEU LYS N2468 R2477 LYS ASN THR GLU GLY
THR GLN LYS GLN LYS E2497 W2505 ASP ILE ASN LEU PRO HIS GLU VAL GLN ASN LEU GLU GLU LYS HIS ILE GLU VAL GLU LEU ALA GLU LYS MET ARG ARG THR SER VAL GLU
• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2
Chain 31-B:
41%
59%
MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE
HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS
MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP SER LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY
CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU
VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU LEU VAL LEU ASN LYS VAL HIS HIS VAL GLN
GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU HIS ARG GLN GLU ASN ASP ASP GLU GLY GLU GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA ALA THR LYS ALA LEU THR HIS
ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN
ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS LEU ILE HIS SER LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA ALA LEU LEU ASN HIS LEU PHE GLU GLY LYS SER LEU ASP ILE ILE
ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU GLU ALA LEU ARG ALA ILE LEU HIS PHE HIS VAL PRO GLY MET PRO GLU GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN
ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASP ASN PHE ASP LEU LYS ILE LEU LYS VAL LEU ILE SER LEU ASN ASN PRO GLY ILE GLN LYS CYS GLY GLY LEU LYS VAL LEU ILE VAL HIS PHE ILE PRO ASP ALA LEU GLU MET LEU SER GLU GLY GLY ALA MET ASP SER VAL LEU HIS LEU THR THR GLN GLN
GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU LEU ALA LYS ILE LEU VAL SER SER LEU LYS ASP VAL ALA GLU ILE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA
SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU ASP GLN ASN
ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY
LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASN ASN SER ILE LEU GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA
ARG MET VAL ILE ARG TYR GLN MET LYS SER SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL SER LYS PHE GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP LEU ASP SER GLU GLY GLU GLU
SER PHE LEU VAL LYS LYS SER ASN SER PRO ASN SER ILE ILE GLN ARG CYS SER GLU ASP LEU LEU LYS ARG LYS HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU SER SER ASP GLU GLU GLY



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 32-A:



Q2462
N2468
R2477
E2497
W2505
F1883
R1915
L1921
A2135
R2142
T2158
N2164
F2253
Q2254
E2305
V2314
E2395
M2408
I1690
Y1332
S1444
A1464
K1468
R1477
G1478
F1479
P1480
R1483
R1514
P1524
D1565
Q1586
D1587
P1588
A1589
L1590
Q1591
Q1648
V1669
G1722
R1723
E1724
I1765
G1837

• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 32-B: 40% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU THR SER GLY LYS ILE THR LEU LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN LYS VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU VAL LEU GLN ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS LYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU GLN ASP

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO SER LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS GLN THR ILE LEU ILE ILE

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU LEU GLY PRO LEU LEU PHE PRO ASP LEU ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

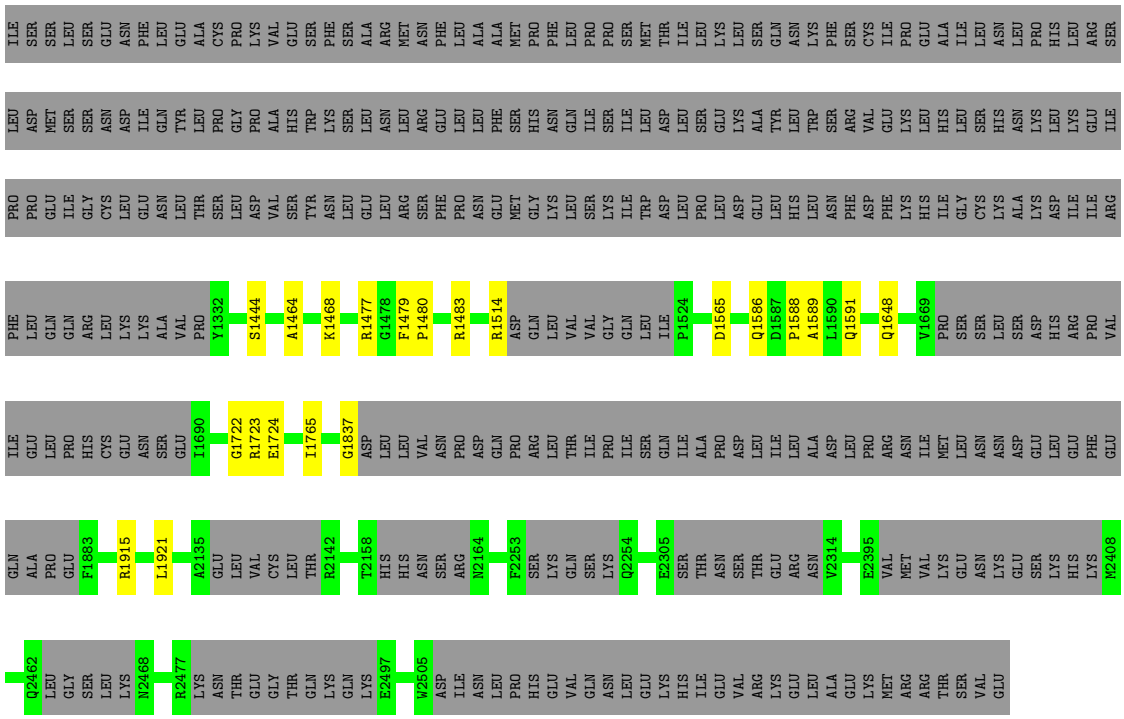
ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ASP ALA GLN ARG LYS ASP ASP LEU ASP SER GLU GLY GLU GLY

SER PHE LEU VAL LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER ASP SER LEU ARG

SER SER LYS LEU GLN HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU SER ALA LEU GLN LYS CYS CYS ILE SER VAL HIS LEU GLU GLU LYS LEU GLU HIS GLN

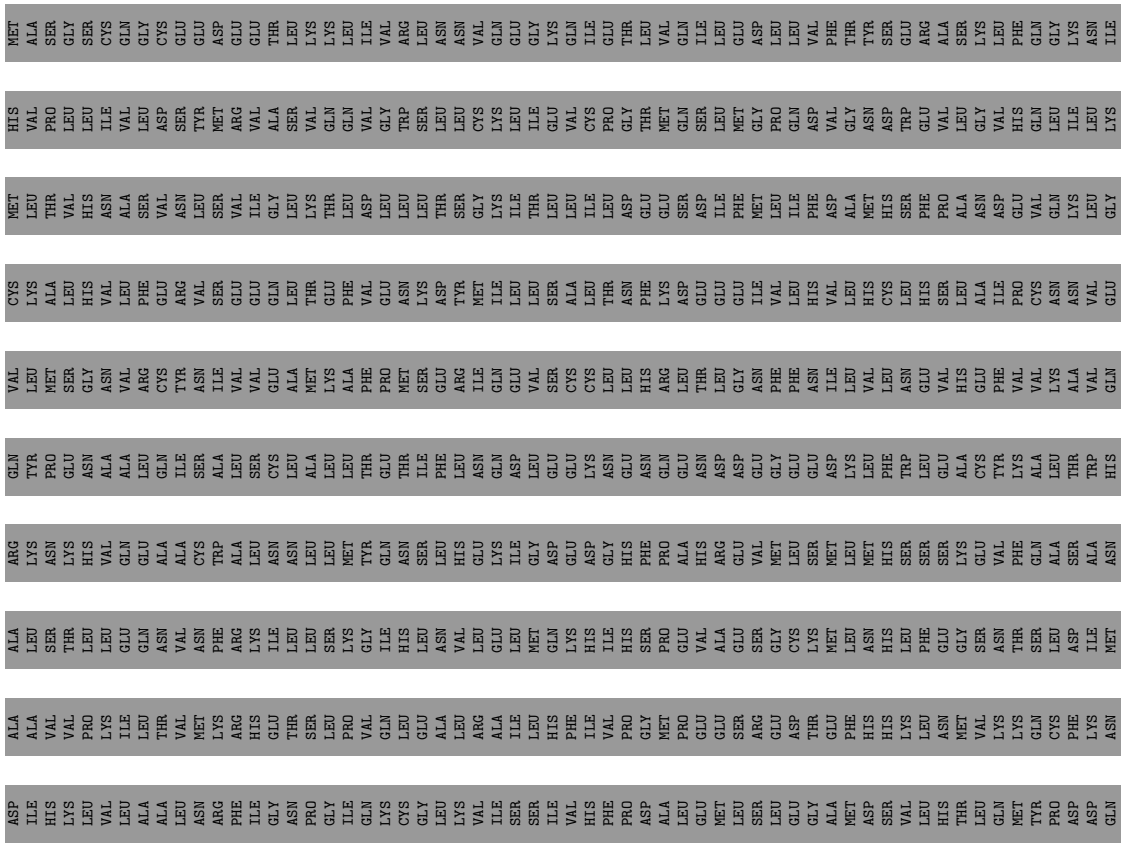
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR ILE HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR MET ASP LEU ALA ILE ASP VAL SER ARG ASN LEU LYS ARG LYS ILE LEU ASP ILE ALA ILE GLY PRO VAL THR ARG LYS ARG LYS LEU LEU ASP SER GLU GLU ASP VAL

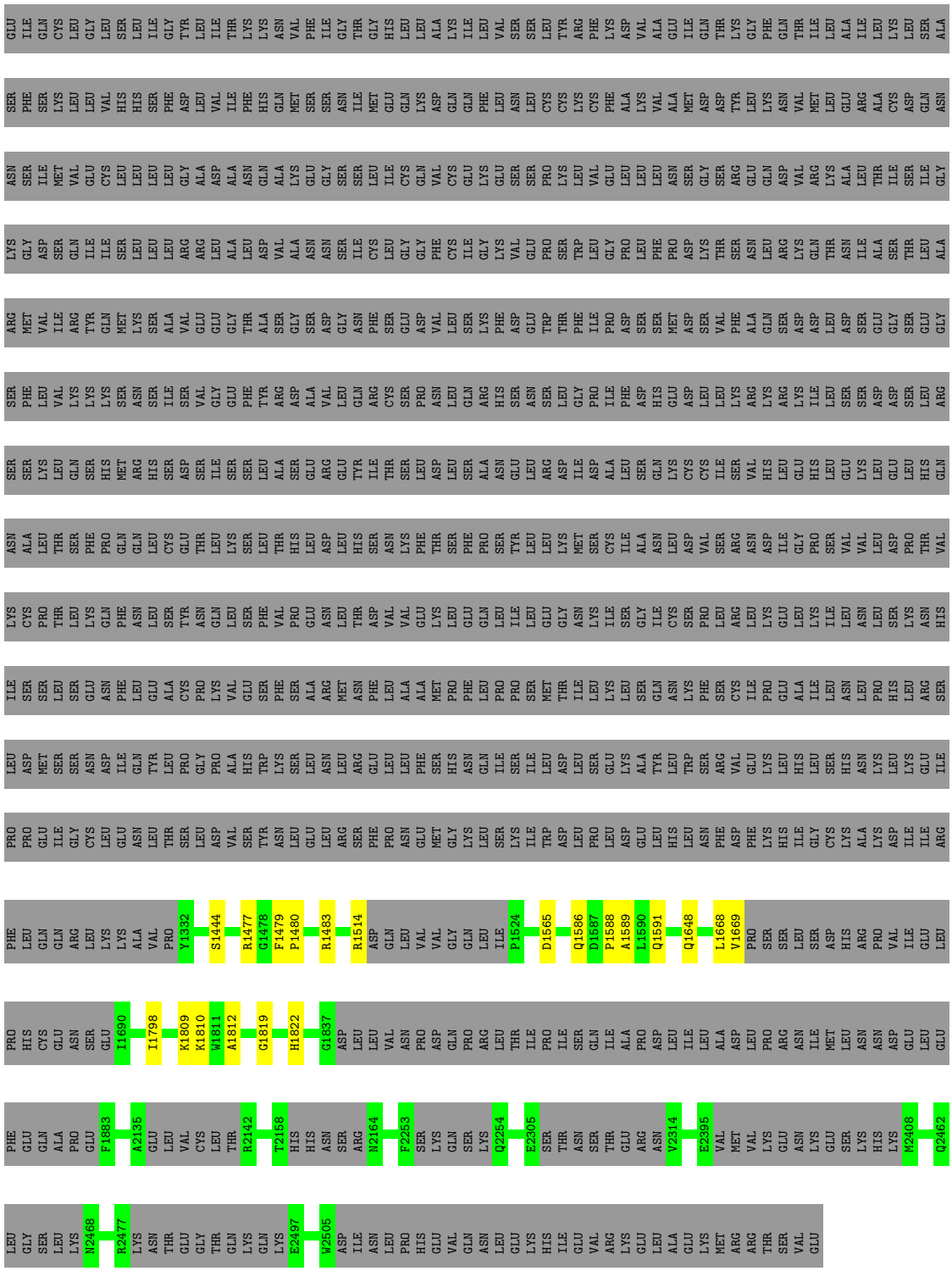
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLN GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 33-A: 40% • 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 33-B:

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

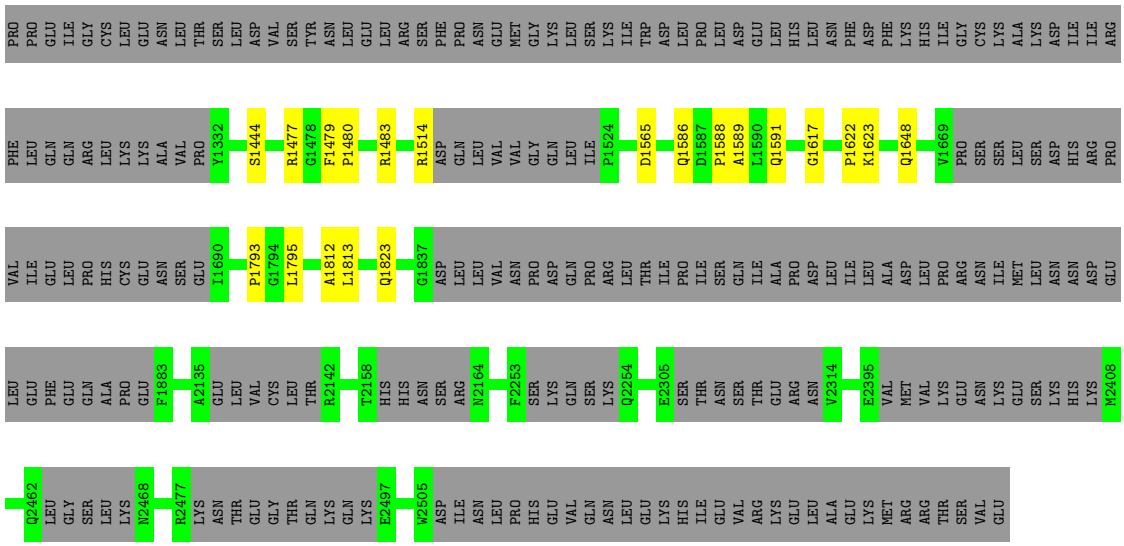
SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

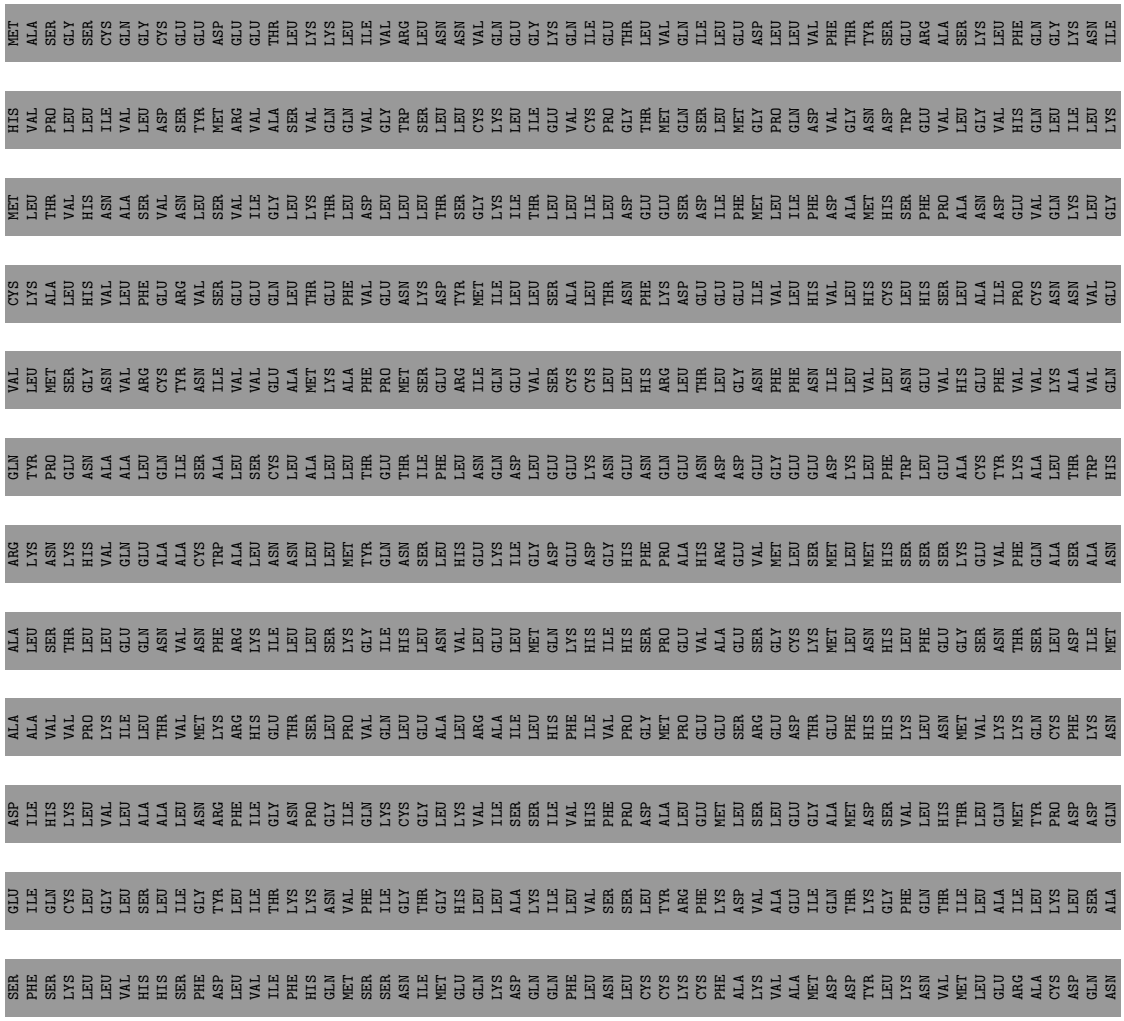
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER

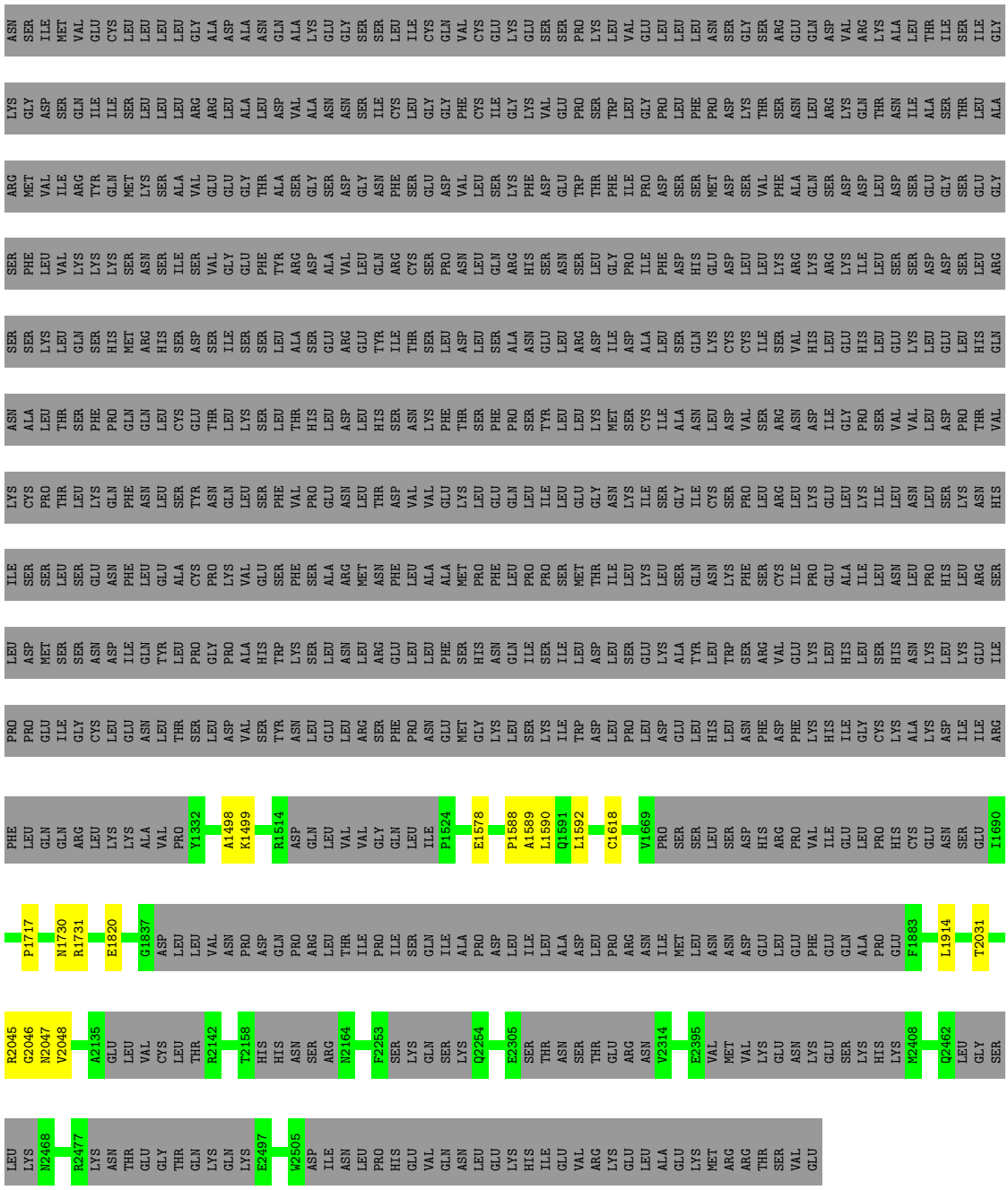
LEU ASP MET SER SER ASN ASP ILE GLN TYR LEU PRO GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG GLU LEU LEU PHE SER HIS ASN GLN ILE SER ILE LEU ASP LEU SER GLU LYS ALA TYR LEU TRP SER ARG VAL GLU LYS LEU HIS LEU SER HIS ASN LYS LEU LYS GLU ILE



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 34-A:

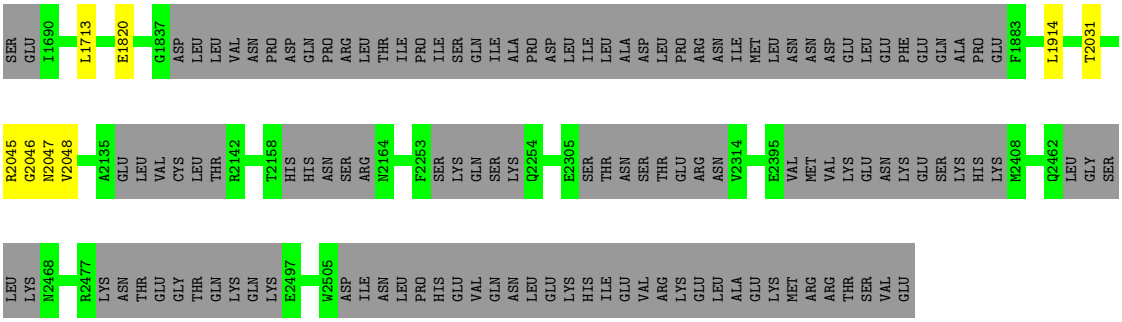




- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

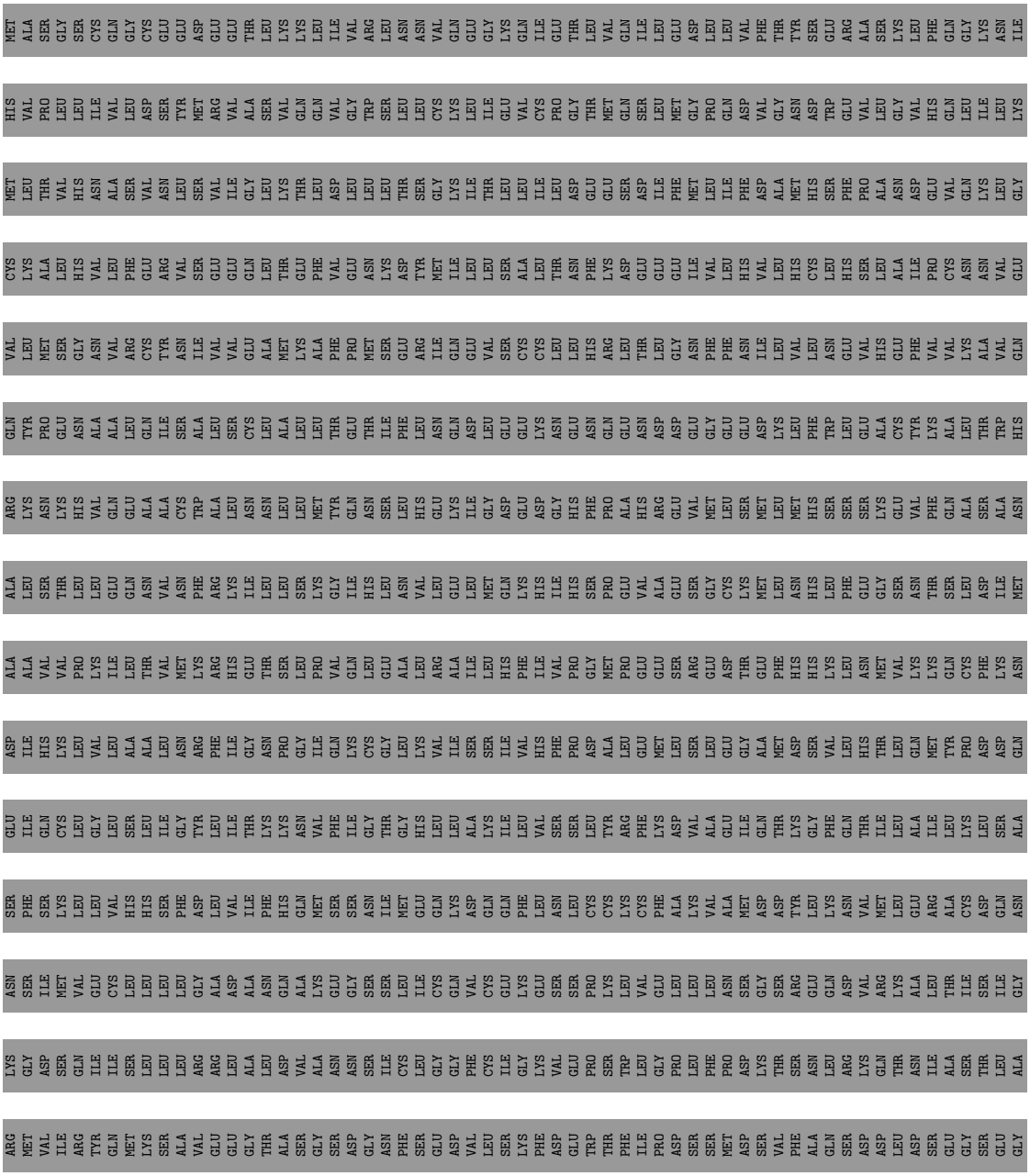
Chain 34-B:

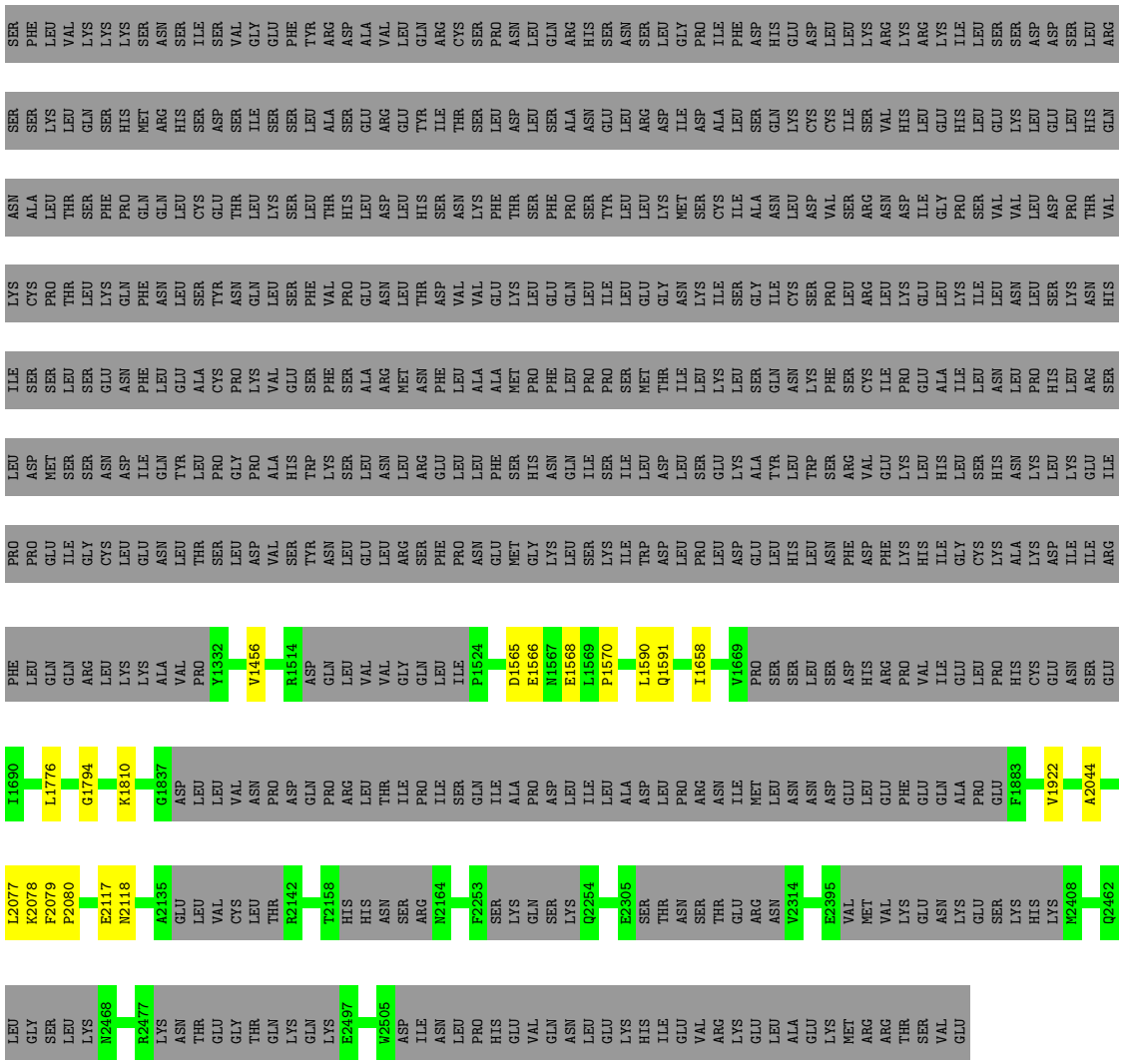
PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA	ARG	GLN	VAL	CYS
LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS	TYR	LEU	LYS
GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN	PRO	MET	ALA
GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS	GLU	SER	LEU
ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS	ASN	GLY	HIS
LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL	ALA	ASN	VAL
LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN	ALA	VAL	LEU
LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU	LEU	ARG	PHE
ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA	GLN	CYS	GLU
VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA	ILE	TYR	ARG
PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS	SER	ASN	VAL
Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP	ALA	ILE	SER
	LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA	LEU	VAL	GLU
A1498	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU	SER	VAL	GLU
K1499	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN	CYS	GLU	GLN
	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN	LEU	ALA	LEU
R1514	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU	ALA	MET	THR
ASP	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU	LEU	LYS	GLU
GLN	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET	LEU	ALA	PHE
LEU	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR	THR	PHE	VAL
VAL	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN	GLU	PRO	GLU
VAL	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN	THR	MET	ASN
GLY	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER	ILE	SER	LYS
GLN	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU	PHE	GLU	ASP
LEU	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS	LEU	ARG	TYR
ILE	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU	ASN	ILE	MET
P1524	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS	GLN	GLN	ILE
	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE	ASP	GLU	LEU
E1578	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY	LEU	VAL	LEU
	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP	GLU	SER	SER
P1588	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU	GLU	CYS	ALA
A1589	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP	LYS	CYS	LEU
L1590	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY	ASN	LEU	THR
Q1591	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS	GLU	LEU	ASN
L1592	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE	ASN	HIS	PHE
	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO	GLN	ARG	LYS
C1618	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA	GLU	LEU	ASP
P1619	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS	ASN	THR	GLU
K1620	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG	ASP	LEU	GLU
H1621	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU	ASP	GLY	GLU
	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL	GLU	ASN	ILE
V1669	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET	GLY	PHE	VAL
PRO	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU	GLU	PHE	LEU
SER	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER	GLU	ASN	HIS
SER	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET	ASP	ILE	VAL
LEU	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU	LYS	LEU	LEU
SER	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET	LEU	VAL	HIS
ASP	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS	PHE	LEU	CYS
HIS	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER	TRP	ASN	LEU
ARG	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER	LEU	GLU	HIS
PRO	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER	GLU	VAL	SER
VAL	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS	ALA	HIS	LEU
ILE	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU	CYS	GLU	ALA
GLU	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL	TYR	PHE	ILE
LEU	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE	LYS	VAL	PRO
PRO	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN	ALA	VAL	CYS
HIS	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA	LEU	LYS	ASN
CYS	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER	THR	ALA	ASN
GLU	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA	TRP	VAL	VAL
ASN	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN	HIS	GLN	GLU



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

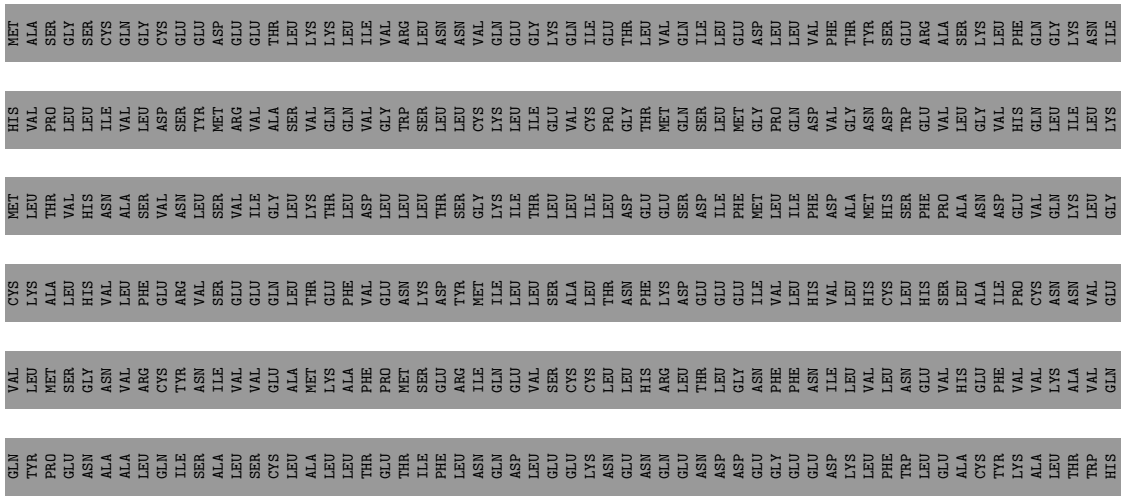
Chain 35-A: 40% • 59%



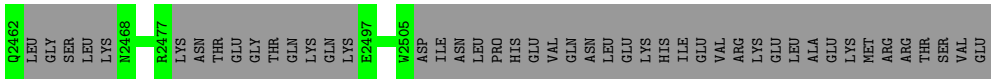


- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 35-B:

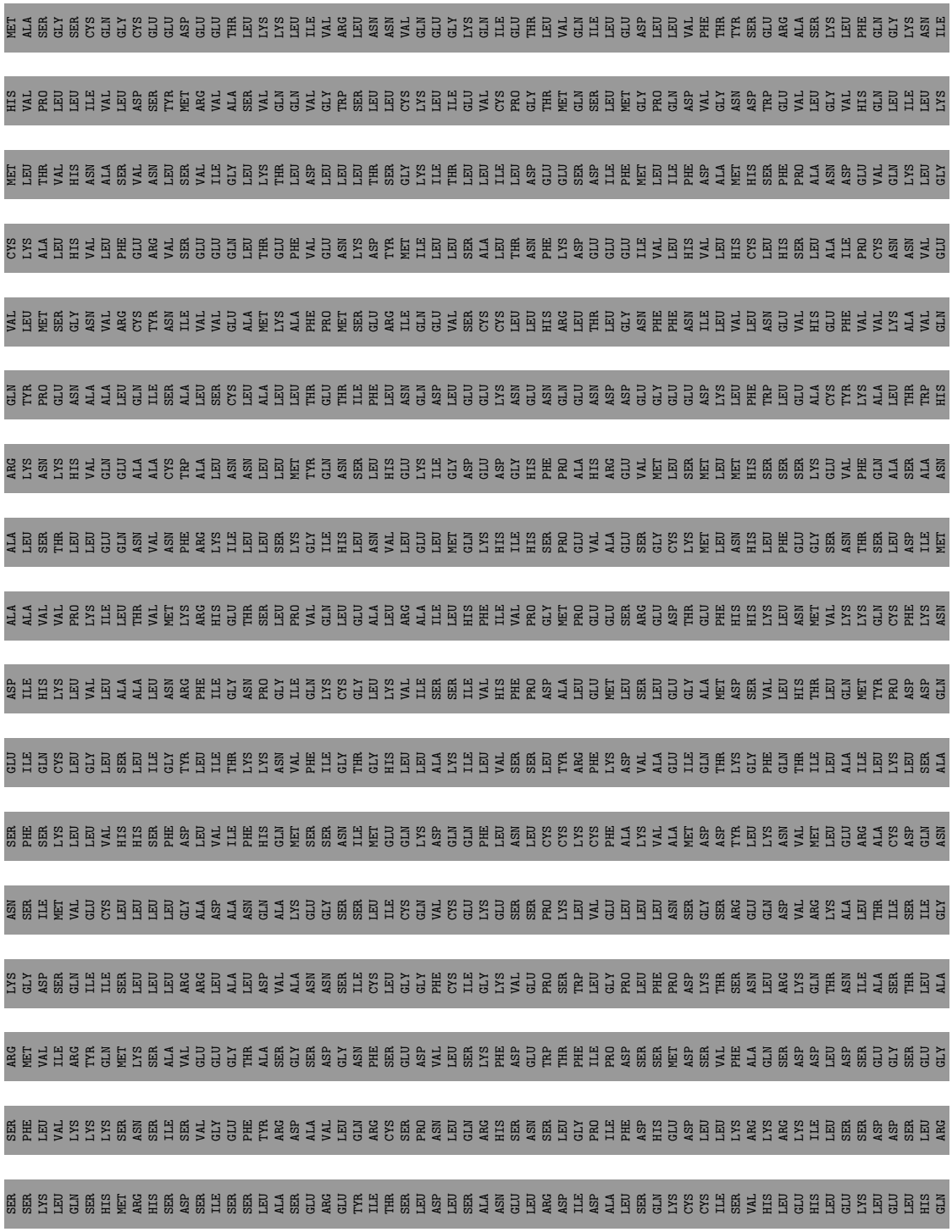


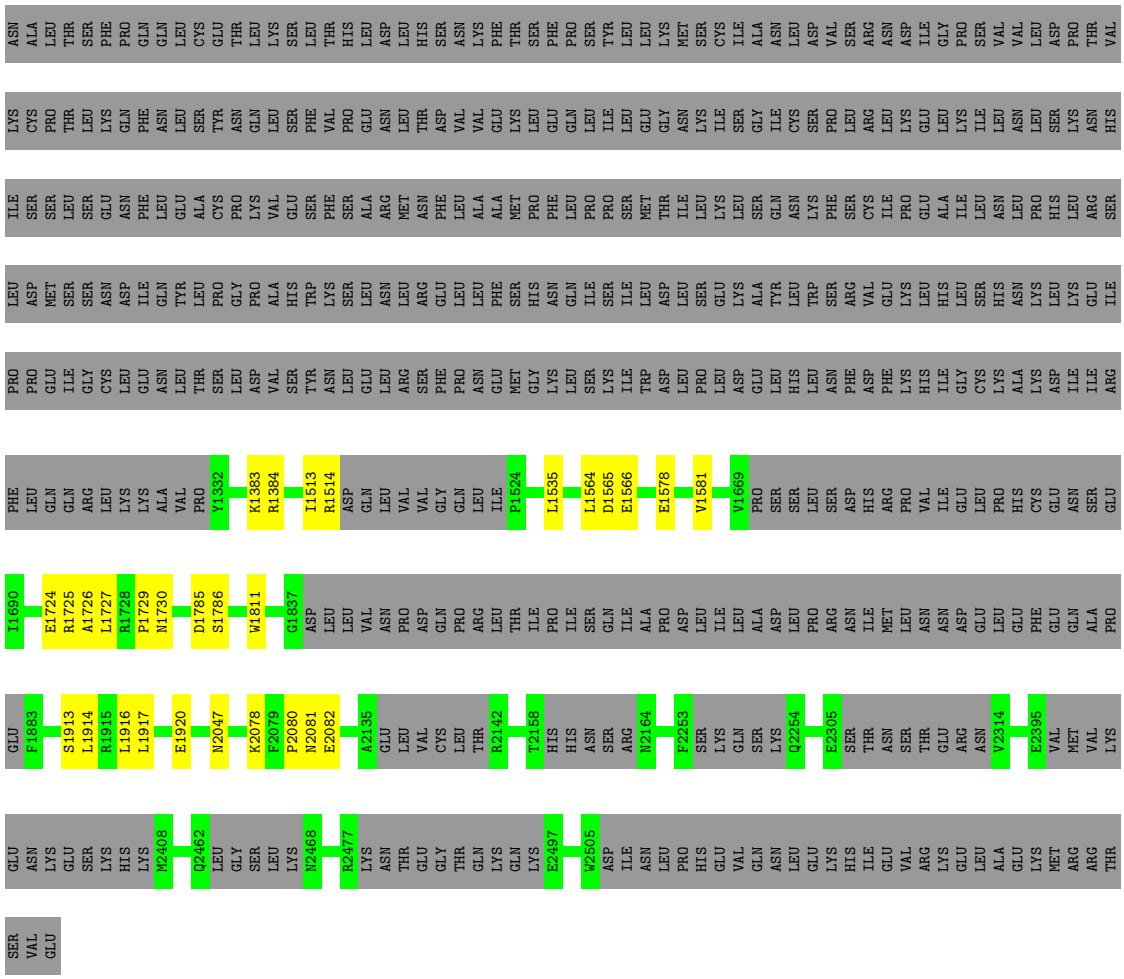
L2077 K2078 F2079 P2080 E2117 N2118 A2135 R2142 T2158 N2164 F2253 Q2254 E2305 V2314 E2395 M2408
L1776 L1795 L1796 K1810 Q1823 G1837 F1883 V1922 A2044
Y1332 R1514 P1524 D1565 E1566 N1567 E1568 L1569 P1570 L1590 Q1591 I1658 V1669 I1690



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

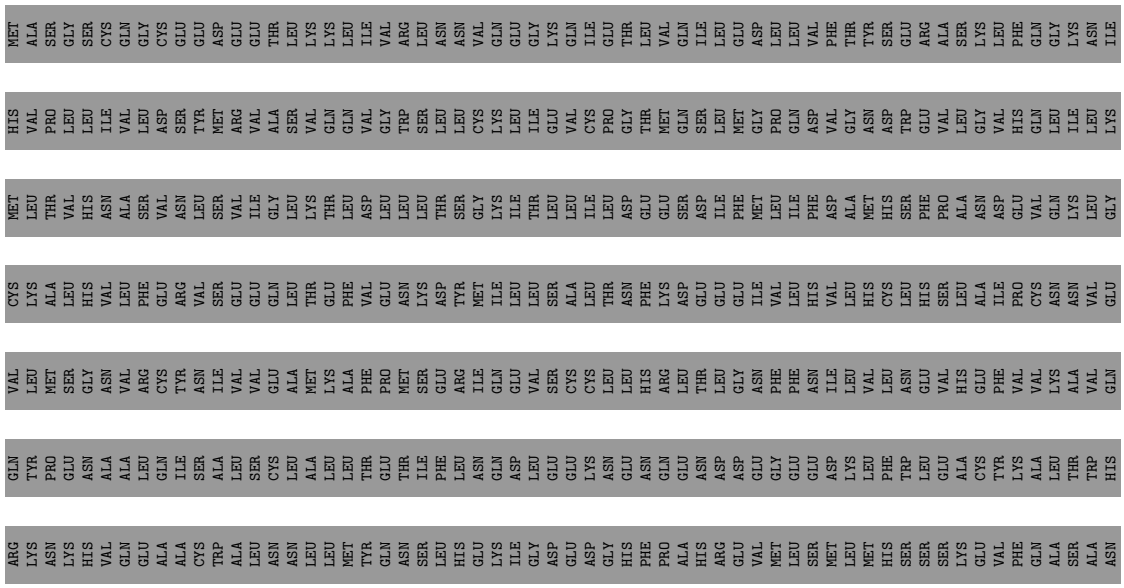
Chain 36-A:





• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 36-B: 40% • 59%



LYS	PRO	I1690	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA
GLU	GLU		LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU
ASN	F1883	E1724	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER
LYS		R1725	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR
GLU	S1913	A1726	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU
SER	L1914	L1727	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU
LYS	R1915	R1728	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU
HIS	L1916	P1729	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN
LYS	L1917	N1730	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN
M2408			VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL
	E1920	I1775	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN
Q2462			Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE
LEU	N2047	K1810		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG
GLY		W1811	K1383	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS
SER	K2078	A1812	R1384	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE
LEU	F2079			SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU
LYS	P2080	G1837	I1513	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU
N2468	N2081	ASP	R1514	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER
	E2082	LEU	ASP	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS
R2477		LEU	GLN	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY
LYS	A2135	VAL	LEU	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE
ASN	GLU	ASN	VAL	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS
THR	LEU	PRO	VAL	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU
GLU	VAL	ASP	GLY	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN
GLY	CYS	GLN	GLN	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL
THR	LEU	PRO	LEU	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU
GLN	THR	ARG	ILE	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU
LYS	R2142	LEU	P1524	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU
GLN		THR		GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET
LYS	T2158	ILE	L1535	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN
E2497	HIS	PRO		LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS
	HIS	ILE	L1564	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS
W2505	ASN	SER	D1565	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE
ASP	SER	GLN	E1566	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS
ILE	ARG	ILE		TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER
ASN	N2164	ALA	E1578	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO
LEU		PRO		LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU
PRO	F2253	ASP	V1581	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL
HIS	SER	LEU		LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA
GLU	LYS	ILE	V1669	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU
VAL	GLN	LEU	PRO	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER
GLN	SER	ALA	SER	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY
ASN	LYS	ASP	SER	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS
LEU	Q2254	LEU	LEU	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS
GLU		PRO	PRO	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET
LYS	E2305	ARG	ASP	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU
HIS	SER	ASN	HIS	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN
ILE	THR	ILE	ARG	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS
GLU	ASN	MET	PRO	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU
VAL	SER	LEU	VAL	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE
ARG	THR	ASN	ILE	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU
LYS	GLU	ASN	GLU	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY
GLU	ARG	ASP	LEU	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER
LEU	ASN	GLU	PRO	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN
ALA	V2314	LEU	HIS	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR
GLU		GLU	CYS	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER
LYS	E2395	PHE	GLU	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU
MET	VAL	GLU	ASN	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP
ARG	MET	GLN	SER	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE
ARG	VAL	ALA	GLU	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET

THR SER VAL GLU

- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 37-A:

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

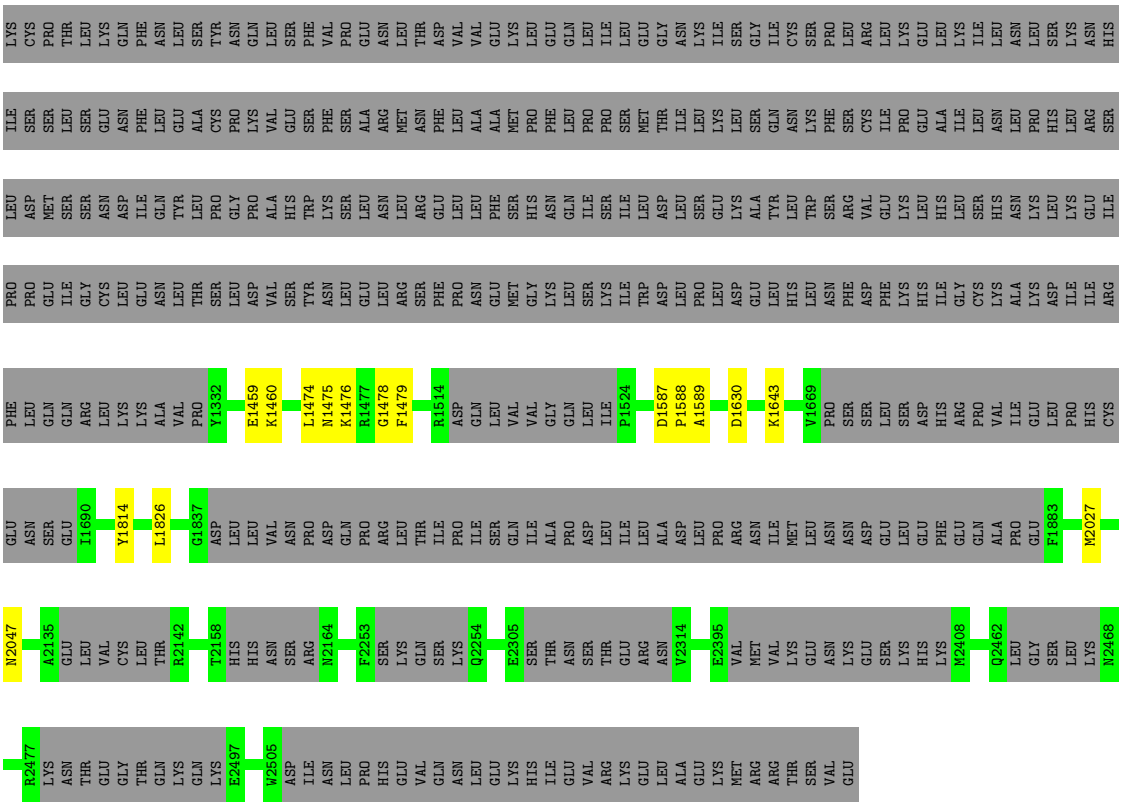
LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

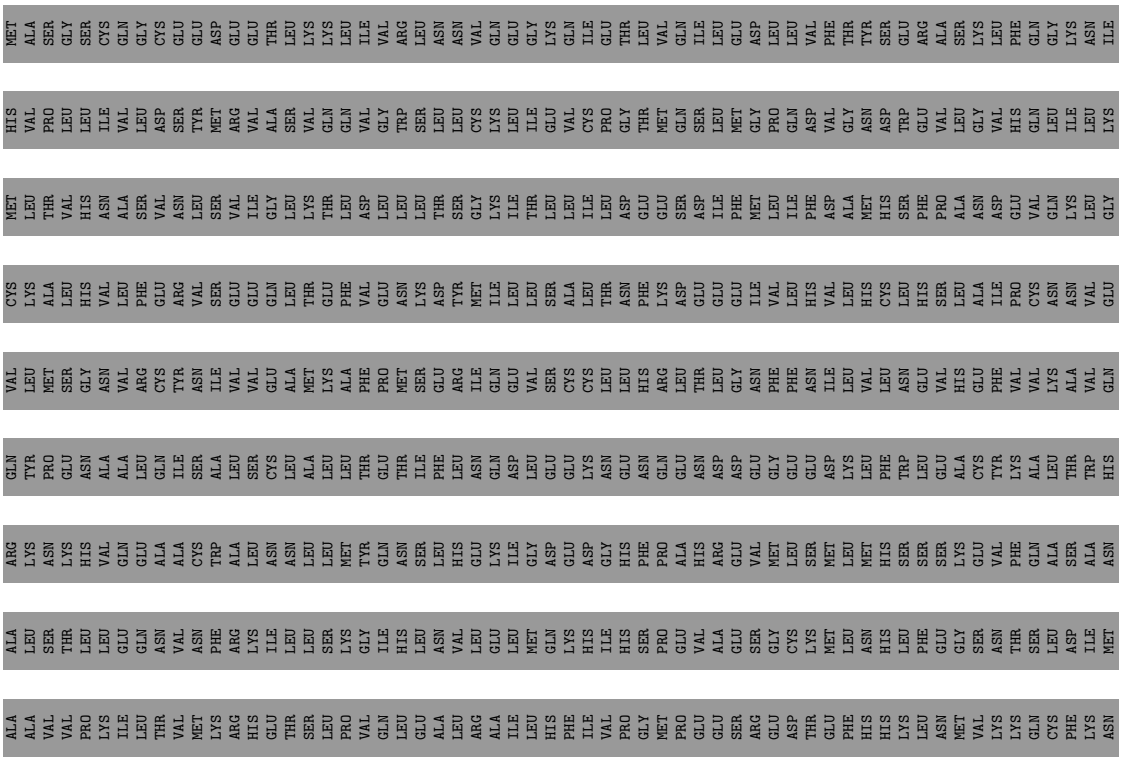
SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

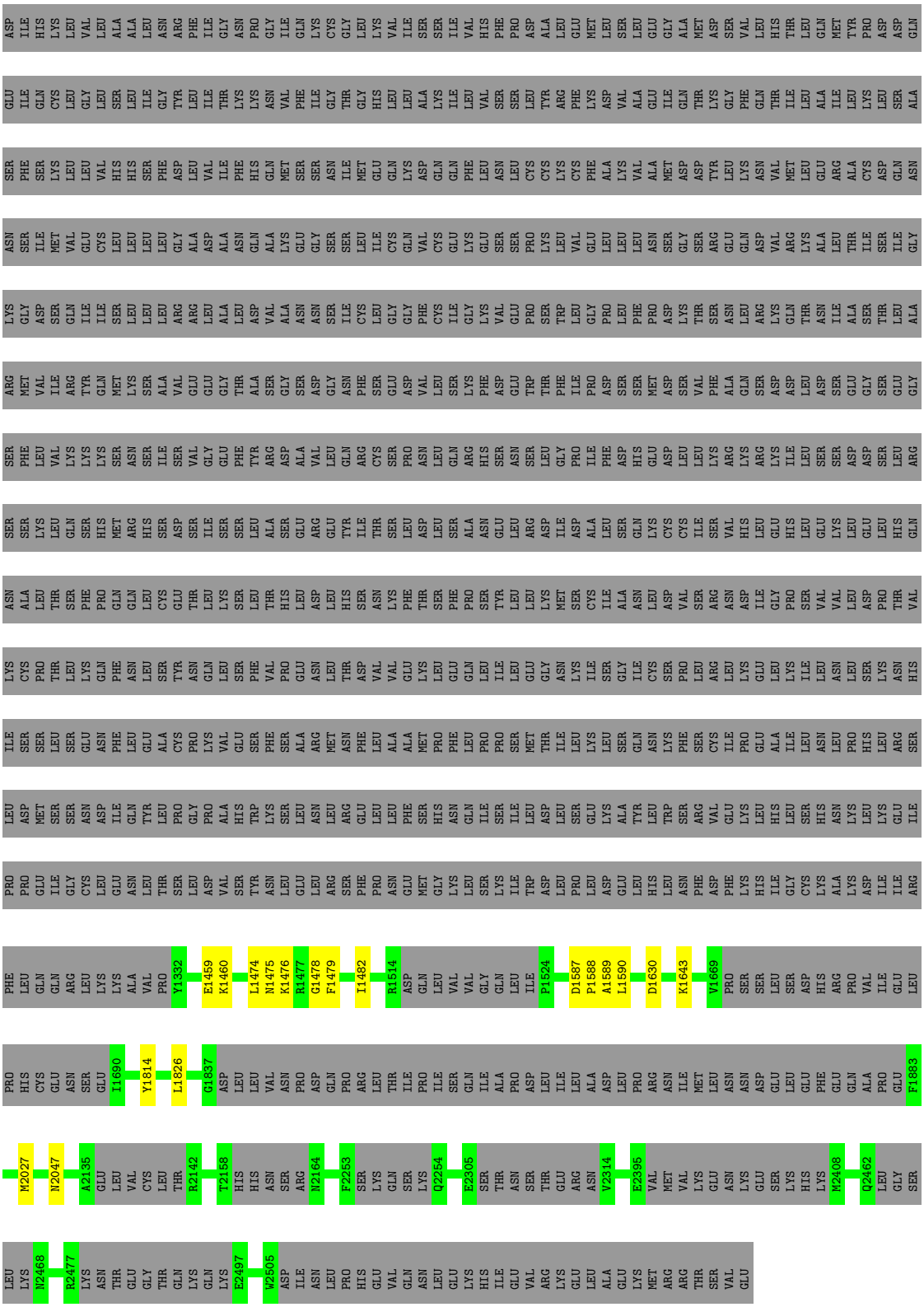
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 37-B: 40% • 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 38-A: 39% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

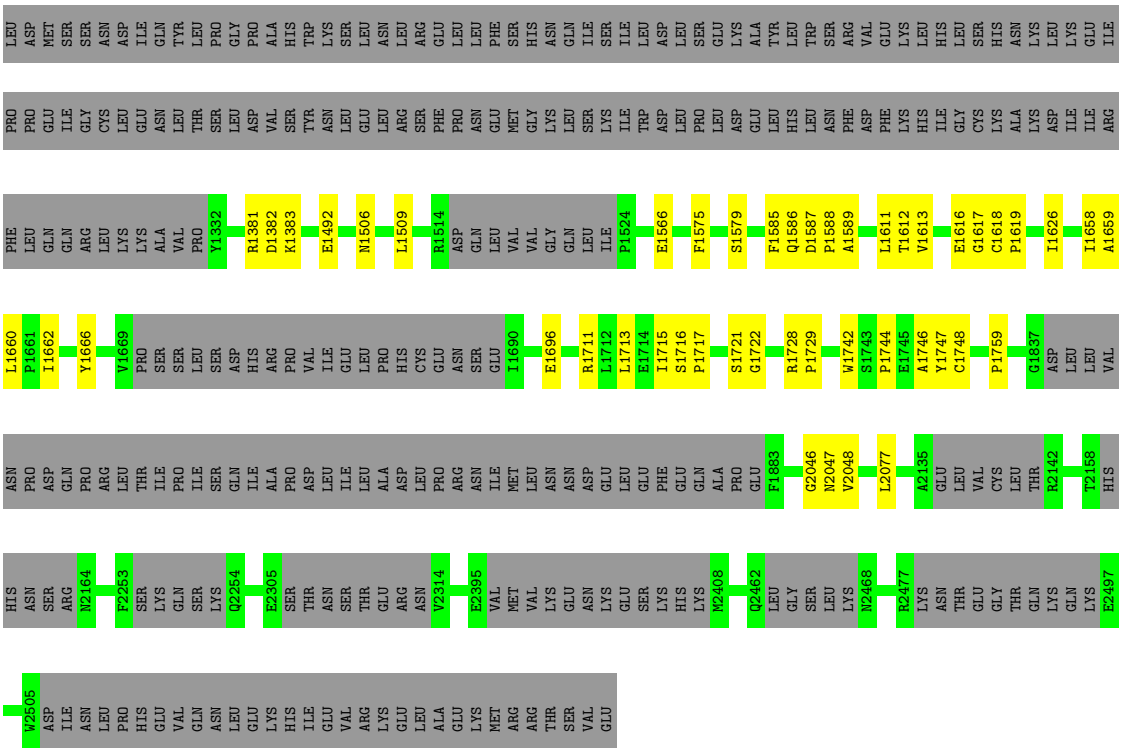
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

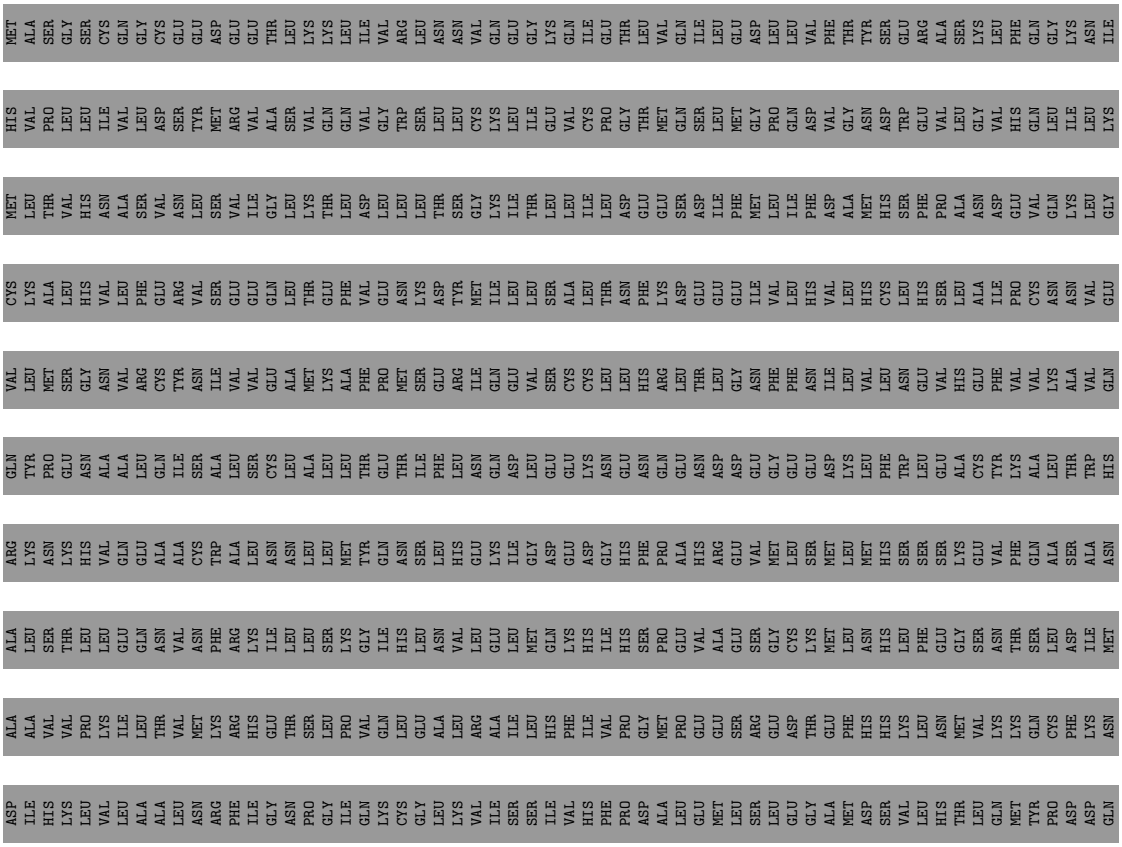
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

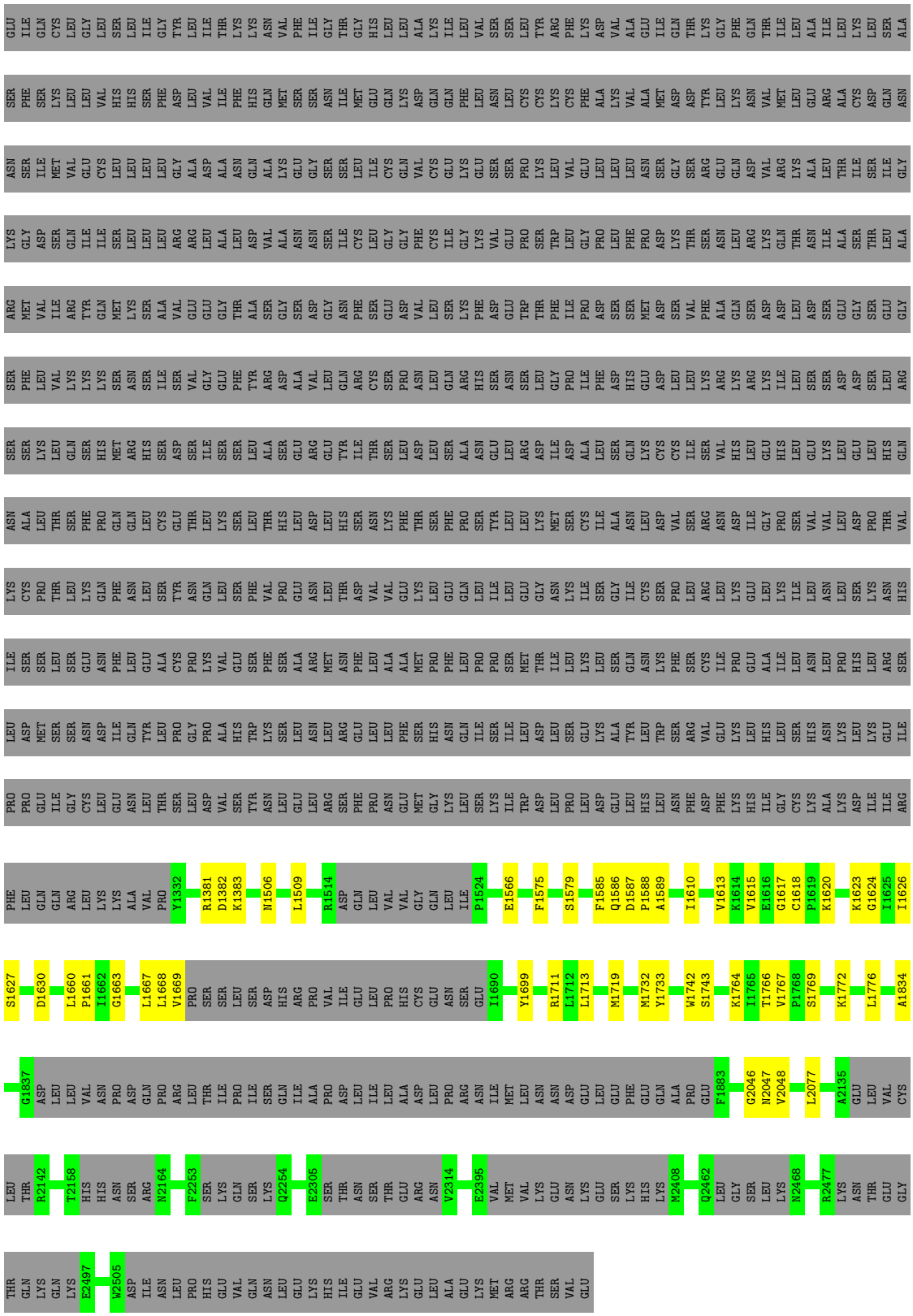
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 38-B:





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 39-A: 40% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLN GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

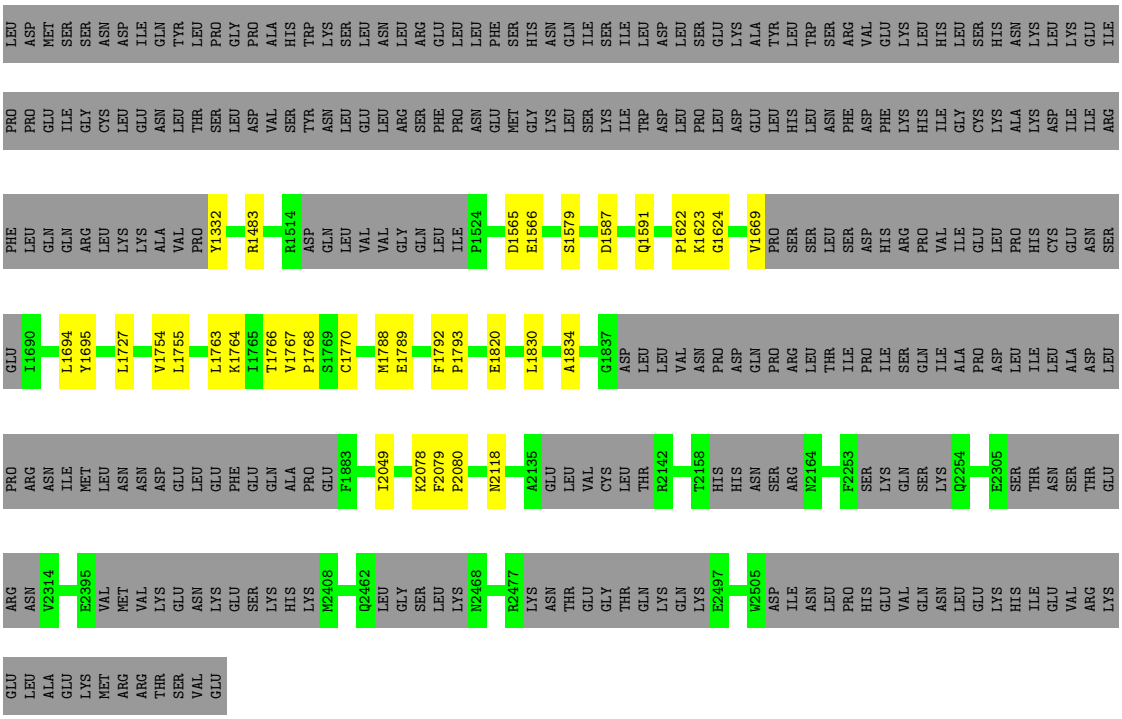
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

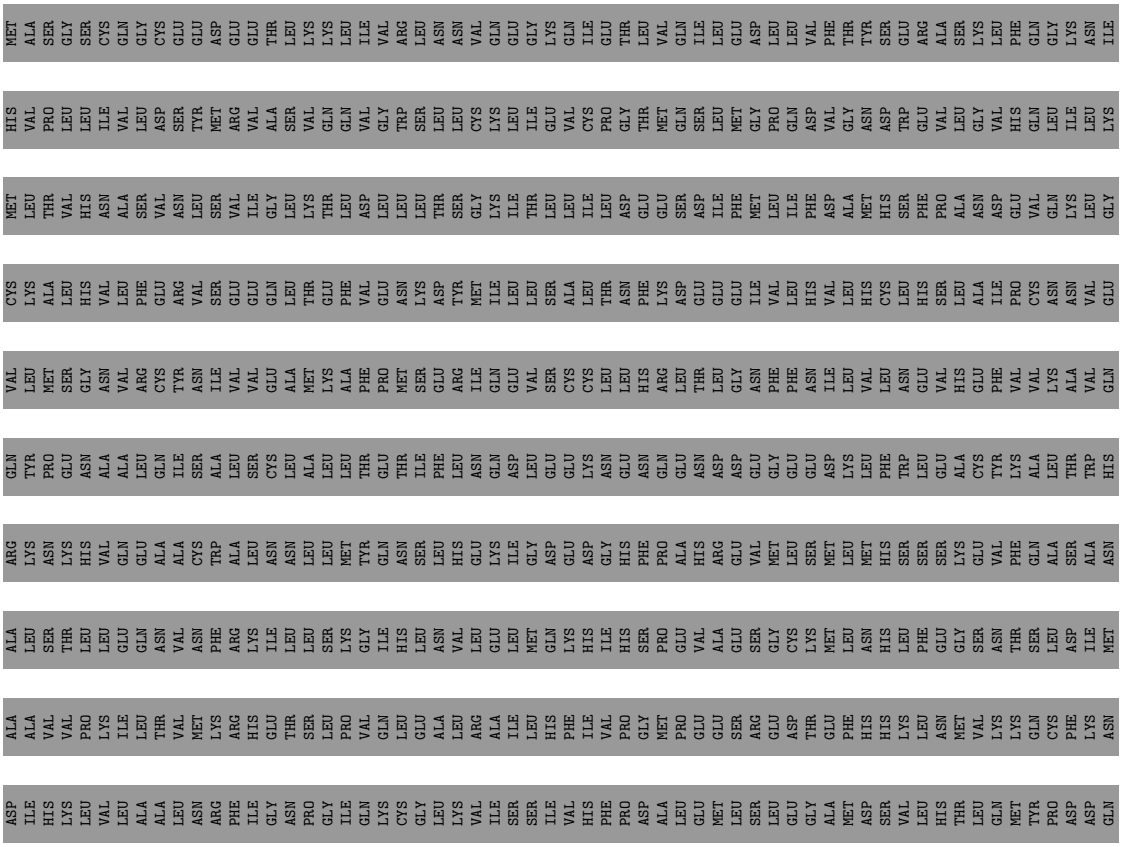
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

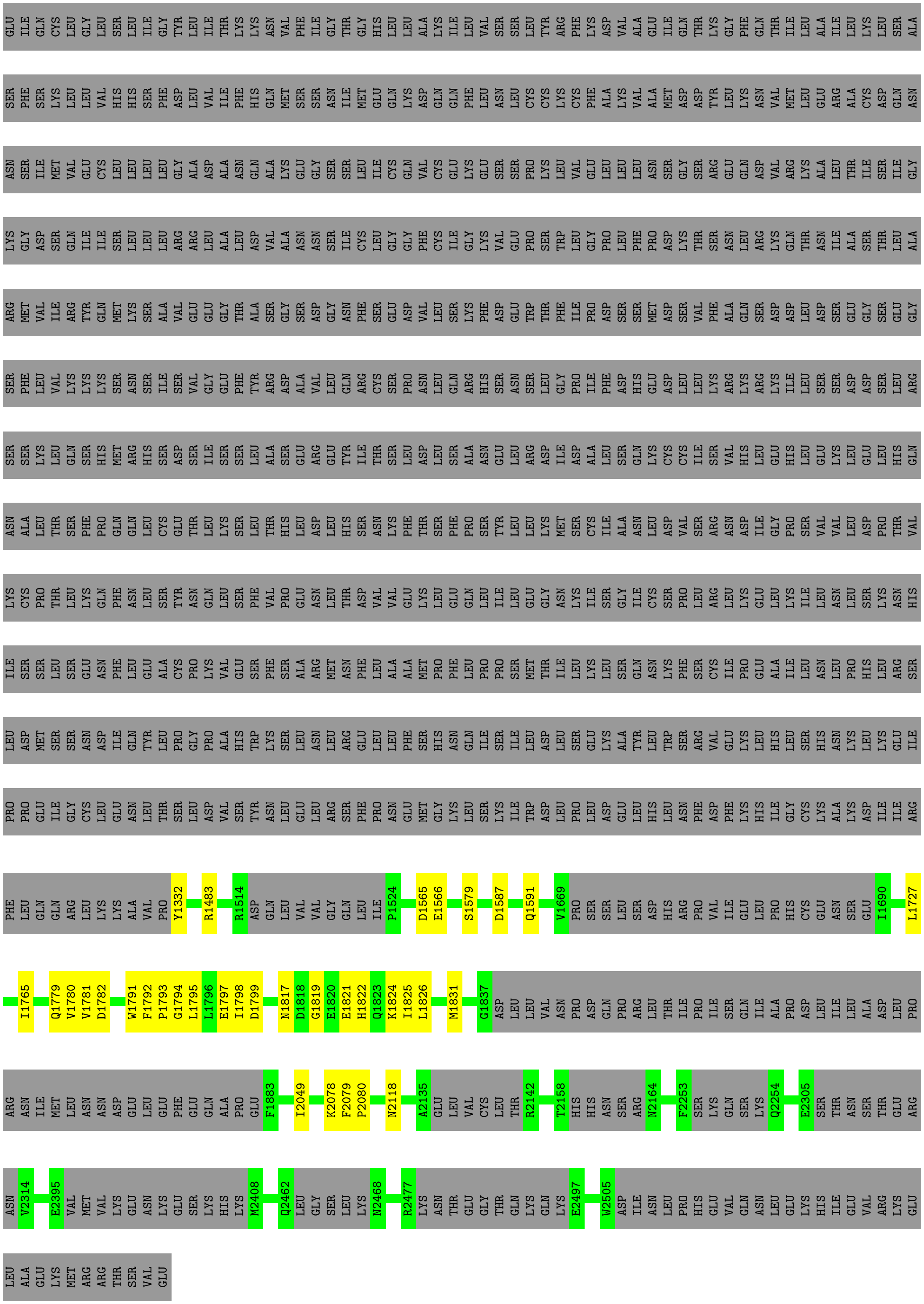
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 39-B: 40% • 59%





• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 40-A:

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

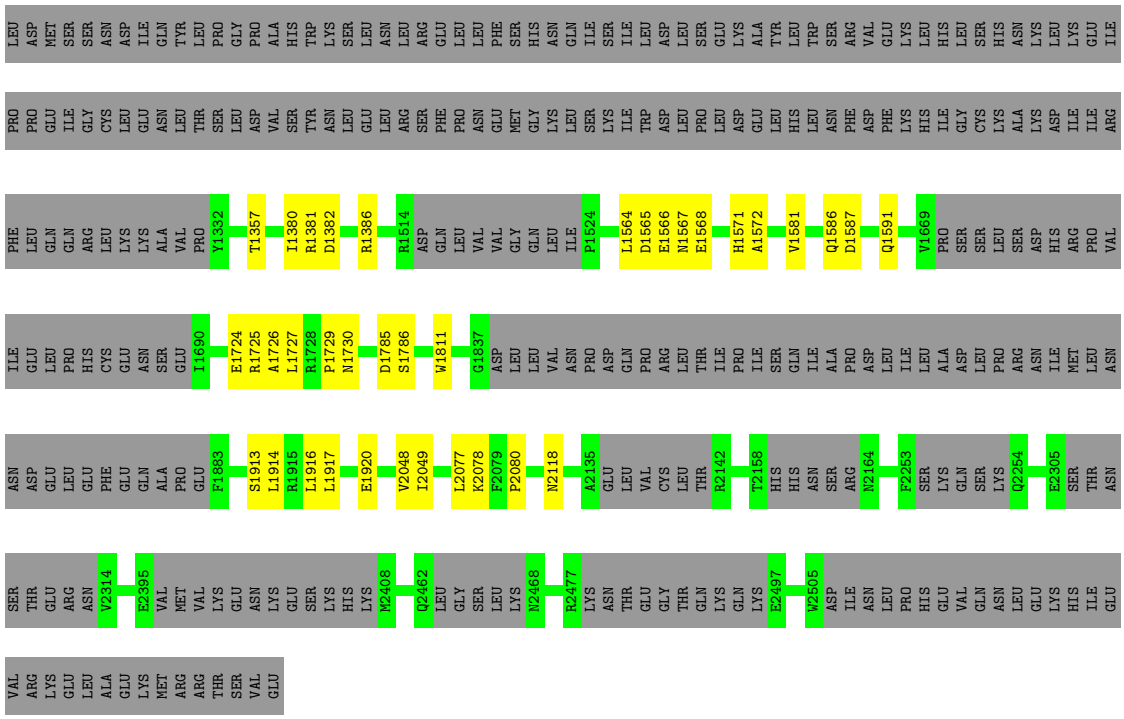
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

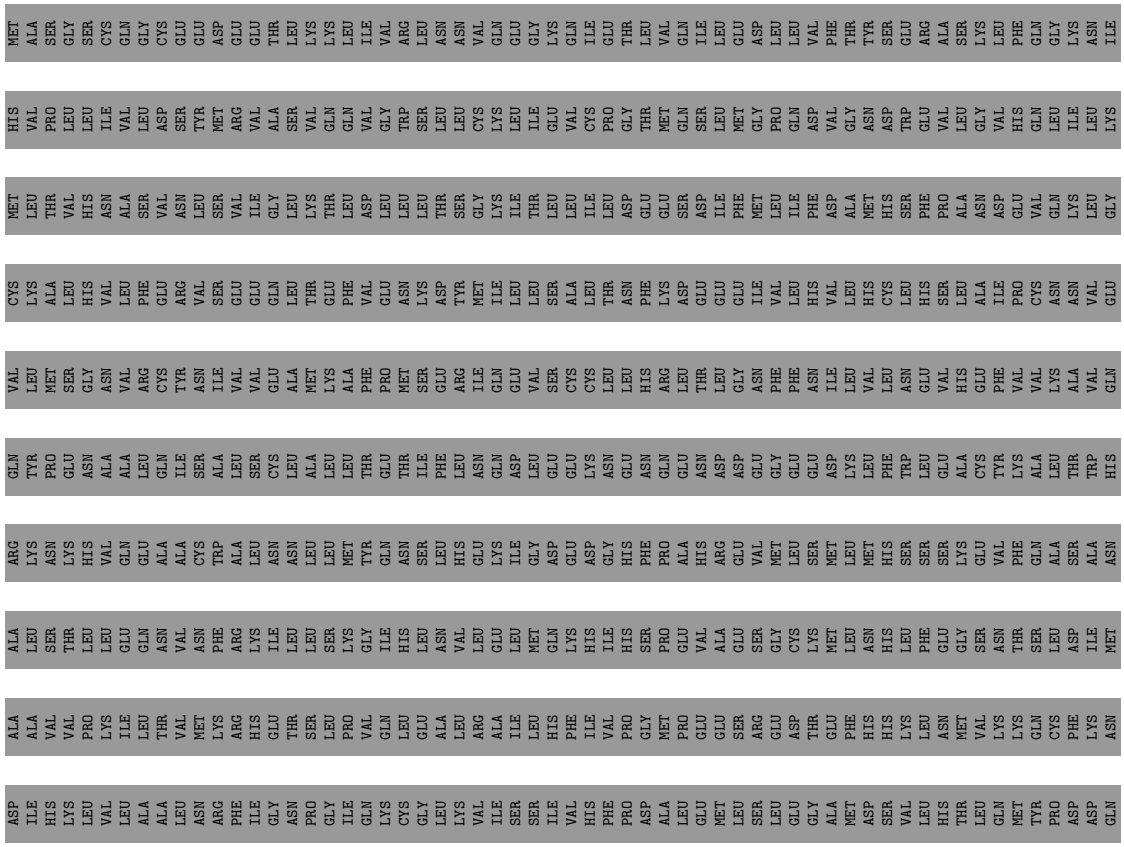
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

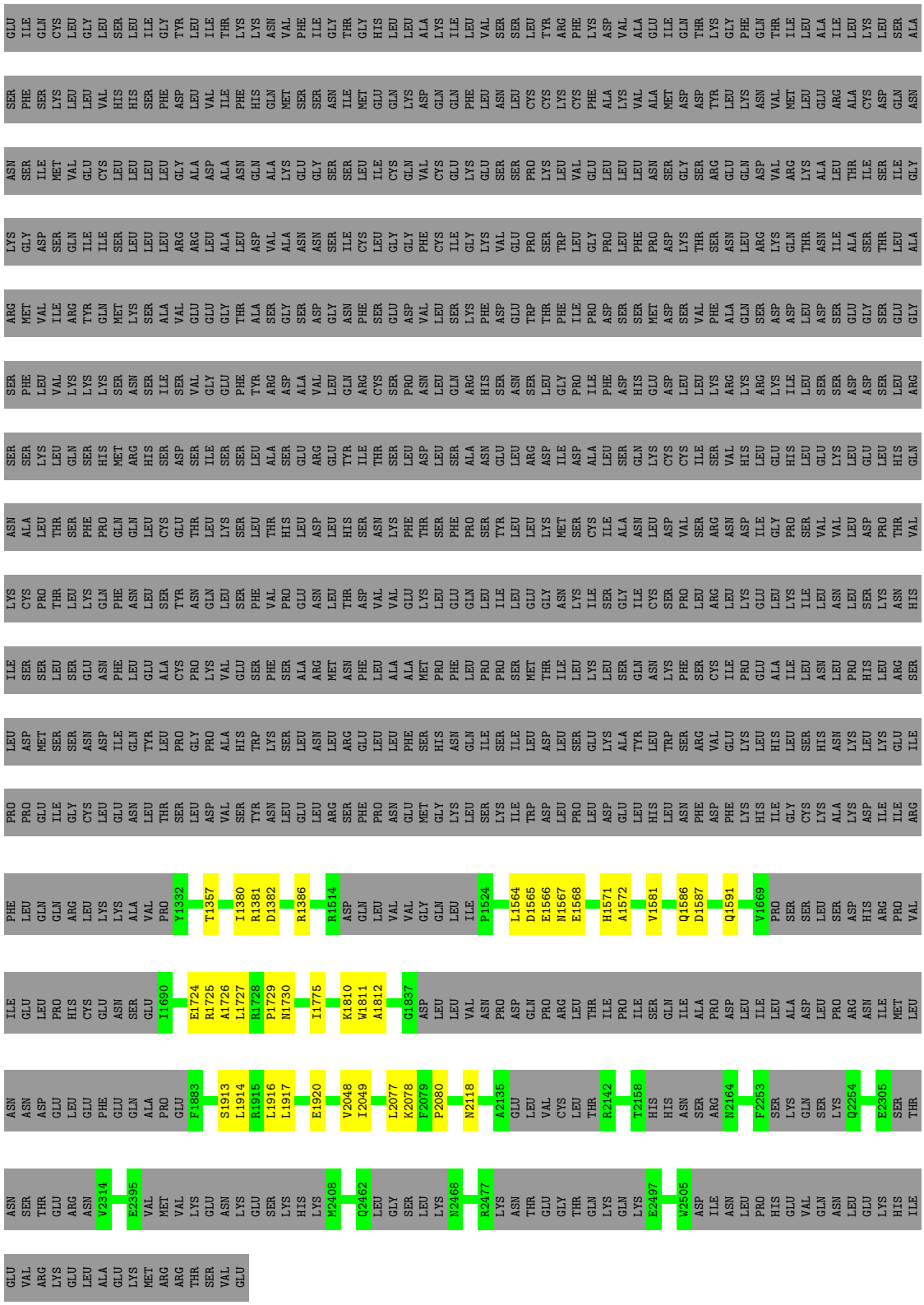
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 40-B: 40% • 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 41-A: 39% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

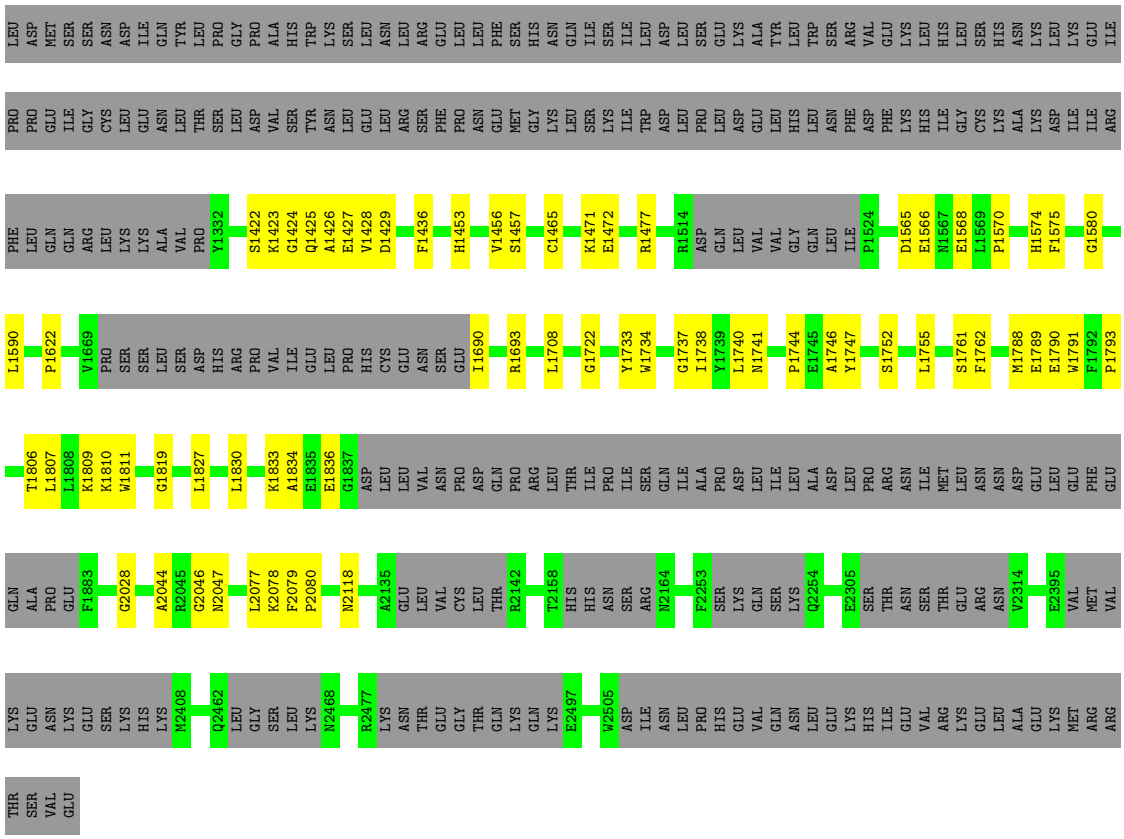
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

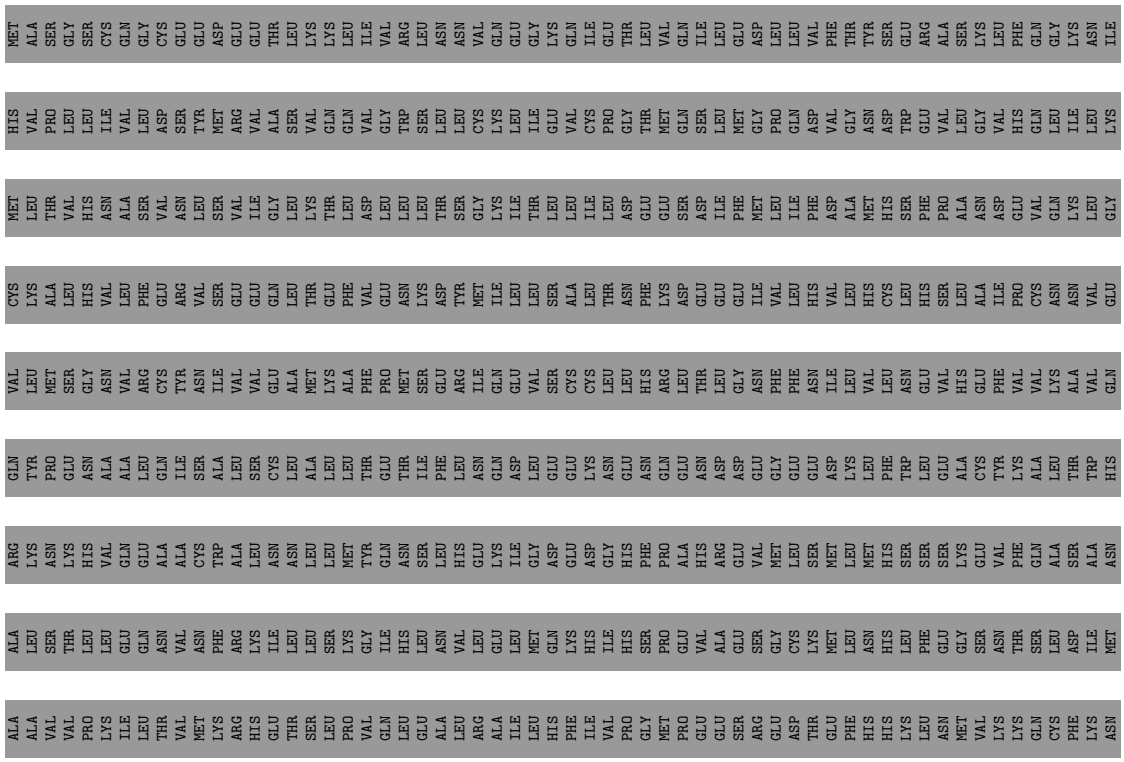
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 41-B: 38% • 59%



MET ARG ARG THR SER VAL GLU
VAL MET VAL LYS GLU ASN LYS GLU SER LYS HIS LYS M2408 Q2462 LEU GLY SER LEU LYS N2468 R2477 LYS ASN THR GLU GLY THR GLN LYS GLN LYS E2497 W2505 ASP ILE ASN LEU PRO HIS GLU VAL GLN ASN LEU GLU LYS HIS ILE GLU VAL ARG LYS GLU LEU ALA GLU LYS
GLU PHE GLU GLN ALA PRO GLU F1883 G2028 A2044 R2045 G2046 N2047 L2077 K2078 P2079 P2080 N2118 A2135 GLU LEU VAL CYS LEU THR R2142 T2158 HIS HIS ASN SER ARG N2164 F2253 SER LYS GLN SER LYS Q2254 E2305 SER THR ASN SER THR GLU ARG ASN ASP GLU LEU
V1754 T1766 E1789 E1790 W1791 C1801 T1806 L1807 L1808 K1809 K1810 W1811 G1819 E1836 G1837 ASP LEU LEU VAL ASN PRO ASP GLN PRO ARG LEU THR ILE PRO ILE SER GLN ILE ILE ALA PRO ASP LEU ILE LEU PRO ARG ASN ILE MET LEU ALA ASP LEU PRO
V1669 PRO SER SER LEU SER ASP HIS ARG PRO VAL ILE GLU LEU PRO HIS CYS GLU ASN SER I1690 I1691 I1692 R1693 P1701 M1702 G1703 F1704 W1705 S1706 R1707 L1708 I1709 S1716 P1717 Y1718 M1719 G1722 R1725 A1726 L1727 R1728 P1729 N1730 R1735 L1740 S1743 A1746 Y1747 C1748
PHE LEU GLN GLN ARG LEU LYS LYS ALA VAL PRO Y1332 S1422 K1423 G1424 Q1425 A1426 E1427 V1428 D1429 F1436 H1453 C1465 K1471 E1472 R1477 R1514 ASP GLN LEU VAL VAL GLY GLN LEU ILE P1524 D1565 E1566 N1567 E1568 L1569 P1570 H1574 F1575 G1580 L1590 P1622
PRO PRO GLU ILE GLY CYS LEU LEU GLU ASN LEU THR SER TYR ASN ASP PHE ARG LEU ASP VAL SER TYR ASN LEU GLU SER PHE VAL SER LYS ILE ILE ASP LEU PRO LYS SER LEU LEU ASN LEU ARG ARG PHE SER ALA ARG GLU ASN PHE PRO ASN GLU MET GLY LYS LEU ILE TRP ASP LEU PRO LEU ASP GLU LEU HIS LEU ASN LYS PHE SER CYS PRO LEU ARG VAL GLU ILE ARG
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLN LEU ILE ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS LYS ILE LEU LYS ILE ASN HIS
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN LEU ASP ILE GLY PRO SER LEU LEU VAL LEU LEU ASP PRO THR VAL
SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU ILE ASP ALA LEU SER GLN LYS CYS CYS ILE ILE LEU SER VAL HIS ARG LYS LYS ILE LEU GLU LYS LEU LEU
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ILE LEU GLY PRO ILE PHE ASP LEU SER LEU LEU LYS ARG LYS ILE LEU LEU
ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER LEU LEU PRO LYS THR LYS SER GLU GLY GLU
LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG LEU ALA ASP VAL ALA ASN ASN SER ILE CYS LEU GLU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN GLN ILE ILE SER LEU LEU ASN LYS ASN VAL ARG LYS GLN THR ASN ILE ALA SER THR ILE LEU ALA
ASN SER ILE MET VAL GLU CYS LEU LEU LEU GLY ALA ASP ASN ASN GLY SER SER ILE LEU ILE CYS GLN VAL CYS GLU LYS GLU SER LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS THR LEU GLU LEU ILE SER GLY
SER PHE SER LYS SER HIS HIS SER HIS GLN MET MET GLU GLN LYS ASP GLN GLN PHE LEU ASN VAL MET LEU GLU ARG ARG GLN ASP SER ASP ASP VAL LEU LYS GLY PHE LYS LYS ARG LYS ILE LEU LYS ILE ILE GLN
GLU ILE GLN CYS LEU GLY LEU SER LEU LEU ILE ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY HIS LEU LEU LEU ILE GLN THR ILE LEU ALA ILE LEU LYS LEU LEU
ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLN LYS CYS GLN LEU VAL ILE SER SER ILE VAL HIS PHE PRO ASP ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP GLN
PHE LEU GLN GLN ARG LEU LYS LYS ALA VAL PRO Y1332 S1422 K1423 G1424 Q1425 A1426 E1427 V1428 D1429 F1436 H1453 C1465 K1471 E1472 R1477 R1514 ASP GLN LEU VAL VAL GLY GLN LEU ILE P1524 D1565 E1566 N1567 E1568 L1569 P1570 H1574 F1575 G1580 L1590 P1622
PRO PRO GLU ILE GLY CYS LEU LEU GLU ASN LEU THR SER TYR ASN ASP PHE ARG LEU ASP VAL SER TYR ASN LEU GLU SER PHE VAL SER LYS ILE ILE ASP LEU PRO LYS SER LEU LEU ASN LEU ARG ARG PHE SER ALA ARG GLU ASN PHE PRO ASN GLU MET GLY LYS LEU ILE TRP ASP LEU PRO LEU ASP GLU LEU HIS LEU ASN LYS PHE SER CYS PRO LEU ARG VAL GLU ILE ARG
LEU ASP MET SER SER ASN ASP ILE GLN LEU TYR LEU ASP PRO HIS GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG ARG GLU ILE LEU LEU PHE SER HIS ASN GLN ILE SER GLU LEU LEU PRO GLY ASN LYS ILE SER GLU LYS LYS ALA TYR LEU TRP SER GLU LYS LEU SER GLN ASN LYS PHE SER ARG VAL GLU LYS LEU LEU ILE LEU LEU ASN LEU LEU LEU ILE LEU ILE GLU
ILE SER SER LEU SER GLU SER ALA ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER LYS MET THR ILE LEU LYS LEU SER GLN LYS PHE SER CYS ILE LEU LEU ASN LEU ARG LEU LYS LYS LEU LEU ASN LEU LEU LEU ILE LEU ASN LEU LEU LEU ILE LEU ARG SER
PHE LEU GLN GLN ARG LEU LYS LYS ALA VAL PRO Y1332 S1422 K1423 G1424 Q1425 A1426 E1427 V1428 D1429 F1436 H1453 C1465 K1471 E1472 R1477 R1514 ASP GLN LEU VAL VAL GLY GLN LEU ILE P1524 D1565 E1566 N1567 E1568 L1569 P1570 H1574 F1575 G1580 L1590 P1622
V1669 PRO SER SER LEU SER ASP HIS ARG PRO VAL ILE GLU LEU PRO HIS CYS GLU ASN SER I1690 I1691 I1692 R1693 P1701 M1702 G1703 F1704 W1705 S1706 R1707 L1708 I1709 S1716 P1717 Y1718 M1719 G1722 R1725 A1726 L1727 R1728 P1729 N1730 R1735 L1740 S1743 A1746 Y1747 C1748
V1754 T1766 E1789 E1790 W1791 C1801 T1806 L1807 L1808 K1809 K1810 W1811 G1819 E1836 G1837 ASP LEU LEU VAL ASN PRO ASP GLN PRO ARG LEU THR ILE PRO ILE SER GLN ILE ILE ALA PRO ASP LEU ILE LEU PRO ARG ASN ILE MET LEU ALA ASP LEU PRO
GLU PHE GLU GLN ALA PRO GLU F1883 G2028 A2044 R2045 G2046 N2047 L2077 K2078 P2079 P2080 N2118 A2135 GLU LEU VAL CYS LEU THR R2142 T2158 HIS HIS ASN SER ARG N2164 F2253 SER LYS GLN SER LYS Q2254 E2305 SER THR ASN SER THR GLU ARG ASN ASN ASP GLU LEU
VAL MET VAL LYS GLU ASN LYS GLU SER LYS HIS LYS M2408 Q2462 LEU GLY SER LEU LYS N2468 R2477 LYS ASN THR GLU GLY THR GLN LYS GLN LYS E2497 W2505 ASP ILE ASN LEU PRO HIS GLU VAL GLN ASN LEU GLU LYS HIS ILE GLU VAL ARG LYS GLU LEU ALA GLU LYS

• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 42-A: 40% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

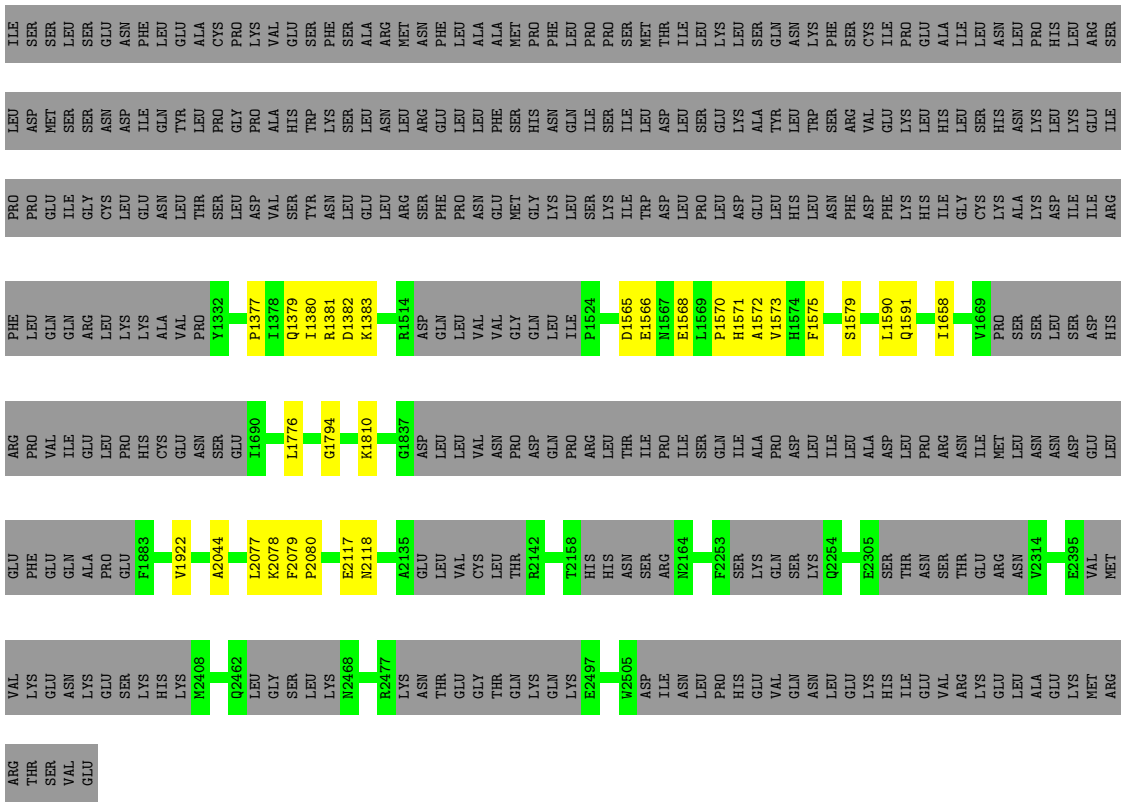
ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLY GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

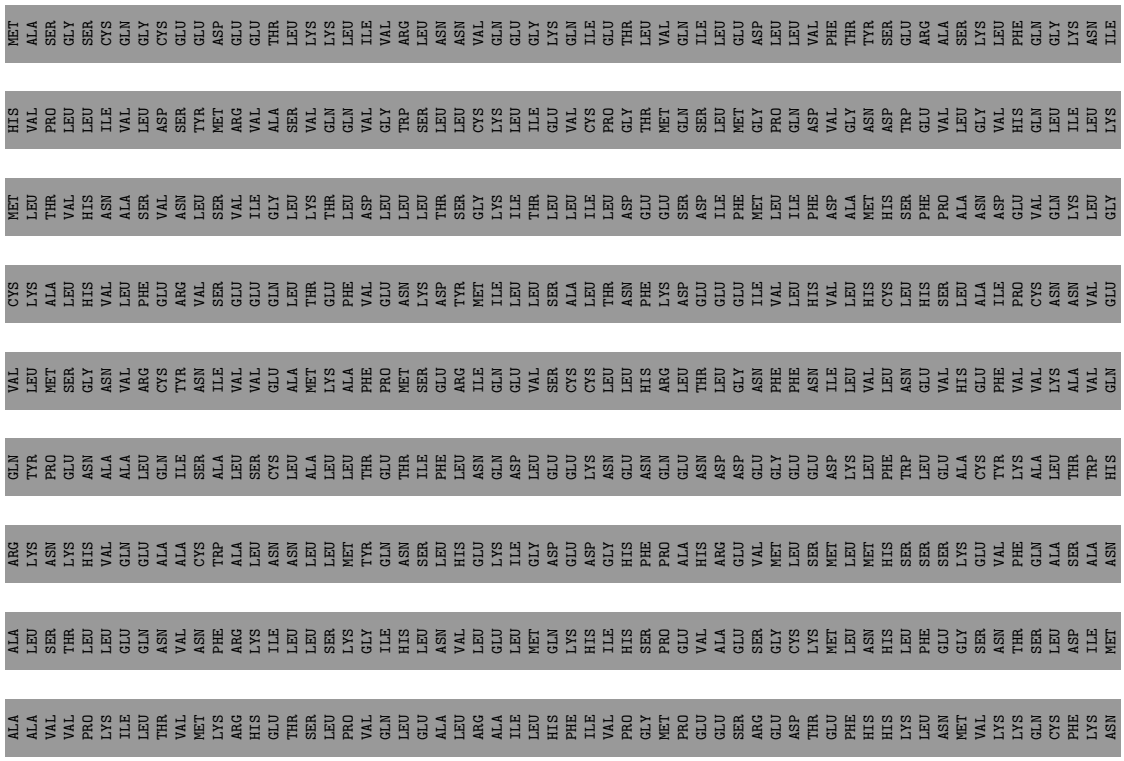
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

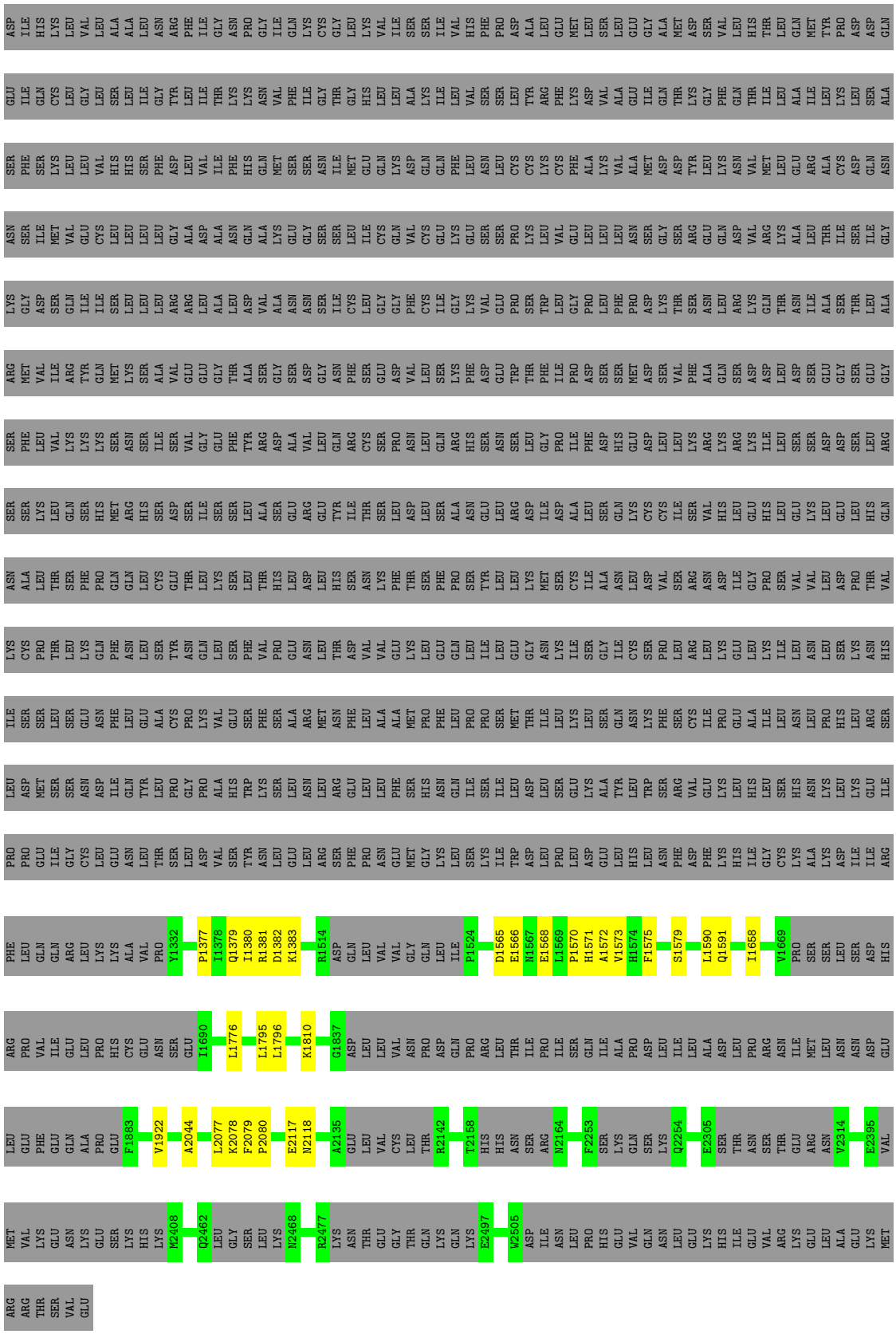
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 42-B: 40% • 59%

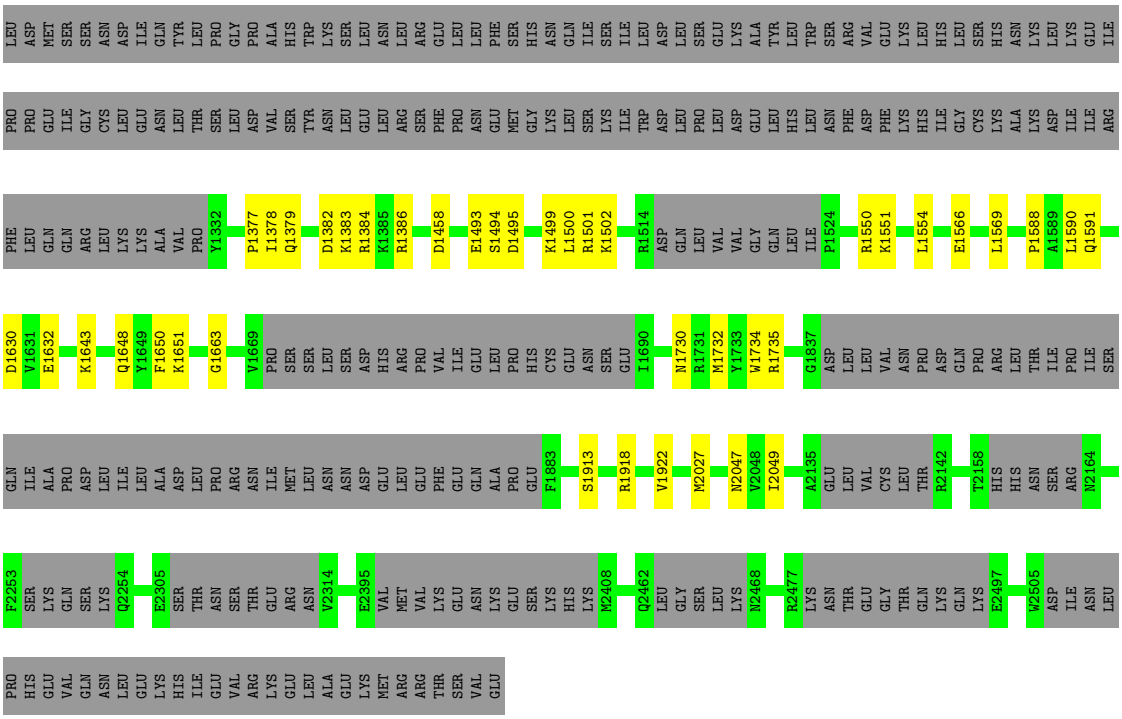




• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

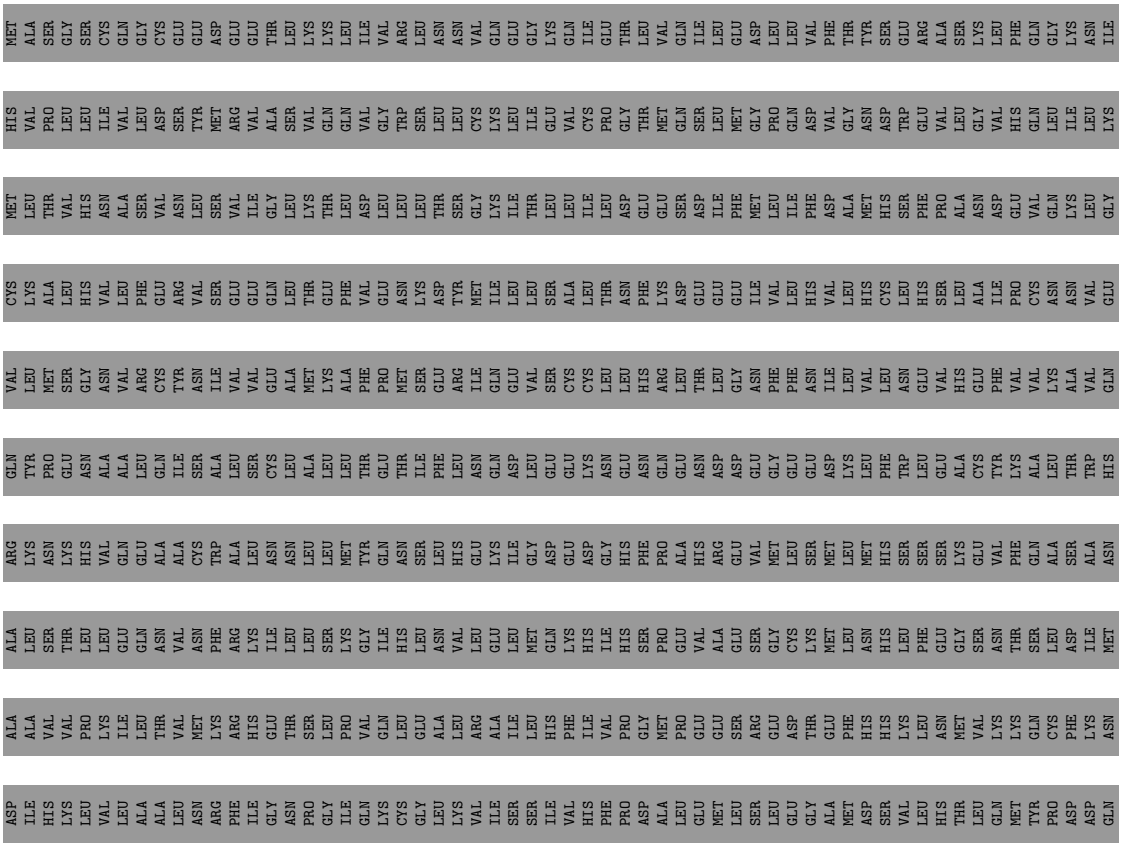
Chain 43-A: 40% 59%

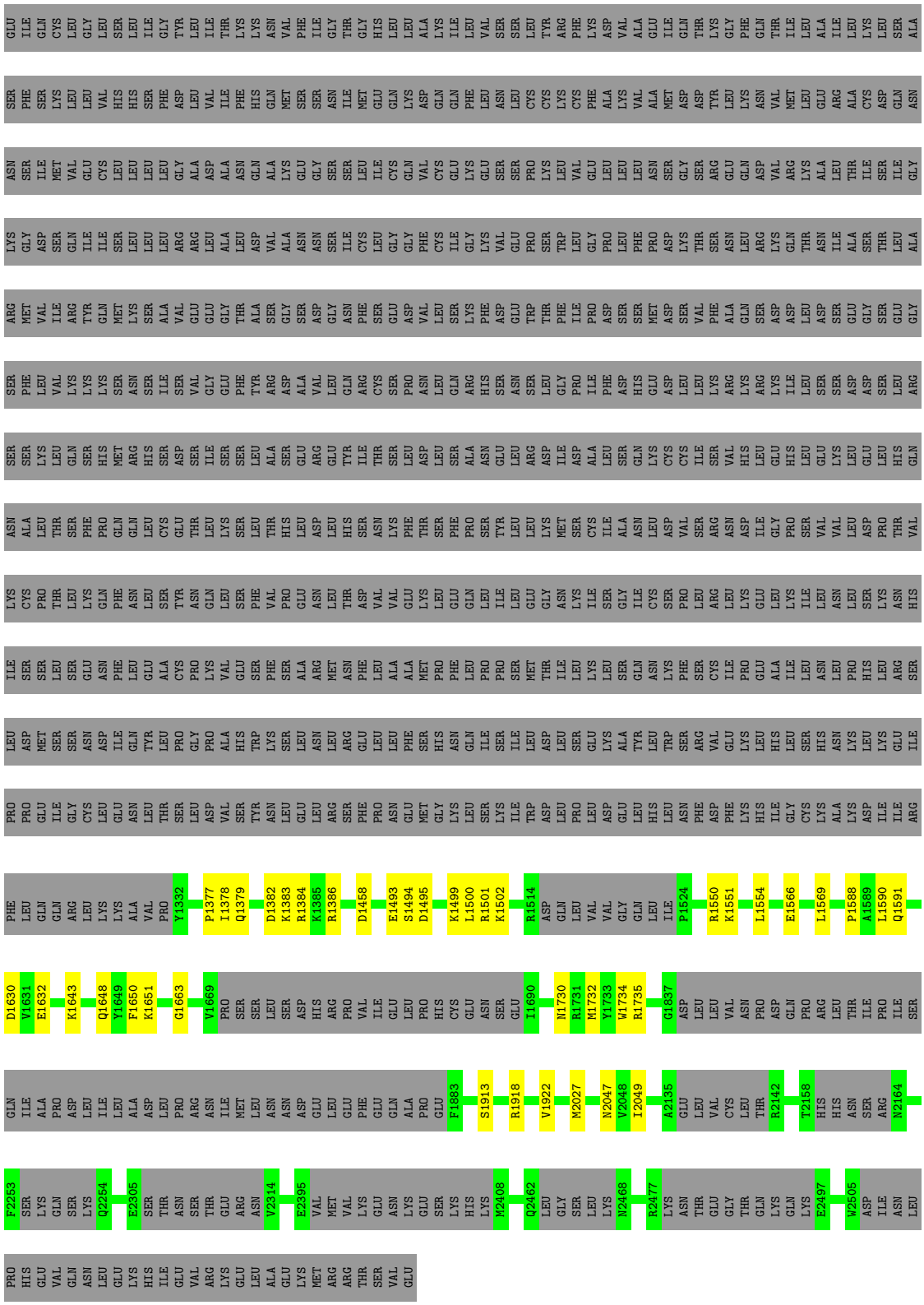
| | | |



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 43-B: 40% • 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 44-A: 41% 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

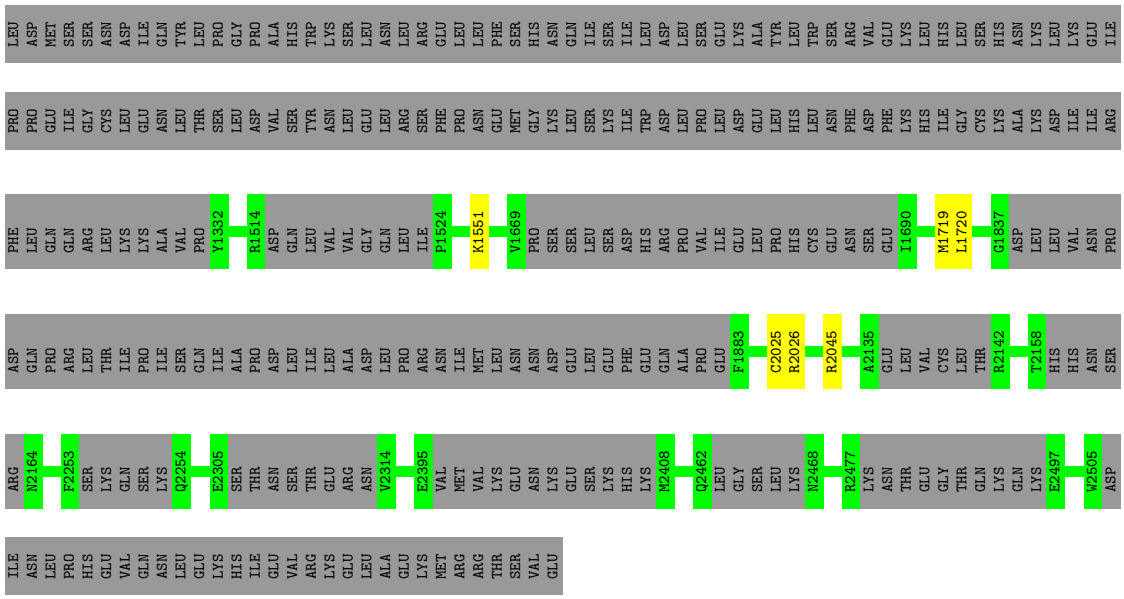
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

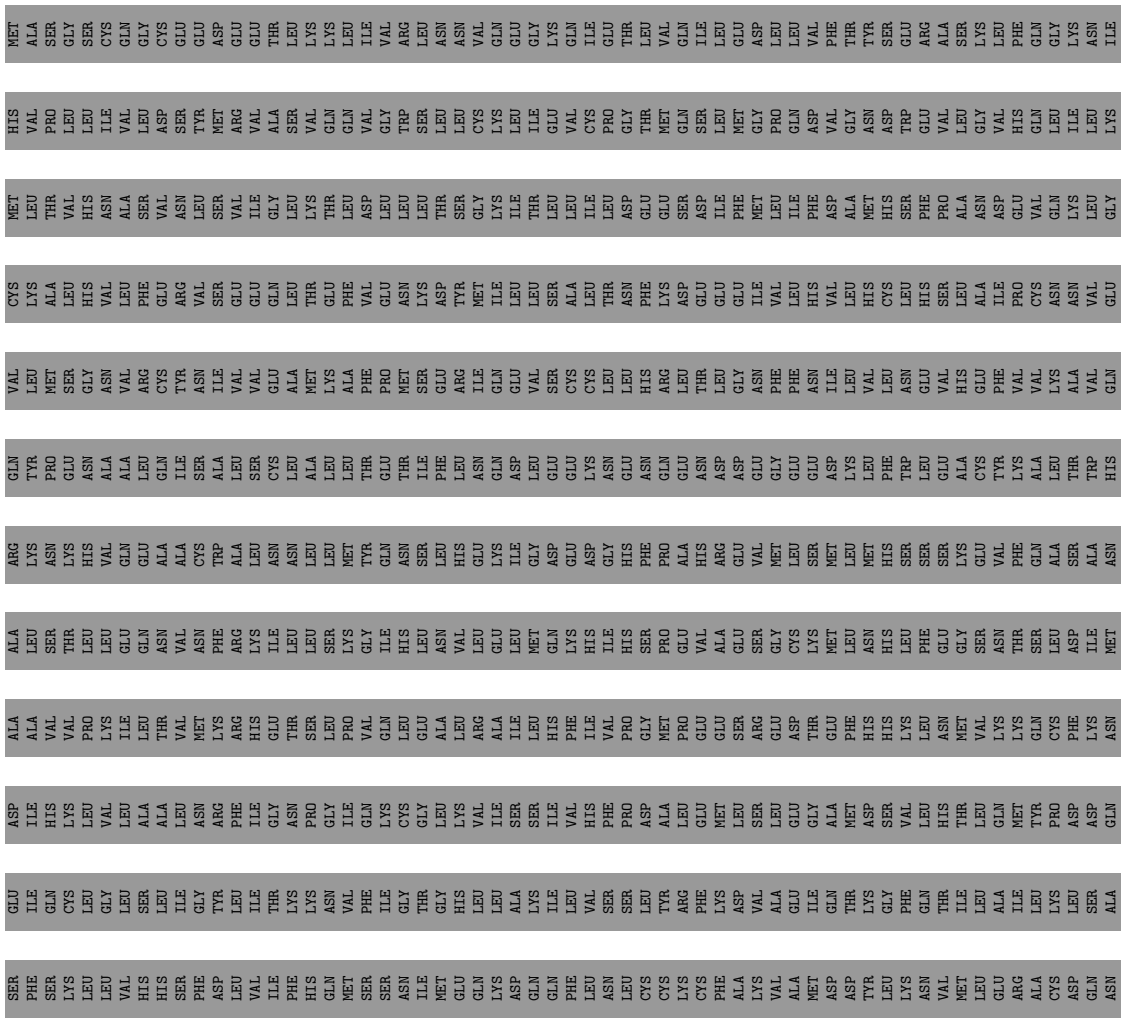
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

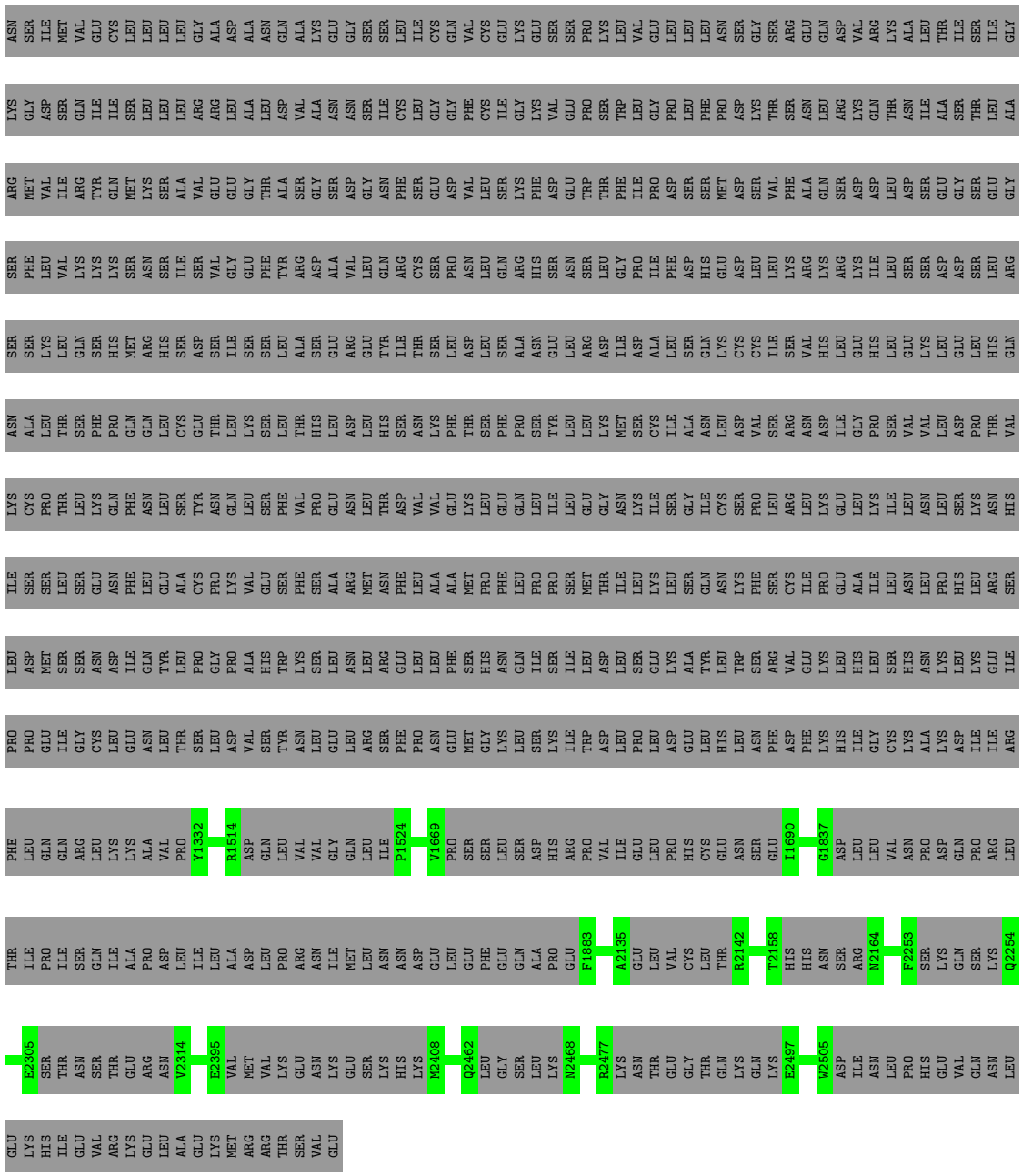
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

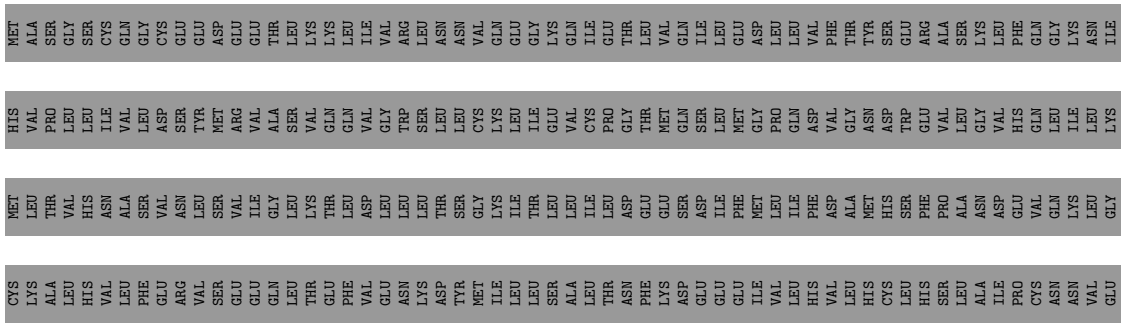
Chain 44-B:



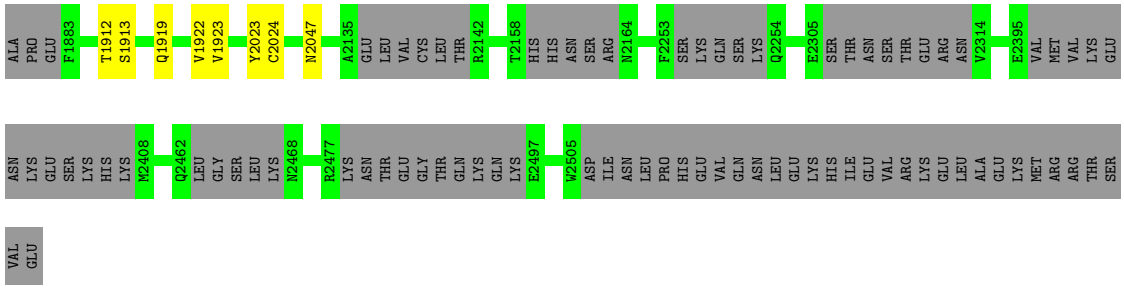


• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 45-A: 40% 59%

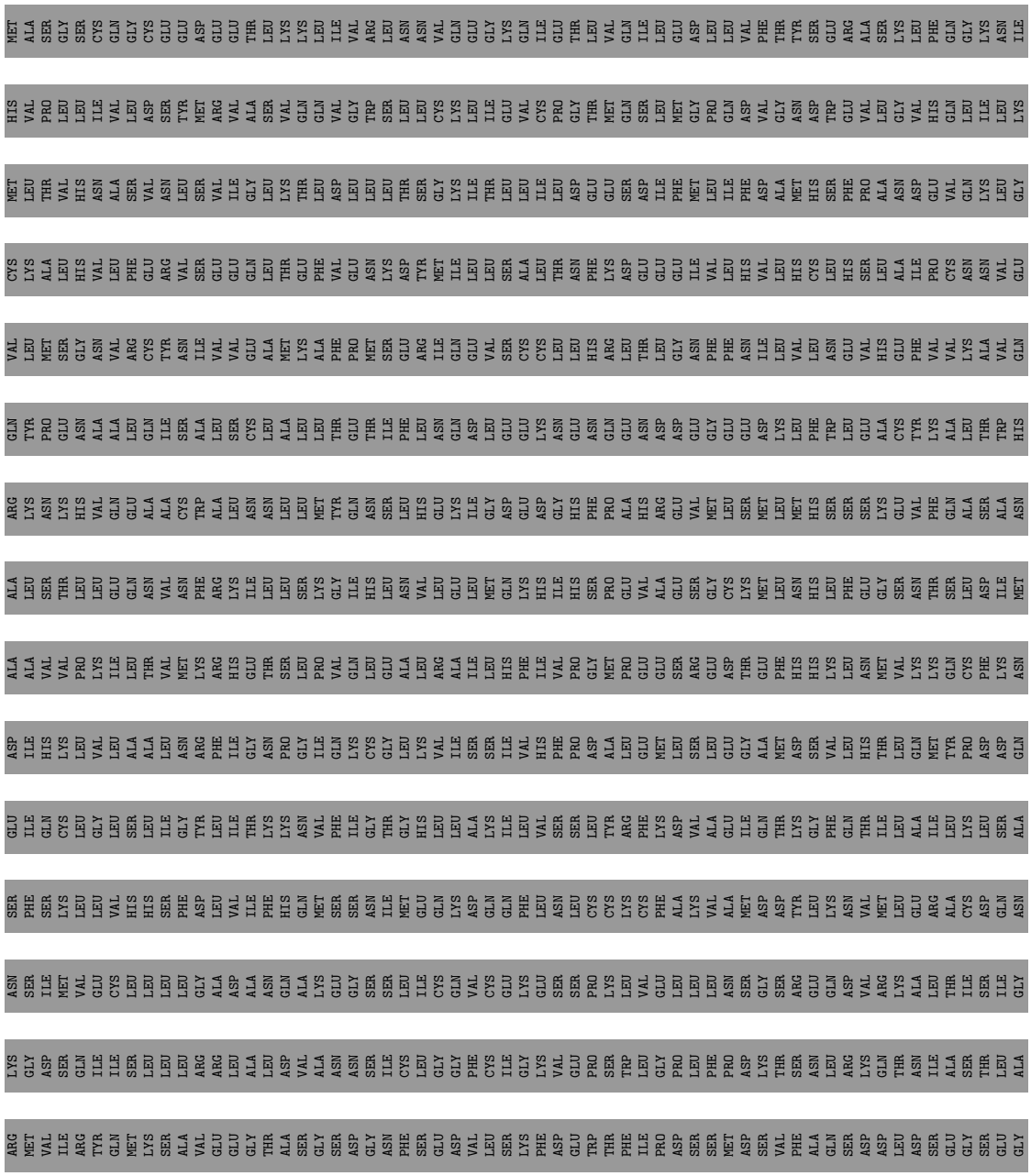


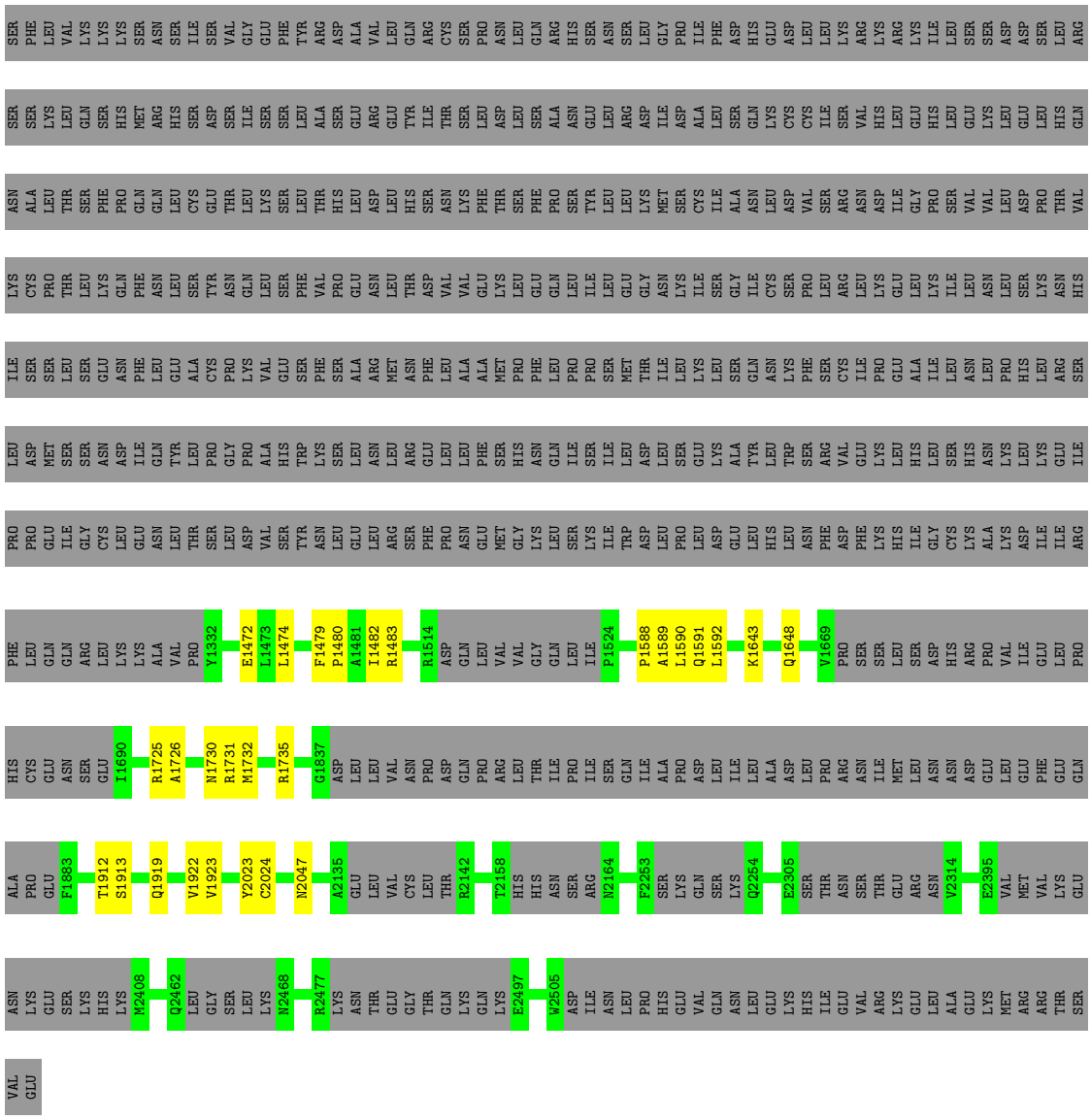
HIS	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA	ARG	GLN	VAL
CYS	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS	TYR	LEU
GLU	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN	PRO	MET
ASN	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS	GLU	SER
SER	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS	ASN	GLY
GLU	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL	ALA	ASN
I1690	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN	ALA	VAL
	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU	LEU	ARG
R1725	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA	GLN	CYS
A1726	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA	ILE	TYR
	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS	SER	ASN
N1730	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP	ALA	ILE
R1731		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA	LEU	VAL
M1732	E1472	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU	SER	VAL
	L1473	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN	CYS	GLU
R1735	L1474	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN	LEU	ALA
		TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU	ALA	MET
G1837	F1479	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU	LEU	LYS
ASP	P1480	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET	LEU	ALA
LEU	A1481	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR	THR	PHE
LEU	I1482	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN	GLU	PRO
VAL	R1483	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN	THR	MET
ASN		SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER	ILE	SER
PRO	R1514	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU	PHE	GLU
ASP	ASP	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS	LEU	ARG
GLN	GLN	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU	ASN	ILE
PRO	LEU	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS	GLN	GLN
ARG	VAL	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE	ASP	GLU
LEU	VAL	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY	LEU	VAL
THR	GLY	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP	GLU	SER
ILE	GLN	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU	GLU	CYS
PRO	LEU	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP	LYS	CYS
ILE	ILE	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY	ASN	LEU
SER	P1524	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS	GLU	LEU
GLN		TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE	ASN	HIS
ILE	P1588	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO	GLN	ARG
ALA	A1589	LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA	GLU	LEU
PRO	L1590	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS	ASN	THR
ASP	Q1591	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG	ASP	LEU
LEU	L1592	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU	ASP	GLY
ILE		GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL	GLU	ASN
LEU	K1643	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET	GLY	PHE
ALA		HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU	GLU	PHE
ASP	Q1648	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER	GLU	ASN
LEU		ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET	ASP	ILE
PRO	V1669	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU	LYS	LEU
ARG	PRO	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET	LEU	VAL
ASN	SER	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS	PHE	LEU
ILE	SER	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER	TRP	ASN
MET	LEU	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER	LEU	GLU
LEU	SER	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER	GLU	VAL
ASN	ASP	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS	ALA	HIS
ASN	HIS	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU	CYS	GLU
ASP	ARG	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL	TYR	PHE
GLU	PRO	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE	LYS	VAL
LEU	VAL	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN	ALA	VAL
GLU	ILE	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA	LEU	LYS
PHE	GLU	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER	THR	ALA
GLU	LEU	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA	TRP	VAL
GLN	PRO	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN	HIS	GLN



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

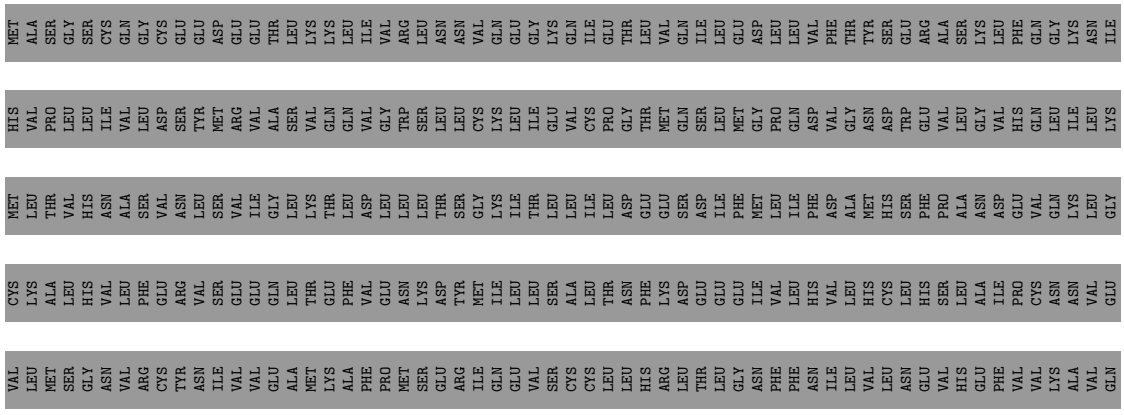
Chain 45-B: 40% • 59%



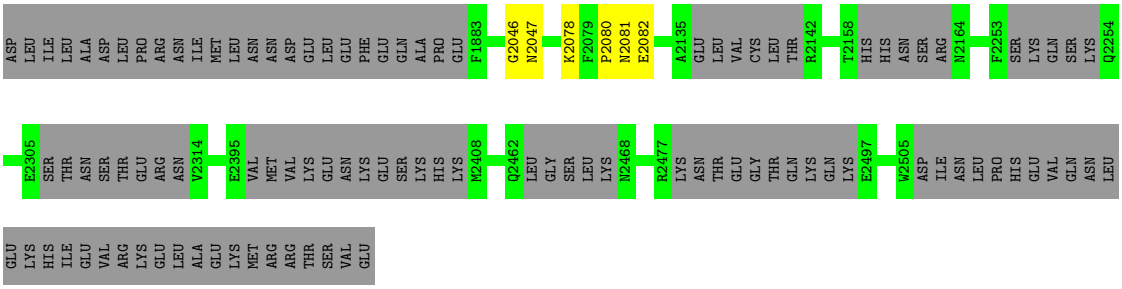


- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 46-A:

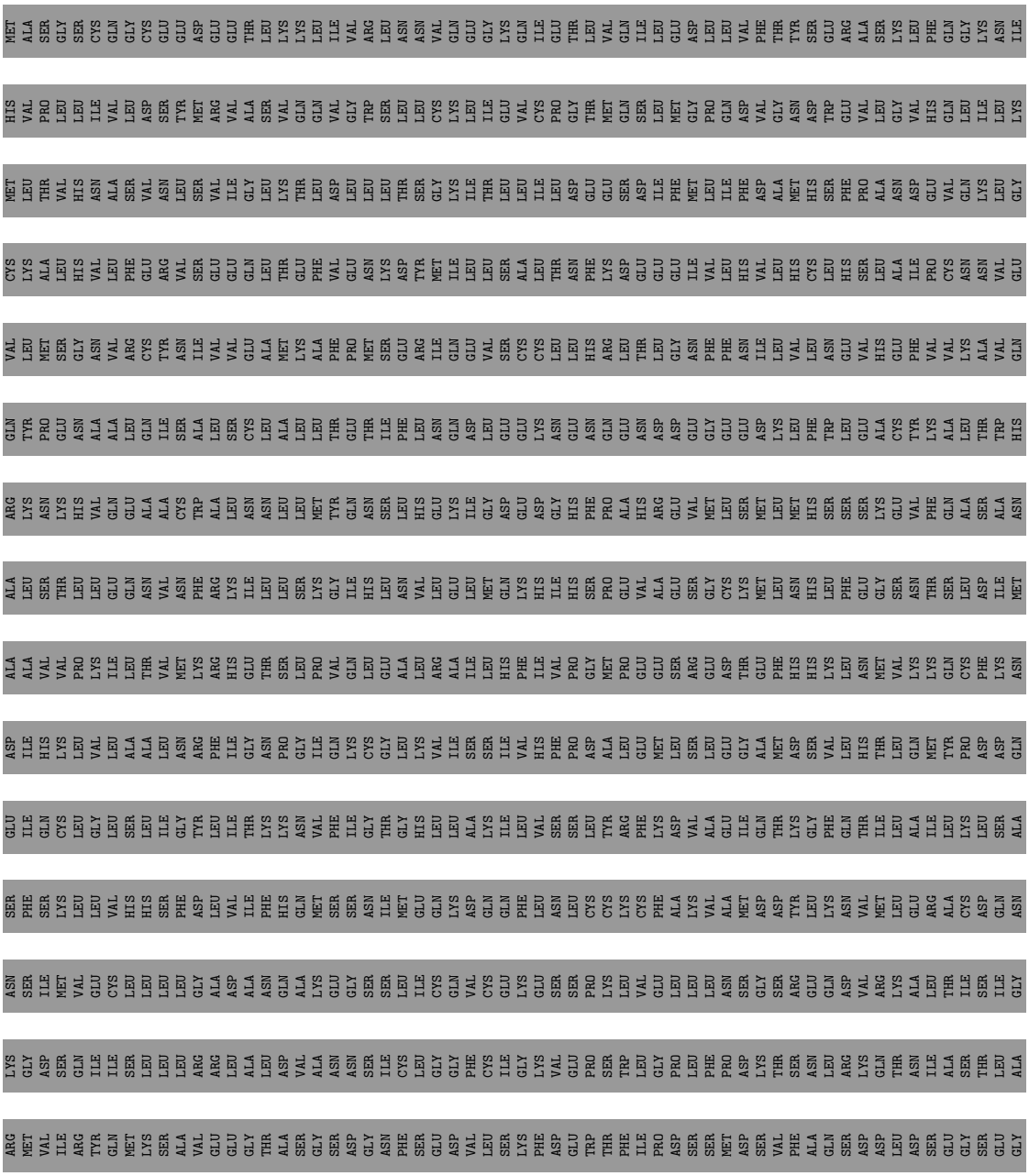


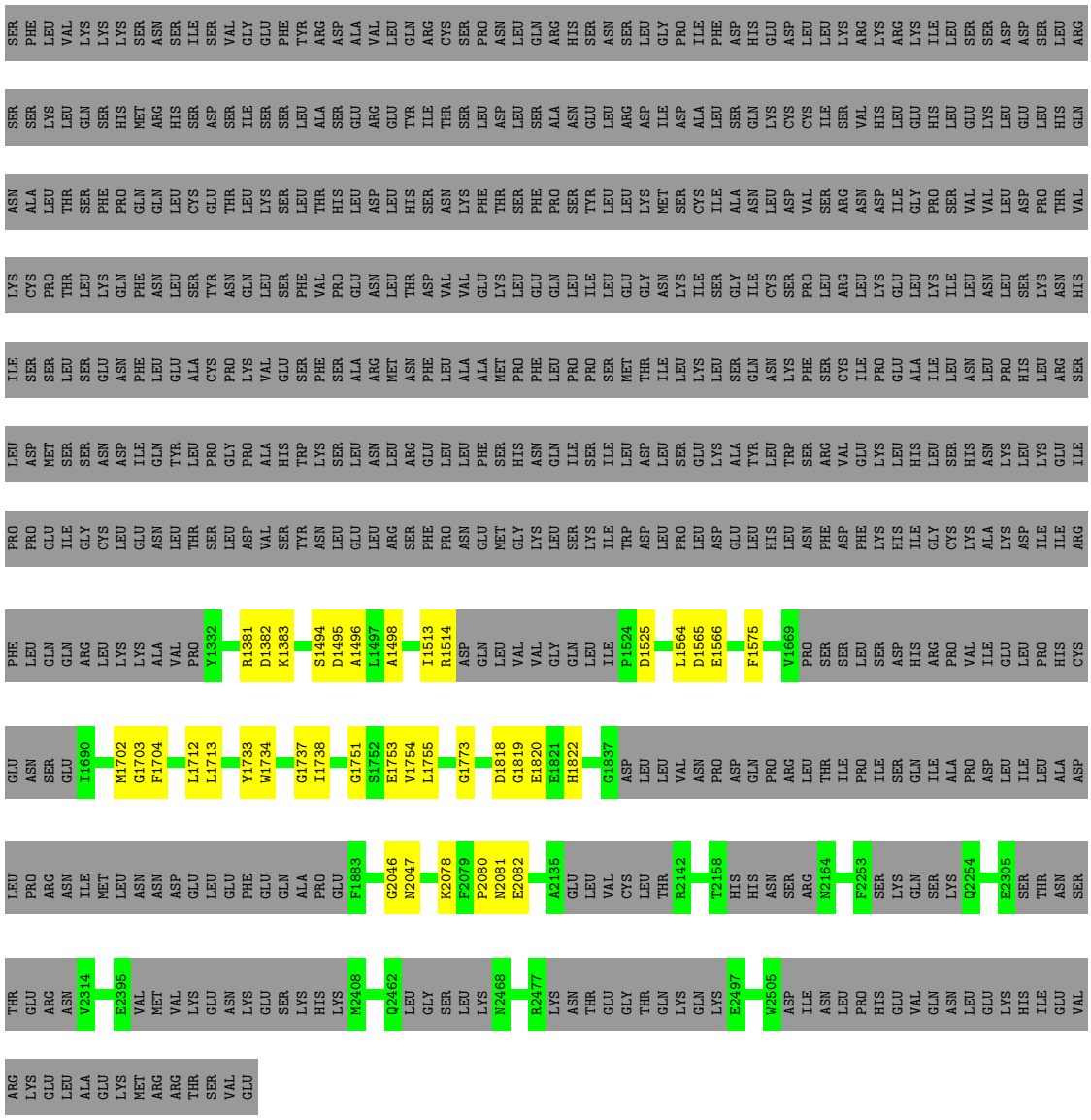
GLU	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA	ARG	GLN
ASN	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS	TYR
SER	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN	PRO
GLU	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS	GLU
I1690	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS	ASN
	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL	ALA
L1694	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN	ALA
Y1695	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU	LEU
E1696	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA	GLN
M1697	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA	ILE
P1698	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS	SER
Y1699	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP	ALA
F1700		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA	LEU
P1701	R1381	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU	SER
	D1382	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN	CYS
S1706	K1383	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN	LEU
R1707		TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU	ALA
L1708	S1494	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU	LEU
	D1495	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET	LEU
R1711	A1496	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR	THR
	L1497	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN	GLU
R1735	A1498	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN	THR
Q1736		SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER	ILE
	I1513	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU	PHE
E1753	R1514	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS	LEU
V1754	ASP	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU	ASN
L1755	GLN	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS	GLN
	LEU	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE	ASP
I1775	VAL	GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY	LEU
L1776	VAL	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP	GLU
L1777	GLY	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU	GLU
G1778	GLN	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP	LYS
	LEU	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY	ASN
D1818	ILE	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS	GLU
G1819	P1524	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE	ASN
E1820	D1525	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO	GLN
E1821		LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA	GLU
H1822	L1564	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS	ASN
	D1565	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG	ASP
G1837	E1566	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU	ASP
ASP		GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL	GLU
LEU	F1575	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET	GLY
LEU		HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU	GLU
VAL	V1669	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER	GLU
ASN	PRO	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET	ASP
PRO	SER	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU	LYS
ASP	SER	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET	LEU
GLN	LEU	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS	PHE
PRO	SER	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER	TRP
ARG	ASP	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER	LEU
LEU	HIS	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER	GLU
THR	ARG	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS	ALA
ILE	PRO	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU	CYS
PRO	VAL	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL	TYR
ILE	ILE	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE	LYS
SER	GLU	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN	ALA
GLN	LEU	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA	LEU
ILE	PRO	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER	THR
ALA	HIS	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA	TRP
PRO	CYS	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN	HIS



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

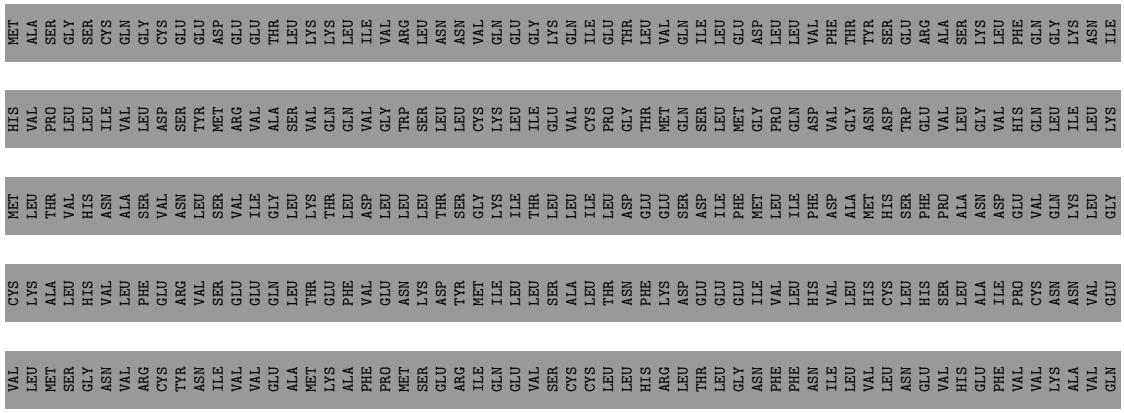
Chain 46-B: 40% • 59%



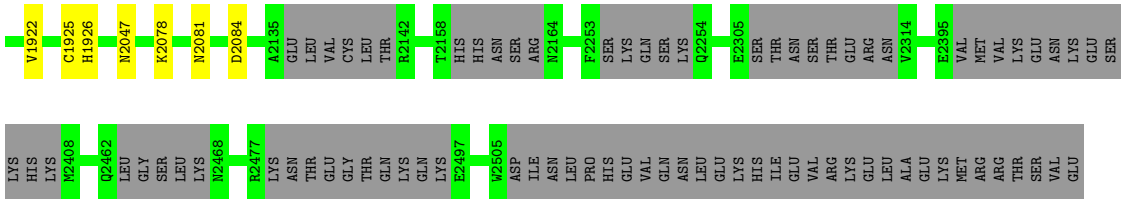


- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 47-A: 40% 59%

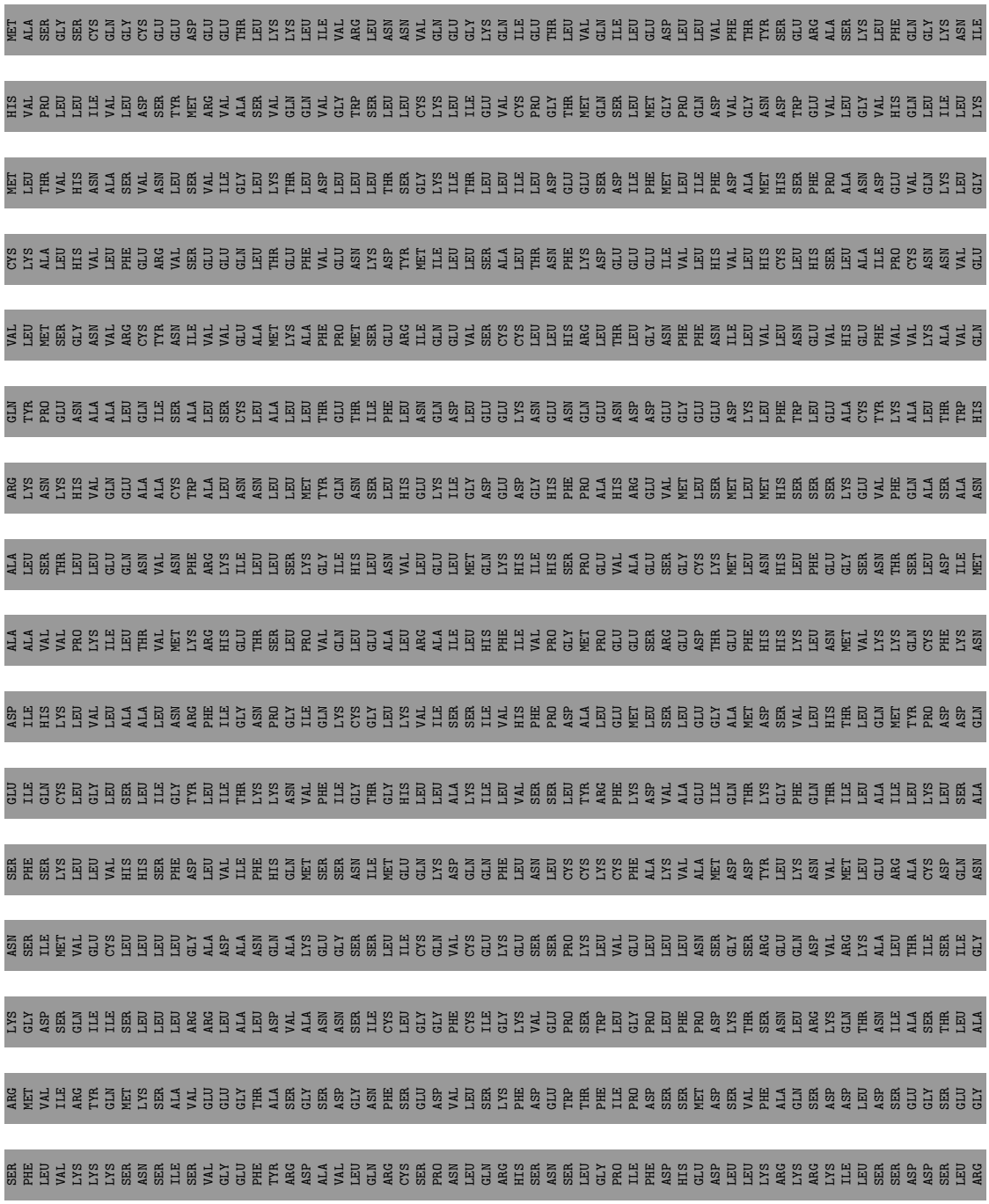


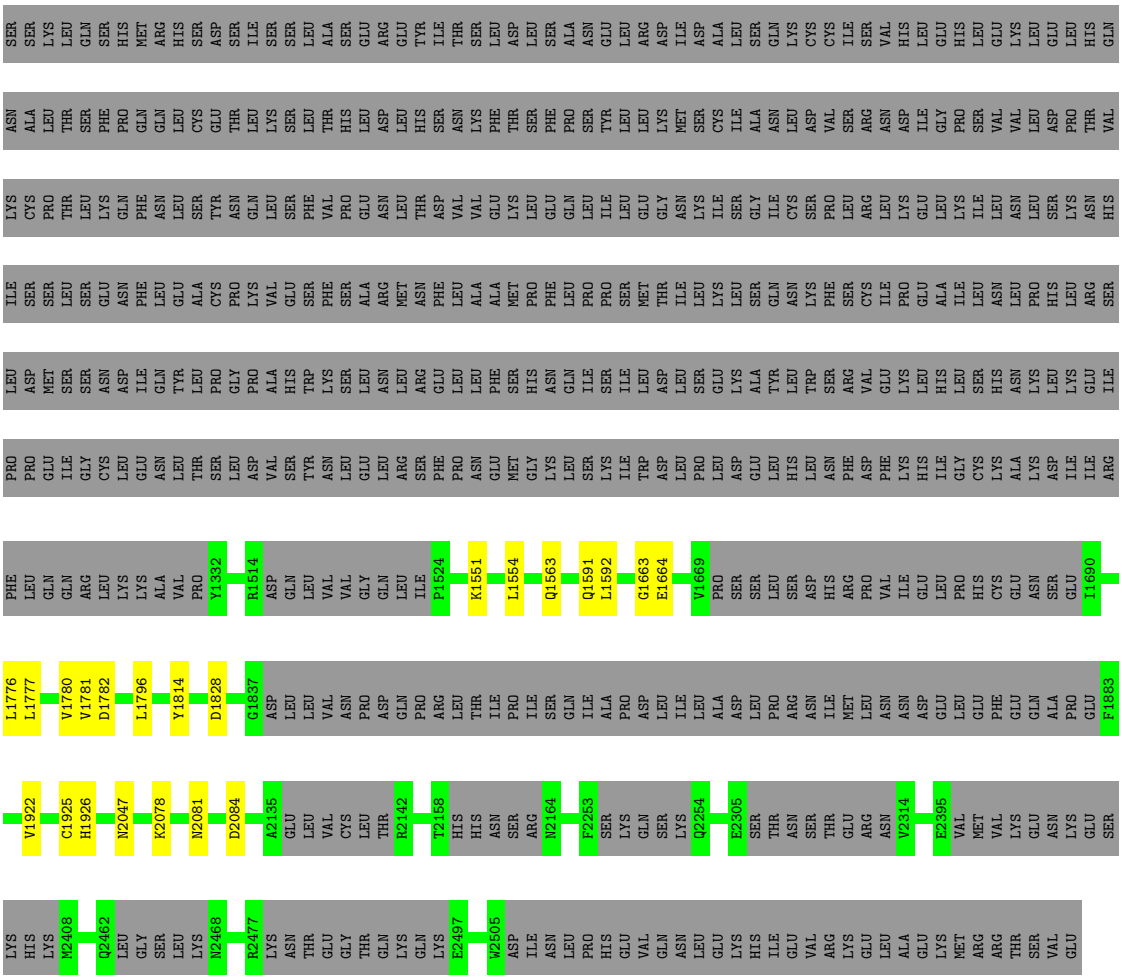
L1776	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA	ARG	GLN
L1777	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU	LYS	TYR
	GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER	ASN	PRO
V1780	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR	LYS	GLU
V1781	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU	HIS	ASN
D1782	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU	VAL	ALA
	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU	GLN	ALA
Y1814	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN	GLU	LEU
	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN	ALA	GLN
E1821	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL	ALA	ILE
	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN	CYS	SER
D1828	Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE	TRP	ALA
		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG	ALA	LEU
G1837	R1514	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS	LEU	SER
ASP	ASP	VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE	ASN	CYS
LEU	GLN	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU	ASN	LEU
LEU	LEU	TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU	LEU	ALA
VAL	VAL	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER	LEU	LEU
ASN	VAL	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS	MET	LEU
PRO	GLY	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY	TYR	THR
ASP	GLN	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE	GLN	GLU
GLN	LEU	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS	ASN	THR
PRO	ILE	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU	SER	ILE
ARG	P1524	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN	LEU	PHE
LEU		PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL	HIS	LEU
THR	K1551	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU	GLU	ASN
ILE		GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU	LYS	GLN
PRO	L1554	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU	ILE	ASP
ILE		GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET	GLY	LEU
SER	Q1563	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN	ASP	GLU
GLN		LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS	GLU	GLU
ILE	Q1591	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS	ASP	LYS
ALA	L1592	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE	GLY	ASN
PRO		ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS	HIS	GLU
ASP	G1663	TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER	PHE	ASN
LEU	E1664	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO	PRO	GLN
ILE		LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU	ALA	GLU
LEU	V1669	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL	HIS	ASN
ALA	PRO	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA	ARG	ASP
ASP	SER	ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU	GLU	ASP
LEU	SER	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER	VAL	GLU
PRO	LEU	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY	MET	GLY
ARG	SER	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS	LEU	GLU
ASN	ASP	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS	SER	GLU
ILE	HIS	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET	MET	ASP
MET	ARG	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU	LEU	LYS
LEU	PRO	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN	MET	LEU
ASN	VAL	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS	HIS	PHE
ASN	ILE	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU	SER	TRP
ASP	GLU	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE	SER	LEU
GLU	LEU	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU	SER	GLU
LEU	PRO	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY	LYS	ALA
GLU	HIS	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER	GLU	CYS
PHE	CYS	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN	VAL	TYR
GLU	GLU	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR	PHE	LYS
GLN	ASN	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER	GLN	ALA
ALA	SER	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU	ALA	LEU
PRO	GLU	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP	SER	THR
GLU	I1690	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE	ALA	TRP
F1883		ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET	ASN	HIS



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

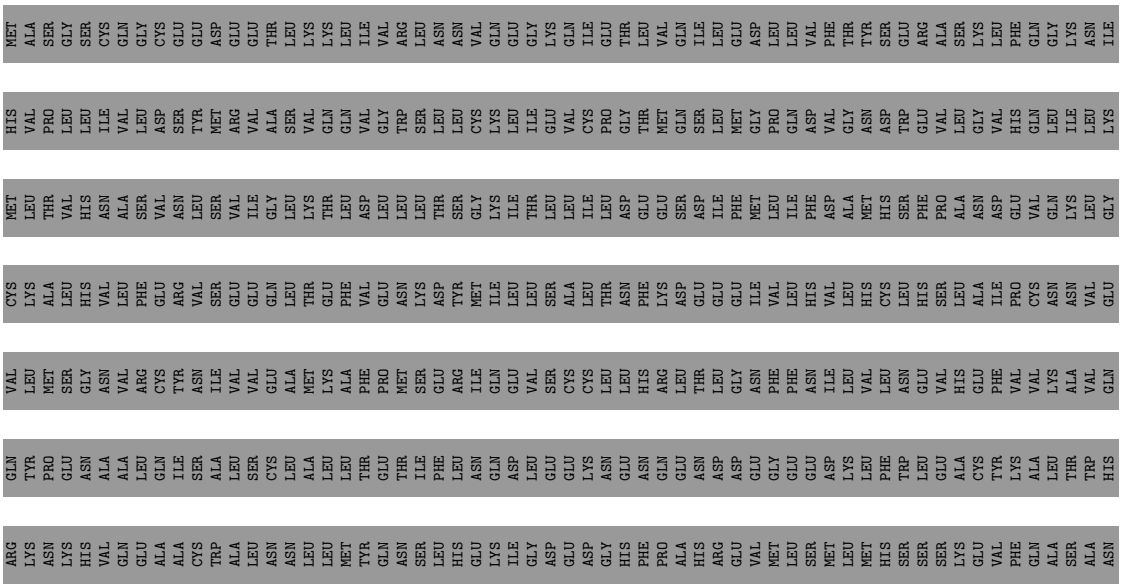
Chain 47-B: 40% • 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 48-A: 40% • 59%



GLU	ASP	GLU	PHE	PRO	LEU	ILE	LYS	ASN	SER	SER	ARG	LYS	ASN	SER	GLU	ASP	ALA	ALA
ARG	LEU	I1690	LEU	PRO	ASP	SER	CYS	ALA	SER	PHE	MET	GLY	SER	PHE	ILE	ILE	ALA	LEU
ASN	PRO		GLN	GLU	MET	SER	PRO	LEU	LYS	LEU	VAL	ASP	ILE	SER	GLN	HIS	VAL	SER
V2314	ARG	L1694	GLN	ILE	SER	LEU	THR	THR	LEU	VAL	ILE	SER	MET	LYS	CYS	LYS	VAL	THR
	ASN	Y1695	ARG	GLY	SER	SER	LEU	SER	GLN	LYS	ARG	GLN	VAL	LEU	LEU	LEU	PRO	LEU
E2395	ILE	E1696	LEU	CYS	ASN	GLU	LYS	PHE	SER	LYS	TYR	ILE	GLU	LEU	GLY	VAL	LYS	LEU
VAL	MET	M1697	LYS	LEU	ASP	ASN	GLN	PRO	HIS	LYS	GLN	ILE	CYS	VAL	LEU	LEU	ILE	GLU
MET	LEU	P1698	LYS	GLU	ILE	PHE	PHE	GLN	MET	SER	MET	SER	LEU	HIS	SER	ALA	LEU	GLN
VAL	ASN	Y1699	ALA	ASN	GLN	LEU	ASN	GLN	ARG	ASN	LYS	LEU	LEU	HIS	LEU	ALA	THR	ASN
LYS	ASN	F1700	VAL	LEU	TYR	GLU	LEU	LEU	HIS	SER	SER	LEU	LEU	SER	ILE	LEU	VAL	VAL
GLU	ASP	P1701	PRO	THR	LEU	ALA	SER	CYS	SER	ILE	ALA	LEU	LEU	PHE	GLY	ASN	MET	ASN
ASN	GLU		Y1332	SER	PRO	CYS	TYR	GLU	ASP	SER	VAL	ARG	GLY	ASP	TYR	ARG	LYS	PHE
LYS	LEU	S1706		LEU	GLY	PRO	ASN	THR	SER	VAL	GLU	ARG	ALA	LEU	LEU	PHE	ARG	ARG
GLU	GLU	R1707	K1476	ASP	PRO	LYS	GLN	LEU	ILE	GLY	GLU	LEU	ASP	VAL	ILE	ILE	HIS	LYS
SER	PHE	L1708		VAL	ALA	VAL	LEU	LYS	SER	GLU	GLY	ALA	ALA	ILE	THR	GLY	GLU	ILE
LYS	GLU		L1509	SER	HIS	GLU	SER	SER	SER	PHE	THR	LEU	ASN	PHE	LYS	ASN	THR	LEU
HIS	GLN	R1711		TYR	TRP	SER	PHE	LEU	LEU	TYR	ALA	ASP	GLN	HIS	LYS	PRO	SER	LEU
LYS	ALA		R1514	ASN	LYS	PHE	VAL	THR	ALA	ARG	SER	VAL	ALA	GLN	ASN	GLY	LEU	SER
M2408	PRO	R1735	ASP	LEU	SER	SER	PRO	HIS	SER	ASP	GLY	ALA	LYS	MET	VAL	ILE	PRO	LYS
	GLU	Q1736	GLN	GLU	LEU	ALA	GLU	LEU	GLU	ALA	SER	ASN	GLU	SER	PHE	GLN	VAL	GLY
Q2462	F1883		LEU	LEU	ASN	ARG	ASN	ASP	ARG	VAL	ASP	ASN	GLY	SER	ILE	LYS	GLN	ILE
LEU		E1753	VAL	ARG	LEU	MET	LEU	LEU	GLU	LEU	GLY	SER	SER	ASN	GLY	CYS	LEU	HIS
GLY	A2044	V1754	VAL	SER	ARG	ASN	THR	HIS	TYR	GLN	ASN	ILE	SER	ILE	THR	GLY	GLU	LEU
SER		L1755	GLY	PHE	GLU	PHE	ASP	SER	ILE	ARG	PHE	CYS	LEU	MET	GLY	LEU	ALA	ASN
LEU	K2078		GLN	PRO	LEU	LEU	VAL	ASN	THR	CYS	SER	LEU	ILE	GLU	HIS	LYS	LEU	VAL
LYS	F2079	I1775	LEU	ASN	LEU	ALA	VAL	LYS	SER	SER	GLU	GLY	CYS	GLN	LEU	VAL	ARG	LEU
N2468	P2080	L1776	ILE	GLU	PHE	ALA	GLU	PHE	LEU	PRO	ASP	GLY	GLN	LYS	LEU	ILE	ALA	GLU
	N2081	L1777	P1524	MET	SER	MET	LYS	THR	ASP	ASN	VAL	PHE	VAL	ASP	ALA	SER	ILE	LEU
R2477		G1778		GLY	HIS	PRO	LEU	SER	LEU	LEU	LEU	CYS	CYS	GLN	LYS	SER	LEU	MET
LYS	A2135		N1567	LYS	ASN	PHE	GLU	PHE	SER	GLN	SER	ILE	GLU	GLN	ILE	ILE	HIS	GLN
ASN	GLU	A1812	E1568	LEU	GLN	LEU	GLN	PRO	ALA	ARG	LYS	GLY	LYS	PHE	LEU	VAL	PHE	LYS
THR	LEU		L1569	SER	ILE	PRO	LEU	SER	ASN	HIS	PHE	LYS	GLU	LEU	VAL	HIS	ILE	HIS
GLU	VAL	E1821	P1570	LYS	SER	PRO	ILE	TYR	GLU	SER	ASP	VAL	SER	ASN	SER	PHE	VAL	ILE
GLY	CYS		H1571	ILE	ILE	SER	LEU	LEU	LEU	ASN	GLU	GLU	SER	LEU	SER	PRO	PRO	HIS
THR	LEU	G1837		TRP	LEU	MET	GLU	LEU	ARG	SER	TRP	PRO	PRO	CYS	LEU	ASP	GLY	SER
GLN	THR	ASP	H1574	ASP	ASP	THR	GLY	LYS	ASP	LEU	THR	SER	LYS	CYS	TYR	ALA	MET	PRO
LYS	R2142	LEU		LEU	LEU	ILE	ASN	MET	ILE	GLY	PHE	TRP	LEU	LYS	ARG	LEU	PRO	GLU
GLN		LEU	E1599	PRO	SER	LEU	LYS	SER	ASP	PRO	ILE	LEU	VAL	CYS	PHE	GLU	GLU	VAL
LYS	T2158	VAL	P1600	LEU	GLU	LYS	ILE	CYS	ALA	ILE	PRO	GLY	GLU	PHE	LYS	MET	GLU	ALA
E2497	HIS	ASN		ASP	LYS	LEU	SER	ILE	LEU	PHE	ASP	PRO	LEU	ALA	ASP	LEU	SER	GLU
	HIS	PRO	V1669	GLU	ALA	SER	GLY	ALA	SER	ASP	SER	LEU	LEU	LYS	VAL	SER	ARG	SER
W2505	ASN	ASP	PRO	LEU	TYR	GLN	ILE	ASN	GLN	HIS	SER	PHE	LEU	VAL	ALA	LEU	GLU	GLY
ASP	SER	GLN	SER	HIS	LEU	ASN	CYS	LEU	LYS	GLU	MET	PRO	ASN	ALA	GLU	GLU	ASP	CYS
ILE	ARG	PRO	SER	LEU	TRP	LYS	SER	ASP	CYS	ASP	ASP	ASP	SER	MET	ILE	GLY	THR	LYS
ASN	N2164	ARG	LEU	ASN	SER	PHE	PRO	VAL	CYS	LEU	SER	LYS	GLY	ASP	GLN	ALA	GLU	MET
LEU		LEU	SER	PHE	ARG	SER	LEU	SER	ILE	LEU	VAL	THR	SER	ASP	THR	MET	PHE	LEU
PRO	F2253	THR	ASP	ASP	VAL	CYS	ARG	ARG	SER	LYS	PHE	SER	ARG	TYR	LYS	ASP	HIS	ASN
HIS	SER	ILE	HIS	PHE	GLU	ILE	LEU	ASN	VAL	ARG	ALA	ASN	GLU	LEU	GLY	SER	HIS	HIS
GLU	LYS	PRO	ARG	LYS	LYS	PRO	LYS	ASP	HIS	LYS	GLN	LEU	GLN	LYS	PHE	VAL	LYS	LEU
VAL	GLN	ILE	PRO	HIS	LEU	GLU	GLU	ILE	LEU	ARG	SER	ARG	ASP	ASN	GLN	LEU	LEU	PHE
GLN	SER	SER	VAL	ILE	HIS	ALA	LEU	GLY	GLU	LYS	ASP	LYS	VAL	VAL	THR	HIS	ASN	GLU
ASN	LYS	GLN	ILE	GLY	LEU	ILE	LYS	PRO	HIS	ILE	ASP	GLN	ARG	MET	ILE	THR	MET	GLY
LEU	Q2254	ILE	GLU	CYS	SER	LEU	ILE	SER	LEU	LEU	LEU	THR	LYS	LEU	LEU	LEU	VAL	SER
GLU		ALA	LEU	LYS	HIS	ASN	LEU	VAL	GLU	SER	ASP	ASN	ALA	GLU	ALA	GLN	LYS	ASN
LYS	E2305	PRO	PRO	ALA	ASN	LEU	ASN	VAL	LYS	SER	SER	ILE	LEU	ARG	ILE	MET	LYS	THR
HIS	SER	ASP	HIS	LYS	LYS	PRO	LEU	LEU	LEU	ASP	GLU	ALA	THR	ALA	LEU	TYR	GLN	SER
ILE	THR	LEU	CYS	ASP	LEU	HIS	SER	ASP	GLU	ASP	GLY	SER	ILE	CYS	LYS	PRO	CYS	LEU
GLU	ASN	ILE	GLU	ILE	LYS	LEU	LYS	PRO	LEU	SER	SER	THR	SER	ASP	LEU	ASP	PHE	ASP
VAL	SER	LEU	ASN	ILE	GLU	ARG	ASN	THR	HIS	LEU	GLU	LEU	ILE	GLN	SER	ASP	LYS	ILE
ARG	THR	ALA	SER	ARG	ILE	SER	HIS	VAL	GLN	ARG	GLY	ALA	GLY	ASN	ALA	GLN	ASN	MET

LYS GLU LEU ALA GLU LYS MET ARG ARG THR SER VAL GLU

- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 48-B: 40% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU LEU LEU GLU LEU VAL HIS GLN ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR THR SER LEU PRO VAL GLN LEU GLU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO GLY MET LEU SER LEU GLU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU LEU ALA LYS ILE LEU VAL SER SER LEU PHE LYS ASP VAL ALA GLU ILE GLN THR THR LYS GLY PHE GLN THR LEU ILE LEU ALA ILE LEU LYS LEU SER SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN GLU ILE MET GLU GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU LEU GLN GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

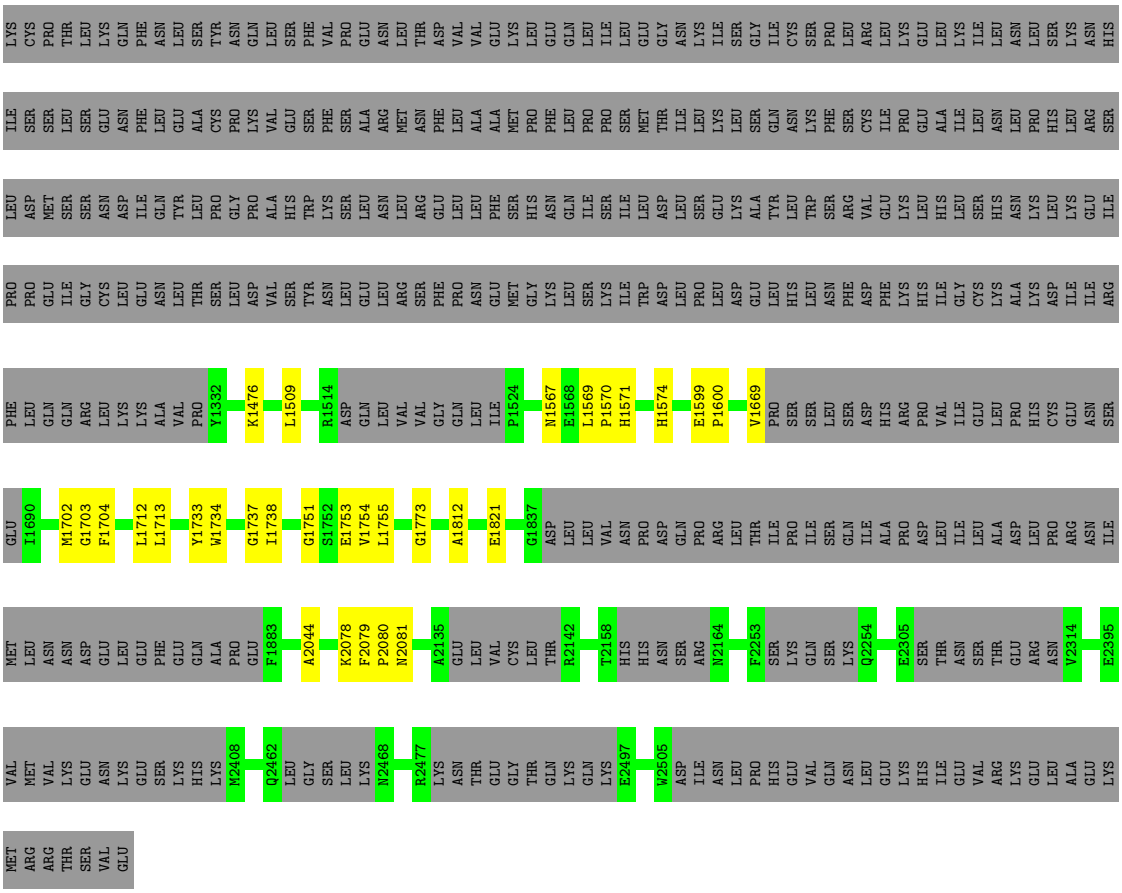
LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU LEU GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN GLU LEU ARG LYS GLN THR ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN GLN ARG CYS SER PRO ASN LEU LEU GLN ARG HIS SER ASN SER LEU GLY PHE HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

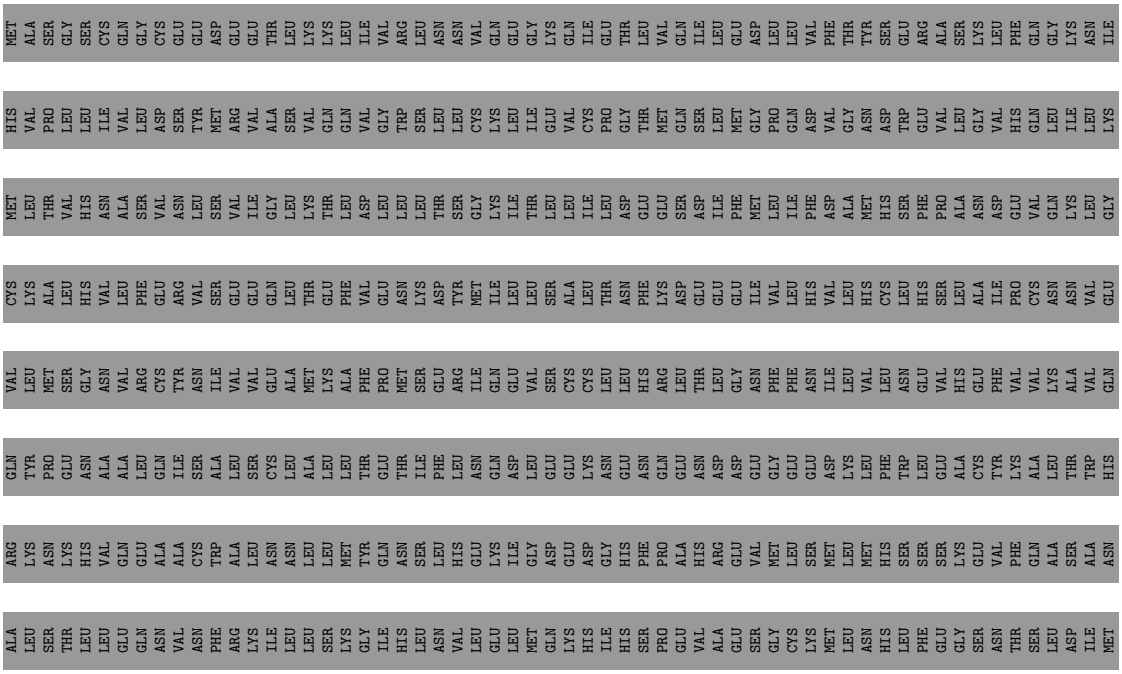
SER SER LYS LEU GLN ILE SER SER LEU ARG HIS SER ASP SER ILE SER SER LEU ALA ILE THR SER LEU ASP LEU SER SER VAL GLU GLU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU LEU GLU LYS LEU LEU GLY

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU THR HIS LEU ASP VAL SER ARG ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO VAL THR



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 49-A: 40% 59%



ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN
ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU VAL LEU HIS LYS LEU ARG THR LYS GLY PHE GLN THR ILE LEU LEU GLN MET ASP SER VAL LEU HIS THR LEU LEU GLN GLN ASN
GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR HIS LEU LEU ILE LEU ILE LYS ASP GLN GLN PHE LEU ASN LEU LEU GLN THR ILE LEU ALA ILE LEU LYS CYS PHE LYS ASP GLN ASN
SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN VAL MET LEU GLU ARG LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL LEU GLY PHE GLN THR ILE LEU LEU GLU ARG ALA CYS ASP GLN ASN
ASN SER ILE MET VAL GLU CYS LEU LEU SER LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS ASN GLU GLY SER SER ILE LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER LEU LEU LEU LEU GLY LYS VAL GLU LEU LEU ASN SER GLY SER GLN GLN PHE LEU ASP VAL GLU LEU GLU ARG ALA ILE SER ILE LEU GLY
LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU LEU ARG ARG LEU ALA LEU LEU ASP VAL ALA ASN ASN SER ILE CYS LEU LEU GLY GLY PHE PHE CYS CYS ILE GLY LYS VAL GLN PRO PRO SER TRP LEU GLY PRO LEU LEU PHE PRO ASP LYS THR SER GLN GLN ASP VAL ARG LYS GLN THR ASN ASN ILE ALA SER THR ILE LEU ALA
ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP TRP THR PHE ILE PRO ASP SER LEU LYS ASP ASP VAL PHE ALA GLN SER ASP ARG LYS THR SER GLU GLU GLY SER GLU GLU GLY
SER PHE LEU VAL LYS LYS LYS SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER LEU LEU ASP PHE PHE ASP HIS GLU SER LYS LEU LEU LYS ARG LYS LYS SER SER LEU LEU ARG
SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU LEU SER ALA ASN GLU ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU LEU GLU GLU LYS LEU LEU GLN HIS GLN
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL LEU LEU VAL PRO THR VAL
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU LEU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU LEU ARG LEU LYS LYS LEU LEU ASN LEU ASN HIS
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE SER LEU LEU ASN LYS PHE SER CYS ILE LEU ILE LEU ARG SER
LEU ASP MET SER SER SER ASN ASP ILE GLN TYR GLU LEU PRO GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG GLU LEU LEU PHE SER HIS ASN GLN ILE SER ILE LEU LYS SER SER GLU LYS ALA TYR LEU TRP SER ARG VAL GLU LYS LEU LEU ASN LYS LEU HIS LYS LEU ILE ILE
PRO PRO GLU ILE GLY CYS LEU LEU GLU ASN LEU THR SER LEU ASP VAL SER TYR ASN LEU LEU ARG SER PHE PRO ASN GLU MET GLY LYS LEU SER LYS ILE THR ASP ASP GLU LEU HIS LEU ASN PHE ASP PHE LYS LYS LEU ASP LYS ILE ILE ARG
PHE LEU GLN GLN ARG LEU LYS LYS ALA VAL PRO Y1332 Q1353 A1367 T1368 V1369 G1370 D1455 N1489 A1490 T1491 E1492 E1493 S1494 R1514 ASP GLN LEU VAL VAL GLY GLN LEU ILE P1524 D1565 E1566 N1567 E1568 L1569 P1570 L1576 N1577 E1578 S1579 G1580 V1581 L1582 L1583 L1590 Q1591
P1600 I1658 V1669 PRO SER SER LEU SER ASP HIS ARG PRO VAL ILE GLU LEU PRO HIS CYS GLU ASN SER GLU I1690 K1764 L1776 G1794 K1810 K1832 G1837 ASP LEU LEU VAL ASN PRO ASP GLN PRO ARG LEU THR ILE PRO ILE SER GLN GLN LEU ALA PRO ASP LEU
ILE LEU ALA ASP LEU PRO ARG ASN ILE MET LEU ASN ASP GLU ILE GLN ALA PRO GLU F1883 V1922 A2044 L2077 K2078 F2079 P2080 E2117 N2118 A2135 GLU LEU VAL CYS LEU THR R2142 T2158 HIS HIS ASN SER ARG N2164 F2253 SER LYS GLN SER LYS
Q2254 E2305 SER THR ASN SER THR GLU ARG ASN V2314 E2395 VAL MET VAL LYS GLU ASN LYS GLU SER LYS HIS LYS M2408 Q2462 LEU GLY SER LEU LYS N2468 R2477 LYS ASN THR GLU GLY THR GLN LYS GLN LYS E2497 W2505 ASP ILE ASN LEU PRO HIS GLU VAL GLN ASN
LEU GLU LYS HIS ILE GLU VAL ARG LYS GLU LEU ALA GLU LYS MET ARG ARG THR SER VAL GLU

• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 49-B: 40% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

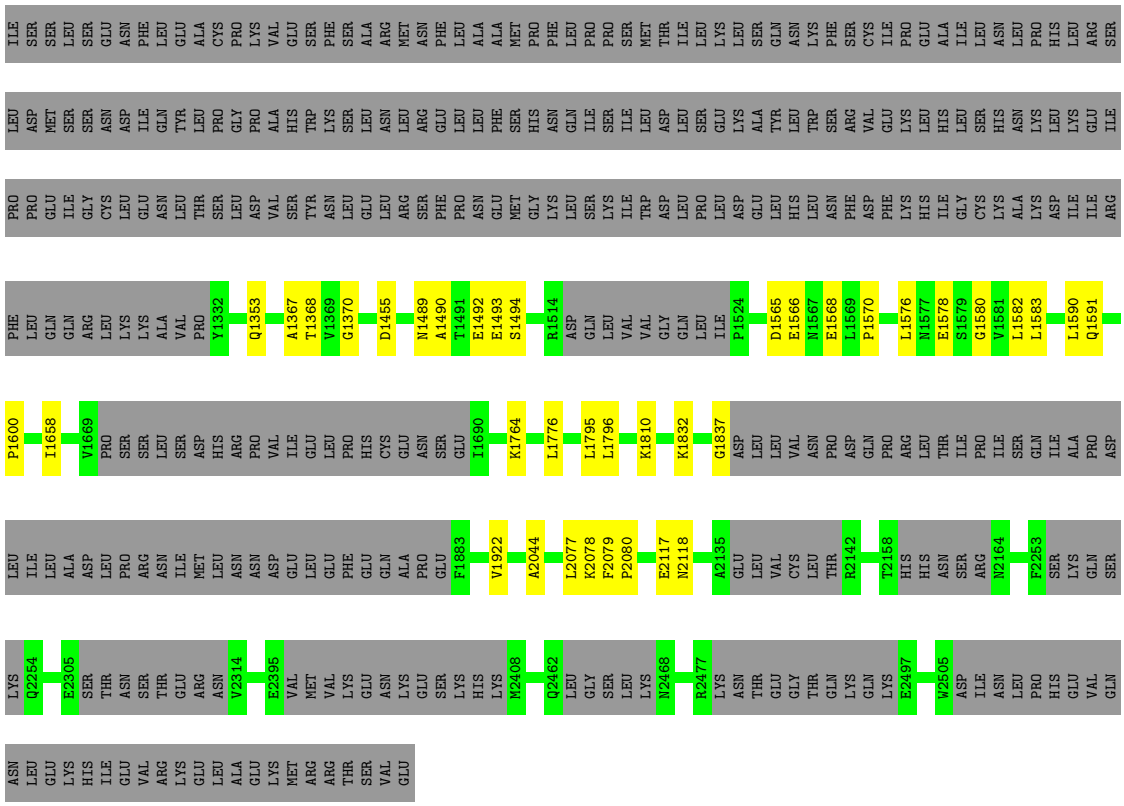
ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

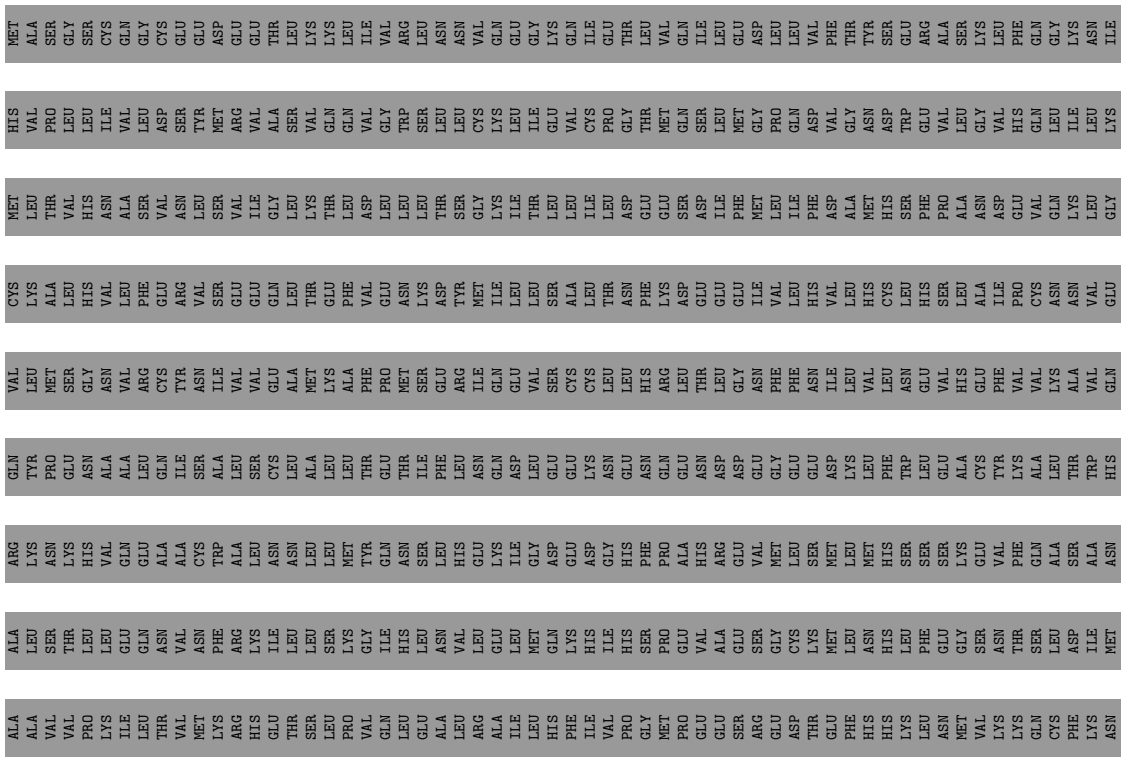
ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

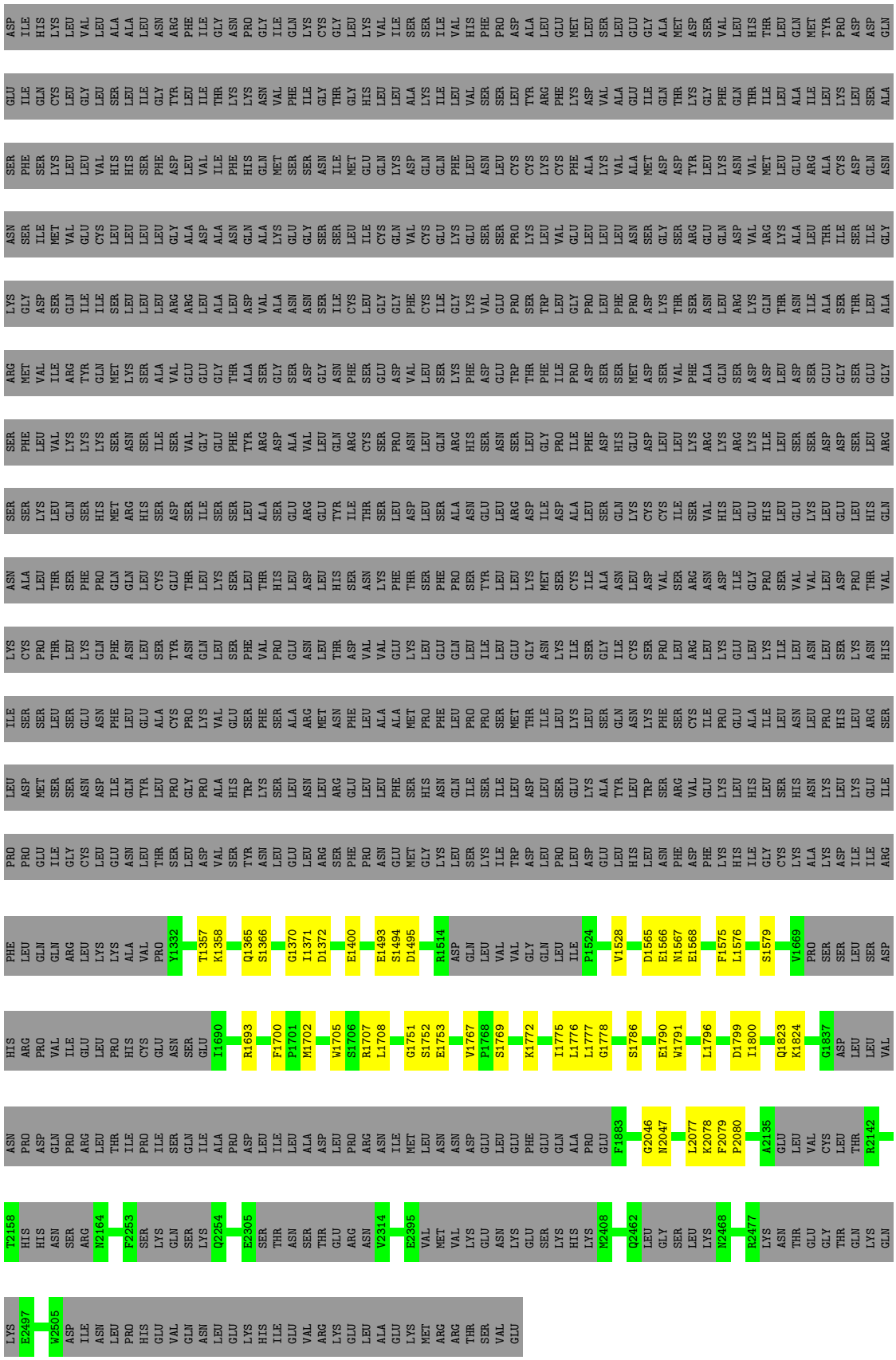
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 50-A: 39% 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 50-B:

39% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLN GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

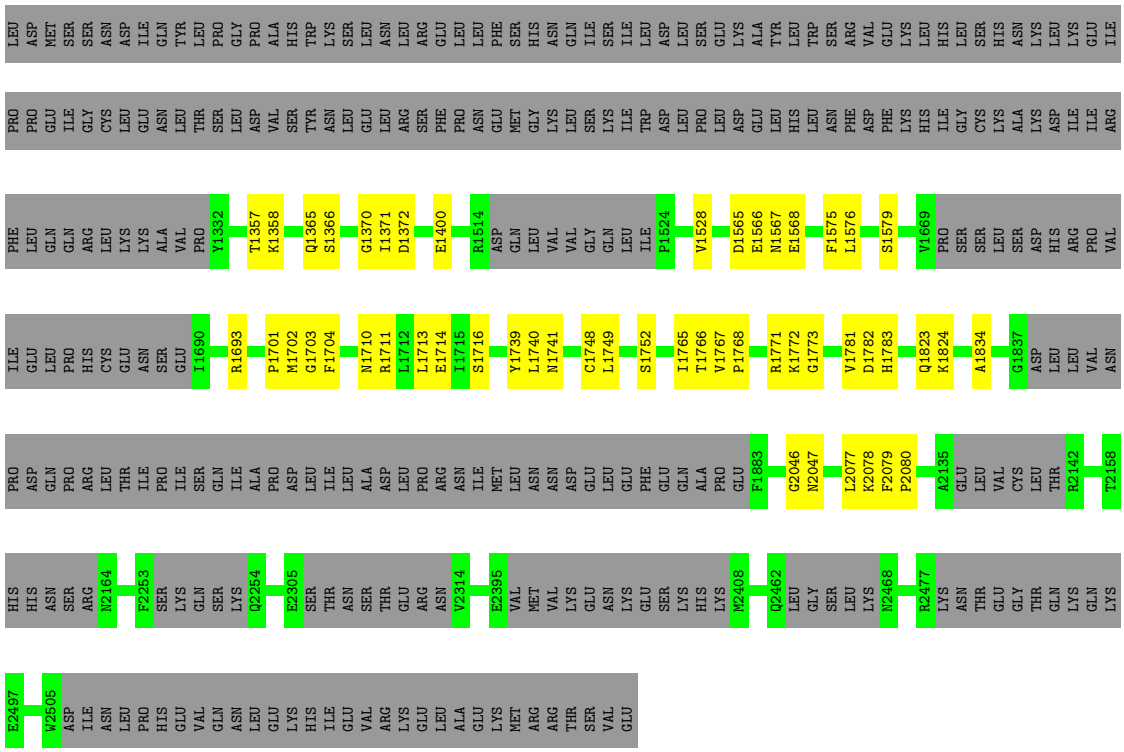
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

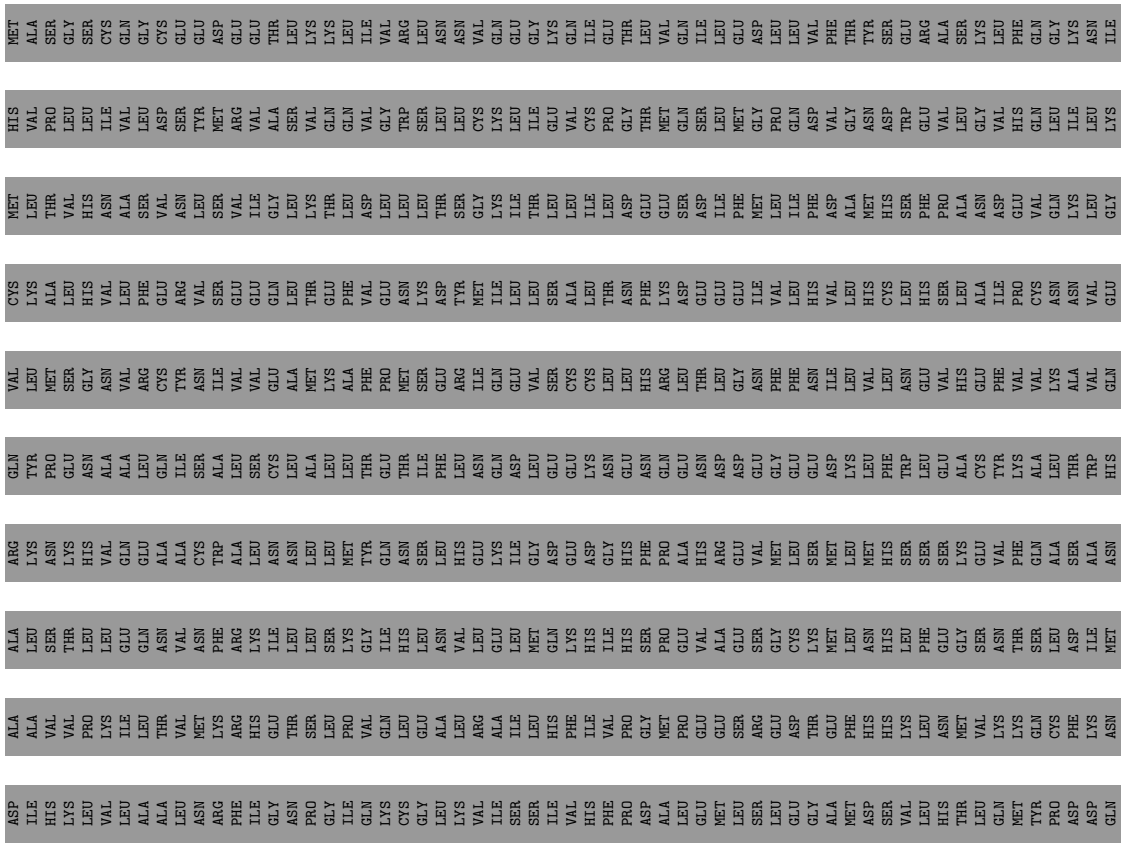
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

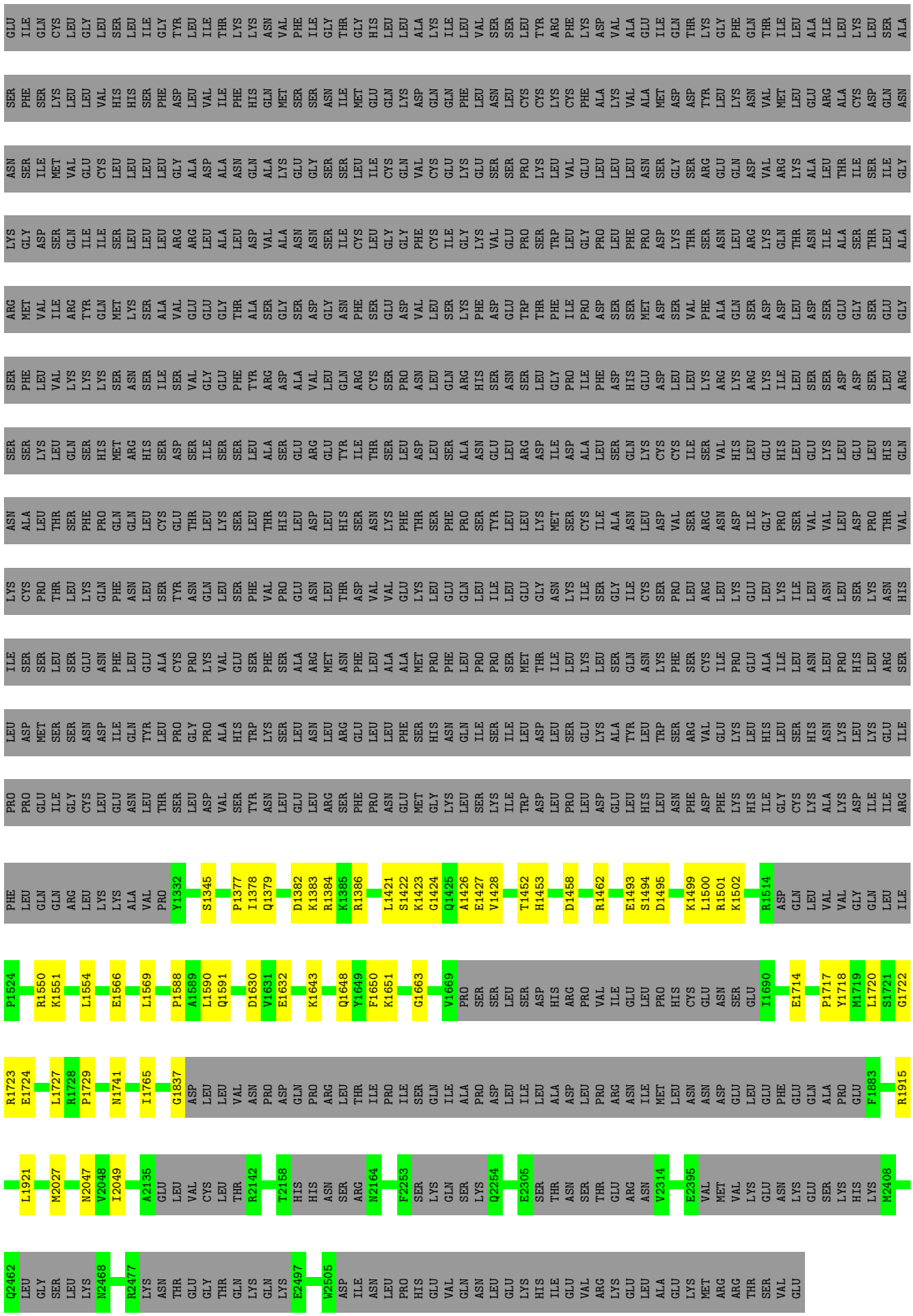
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 51-A:





• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 51-B: 39% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLN GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

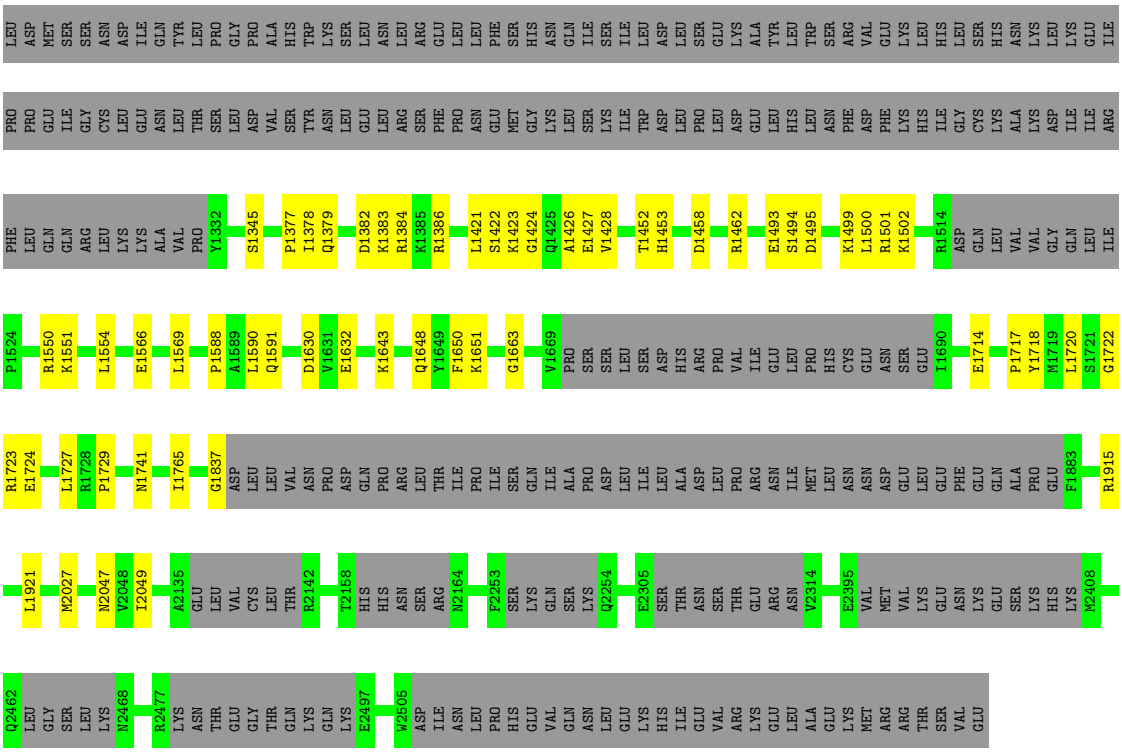
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

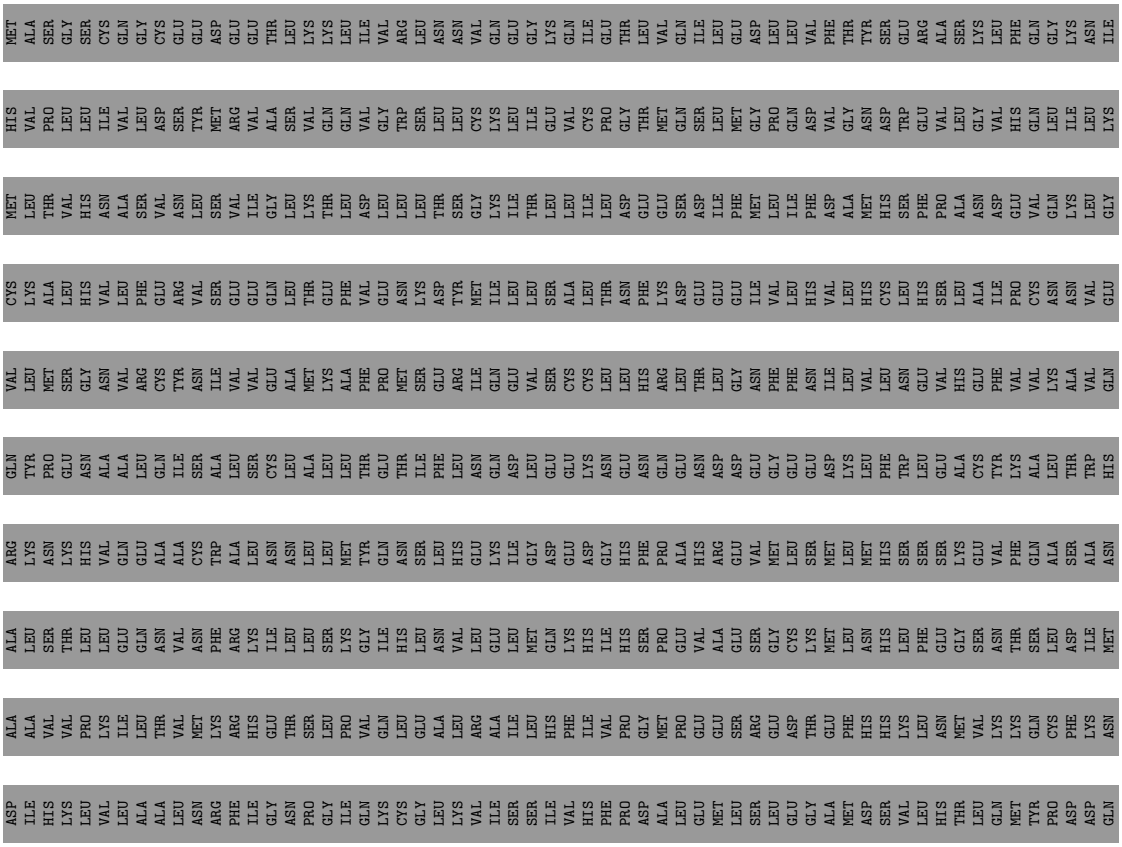
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

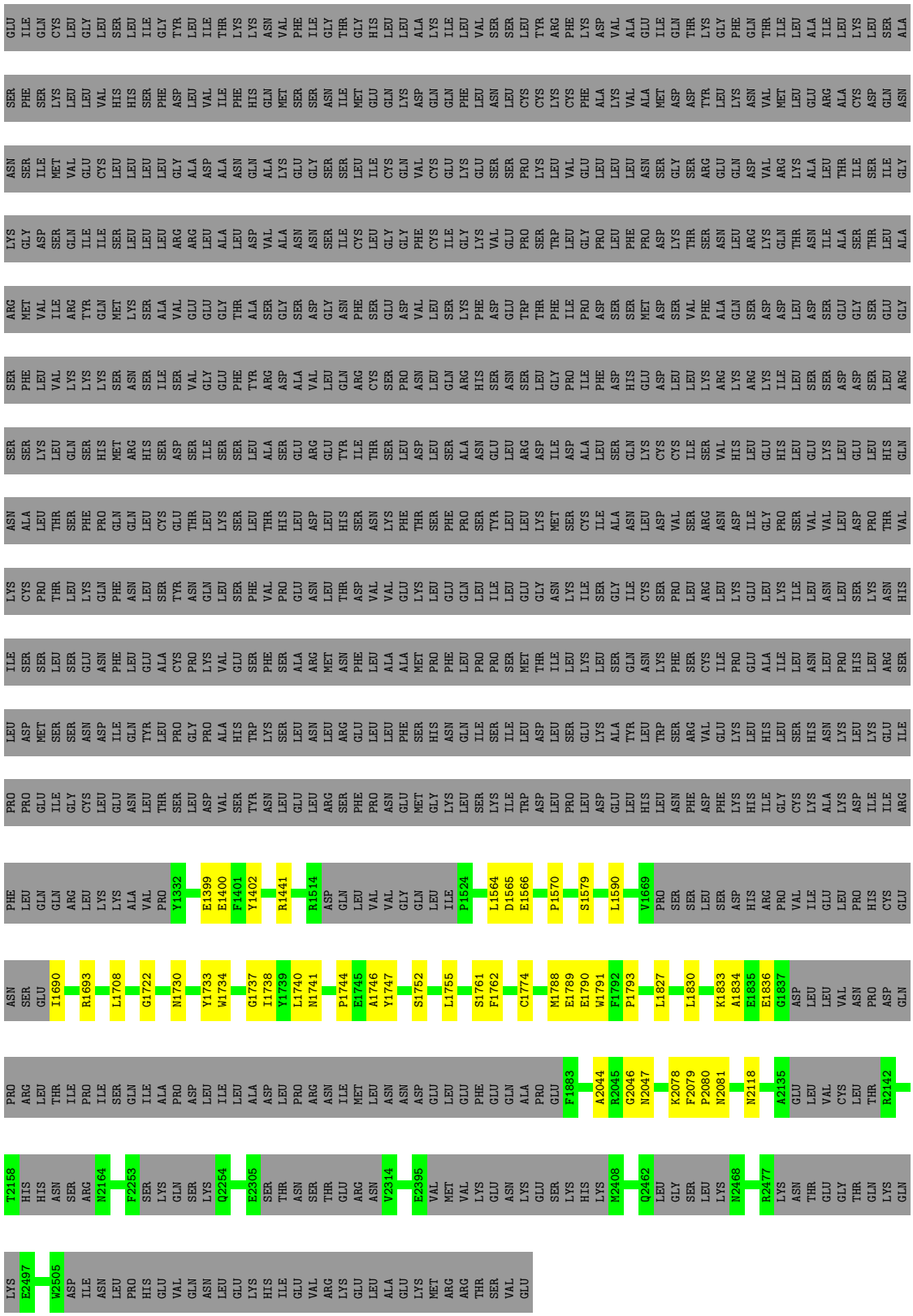
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER



• Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 52-A: 39% • 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 52-B: 39% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

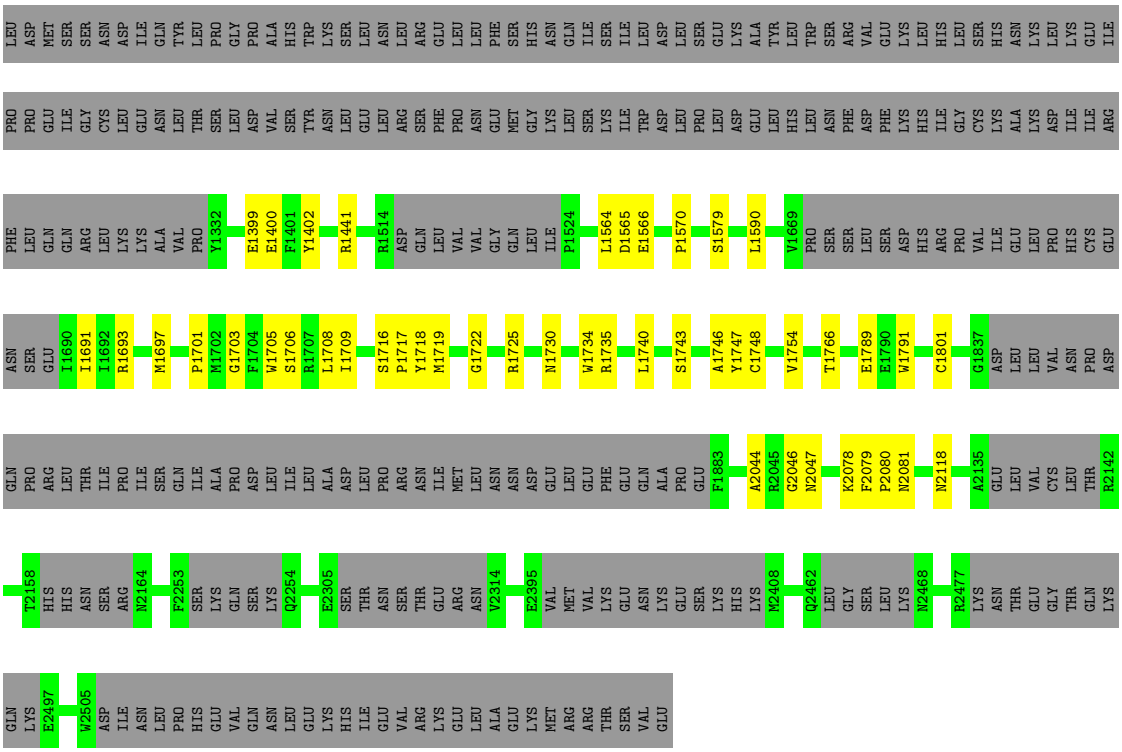
SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

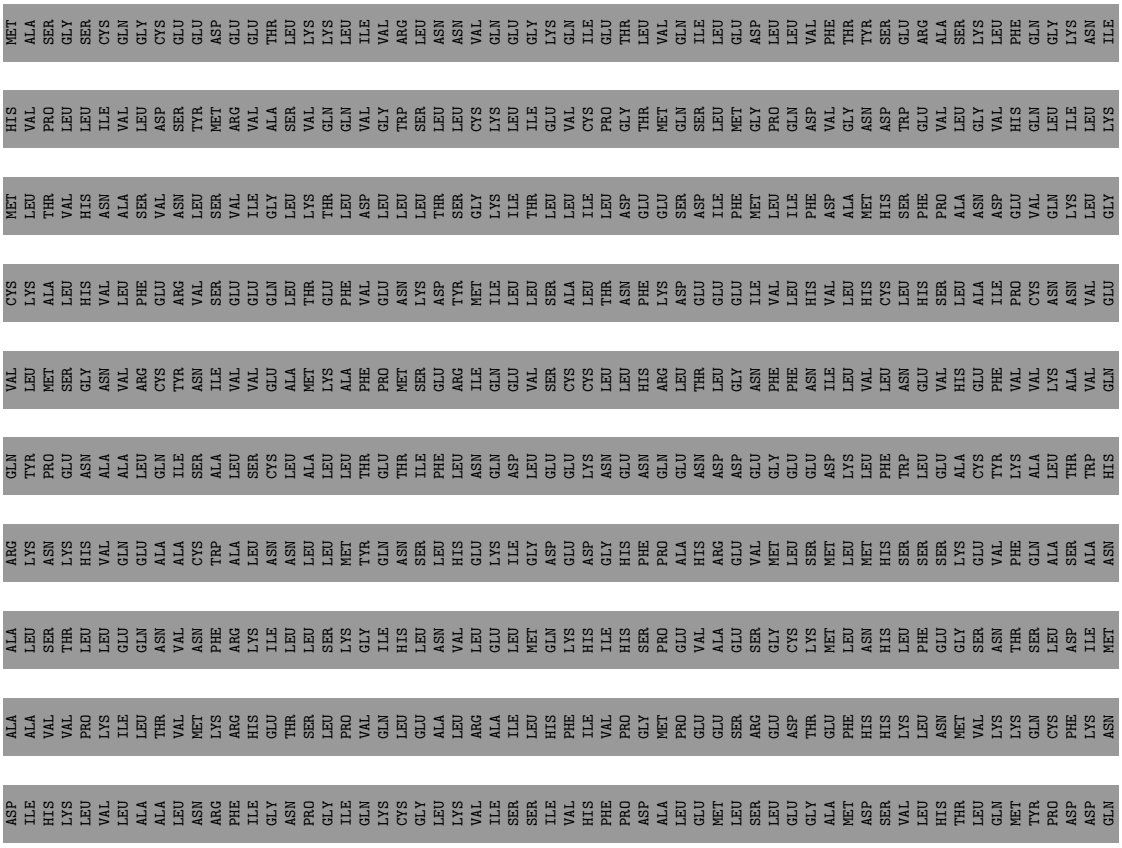
LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

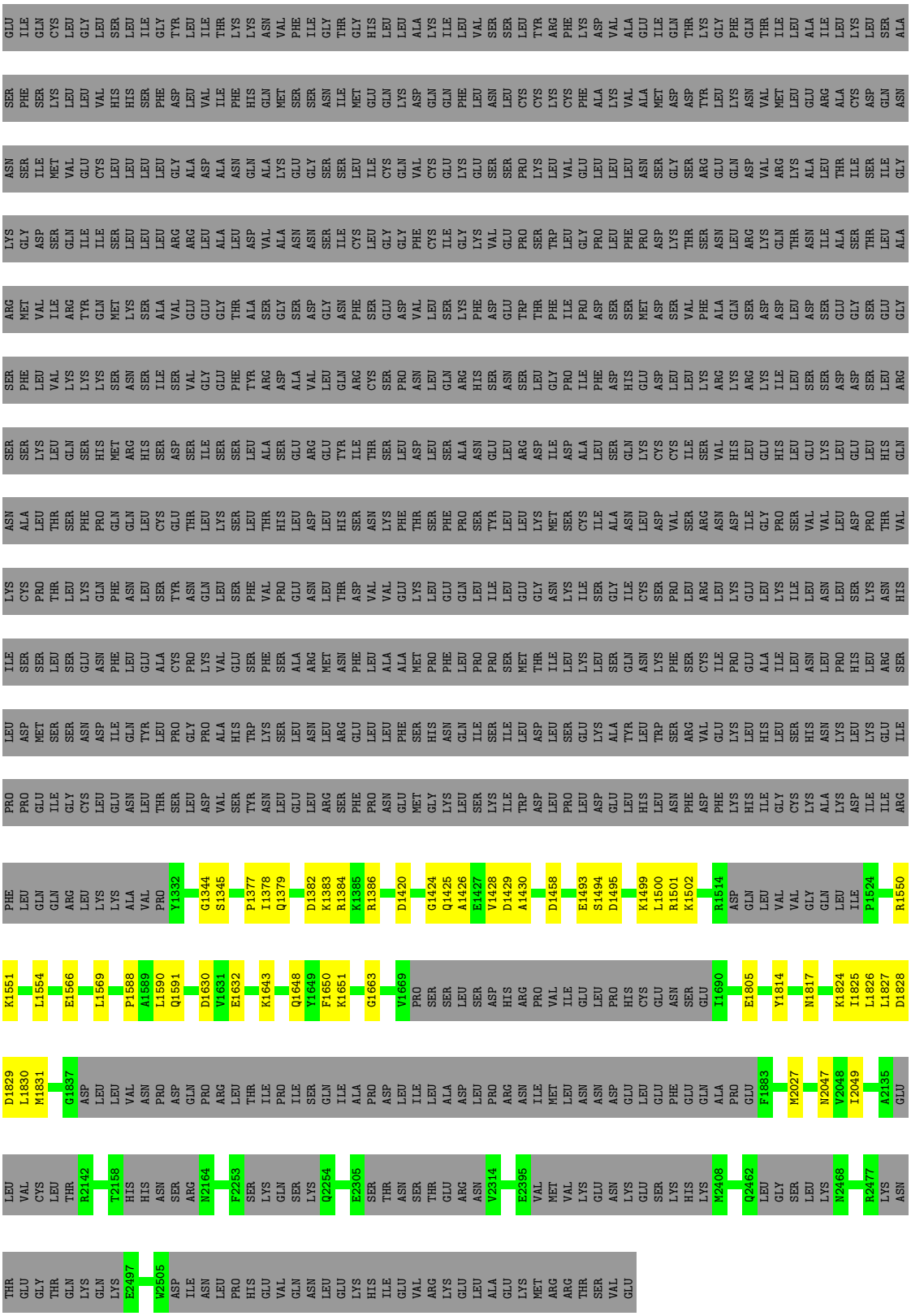
ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER



- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 53-A: 39% • 59%





- Molecule 1: Leucine-rich repeat serine/threonine-protein kinase 2

Chain 53-B: 39% • 59%

MET ALA SER GLY SER CYS GLN GLY CYS GLU GLU ASP GLU GLU THR LEU LYS LYS LEU ILE VAL ARG LEU ASN ASN VAL GLN GLU GLY LYS GLN ILE GLU THR LEU VAL GLN ILE LEU GLU ASP LEU LEU VAL PHE THR TYR SER GLU ARG ALA SER LYS LEU PHE GLN GLY LYS ASN ILE

HIS VAL PRO LEU LEU ILE VAL LEU ASP SER TYR MET ARG VAL ALA SER VAL GLN GLN VAL GLY TRP SER LEU LEU CYS LYS LEU ILE GLU VAL CYS PRO GLY THR MET GLN SER LEU MET GLY PRO GLN ASP VAL GLY ASN ASP TRP GLU VAL LEU GLY VAL HIS GLN LEU ILE LEU LYS

MET LEU THR VAL HIS ASN ALA SER VAL ASN LEU SER VAL ILE GLY LEU LYS THR LEU ASP LEU LEU LEU THR SER GLY LYS ILE THR LEU LEU ILE LEU ASP GLU GLU SER ASP ILE PHE MET LEU ILE PHE ASP ALA MET HIS SER PHE PRO ALA ASN ASP GLU VAL GLN LYS LEU GLY

CYS LYS ALA LEU HIS VAL LEU PHE GLU ARG VAL SER GLU GLU GLN LEU THR GLU PHE VAL GLU ASN LYS ASP TYR MET ILE LEU LEU SER ALA LEU THR ASN PHE LYS ASP GLU GLU GLU ILE VAL LEU HIS VAL LEU HIS CYS LEU HIS SER LEU ALA ILE PRO CYS ASN ASN VAL GLU

VAL LEU MET SER GLY ASN VAL ARG CYS TYR ASN ILE VAL VAL GLU ALA MET LYS ALA PHE PRO MET SER GLU ARG ILE GLN GLU VAL SER CYS CYS LEU LEU HIS ARG LEU THR LEU GLY ASN PHE PHE ASN ILE LEU VAL LEU ASN GLU VAL HIS GLU PHE VAL VAL LYS ALA VAL GLN

GLN TYR PRO GLU ASN ALA ALA LEU GLN ILE SER ALA LEU SER CYS LEU ALA LEU LEU THR GLU THR ILE PHE LEU ASN GLN ASP LEU GLU GLU LYS ASN GLU ASN GLN GLU ASN ASP ASP GLU GLY GLU GLU ASP LYS LEU PHE TRP LEU GLU ALA CYS TYR LYS ALA LEU THR TRP HIS

ARG LYS ASN LYS HIS VAL GLN GLU ALA ALA CYS TRP ALA LEU ASN ASN LEU LEU MET TYR GLN ASN SER LEU HIS GLU LYS ILE GLY ASP GLU ASP GLY HIS PHE PRO ALA HIS ARG GLU VAL MET LEU SER MET LEU MET HIS SER SER SER LYS GLU VAL PHE GLN ALA SER ALA ASN

ALA LEU SER THR LEU LEU GLU GLN ASN VAL ASN PHE ARG LYS ILE LEU LEU SER LYS GLY ILE HIS LEU ASN VAL LEU GLU LEU MET GLN LYS HIS ILE HIS SER PRO GLU VAL ALA GLU SER GLY CYS LYS MET LEU ASN HIS LEU PHE GLU GLY SER ASN THR SER LEU ASP ILE MET

ALA ALA VAL VAL PRO LYS ILE LEU THR VAL MET LYS ARG HIS GLU THR SER LEU PRO VAL GLN LEU GLU ALA LEU ARG ALA ILE LEU HIS PHE ILE VAL PRO GLY MET PRO GLU GLU SER ARG GLU ASP THR GLU PHE HIS HIS LYS LEU ASN MET VAL LYS LYS GLN CYS PHE LYS ASN

ASP ILE HIS LYS LEU VAL LEU ALA ALA LEU ASN ARG PHE ILE GLY ASN PRO GLY ILE GLN LYS CYS GLY LEU LYS VAL ILE SER SER ILE VAL HIS PHE PRO ASP ALA LEU GLU MET LEU SER LEU GLU GLY ALA MET ASP SER VAL LEU HIS THR LEU GLN MET TYR PRO ASP ASP GLN

GLU ILE GLN CYS LEU GLY LEU SER LEU ILE GLY TYR LEU ILE THR LYS LYS ASN VAL PHE ILE GLY THR GLY HIS LEU LEU ALA LYS ILE LEU VAL SER SER LEU TYR ARG PHE LYS ASP VAL ALA GLU ILE GLN THR LYS GLY PHE GLN THR ILE LEU ALA ILE LEU LYS LEU SER ALA

SER PHE SER LYS LEU LEU VAL HIS HIS SER PHE ASP LEU VAL ILE PHE HIS GLN MET SER SER ASN ILE MET GLU GLN LYS ASP GLN GLN PHE LEU ASN LEU CYS CYS LYS CYS PHE ALA LYS VAL ALA MET ASP ASP TYR LEU LYS ASN VAL MET LEU GLU ARG ALA CYS ASP GLN ASN

ASN SER ILE MET VAL GLU CYS LEU LEU LEU LEU GLY ALA ASP ALA ASN GLN ALA LYS GLU GLY SER SER LEU ILE CYS GLN VAL CYS GLU LYS GLU SER SER PRO LYS LEU VAL GLU LEU LEU LEU ASN SER GLY SER ARG GLU GLN ASP VAL ARG LYS ALA LEU THR ILE SER ILE GLY

LYS GLY ASP SER GLN ILE ILE SER LEU LEU ARG ARG LEU ALA LEU ASP VAL ALA ASN ASN SER ILE CYS LEU GLY GLY PHE CYS ILE GLY LYS VAL GLU PRO SER TRP LEU GLY PRO LEU PHE PRO ASP LYS THR SER ASN LEU ARG LYS GLN THR ASN ILE ALA SER THR LEU ALA

ARG MET VAL ILE ARG TYR GLN MET LYS SER ALA VAL GLU GLU GLY THR ALA SER GLY SER ASP GLY ASN PHE SER GLU ASP VAL LEU SER LYS PHE ASP GLU TRP THR PHE ILE PRO ASP SER SER MET ASP SER VAL PHE ALA GLN SER ASP ASP LEU ASP SER GLU GLY SER GLU GLY

SER PHE LEU VAL LYS LYS LYS SER ASN SER ILE SER VAL GLY GLU PHE TYR ARG ASP ALA VAL LEU GLN ARG CYS SER PRO ASN LEU GLN ARG HIS SER ASN SER LEU GLY PRO ILE PHE ASP HIS GLU ASP LEU LEU LYS ARG LYS ARG LYS ILE LEU SER SER ASP ASP SER LEU ARG

SER SER LYS LEU GLN SER HIS MET ARG HIS SER ASP SER ILE SER SER LEU ALA SER GLU ARG GLU TYR ILE THR SER LEU ASP LEU SER ALA ASN GLU LEU ARG ASP ILE ASP ALA LEU SER GLN LYS CYS CYS ILE SER VAL HIS LEU GLU HIS LEU GLU LYS LEU GLU LEU HIS GLN

ASN ALA LEU THR SER PHE PRO GLN GLN LEU CYS GLU THR LEU LYS SER LEU THR HIS LEU ASP LEU HIS SER ASN LYS PHE THR SER PHE PRO SER TYR LEU LEU LYS MET SER CYS ILE ALA ASN LEU ASP VAL SER ARG ASN ASP ILE GLY PRO SER VAL VAL LEU ASP PRO THR VAL

LYS CYS PRO THR LEU LYS GLN PHE ASN LEU SER TYR ASN GLN LEU SER PHE VAL PRO GLU ASN LEU THR ASP VAL VAL GLU LYS LEU GLU GLN LEU ILE LEU GLU GLY ASN LYS ILE SER GLY ILE CYS SER PRO LEU ARG LEU LYS GLU LEU LYS ILE LEU ASN LEU SER LYS ASN HIS

ILE SER SER LEU SER GLU ASN PHE LEU GLU ALA CYS PRO LYS VAL GLU SER PHE SER ALA ARG MET ASN PHE LEU ALA ALA MET PRO PHE LEU PRO PRO SER MET THR ILE LEU LYS LEU SER GLN ASN LYS PHE SER CYS ILE PRO GLU ALA ILE LEU ASN LEU PRO HIS LEU ARG SER

LEU ASP MET SER SER ASN ASP ILE GLN TYR LEU PRO GLY PRO ALA HIS TRP LYS SER LEU ASN LEU ARG GLU LEU LEU PHE SER HIS ASN GLN ILE SER ILE LEU ASP LEU SER GLU LYS ALA TYR LEU TRP SER ARG VAL GLU LYS LEU HIS LEU SER HIS ASN LYS LEU LYS GLU ILE
PRO PRO GLU ILE GLY CYS LEU GLU ASN LEU THR SER LEU ASP VAL SER TYR ASN LEU GLU LEU ARG SER PHE PRO ASN GLU MET GLY LYS LEU SER LYS ILE TRP ASP LEU PRO LEU ASP GLU LEU HIS LEU ASN PHE ASP PHE LYS HIS ILE GLY CYS LYS ALA LYS ASP ILE ILE ARG
PHE LEU GLN GLN ARG LEU LYS LYS ALA VAL PRO Y1332 G1344 S1345 P1377 I1378 Q1379 D1382 K1383 R1384 K1385 R1386 D1420 G1424 Q1425 A1426 E1427 V1428 D1429 A1430 D1458 E1493 S1494 D1495 K1499 L1500 R1501 K1502 R1514 ASP GLN LEU VAL VAL GLY GLN LEU ILE P1524 R1550
K1551 L1554 E1566 L1569 P1588 A1589 L1590 Q1591 D1630 Y1631 E1632 K1643 Q1648 Y1649 F1650 K1651 G1663 V1669 PRO SER SER LEU SER ASP HIS ARG PRO VAL ILE GLU LEU PRO HIS CYS GLU ASN SER GLU I1690 E1805 Y1814 N1817 K1824 I1825 L1826 L1827 D1828
D1829 L1830 M1831 G1837 ASP LEU LEU VAL ASN PRO ASP GLN PRO ARG LEU THR ILE PRO ILE SER GLN ILE ALA PRO ASP LEU ILE LEU ALA ASP LEU PRO ARG ASN ILE MET LEU ASN ASN ASP GLU LEU GLU PHE GLU GLN ALA PRO GLU F1883 M2027 N2047 V2048 I2049 A2135 GLU
LEU VAL CYS LEU THR R2142 T2158 HIS HIS ASN SER ARG N2164 F2253 SER LYS GLN SER LYS Q2254 E2305 SER THR ASN SER THR GLU ARG ASN V2314 E2395 VAL MET VAL LYS GLU ASN LYS GLU SER LYS HIS LYS M2408 Q2462 LEU GLY SER LEU LYS N2468 R2477 LYS ASN
THR GLU GLY THR GLN LYS GLN LYS E2497 W2505 ASP ILE ASN LEU PRO HIS GLU VAL GLN ASN LEU GLU LYS HIS ILE GLU VAL ARG LYS GLU LEU ALA GLU LYS MET ARG ARG THR SER VAL GLU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	4307	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.209	Depositor
Minimum map value	-0.128	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	281.6, 281.6, 281.6	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.2, 2.2, 2.2	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-A	1040	0	0	2	0
1	1-B	1040	0	0	2	0
1	2-A	1040	0	0	0	0
1	2-B	1040	0	0	2	0
1	3-A	1040	0	0	7	0
1	3-B	1040	0	0	2	0
1	4-A	1040	0	0	12	0
1	4-B	1040	0	0	7	0
1	5-A	1040	0	0	17	0
1	5-B	1040	0	0	16	0
1	6-A	1040	0	0	4	0
1	6-B	1040	0	0	4	0
1	7-A	1040	0	0	42	0
1	7-B	1040	0	0	42	0
1	8-A	1040	0	0	19	0
1	8-B	1040	0	0	19	0
1	9-A	1040	0	0	6	0
1	9-B	1040	0	0	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	10-A	1040	0	0	20	0
1	10-B	1040	0	0	20	0
1	11-A	1040	0	0	1	0
1	11-B	1040	0	0	0	0
1	12-A	1040	0	0	11	0
1	12-B	1040	0	0	11	0
1	13-A	1040	0	0	18	0
1	13-B	1040	0	0	18	0
1	14-A	1040	0	0	32	0
1	14-B	1040	0	0	32	0
1	15-A	1040	0	0	14	0
1	15-B	1040	0	0	14	0
1	16-A	1040	0	0	31	0
1	16-B	1040	0	0	31	0
1	17-A	1040	0	0	7	0
1	17-B	1040	0	0	7	0
1	18-A	1040	0	0	11	0
1	18-B	1040	0	0	11	0
1	19-A	1040	0	0	34	0
1	19-B	1040	0	0	34	0
1	20-A	1040	0	0	10	0
1	20-B	1040	0	0	10	0
1	21-A	1040	0	0	18	0
1	21-B	1040	0	0	18	0
1	22-A	1040	0	0	13	0
1	22-B	1040	0	0	13	0
1	23-A	1040	0	0	7	0
1	23-B	1040	0	0	7	0
1	24-A	1040	0	0	39	0
1	24-B	1040	0	0	39	0
1	25-A	1040	0	0	42	0
1	25-B	1040	0	0	42	0
1	26-A	1040	0	0	7	0
1	26-B	1040	0	0	7	0
1	27-A	1040	0	0	26	0
1	27-B	1040	0	0	26	0
1	28-A	1040	0	0	16	0
1	28-B	1040	0	0	16	0
1	29-A	1040	0	0	22	0
1	29-B	1040	0	0	22	0
1	30-A	1040	0	0	17	0
1	30-B	1040	0	0	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	31-A	1040	0	0	7	0
1	31-B	1040	0	0	7	0
1	32-A	1040	0	0	12	0
1	32-B	1040	0	0	12	0
1	33-A	1040	0	0	17	0
1	33-B	1040	0	0	17	0
1	34-A	1040	0	0	15	0
1	34-B	1040	0	0	15	0
1	35-A	1040	0	0	13	0
1	35-B	1040	0	0	14	0
1	36-A	1040	0	0	23	0
1	36-B	1040	0	0	23	0
1	37-A	1040	0	0	10	0
1	37-B	1040	0	0	11	0
1	38-A	1040	0	0	49	0
1	38-B	1040	0	0	49	0
1	39-A	1040	0	0	31	0
1	39-B	1040	0	0	31	0
1	40-A	1040	0	0	26	0
1	40-B	1040	0	0	26	0
1	41-A	1040	0	0	62	0
1	41-B	1040	0	0	62	0
1	42-A	1040	0	0	20	0
1	42-B	1040	0	0	21	0
1	43-A	1040	0	0	24	0
1	43-B	1040	0	0	24	0
1	44-A	1040	0	0	4	0
1	44-B	1040	0	0	0	0
1	45-A	1040	0	0	17	0
1	45-B	1040	0	0	17	0
1	46-A	1040	0	0	38	0
1	46-B	1040	0	0	38	0
1	47-A	1040	0	0	13	0
1	47-B	1040	0	0	13	0
1	48-A	1040	0	0	34	0
1	48-B	1040	0	0	34	0
1	49-A	1040	0	0	23	0
1	49-B	1040	0	0	24	0
1	50-A	1040	0	0	50	0
1	50-B	1040	0	0	50	0
1	51-A	1040	0	0	36	0
1	51-B	1040	0	0	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	52-A	1040	0	0	46	0
1	52-B	1040	0	0	46	0
1	53-A	1040	0	0	34	0
1	53-B	1040	0	0	34	0
All	All	110240	0	0	1840	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

The worst 5 of 1840 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1591:GLN:CA	1:A:2118:ASN:CA	1.75	1.65
1:A:1428:VAL:CA	1:A:1811:TRP:CA	1.75	1.64
1:A:1458:ASP:CA	1:A:1601:LYS:CA	1.77	1.63
1:B:1426:ALA:CA	1:B:1807:LEU:CA	1.76	1.63
1:A:1740:LEU:CA	1:B:1754:VAL:CA	1.76	1.62

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

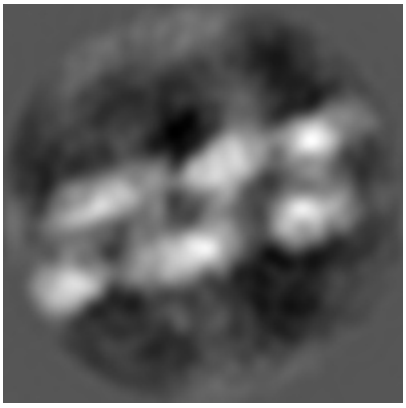
6 Map visualisation (i)

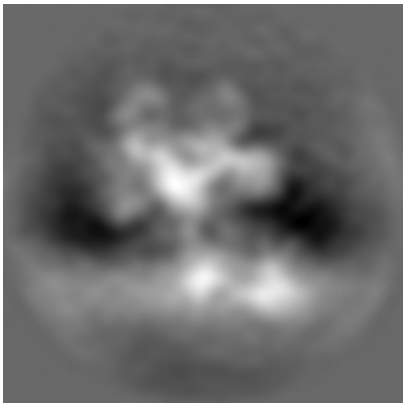
This section contains visualisations of the EMDB entry EMD-20825. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary map


X

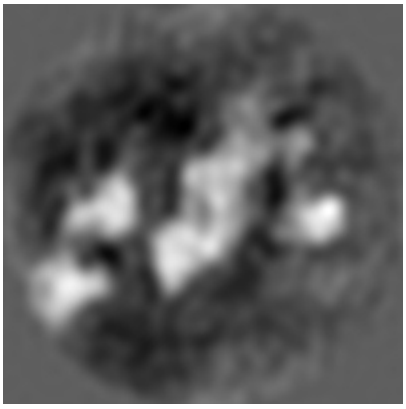

Y

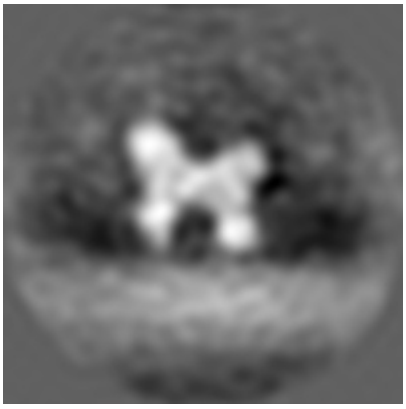
Z

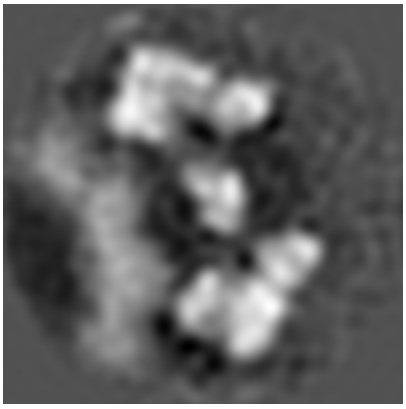
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map


X Index: 64

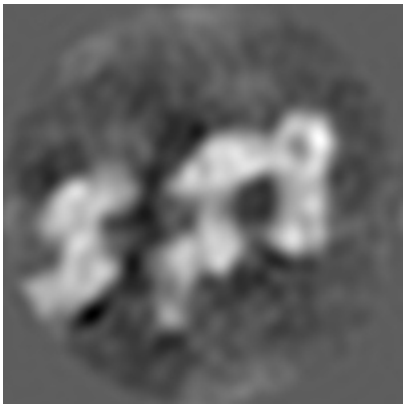

Y Index: 64

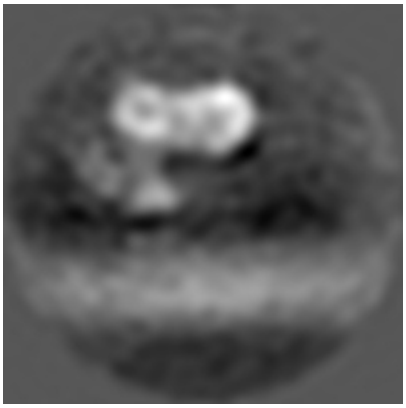

Z Index: 64

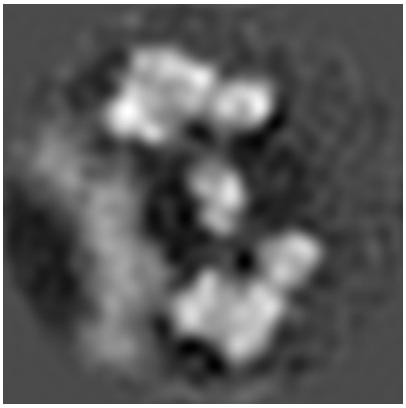
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map


X Index: 76

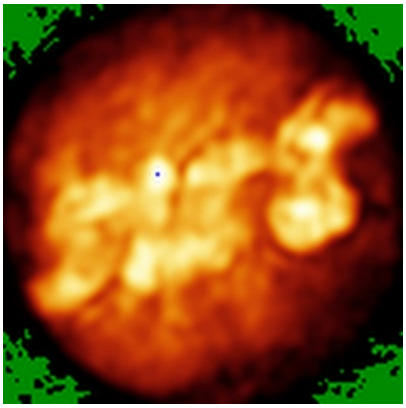

Y Index: 49

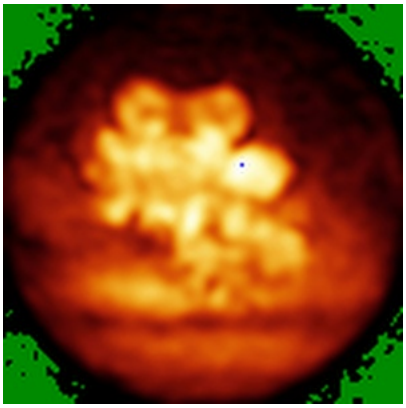

Z Index: 62

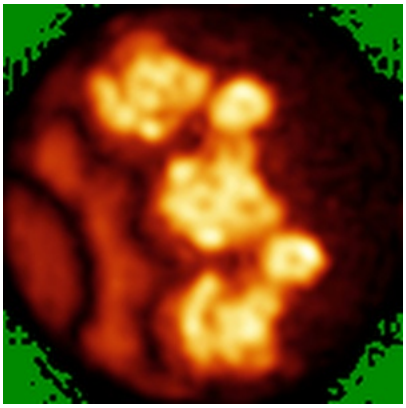
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map


X

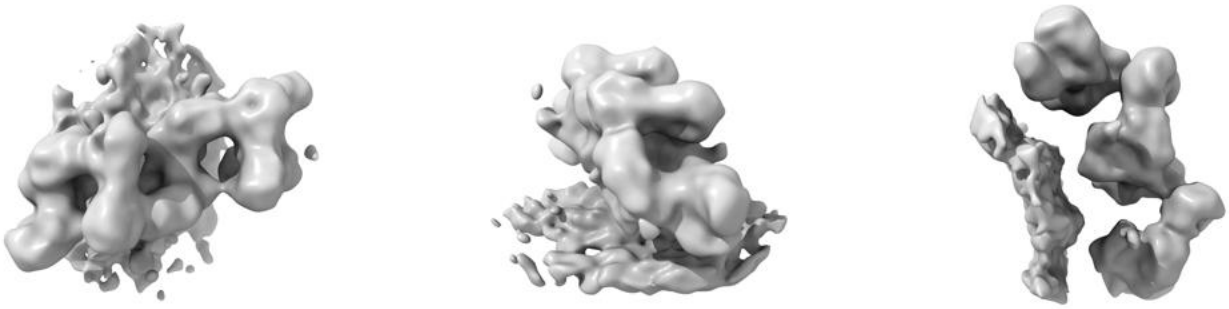

Y


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

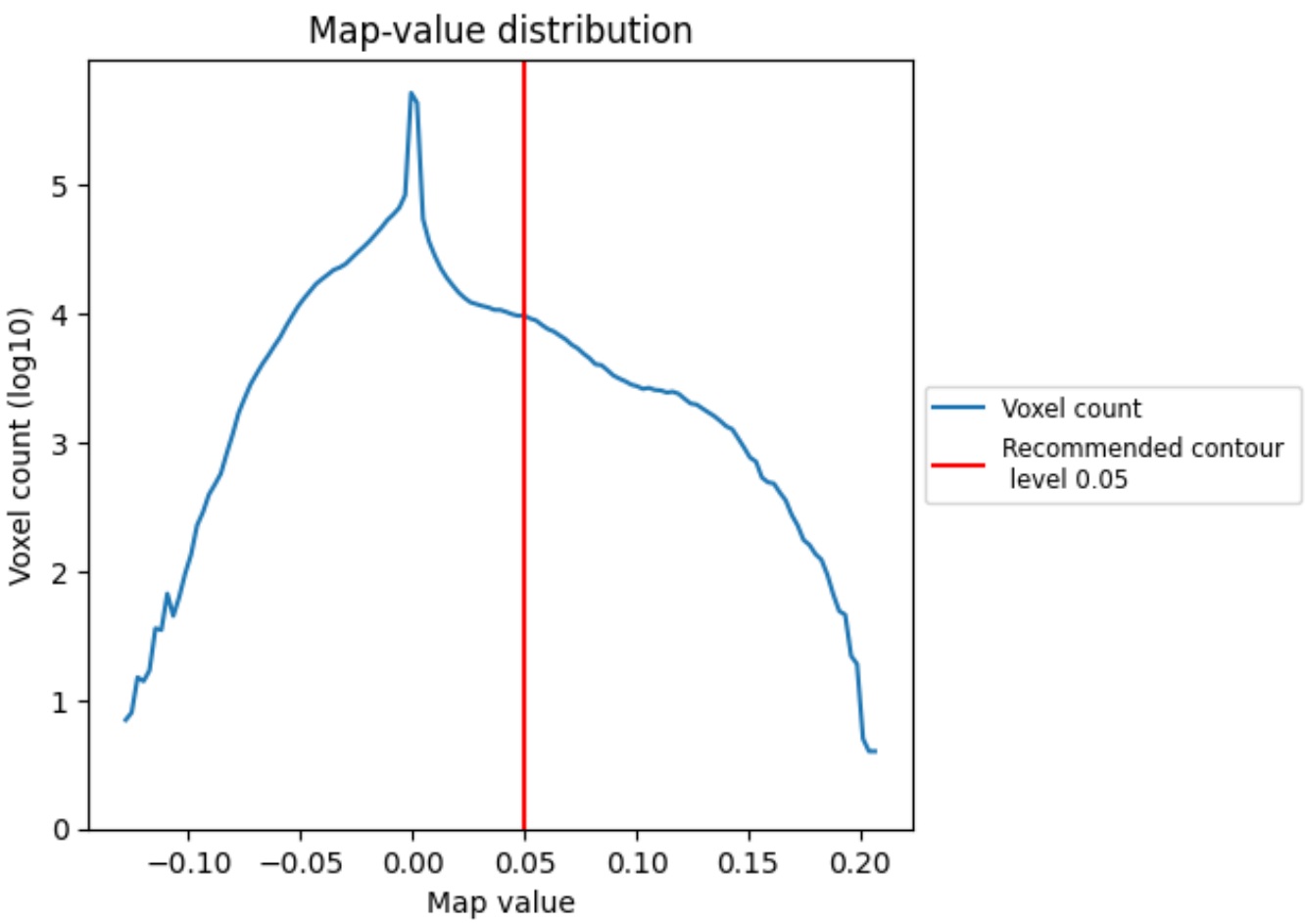
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis (i)

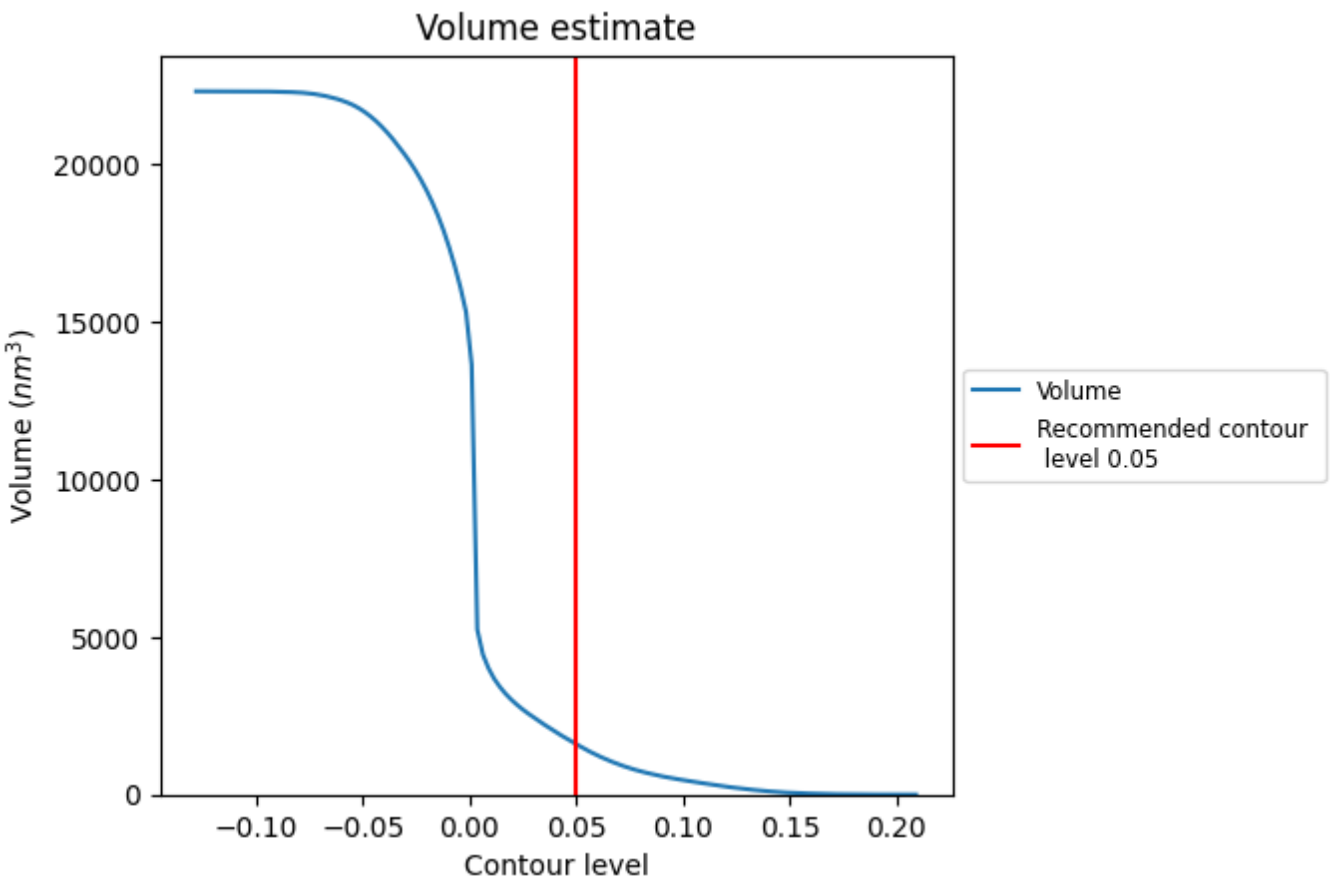
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

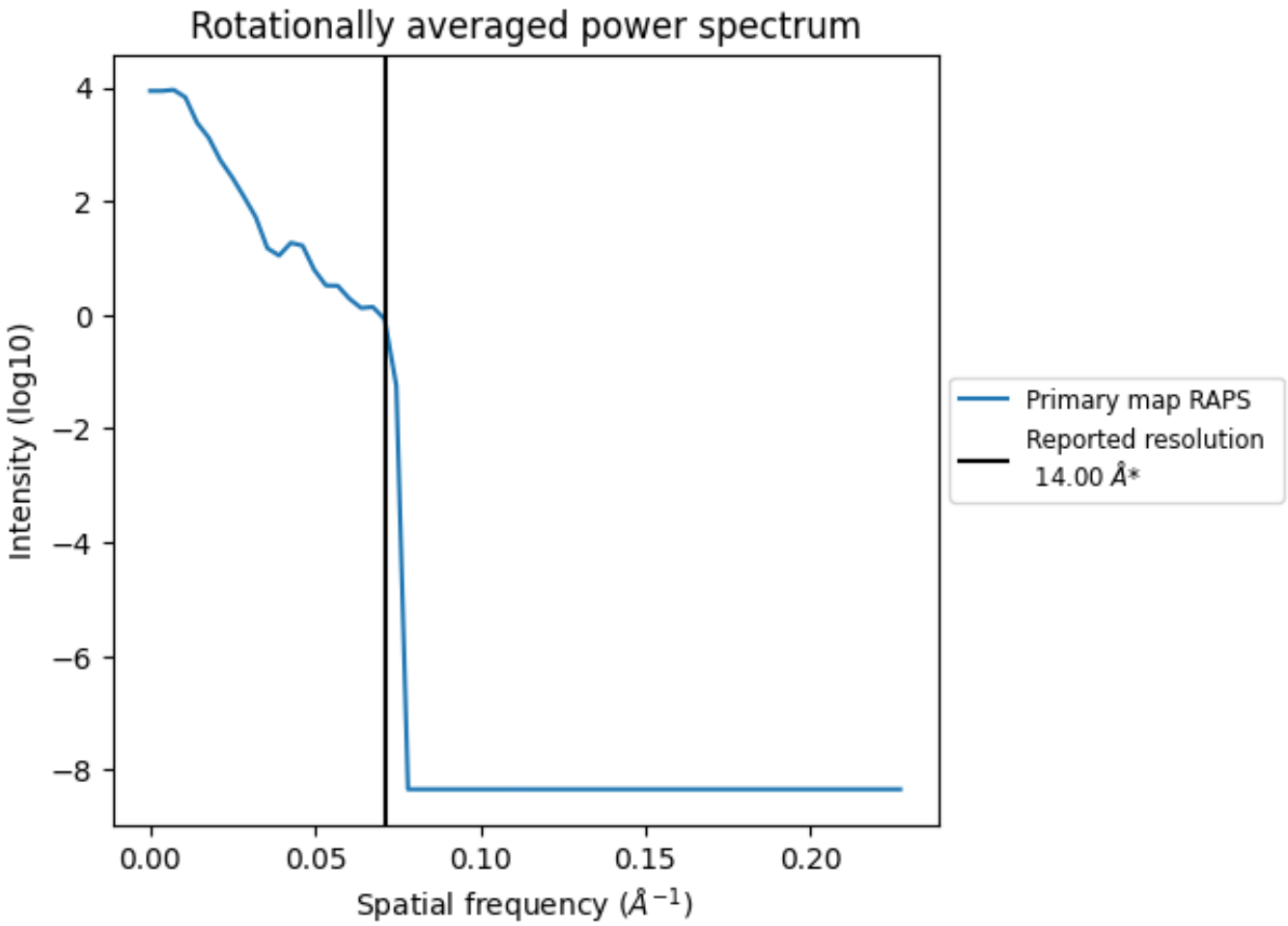
7.2 Volume estimate (i)



The volume at the recommended contour level is 1604 nm^3; this corresponds to an approximate mass of 1449 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.071 Å^{-1}

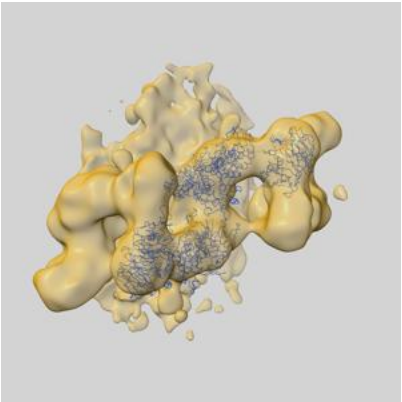
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

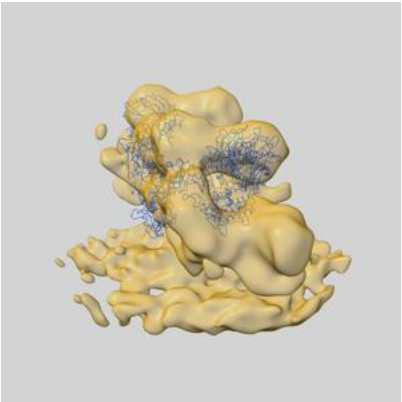
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-20825 and PDB model 6XR4. Per-residue inclusion information can be found in section 3 on page 13.

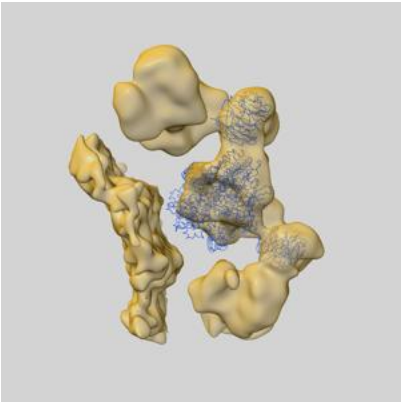
9.1 Map-model overlay (i)



X



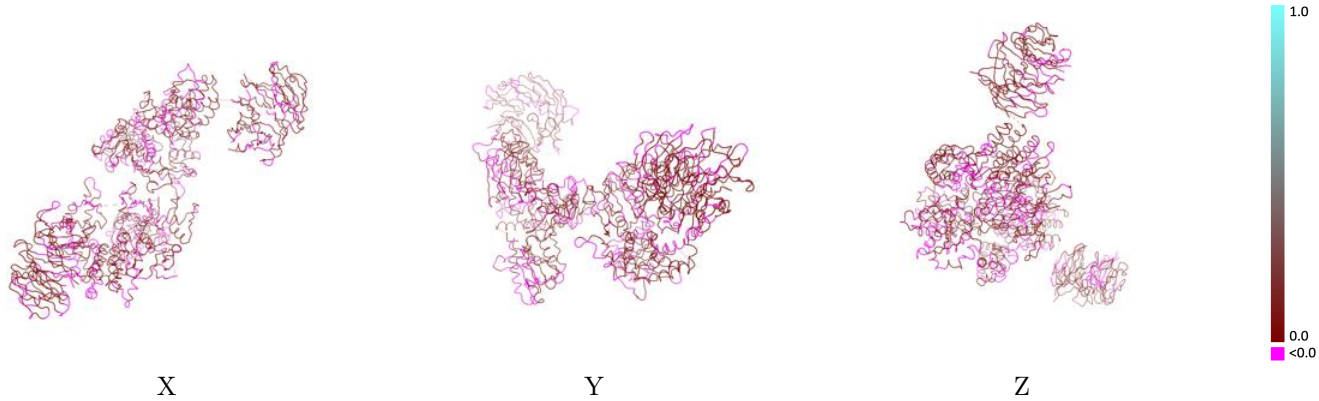
Y



Z

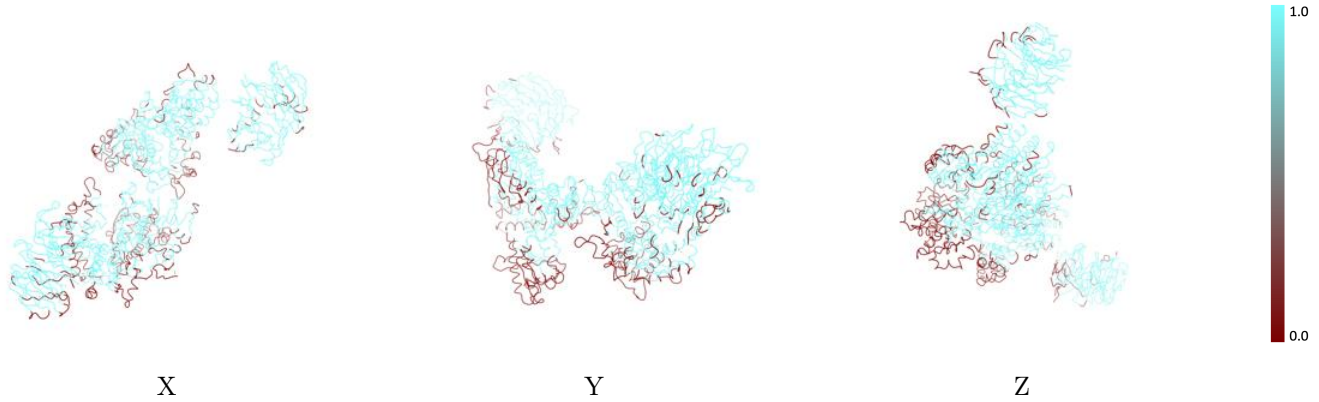
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



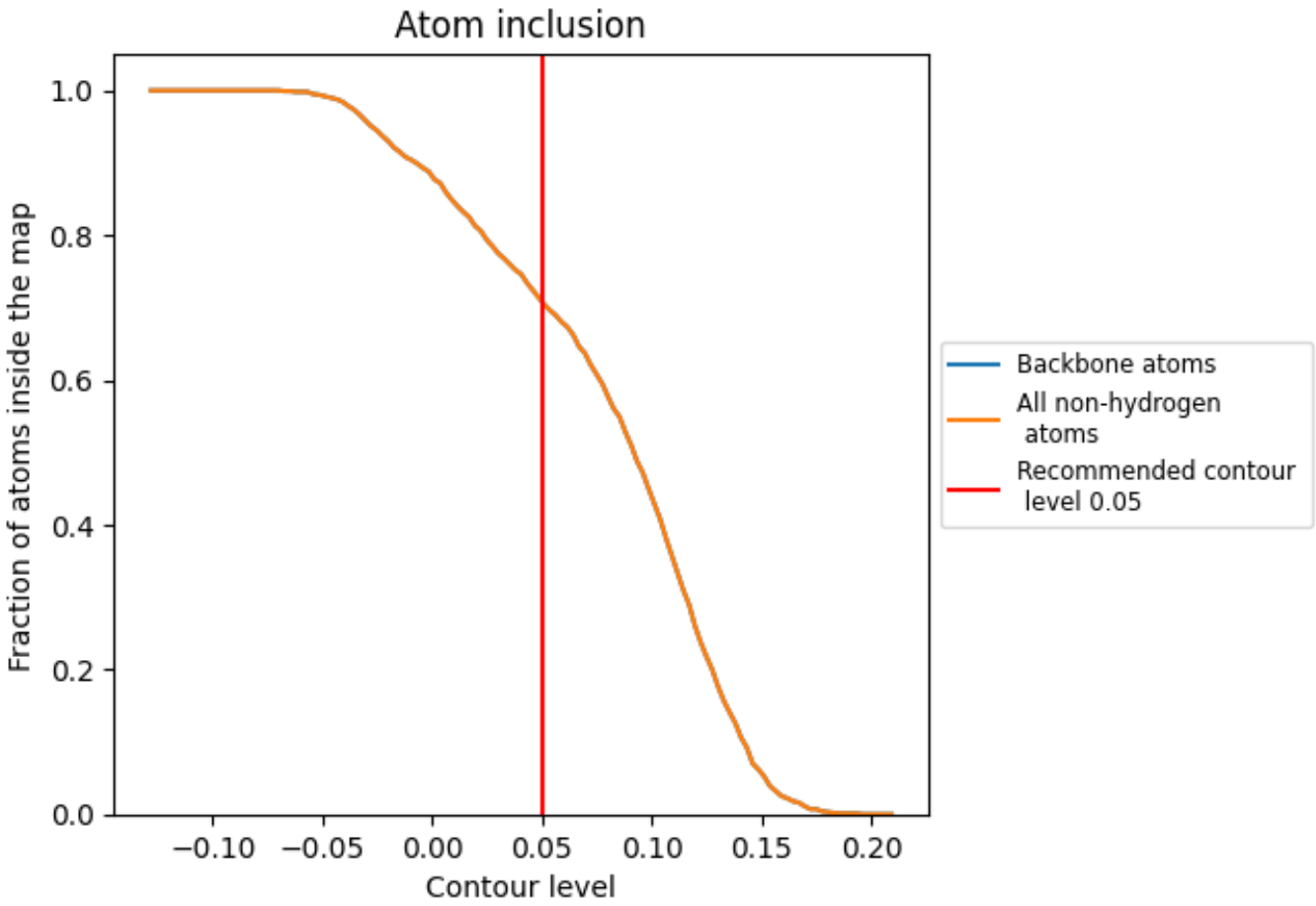
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion (i)



At the recommended contour level, 71% of all backbone atoms, 71% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7080	0.0370
A	0.7670	0.0390
B	0.6480	0.0340