**Supporting Information S2.** **The benchmark dataset used for studying the PPIs in *H. pylori*.** It contains 2,916 protein pairs, of which 1,458 are interactive and the other 1,458 are non-interactive pairs. (I) Each pair is represented by two protein codes with a hyphen “-” between. (II) The detailed sequence for each of the codes. For further information, refer to Martin et al. (Bioinformatics, 2005, 21, 218-226).

**(I) Pair codes**

**The positive subset contains 1,458 interactive pairs**

564-192 1119-729 1375-603 505-999

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1069-466 245-244 1099-773 1385-937

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223-1563 980-82 1399-389 1306-997

332-1261 287-121 1055-1494 1325-140

874-1 1190-894 300-1368 838-1140

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891-704 758-73 1542-929 1557-240

503-73 131-788 890-243 884-188

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1475-1180 1006-1259 459-495 623-1174

228-404 792-871 103-1149 972-565

1038-1168 644-507 1382-1469 928-184

130-680 1366-1060 1168-587 1265-291

902-240 176-1212 954-423 468-108

342-513 216-838 1520-1184 457-486

358-1464 912-629 1086-409 1234-820

208-320 1544-9 1531-865 886-1106

1352-578 1366-1140 639-684 426-63

1235-1444 1062-788 1397-960 390-347

1091-670 1541-434 288-1063 1184-1464

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960-726 524-1105 455-902 350-933

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305-142 1155-502 317-1277 1245-443

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64-296 202-1560 458-1033 960-895

1006-739 763-879 1066-267 1272-292

496-1548 1072-473 776-398 727-845

427-1485 269-639 597-43 322-963

944-333 963-1488 838-1021 947-1543

57-782 989-1231 591-429 491-1562

704-397 761-471 1104-617 672-1136

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160-735 28-530 908-1560 953-1056

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251-268 83-490 1522-41 1129-1260

940-631 487-265 237-1361 1023-1202

424-842 601-1335 297-234 65-22

779-1210 1566-1092 1004-987 137-216

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759-1224 1564-1144 1205-519 140-1185

674-873 829-1130 1308-382 1486-1476

726-845 148-62 275-826 832-461

651-858 1137-1221 68-1322 1275-321

859-778 511-1334 858-214 104-478

793-356 1529-838 1006-303 126-1051

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1112-1151 1335-9 917-156 1517-538

377-1092 1321-320 1527-1376 1201-84

616-1187 797-1405 498-1321 1503-676

245-239 288-750 1382-286 53-1257

235-750 492-1010 1409-1389 597-553

884-143 823-118 566-589 660-1396

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340-498 682-1499 697-1542 357-454

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202-1280 1354-744 1319-464 512-199

1514-661 1490-1366 1078-1316 1146-922

184-895 955-1456 771-1150 821-1503

326-80 240-1239 207-859 317-1205

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223-958 1474-1467 775-969 29-131

343-1546 857-416 1433-687 369-182

295-647 918-778 1568-86 719-1489

822-377 1223-728 358-1418 252-522

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240-875 1145-1344 8-953 1205-475

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207-842 1490-15 200-824 757-144

423-232 178-398 1275-796 647-1530

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530-512 1006-807 1116-1316 1372-1443

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1324-1397 286-821 41-893 1266-967

808-136 507-1384 1349-730 309-1212

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545-688 19-1284 1061-1452 921-971

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555-1183 1445-745 681-1151 1543-1174

1153-514 1453-446 246-87 1384-79

1445-1182 1544-875 1213-539 804-181

624-189 893-439 971-587 1229-1315

363-906 463-891

**The negative subset contains 1,458 non-interactive pairs**

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307-308 307-583 307-954 288-351

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288-741 288-82 288-1179 288-1418

288-169 288-347 288-1227 288-1262

288-1567 288-583 288-579 47-746

47-1417 47-1354 47-1044 47-1256

46-46 46-583 588-588 588-591

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464-419 464-116 464-386 464-95

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1105-23 1105-29 1105-335 1105-1276

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1382-1342 601-1307 601-129 601-583

602-602 602-1387 602-633 602-901

602-583 604-603 1307-1307 453-451

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455-583 455-1282 455-1288 455-1539

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450-87 450-1096 450-1339 450-305

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449-1316 449-98 449-456 148-148

310-1481 310-1223 351-46 351-351

351-1392 351-1096 351-1407 351-1500

351-154 351-1097 351-6 351-1098

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624-214 624-223 624-1090 624-37

624-1187 624-1200 624-1515 624-1042

624-890 624-345 624-80 625-1005

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1377-1072 1377-85 1377-1286 1377-961

1377-1290 1377-963 445-207 445-1234

980-600 980-1026

**(II) The detailed sequences for the proteins coded in (I).** Note that each code is indicated by a number right after the symbol “>”.

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MGYQLFEFENLKDCHKALTERFKEFFNTALKKHHQISIAFSGGRSPISLLQKLSVLNLKWHECLISLVDE

RIIDTSHDDSNTKLLHDYLLQNNALKASFIPLLPEKISSDTNALFNFANQHFKQPHLAILGMGTDGHTAS

LFPETSAFLNEEKENIVLTKPINAPYERLSMSVNALENCEKLFLSISGVEKRGVLEKALKENAPYSLPIA

RILHSQKVTTEVFYAKN

>2

MAVYLDFENHIKEIQNEIELALIRGDEDAKEILEKRLDKEVKSIYSNLTDFQKLQLARHPDRPYAMDYID

LILKDKYEVFGDRHYNDDKAIVCFVGKIDNVPVVVIGEEKGRGTKNKLLRNFGMPNPCGYRKALKMAKFA

EKFNLPILMLVDTAGAYPGIGAEERGQSEAIAKNLQEFASLKVPTISVIIGEGGSGGALAIAVADKLAMM

EYSIFSVISPEGCAAILWDDPSKTEVAIKAMKITPRDLKEAGLIDDIILEPSKGAHRDKFSAANTIKEYF

LDALRTIQQDPHFLDNRYQKLMSLGSFVESMN

>3

MKDFLEDYKKSVSERGSEGIPPLPLNAKQVQAVVEILTKDPTNAAFAKELLIHRVSPGVDEGAKVKAEFL

AKLSQKKLECVHISALEATTLLGTMLGGYNVEPLIMGLESQDKNIAKESAKALKTTLLVYGSFDKIAAMS

KTNALAKEVLESWANAEWFLNKEPLNECIEACVFKIDGETNTDDLSPASDAFTRSDIPLHAKAMLKNRIE

NYEQRIKAIKTKGVPVAYVGDVVGTGSSRKSATNSIMWHFGKDIPFVPNKRSGGIVIGGVIAPIFFATCE

DSGALPIVADVKDLKEGDLIKIYPYKGEITLNDKVVSTFKLEPETLLDEVRASGRIPLIIGRGLTNKARK

FLGLGESEAFKKPSAPKSDAKGYTLAQKIVGHACGVKGILPGTYCEPKVTTVGSQDTTGAMTRDEVKELA

SLKFDAPFVLQSFCHTAAYPKPSDVSLHATLPGFITQRGGVALHPGDGVIHTWLNRMGLPDTLGTGGDSH

TRFPLGISFPAGSGLVAFAAVTGTMPLNMPESVLVRFKGEMNPGITLRDLVNAIPYYAIKKGLLTVEKKG

KINVFNGRILEIEGLPDIKMEQAFELSDASAERSAAACVVRLNKEPMIEYLKSNIKLIDEMIASGYEDKE

TLKKRRDAMQAWVDNPVLLEPDSNAQYAAVIEIDVAEITEPILACPNDPDDVATLSEVLADTTGKRPHAI

DEVFIGSCMTNIGHFRAFGEIVKNAPPSQARLWVVPPSKMDEQELINEGYYAIFGAAGARTEVPGCSLCM

GNQARVRDNAVVFSTSTRNFDNRMGRGAKVYLGSAELGAACALLGRIPTKEEYMNLVSEKLESQKDKIYR

YMNFNLMENFRL

>4

MIGIDIVSIARIEKCVKRFKMKFLERFLSPSEIVLCKDKSSSIAGFFALKEACSKALQVGIGKELSFLDI

KISKSPKNAPLITLSKEKMDYFNIQSLSASISHDAGFAIAVVVVSSSNE

>5

MALFEDIQAVIAEQLNVDAVQVTPEAEFVKDLGADSLDVVELIMALEEKFGVEIPDEQAEKIINVGDVVK

YIEDNKLA

>6

MQLDEDLEFAKKIFNPNRAFAKQARIKNMCEYKDLVHEANEDYEHFWGDLAKQKLTWFKPFDKVLNSDNA

PFFKWFENGKINVSYNCIDRHLKDKKNKVAIIFEGEMGDYNVITYRKLHSEVNKTANLLKNEFNVKKGDR

VIIYMPMIVESVYMMLACTRIGAIHSIVFAGFSPEALRDRINDAQAKLVITADGTFRKGKPYMLKPALDK

ALENNACPSVEKALIVIRNAKEIDYVRGRDFVYNEMVNYQSDKCEPEMMDSEDPLFLLYTSGSTGKPKGV

QHSSAGYLLWAQMTMEWVFDIRDNDNFWCTADIGWITGHTYVVYGPLACGATTLILEGTMSYPDYGRWWR

MIEEYRVDKFYTSPTAIRMLHAKGENEPSKYNLESLKVLGTVGEPINPTAWKWFYEKIGNSKCSIVDTWW

QTETGGHIISPLPGATPIRASCATLPLPGIHAEVLNEDGTKTKPGEQGFLCITKPWPSMIRNIWGDEKRY

IDSYFSQIKLNGEYVYLSGDGAIVDENGYITIIGRTDDIVNVSGHRIGTAEVESAISKHEMVAECAVVGI

PDAIKGEGLFAFVVLCDGAKCNLGESLELLKEMNHILSIEIGKIAKLDNVMYVPGLPKTRSGKIMRRLLK

SIAKKEPITQDLSTLEDVNVVKEIMSIAQMEE

>7

MLIVQKYGGTSMGSIERIHNVAQRVLESVTLGHQVVVVVSAMSGETDRLLEFGKNFSHNPNKREMDRIVS

VGELVSSAALSMALERYGHRAISLSGKEAGILTSSHFQNAVIQSIDTKRITELLEKNYIVVIAGFQGADI

QGETTTLGRGGSDLSAVALAGALKAHLCEIYTDVDGVYTTDPRIEEKAQKIAQISYDEMLELASMGAKVL

LNRSVELAKKLSVKLVTRNSFNHSEGTLIVAEKDFKGERMETPIVSGIALDKNQARVSMEGVEDRPGIAA

EIFGALAEYRINVDMIVQTIGRDGKTDLDFTIVKTQIEETKQALKPFLAQMDSIDYDENIAKVSIVGVGM

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>8

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IEDNISVDEKDAVLVNPKEAEQFVKESQVDYLAPAIGTSHGAFKFKGEPKLDFERLQEVKRLTNIPLVLH

GASAIPDNVRKSYLDAGGDLKGSKGVPFEFLQESVKGGINKVNTDTDLRIAFIAEVRKVANEDKSQFDLR

KFFSPAQLALKNVVKERMKLLGSANKI

>9

MLKRASFVEVDTASLRHNFSAVKSIVPKDACVMAVVKANAYGAGAIKASEIFLQEGANYLGVATLDEALE

LRSHFSKTPILILGYSPNANASMLVDNDLSAMIFSLEQAEVFSQMALKSQKRLKVHIKIDTGMHRLGLEP

NFKSIETIKKIRALKGLEIEGIFTHLSNADAKIKTHAKNQMKAFNAFLEQLLDQKIEFQYRHAYNSAGIL

SLCNGNENRLLNLYRPGIMLYGFYPSNGMKESCPTILKNVISLKAQIVQIRSVKKGEFIGYGEHFYTNEE

TLVGVLALGYADGLMRALGNRIQVAINNQLAPLIGKVCMDQCFVKLNNIQAKEGDEVILFGDKSAKANDA

SEIXALLNTIAYETISTLSKRLERVYI

>10

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ECWYPGDKTYVVDGPKGLKVSLIICDDGNYPEIWRDCAMRGAELIVRCQGYMYPAKEQQIAIVKAMAWAN

QCYVAVANATGFDGVYSYFGHSSIIGFDGHTLGECGEEENGLQYAQLSVQQIRDARKYDQSQNQLFKLLH

RGYSGVFASGDGDKGVAECPFEFYKTWVNDPKKAQENVEKITRPSVGVAACPVGDLPTK

>11

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WLSEEFLLDVPGKETELYAKACKEAKVYGVFSIMERNPDSNKNPYNTAIIIDPQGEIILKYRKLFPWNPI

EPWYPGDLGMPVCEGPGGSKLAVCICHDGMIPELAREAAYKGCNVYIRISGYSTQVNDQWILTNRSNAWH

NLMYTVSVNLAGYDNVFYYFGEGQICNFDGTTLVQGHRNPWEIVTGEIYPKMADNARLSWGLENNIYNLG

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>12

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ALELHKPCEKTCANSLEKSAKEALKYAEIMTESLNIVKDLVNTPPMIGTPVYMAEVAQKVAKENHLEIHV

HDEKFLEEKKMNAFLAVNKASLSVNPPRLIHLVYKPKKAKKKIALVGKGLTYDCGGLSLKPADYMVTMKA

DKGGGSAVIGLLNALAKLGVEAEVHGIIGATENMIGPAAYKPDDILISKEGKSIEVRNTDAEGRLVLADC

LSYAQDLNPDVIVDFATLTGACVVGLGEFTSAIMGHNEELKNLFETSGLESGELLAKLPFNRHLKKLIES

KIADVCNISSSRYGGAITAGLFLNEFIRDEFKDKWLHIDIAGPAYVEKEWDVNSFGASGAGVRACTAFVE

ELLKKA

>13

MAISIKSPKEIKALRKAGELTAQALALLEREVRPGVSLLELDKMAEDFIKSSHARPAFKGLYGFPNSVCM

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GMHFKELSQILESTITERGFVPLKGFCGHGIGKKPHEEPEIPNYLEKGVKPNSGPKIKEGMVFCLEPMVC

QKQGEPKILADKWSVVSVDGLNTSHHEHTIAIVGNKAVILTER

>14

MSNSMLDKNKAILTGGGALLLGLIVLFYLAYRPKAEVLQGFLEAREYSVSSKVPGRIEKVFVKKGDHIKK

GDLVFSISSPELEAKLAQAEAGHKAAKALSDEVKRGSRDETINSARDVWQAAKSQATLAKETYKRVQDLY

DNGVASLQKRDEAYAAYESTKYNESAAYQKYKMALGGASSESKIAAKAKESAALGQVNEVESYLKDVKAT

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>15

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>16

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GSPLKACHYESPIASAQVKSAFILSALQAQGASTYKESELSRNHTEIMLKSLGADIHNQDGVLKISPLEK

PLEAFDFTIANDPSSAFFFALACAITPKSRLLLKNVLLNPTRIEAFEVLKKMGASIEYAIQSKDLEMIGD

IYVEHAPLKAINIDQNIASLIDEIPALSIAMLFAKGKSMVKNAKDLRAKESDRIKAVVSNFKALGIECEE

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>17

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>18

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>19

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>20

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>21

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>22

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>23

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>25

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RKVLEEFKLTYSE

>26

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>27

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>28

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>29

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>31

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>32

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>33

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LLAKEFLPNARLMVAGGREVVFKDNDKKEAKLFEYGINAVVLGDYLTTKGKAPKKDIEKLLSYGLTMATS

CH

>34

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VLMSFALK

>35

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>36

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>37

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>38

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KEY

>39

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>41

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>42

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>43

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>44

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>45

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>46

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>47

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>49

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QVYVGD

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>76

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>78

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>86

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>87

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>88

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>89

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>90

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>91

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>92

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ALQMK

>93

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>94

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>95

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>96

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>97

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>98

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>99

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>100

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>101

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>102

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RIMKK

>103

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>104

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>105

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>106

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>107

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>108

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>109

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>110

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>111

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>112

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>113

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>114

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>115

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>116

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>117

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>118

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>119

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>120

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>121

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>122

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>123

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>124

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>125

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>126

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>127

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>128

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>129

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>130

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>131

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>132

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>133

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>134

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>135

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>136

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>137

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KPLYQ

>138

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>139

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>140

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>141

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>142

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>143

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>144

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>145

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>146

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>147

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>148

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>149

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>151

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>152

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>153

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>154

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>155

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>156

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>157

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>158

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>159

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>160

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>161

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>162

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>163

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>164

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>165

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>167

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>168

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>169

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>171

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>172

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>173

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>174

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>175

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>176

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>177

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>178

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>179

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>180

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>184

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>190

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>196

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>200

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>202

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>203

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>204

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>207

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>208

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>209

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>210

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>212

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>214

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>215

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>217

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>218

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>219

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>221

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>222

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>223

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>224

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>225

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>227

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>228

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>229

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>230

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>235

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>237

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>238

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>240

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>241

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>242

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LETIVPLLENFYGVKGRLEIVHSKPLVVVDFAHTIDGMQQVFESFKNQKITALFGAGGDRDKTKRPEMGA

IASYYAHKIILTSDNPRSENEEDIIKDILKGINDSSKVIVEKDRKKAILNALENLKDDEVLLILGKGDEN

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>243

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CGPNSYEQVRFFYQELGLLDKIELFAFHNNITEIMHRADLCVSRAGASSVWELCANGLPTIFIPYPFASN

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LSA

>244

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>245

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LFDDEGKIKQGANATLDALNESLNRLKKESVKIIHHYARSKELAPYLVDTQSHLKHGYECLLLKSGFSGA

IKGVVLERSANGYFYLLPESAQKIAQKIAQIGNEIDCCIVEMCQTLSHSLQKHLLFLKFLFKEFDFLDSL

QARLNFAKAYNLEFVMPSFTQKKMILENFSHPILKEPKPLNLKFEKSMLAVTGVNAGGKTMLLKSLLSAA

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>246

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>247

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>248

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>249

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>250

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>251

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AHLA

>252

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>253

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ASSFEYNE

>254

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>255

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VYRQVIAYFKREGYL

>256

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>257

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>258

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>259

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>261

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>262

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>263

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>264

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>265

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>266

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>267

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>268

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>269

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>270

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>271

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>272

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SKKR

>273

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>274

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>275

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>276

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>277

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>278

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>279

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>280

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>281

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KEYS

>282

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>283

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>286

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>287

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>290

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>291

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>292

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>294

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>295

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>296

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>297

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>299

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>300

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>302

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>303

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>305

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>306

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>311

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>314

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>315

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>316

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>317

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>323

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>334

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>337

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>338

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>339

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>340

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>355

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>367

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>368

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>369

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>371

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>373

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>374

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>377

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>378

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>379

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>380

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>381

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>383

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>384

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>385

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>387

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>388

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>389

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>391

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>392

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>393

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>394

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>395

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>396

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>397

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>398

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>399

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>400

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>401

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>402

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I

>403

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>404

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KRCEQVLKER

>405

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>406

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>407

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>408

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>409

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>410

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>411

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>412

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>413

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>414

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>415

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>416

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>417

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>418

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>419

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>420

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>421

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>422

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>423

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>424

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>425

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>426

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>427

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>428

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>429

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>430

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>431

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>432

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>433

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>434

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>435

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>436

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>437

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>438

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>440

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>441

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>442

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>443

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>444

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>445

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>446

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>447

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>448

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>449

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>450

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>454

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>455

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>456

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>457

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>458

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>459

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>535

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>583

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>605

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>607

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>620

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>628

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>632

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>633

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>634

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>635

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>637

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>701

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>703

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>704

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>705

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>706

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>713

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>714

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>716

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>717

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>718

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>719

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>720

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>721

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>722

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>723

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>724

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>725

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>726

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>728

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>729

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>730

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>731

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>732

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>733

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>734

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>735

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>736

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>737

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>738

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>739

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>740

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>741

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>742

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>743

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>744

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>762

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>790

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>793

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>794

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>797

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>906

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>907

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>908

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>911

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NAYNNPSTMDVIL

>912

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>915

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>921

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>926

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>930

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>931

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>935

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>937

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>940

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>949

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>950

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>955

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>956

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>958

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>959

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>960

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>961

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>962

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>963

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>964

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LNKRL

>965

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>966

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>967

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>968

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>996

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>1015

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>1016

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>1019

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>1020

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>1021

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HKETS

>1022

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>1023

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>1024

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>1025

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>1026

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>1027

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>1028

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>1029

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>1030

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>1032

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>1033

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>1034

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ALASKF

>1035

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>1036

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>1037

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>1038

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>1039

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>1040

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>1041

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KG

>1042

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>1043

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>1044

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>1045

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>1046

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>1047

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>1048

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>1049

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>1050

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>1051

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>1052

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RIYTKYAQTFHSNPYTNQKTPNSDLYYPALNEGNSFSIQIMGISVAELLKSKKFLSLDVSFKKGSVLWGG

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>1053

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NQDTTVEKGTLKAADLSLSGKVSSIAASISSSRQRLDYDFTLSLTNRKTGEEVWSDVKPIVKNASNKRMF

>1054

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>1055

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TMWFV

>1056

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>1057

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>1058

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LYEKSSL

>1059

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>1060

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>1061

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>1062

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>1063

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>1064

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>1065

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>1066

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>1067

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>1068

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>1069

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SDAYLAQTLGENIEKIKEAKTASDIYALVPIDEQFNAIEQDEITKKIEAEELLEHVQKALNQMSEREQIL

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>1070

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>1072

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>1073

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KSLRK

>1074

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>1075

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>1076

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>1077

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>1078

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NSRSELL

>1079

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>1080

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>1081

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>1082

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>1083

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>1084

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>1085

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>1086

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>1087

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>1088

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>1089

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>1090

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>1091

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>1131

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>1132

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>1133

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>1134

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>1137

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>1138

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>1139

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>1140

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>1141

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>1142

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>1143

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>1144

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>1145

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>1146

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>1147

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>1148

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>1149

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>1150

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>1151

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>1152

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>1153

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>1154

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>1155

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>1157

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>1158

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>1159

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>1160

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>1161

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>1162

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>1163

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>1164

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>1166

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>1167

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>1168

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>1169

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>1170

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>1171

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>1172

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GLGS

>1245

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RM

>1246

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>1247

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>1248

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AYKIPVALSKQVVFSINDCKENEKTLVIGGGNSAVEYAIALCKTTPTTLNYRKKEFSRINEDNAKNLQEV

LNNNTLKSKLGVDIESLEEDNTQIKVNFTDNTSESFDRLLYAIGGSTPLEFFKRCSLELDPSTNIPVVKE

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>1249

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TDENGNGTTINCGGSTNSNGTHSSSGTNTLKADKNVSLSIEQYEKIHEAYQILSKALKQAGLAPLNSKGE

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>1250

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VGGFLGMEHLSLGLILGTLLKPLAFMLGIPWSQAGIAGEIIGIKIALNEFVGYMQLLPYLGDNPPLILSE

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>1251

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>1252

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>1253

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VLAIGFEEGKENPNLDPILEGIQKKQNFKEVALDAFLPKSINYYHLTALSPLLLAQRGWHGL

>1254

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>1255

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>1256

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>1257

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KDIYAFLKNLDKENFDSRENQRERIESLLESVNRHKIPLNEQELQAFDLAIKANSSYYKLSYNLLPLLLS

LLSKKKTP

>1258

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>1259

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>1260

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>1261

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>1262

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>1263

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>1264

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>1265

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WDMAYQS

>1266

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>1267

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>1268

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>1269

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>1270

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FSDALAQTLTYSLFLAKLNHPSEKINLDNVRSLIPKNFAVIREMADFLKKLDEIKEIQWLLNEILSSINH

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>1271

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KNG

>1272

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ALKEALIW

>1273

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>1274

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>1275

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>1276

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>1277

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TF

>1278

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>1311

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>1312

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>1314

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>1315

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>1316

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>1317

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>1318

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>1319

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>1320

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>1321

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>1322

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>1323

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>1324

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>1325

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>1326

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>1327

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>1330

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>1331

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>1332

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>1333

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>1334

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>1335

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>1336

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>1337

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>1338

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>1339

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>1340

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>1341

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>1342

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VRIDPHSRSVKLGPDSAGYRVGTCWKDSGLDTVSVTDCHIVLGYLNPDNFLGGLIKLDVDRAKKHIKEQI

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LDKHRLFHLKEIK

>1343

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ELIEEIKSEFEIKSVELL

>1344

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>1345

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>1346

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>1347

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>1348

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>1349

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ARMNETQ

>1350

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>1351

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>1352

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>1353

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GENLKT

>1354

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>1355

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>1356

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>1357

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>1358

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>1359

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>1360

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>1361

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>1362

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>1363

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>1364

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>1365

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>1366

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>1367

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>1368

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>1369

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>1370

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>1371

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>1372

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>1373

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>1374

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>1375

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>1376

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>1377

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>1378

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>1379

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>1380

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>1381

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>1382

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>1383

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DDALLECAKDIQKGKIIALKGLGGFALLCDGRNFQTIERLRLLKNRPLKPFALMFKDLNTAKQHAFLNAL

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GGQKAIKEPRRLVLEIALKHQLNKLLKRVQKHFKEDELEIFQQMHDKKIQSIATNSIGRLFDIVAFSLDL

TGTISFEAESGQVLENLALQSDEIAFYPFEIKNSVVCLKEFYQAFEKDLGVLEPERIAKKFFNSLVEIIT

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>1384

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>1385

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>1386

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>1387

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NLFKT

>1388

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>1389

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>1390

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>1391

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>1392

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>1393

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>1394

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>1395

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>1396

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>1397

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>1398

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>1399

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>1400

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>1401

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>1402

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>1403

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>1404

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>1405

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>1406

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>1407

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>1408

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>1409

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>1410

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>1411

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>1412

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>1413

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>1415

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>1416

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>1417

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>1418

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>1419

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>1420

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>1423

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>1424

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>1426

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>1427

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IEDKK

>1428

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>1429

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>1430

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>1431

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>1432

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>1433

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>1434

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>1435

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>1436

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>1437

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>1438

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>1439

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>1440

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>1442

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>1443

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>1444

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>1445

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>1446

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>1447

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>1448

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>1450

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>1451

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>1452

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>1454

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>1455

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>1456

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>1457

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>1458

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RKHKY

>1459

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>1460

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>1461

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>1462

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>1463

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>1464

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>1465

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>1466

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>1467

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>1468

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KEK

>1469

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>1470

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>1471

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RR

>1472

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>1474

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>1475

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>1476

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>1477

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>1478

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>1479

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>1480

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>1481

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>1482

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>1483

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>1484

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>1485

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>1486

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>1487

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>1488

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>1489

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>1490

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>1506

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>1526

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>1530

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>1531

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>1532

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KEQA

>1533

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>1535

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>1536

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>1537

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>1538

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>1539

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>1540

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>1541

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>1542

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>1543

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>1544

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>1545

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>1547

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>1548

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>1549

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>1550

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>1551

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>1552

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>1553

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>1555

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>1556

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>1557

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>1559

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>1560

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QTYIQMANMMMAAAMLGIDSCPIEGYDQEKVEAYLEEKGYLNTAEFGVSVMACFGYRNQEITPKTRWKTE

VIYEVIE

>1561

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LSVMKYCEYVSAEKGVFYKTLVPCNLYGEFDKFEEKIAHMIPGLIARMHTAKLKNEKEFAMWGDGTARRE

YLNAKDLARFISLAYENIASIPSVMNVGSGVDYSIEEYYEKVAQVLDYKGVFVKDLSKPVGMQQKLMDIS

KQRALKWELEIPLEQGIKEAYEYYLKLLEV

>1562

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SNNKASFDYGSFSGWLGSVLNNGGAILENCQGAIQNAISTQLKSGVGSVGAISNHLIEVNLLKESPLNAV

VFLEFLGSSYSLEKLKAFEAKFKELKDLEDKKLKAALAVHAPYSVQKDMALSVIQLAKDSQSLLSTHFLE

SLEELEWVENSKGWFENFYQHFLKESHFKSLYKGANDYIDMFKDTHTLFVHNQFASLEALKRIKSQVKNA

FLITCPFSNRLLSGQALDLERTKEAGLSVSVATDGLSSNISLSLLDELRAFLLTHNMPLLELAKIALLGA

TRHGAKALALNNGEIEANKRADLSVFGFNEKFTKEQAILQFLLHAKEVECLFLGGKRVI

>1563

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EKEKSQNILKELEEKYHLDPSLVQNSAPKIYQRFLNAEIRISTIDAFFQSILRKFCWFVGLSANFEVNED

TKAHQQQLNEGFLSALNGEQLEALSVFIAQCLSYDSYTSDSILERLRFLKNKLYLFDPNKKEPAFDEKDF

LEKLRSLNEQIQSIETASDRAKTAIKCDDFRGFLNSSLTWLEKKSEYQSFKKLKSEIPTLESECEEIEND

LKRYYEAKETAIFKKFPKFIQLYDNATSKIQALDFDAIKDKVHVLLNGYEEMPAEFFYFRLDSKIAHILI

DEFQDTSLNDYKILAPFIDEIKAGIGQAKWHRSVFFVGDVKQSIYAFRGSFSSLFESVSKDFYHDNLEFN

HRSAPLIINYVNTIFKKAYQNSPTAYLEQKYPKTSQNKHVTDGYVKVSLVADERELLLDQVLQEAQNLLE

HRIEPKDITILCATNDDALEIKNYLQERLSAIRPSTESSAKLSQFVESKIIKNALEYALAEEPYKPFYKH

SVLKLAGYLHDDAIALAGFNPKKESVAGFVWKVMEQFELYGEPAQSCLELAVGCEDADGFLEKLETKAIA

SSHSKGAQIMTIHKSKGMQFPYVIVCERLGKPNSSHSNQLLEEYDGTELLRLYYRMKNREVVDKDYARAL

DKEEAAKDHEEINVYYVAFTRAELGLIVVAKDKKESKKESKNKTMREKLDLVPLEEGEIAPVISPQKEPL

ITSTLIKPHAYGEQVQEIEEEPSDYEKNNDQEAINFGIALHKGLEYQYAYNIPKQSVLEYLNYHHGFYGL

DYQALEESLELFENDAEIQALFKNLPLKGEAAFLFQGVVSRIDVLLWDRGQNLYVLDYKSSQNYQQSHKA

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>1564

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AIAKSEKATLFAARPLHVFWVVFYPVVRLFDVIAHFFLKKMGINPKEHDGTHSEEELKIIVGESLREGII

DSVEGEIIKNAXDFSDTSAKEIMTPRKDMVCLDEENSYEENIDIVLKGHFTRYPYCKGSKDNIIGMVHIR

DLLSRSIFTPKMHDFNQIVRKMIIVPESASISQILIKMKKEQIHTALVIDEYGGTAGLLTMEDIIEEIMG

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>1565

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TAPYKLKDNSLYALKKPSHHFKENHPNLCAVVNDESDLLKRGFASFVASNANAPMRNAFYDALNSIEPVT

GGGSVRNTLGYKVGNKSEFLSQYKFNLCFENSQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKSFV

NVHDFNNFDEAIDYIKYLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHKFS

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KKLGL

>1566

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TAPYKLKDNSLYALKKPSHHFKENHPNLCAVVNDESDLLKRGFASFVASNANAPMRNAFYDALNSIEPVT

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NVHDFNNFDEAIDYIKYLHTHPNAYLDMLYENPLNTLDGKAYFYQDLSFKKILDFFKTILENDTIYHNNP

FIFYRDLHEPLISIDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNY

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>1567

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KSGDNILKINNESTLSMSIDDAINLMRGKPKTPIQITVVRKNEPKPLVFNIIRDIIKLPSVYVKKIKETP

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KEITPKMINDDIQLKTAIDSLKTWSIVDEKMDEKAPKKK

>1568

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>1569

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>1570

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KPLKEIPEKANALEAYQRYLIKDFKHLKNLKYKIALDFGNGVGALGLEPILKALNIDFNSLYSDPDGNFP

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LEQTPSDLENTIKNLPYSYTTPEEKIAVSEEEKFEIIHNLQETLKNPPSHFPKIKEIISIDGVRVVFEHG

FGLIRASNTTPYLVSRFEGKDETTALEYKRALLNLLEKL