B56δ-related protein phosphatase 2A dysfunction identified in patients with intellectual disability

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Introduction

Unlike protein kinases, mutations in serine/threonine (Ser/Thr) protein phosphatases have not commonly been associated with disorders of human development. There are 2 major Ser/Thr protein phosphatase families in the cell: protein phosphatase 1 (PP1) and protein phosphatase 2A (PP2A), together accounting for more than 90% of all phospho-Ser/Thr dephosphorylations. PP2A consists of a catalytic subunit (C), a substrate binding regulatory subunit (B), and a scaffolding subunit (A) that links B and C. Unlike the generally expressed A and C subunits, there is a plethora of B subunits with different expression patterns (1). The differential substrate preferences of the nearly 100 different PP2A holoenzymes that, in theory, can be formed by 2 C isoforms, 2 A isoforms, and at least 23 types of B subunits is largely unknown (2), particularly within the context of a whole organism. Apparently, PP2A-dependent protein dephosphorylation has a potential for regulation that may be just as fine-tuned as protein phosphorylation. Unlike protein phosphorylation, associations between mutations in PP2A subunits and genetic diseases or syndromes have not been described until recently, when 4 de novo PPP2R5D and 3 de novo PPP2R1A mutations were found among the first 1,133 parent-child trios sequenced in the United Kingdom Deciphering Developmental Disorders project (3).

Here we report inherited dysregulation of protein phosphatase activity as a cause of intellectual disability (ID). De novo missense mutations in 2 subunits of serine/threonine (Ser/Thr) protein phosphatase 2A (PP2A) were identified in 16 individuals with mild to severe ID, long-lasting hypotonia, epileptic susceptibility, frontal bossing, mild hypertelorism, and downslanting palpebral fissures. PP2A comprises catalytic (C), scaffolding (A), and regulatory (B) subunits that determine subcellular anchoring, substrate specificity, and physiological function. Ten patients had mutations within a highly conserved acidic loop of the PPP2R5D-encoded B56δ regulatory subunit, with the same E198K mutation present in 6 individuals. Five patients had mutations in the PPP2R1A-encoded scaffolding subunit, with the same R182W mutation in 3 individuals. Some Au cases presented with large ventricles, causing macrocephaly and hydrocephalus suspicion, and all cases exhibited partial or complete corpus callosum agenesis. Functional evaluation revealed that mutant A and B subunits were stable and uncoupled from phosphatase activity. Mutant B56δ was A and C binding–deficient, while mutant Aa subunits bound B56δ well but were unable to bind C or bound a catalytically impaired C, suggesting a dominant-negative effect where mutant subunits hinder dephosphorylation of B56δ-anchored substrates. Moreover, mutant subunit overexpression resulted in hyperphosphorylation of GSK3β, a B56δ-regulated substrate. This effect was in line with clinical observations, supporting a correlation between the ID degree and biochemical disturbance.

Authorship note: Gunnar Houge and Dorien Haesen contributed equally to this work.

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Taken together, of the 11 mutations in PPP2R5D, 6 mutations and 2 mutations were identical; 3 of the 5 mutations in PPP2R1A were also identical. All AA mutations and all but one of the B56δ mutations had the potential to hinder access of catalytically competent C subunits to B56δ-regulated substrates, suggesting a common dominant-negative disease mechanism mainly affecting B56δ-regulated Ser/Thr dephosphorylation.

Results

In cases with intellectual disability (ID) of unknown etiology, parent-child trio exome sequencing was performed to find de novo and recessive mutations that could explain the condition. De novo missense mutations in 2 subunits of the Ser/Thr phosphatase PP2A were identified in 16 individuals from the United Kingdom (7 cases), the Netherlands (7 cases), Israel (1 case), and Norway (1 case).

The 7 United Kingdom cases were found among 1,133 chromosomally normal parent-child trios (3). This suggests that the prevalence of PP2A subunit mutations in the moderate-to-severe ID group without pathogenic copy number aberrations is around 0.6%. In the United Kingdom, this was part of the large DDD project (http://www.ddduk.org); in other cases, this was done as part of routine diagnostics. In 11 cases, de novo missense mutations in PPP2R5D, encoding the regulatory B56δ PP2A subunit, were found. In 5 other cases, a de novo missense mutation in PPP2R1A, encoding the scaffolding AA subunit of PP2A, was found. Six mutations and 2 mutations in PPP2R5D were identical, and 3 PPP2R1A mutations were identical. Details on all mutations can be found in Table 1. Other trio exome sequencing results indicating a de novo change of possible relevance or a recessive condition of potential interest can be found in Supplemental Table 1 (supplemental material available online with this article; doi:10.1172/JCI79860DS1). In 10 cases, such findings were made, but based on bioinformatic evaluation of the variants and the clinical features of the patients, all but one of these findings could easily be excluded as causative factors for the phenotype. The exception was case 15, which had heterozygosity for a TMEM67 splice mutation and a few signs that were compatible with a ciliopathy (e.g., unilateral postaxial polydactyly). However, this could also be a random finding, since a second TMEM67 mutation was not found upon Sanger sequencing. In addition, detecting the same de novo missense mutations in patients with identical clinical features is, in itself, evidence in support of causality, especially when supported by functional data (see below). As a crude estimation, the likelihood of finding 10 de novo missense mutations in the same 9–amino acid stretch of B56δ by chance should be less than 10−6 (see Statistics).

The clinical features of the 11 PPP2R5D cases and the 5 PPP2R1A cases are summarized in Tables 2 and 3, respectively. Despite mutations occurring in 2 different PP2A subunit genes with different biochemical functions (regulatory and scaffolding), there are clinical similarities between the cases. All patients were born after a normal pregnancy, and 15/16 cases had birth weights within normal range. In 2 cases, breech deliveries were reported, and in 2 other cases, emergency caesarean sections had to be performed. After birth, ID and hypotonia were common features in all cases. Despite pronounced and long-lasting hypotonia, feeding difficulties were usually not a major problem, and only one case had gastrosome. In 12/16 cases, the degree of ID was severe, and this correlated with very late independent walking, usually around age 6–7 years. The exceptions were the 4 patients with E200K, P201R, or W207R PPP2R5D mutations (see below for functional explanation), who learned to walk between 1½ and 2½ years of age and had mild/moderate ID (Table 2). These 4 cases were also the only ones with language development beyond a few words. Seven out of 16 patients had epilepsy, including one of the mild ID cases. Only one patient had short stature (case 1 with a P53S mutation, see Table 2), and he was the only PPP2R5D case that was microcephalic. In the other PPP2R5D cases, head circumferences were from upper-normal range to pronounced macrocephaly, and in the latter cases, hydrocephalus was suspected. In contrast, most PPP2R1A cases were normocephalic or microcephalic, and hydrocephalus was initially suspected in only one case (Table 3). In all these patients, the corpus callosum was absent or almost absent, a feature that distinguished PPP2R1A cases from PPP2R5D cases. In contrast, facial features were overlapping (Figure 1): A hypotonic and sometimes also elongated face with tented upper lip, mild hypertelorism with downsloping palpebral fissures, and frontal bossing in the PPP2R5D cases.

The finding of recurrent and clustered de novo missense mutations in 2 PP2A subunit genes (PPP2R5D and PPP2R1A) suggested a dominant-negative– or gain-of-function–related disease mechanism, rather than haploinsufficiency or loss-of-function. All but one of the PPP2R5D mutations (E198K, E200K, P201R, and...
and W207R) clustered in a highly conserved acidic loop that faces the A and C subunits (4–6). This acidic surface corresponds to the extended loop between α-helices 3 and 4 of HEAT domain 2 in the crystal structure of the highly related B56γ isoform (Figure 2A). Only the P53S mutation (case 1 in Table 2) localized outside this loop, i.e., in the B56δ-specific N-terminal domain.

To investigate if the PPP2R5D missense mutations affected subunit interactions, a human embryonic kidney cell line — HEK293 cells, a well-known model from previous PP2A subunit interaction studies (7) — was transfected with EGFP-tagged WT or mutant B56δ subunits in order to study subunit interactions. All ID-associated B56δ mutants except P53S showed deficient holoenzyme formation, i.e., A- or C-to-B56δ association (Figure 2B). To check if others had discovered missense variants in the same acidic B56δ loop, Broad institute’s ExAC browser (http://exac.broadinstitute.org/) was consulted. Only 2 other missense variants (P196L and P201S) were reported. Interestingly, the latter variant was in the same residue as the de novo mutation (P201R) in case 10, although the amino acid change was different. Unlike P201R, we found that P201S failed to show any significant A or C binding defects (Supplemental Figure 1), further strengthening our working hypothesis that a charge change in the acidic B56δ loop could be pathogenic.

Our cellular binding assays with Glutathione S-Transferase–tagged (GST-tagged) B subunits and HemAgglutinin-tagged (HA-tagged) WT or mutant Aα subunits revealed that all 3 PPP2R1A mutations also affected PP2A holoenzyme formation (Figure 3). Surprisingly, interaction with the C subunit was hindered, despite the Aα mutations being in HEAT domains predicted to interact with B (Figure 3A). The mutations’ effect on B subunit binding was complex (Figure 3B). All Aα mutants lacked significant binding to the B55 (also called B) family members tested (isoforms B55α and B55β), as well as to the B56 (also called B’ or PR61) family members tested (B56α and B56γ). On the other hand, binding to B56δ was almost entirely retained, whereas B56ε bound significantly less. For PR72, a member of the B’’ family of PP2A regulatory subunits, binding was retained to Aα-P179L but was completely lost to the Aα-R182W and Aα-R258H mutants (Figure 3B). These (mutant) Aα binding characteristics were confirmed for endogenous B55α and B56δ subunits, for which good-quality, isoform-specific antibodies are available (Figure 4A). These data could be compatible with a dominant-negative effect on, notably, B56δ for all Aα mutants, and on PR72...
for Aα-P179L, provided that C binding would be lost or diminished in the B56α-Aα mutant complex. To provide direct evidence that mutant Aα can complex with B56δ without C, we expressed HA-Aα mutants or HA-Aα (WT) in HEK293 cells stably expressing EGFP-TEV-B56δ (WT) and analyzed the presence of endogenous C in anti-HA immunoprecipitates from the tobacco etch virus–cleaved δ subunit was clearly present in B56α (WT) and analyzed the presence of endogenous C

In genes encoding PP2A subunits may cause syndromic ID — and therefore may be of therapeutic importance. A-C binding–defective Aα mutants, or C binding–defective Aα-mutants, or B56δ–mutant A-C complexes is catalytically impaired. Furthermore, protein-synthesis–blocking experiments showed that the ID-associated B56δ (P53S, E198K) or Aα (P179L, R182W) mutants tested appeared more long-lived than the WT subunits in our assay (Supplemental Figure 2).

Taken together, for all but one (P53S in PPP2R5D) of the de novo mutations identified, our biochemical data are consistent with a common defect in PP2A-B56δ–dependent dephosphorylation. A-C binding—defective B56δ mutants, or C binding— but not B56δ binding—defective Aα-mutants, and B56δ binding Aα-mutants harboring a catalytically impaired C subunit, may all block dephosphorylation of PP2A-B56δ–specific substrates and interfere with phosphorylation–dephosphorylation dynamics in the brain. In line with this hypothesis, overexpression of the E198K B56δ mutant or the R182W Aα mutant in HEK293 cells resulted in increased dephosphorylation of GSK-3β Ser9, an established PP2A-B56δ substrate in this cell line (Figure 5 and ref. 10).

Discussion
The presented work demonstrates that de novo missense mutations in genes encoding PP2A subunits may cause syndromic ID — and

| Table 2. Clinical features in cases with de novo PPP2R5D missense mutations |

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Case 1</th>
<th>Case 2</th>
<th>Case 3</th>
<th>Case 4</th>
<th>Case 5</th>
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<td>Severe</td>
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<td>5–10th</td>
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<tr>
<td>Head circumference</td>
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<td>50th</td>
<td>5 cm &gt; 97th at age 3½ yr</td>
<td>50th</td>
<td>97th</td>
<td>99th</td>
<td>99th</td>
<td>1 cm &gt; 97th</td>
<td>75th</td>
<td>97th</td>
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<td>Normal</td>
<td>Normal</td>
<td>Normal</td>
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<td>10 kg &gt; 97th</td>
<td>75th</td>
<td>60th</td>
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<td>Hydrocephalus</td>
<td>Mild ventricular dilatation</td>
<td>Mild ventricular dilatation</td>
<td>Small CC</td>
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Other findings
- Cataract
- Hypoglycemia
- Abnormal fat oxidation
- Bilateral 6th nerve palsies
- Narrow palate
- Mild 2/3 and 3/4 finger syndactyly
- Scoliosis
- Neonatal nonepileptic myoclonus
- Fatigue
- Ptosis
- Strabismus
- Gastric reflux
- Hip dysplasia
- Scoliosis Hip dysplasia

Fatigue, Ptosis, Strabismus, and Hip dysplasia are common features in cases with de novo PPP2R5D missense mutations. The presence of these features may indicate a common pathogenic mechanism in these cases.
Probably also nonsyndromic ID, since the facial dysmorphism in these cases is subtle (Figure 1). The PPP2R5D and PPP2R1A mutations disrupt B56δ-dependent dephosphorylation dynamics and link PP2A dysfunction to congenital brain dysfunction.

In general, the Aα cases were more severely affected than the B56δ cases. All had severe ID, absent speech, diminished brain growth, and partial or complete agenesis of the corpus callosum (Table 3). This is in line with the expected greater difficulty to link PP2A dysfunction to congenital brain dysfunction.

Besides its scaffolding function, Aα is a major player in the biogenesis of active PP2A holoenzymes (14). This highly regulated but incompletely understood process does not only involve simple trimeric assembly of the A, B, and C subunits, but it also involves several activation steps of the C subunit, which is de novo translated as an inactive enzyme (15). It has been suggested that some of these activation steps require or are facilitated by the A subunit (16, 17), explaining why A-subunit mutations may affect the specific activity of the associated C subunit, as observed here within the B56δ-(mutant A)-C complexes (Figure 4C). Additional activity measurements performed directly in anti-HA immunoprecipitates of HA-tagged (mutated) A subunits seem to further confirm this hypothesis (Supplemental Figure 3). Hence, it can be further rationalized why mutations in the A subunit have a much more severe effect on the PP2A system as a whole, as opposed to mutations in B56δ, which affect a single PP2A holoenzyme complex.

PPP2R5D encodes the longest isoform of the B′ family of PP2A regulatory subunits and harbors unique N- and C-terminal extensions, which are predicted to be important for substrate recognition and/or subcellular targeting (18). Ten out of 11 PPP2R5D mutations were located in a conserved acidic loop of B56δ needed for holoenzyme formation (Table 1), and all mutations introduced a positively charged residue (either arginine or lysine). Only one mutation (P53S) was atypical, and this case also had a different clinical picture: it was the only PPP2R5D case with short stature (Table 2) and was analyzed and visualized with Molsoft MolBrowser 3.7. (B) Cellular binding assays of ID-associated B56δ mutants and endogenous A and C subunits. EGFP-tagged WT B56δ, 5 ID-associated B56δ mutants (P53S, E198K, E200K, P201R, and W207R), or EGFP alone (−) were ectopically expressed in HEK293 cells. Following EGFP trapping, the presence of endogenous A and C subunits in the trapped complexes was examined by immunoblotting (IB). After quantification of the band intensities with ImageJ software, the ratios between EGFP and C signals — and between EGFP and A signals — were determined and calculated relative to B56δ WT control. Mean values and a representative image of 4 independent experiments are shown (1-way multiple-comparisons ANOVA; *P < 0.05, **P < 0.01).
Table 3. Clinical features in cases with de novo PPP2R1A missense mutations

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<tr>
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<td>CC hypoplasia</td>
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<td>CC agenesis Delayed myelination</td>
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<td>Scoliosis</td>
<td>Scoliosis Hip dysplasia Physically strong</td>
<td>Cortical visual impairment Unilateral postaxial polydactyly</td>
<td>Hyperactivity Obstipation Entropion of eyelids</td>
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</table>

Height, head circumference, and weight are given relative to centiles (the 3rd and 97th centile correspond to ± 2 SD). Abbreviations: y, years; CC, corpus callosum; C/S, cesarean section; –, unknown or not done.

except B56δ and PR72, have been shown to make stabilizing contacts with the C subunit tail (5, 19), C-subunit binding to B56δ, and thereby with control of localized δ anchoring of PP2A via B56δ does not appear essential for mammalian brain development (22). Nevertheless, other malformations than severe corpus callosum hypogenesis were not found in the 5 PPP2R1A cases (Table 3). The restricted phenotype may be related to our finding that mutated A subunits bound most tightly to B56δ and (for P179L) also PR72 (Figure 3B), both of which are expressed in the brain, notably in the striatum where both B56δ and PR72 (encoded by PPP2R3A) control the dephosphorylation of the neural dopamine-regulated inhibitor of PP1 (DARPP-32) (23–25).

Despite the severe intellectual dysfunction in most patients, B56δ does not appear essential for mammalian brain development, since Ppp2r5d knockout mice have intact learning and memory despite ataxia and tauopathy (21). This also suggests that our patients’ ID was not caused by haploinsufficiency or a mere loss of function. It is therefore tempting to speculate that the mutated B56δ subunits may not only interfere in a dominant manner with dephosphorylation of B56δ binding PP2A substrates, as shown for GSK-3β in HEK293 cells (Figure 5), but also with subcellular anchoring of PP2A via B56δ, and thereby with control of localized signaling. Thus, A-C binding–deficient B56δ mutants may still form complexes with B56δ partners, but without promoting dephosphorylation. Such dysphosphorylation may have far-reaching consequences for regulation of localized signaling. One example could be the signaling complex scaffolded by the neural variant of the cAMP-dependent PKA anchoring protein mAKAP, that binds B56δ and several other phosphatases (PP1, PP2B) and kinases (PKA, PKD1, RSK3, ERK5) (26, 27). Dephosphorylation of PP2A-B56δ substrates may also be hindered, e.g., the transcription factor and PKA-substrate HAND (28), the neural cyclin-dependent kinase 5 (CDK5) activator CDK5R1 (21), and DARPP-32 (24, 25). PKA activates DARPP-32 directly by Thr-34 phosphorylation and indirectly by PP2A-B56δ–dependent activation through Thr-75 dephosphorylation (24). B56δ has several sites for PKA phosphorylation that activate PP2A-B56δ phosphatase activity (24, 29). Moreover, PKA-activated PP2A-B56δ–dependent dephosphorylation of another DARPP-32 phosphorylation site (Ser-97) induces nuclear import — mediating dopamine-dependent epigenetic functions (25) — and lack of nuclear PP2A-B56δ targeting has been associated with juvenile myoclonic epilepsy (30). There is also evidence that PP2A-B56δ regulates both expression (30) and activity (31) of tyrosine hydroxylase, the rate-limiting enzyme in catecholamine synthesis. Which of these candidate substrates will eventually be of pathologic relevance in our ID patients remains to be further determined in appropriate cellular and animal models.

A model for a common dominant-negative effect of mutant B56δ and Aa subunits is depicted in Figure 6. This model explains why all our biochemical findings are compatible with B56δ-dependent PP2A dysregulation. Our model is also supported by a recent paper showing that Aa can form a tight complex in vitro with members of the B” subunit family, including PR72, in
Figure 3. Binding of mutant and WT Aα to C and B subunits. (A) PP2A-C subunit binding assays: HA-tagged WT Aα, 3 ID-associated Aα mutants (P179L, R182W, and R258H), or an empty HA-vector (–) were transfected into HEK293 cells. Following anti-HA immunoprecipitation, the presence of endogenous C subunit in the immunoprecipitates was examined by immunoblotting (IB). After quantification of the band intensities with ImageJ software, the ratios between HA and C signals were determined and calculated relative to WT Aα control. Mean values and a representative image of 3 independent experiments are shown (1-way multiple-comparisons ANOVA, ** P < 0.01). (B) PP2A B subunit binding assays: Several GST-tagged B subunits, belonging to 3 different families (B55 or B, B56 or B′, and B′′) or GST alone (–) were coexpressed in HEK293 cells with HA-tagged WT Aα, or ID-associated Aα-P179L, R182W, and R258H mutants. The presence of HA-Aα (WT or mutant) in the complete lysates and the isolated GST pulldown complexes was determined by IB. After quantification of the band intensities with ImageJ software, the ratios between GST and HA signals were determined and calculated relative to WT Aα control (which were set to 100% for each B-type subunit pulldown). Mean values and a representative image of 3 independent experiments are shown (1-way multiple-comparisons ANOVA; * P < 0.05, ** P < 0.01, *** P < 0.001).
the absence of the C subunit (32). It may be of interest to study if fingolimod (FTY720), a PP2A activator and immunosuppressant that is licensed for treatment of multiple sclerosis (33–35), or empty HA-vector (−), eventually turn out to be solely paternal (40). Since 88% of the cancer-associated Aα mutations are of the missense-variant, a dominant-negative effect also in cancer promotion is likely. None of our patients have been diagnosed with or treated for cancer. The cancer risk might not be increased, in line with what is usually the case for congenital gain-of-function mutations in other cancer-related pathways like the RAS/MAPK pathway or the PI3K/akt cascade. Only further patients and patient follow-ups will answer this question, but a major cancer risk seems unlikely.

The tumor-suppressor effect of PP2A may operate by KRAS/MAPK cascade inhibition, KRAS/ARF/TP53 cascade inhibition, or PI3K/akt/TP53 cascade inhibition (33). Somatic mosaic activation of the PI3K/akt cascade causes the megalencephaly-capillary malformation-polymicrogyria (MCAP) and megalencephaly-polymicrogyria-polydactyly-hydrocephalus (MPPH) group of overgrowth syndromes (41).

These patients have variable ID, a tendency to develop hydrocephalus and epilepsy, and dysmorphic facial features, including frontal bossing with hypotonia, tented upper lip, and deep-set eyes. The latter features are shared with several of our patients (Figure 1). It is therefore relevant to consider B56δ-dependent PP2A dysregulation syndrome (which we propose to be designated B56deltopathies) among the differential diagnoses to the MCAP/MPPH group of syndromes, at least in some cases. It is conceivable that the B56δ mutations may affect only a subgroup of PP2A substrates located distally in the PIK3 signaling cascade — such as OSK-3β Ser9, a well-established Akt phosphorylation site — since the proximal steps do not appear to be subject to B56δ-dependent dephosphorylation (42).

In summary, we have demonstrated that de novo missense mutations in the PPP2R5D and PPP2R1A genes encoding PP2A activators (36) may improve brain function in these patients.

For future evaluation of de novo mutation origin (paternal or maternal)(37), it is of interest that all 3 PPP2R1A mutations also are found in the Sanger Institute’s Catalogue of Somatic Mutations in Cancer (the COSMIC database; http://cancer.sanger.ac.uk/cosmic), mainly in endometrial and ovarian cancers (38, 39). Aα P179L/P179R, R182W, and R258H are by far the most prevalent mutations. A growth advantage may also explain mutation recurrence if these de novo mutations turn out to be solely paternal (40).
of patient-parent trios. These patients showed no pathogenic copy number changes (high-resolution copy number array). Putative de novo variants were validated by Sanger sequencing of blood DNA. In 4 of 7 cases, other de novo variants were identified, but none of these were likely to cause the phenotype (Supplemental Table 1). A possible exception was case 16, in which heterozygosity for a likely pathogenic mutation in the TMEM67 was identified. The patient had clinical features partly consistent with a ciliopathy (unilateral postaxial polydactyly, unilateral kidney agenesis, and absent uterus). However, a second TMEM67 mutation was not identified after Sanger sequencing. The 7 United Kingdom patients (cases 3–5, 10, and 12–14 in Tables 2 and 3) were recruited to the DDD study by the United Kingdom National Health Service or the Republic of Ireland Regional Genetics Service (3). Recruitment criteria were patients with neurodevelopmental disorders and/or congenital anomalies, abnormal growth parameters, dysmorphic features, and unusual behavior. DNA samples from patients and parents were analyzed by the Wellcome Trust Sanger Institute using high-resolution microarray analysis (array-CGH and SNP-genotyping) to investigate copy number variations (CNVs) in the child, and exome sequencing to investigate single nucleotide polymorphisms (SNPs) and small insertions/deletions (indels). Putative de novo sequence variants were validated using targeted Sanger sequencing of blood-sample DNA. All genomic variants were annotated with the most severe consequence predicted by Ensembl Variant Effect Predictor (VEP) (45) and their minor allele frequencies observed in diverse population samples. Likely, diagnostic variants were fed back to referring clinical geneticists for validation and discussion with the family via the patient’s record in Database of Chromosomal Imbalance and Phenotype in Humans Using Ensembl Resources (DECIPHER; Ensembl) (46), where they can be viewed in an interactive genome browser. Full genomic datasets were also deposited under accession number EGAS00001000775 in the European Genome-Phenome Archive (www.ebi.ac.uk/ega).

Figure 5. Increased phosphorylation of GSK-3β Ser9 upon expression of B56δ-E198K or Aα-R182W. GFP-tagged WT B56δ, E198K mutant B56δ, or GFP alone (–) (left); or HA-tagged WT Aα, R182W mutant Aα, or HA alone (–) (right) were expressed in HEK293 cells, and the effect on GSK-3β phosphorylation determined by immunoblotting (IB) with the indicated antibodies. Total GSK-3β and phospho-Ser9 GSK-3β signals were determined on different blots, which were both developed for vinculin to correct for loading differences. In cells expressing the ID-associated mutants, higher phospho/total GSK-3β ratios were found, relative to cells transfected with empty expression vector (in which case, this ratio was set to 100%) or cells expressing WT subunits. Mean values and one representative image of 3 independent experiments are shown (1-way multiple-comparisons ANOVA; *P < 0.05, **P < 0.01).
All mutations were confirmed by sequencing (LGC Limited). Thereafter, HEK293 cells (ATCC) were transfected with PEI transfection reagents according to standard protocol. Forty-eight hours after transfection, cells were rinsed with PBS, lysed in 200 μL NET buffer (50 mM Tris pH 7.4, 150 mM NaCl, 15 mM EDTA, and 1% Nonidet P-40) containing protease and phosphatase inhibitor cocktail (Roche Applied Science), and centrifuged for 15 minutes at 13,000 g. In case phosphatase activity needed to be measured, phosphatase inhibitors were omitted from the lysis buffer.

For EGFP trapping, cell lysates were incubated at 4°C for 1 hour with wash buffer (10 mM Tris-HCl pH 7.5, 0.5 mM EDTA, and 150 mM NaCl) and 15 μL HA-agarose beads (ChromoTek GmbH) on a rotating wheel. The beads were washed 4 times with 0.3 mL of wash buffer.

For GST pulldown, cell lysates were incubated at 4°C for 1 hour with NENT 100 buffer (20 mM Tris-HCl pH 7.4, 1 mM EDTA, 0.1% Nonidet P-40, 25% glycerol, and 100 mM NaCl) containing 1 mg/mL bovine serum albumin and 25 μL glutathione-Sepharose beads (GE Healthcare) on a rotating wheel. The beads were washed 2 times with 0.3 mL of NENT 100 containing 1 mg/mL bovine serum albumin, and 2 times with 0.3 mL of NENT 100 containing 300 mM NaCl.

For HA immunoprecipitation, the lysates were precleared with Protein A-Sepharose beads (GE Healthcare) for 1 hour, and incubated on a rotating wheel at 4°C for 2 hours with 1 μg HA antibody (Sigma-Aldrich) in TBS/1% Nonidet P-40. Protein A-Sepharose beads were added for 1 hour, and beads were washed 2 times in NENT 100 and 2 times in TBS/0.1% Nonidet P-40. Alternatively, 25 μL HA-agarose beads (Sigma-Aldrich) were directly added to the lysates and incubated on a rotating wheel in 500 μL TBS/0.1% Nonidet P-40 for 1.5 hours at 4°C. Beads were washed 4 times in TBS/0.1% Nonidet P-40.

In all cases, bound proteins were eluted by the addition of NuPAGE sample buffer (Invitrogen) and boiling. The eluted proteins were subsequently analyzed by SDS-PAGE on 4%-12% (wt/vol) Bis-Tris gels (Bio-Rad) and Western blotting. The membranes were blocked in 5% milk solution in TBS/0.1% Tween 20 for 1 hour at room temperature and subsequently incubated with the primary antibody overnight at 4°C. The following primary antibodies were used: mouse monoclonal anti-GST (Sigma-Aldrich), anti-HA (Sigma-Aldrich), anti-GFP (Corning), anti-PP2A-A subunit (supplied by S. Dilworth, Middlesex University, London, United Kingdom), anti-PP2A-C subunit (BD Biosciences); and rabbit polyclonal anti-B55α (Cell Signaling Technology), and anti-B56δ (20). After washing in TBS/0.1% Tween 20, the membranes were incubated at room temperature for 1 hour with horseradish peroxidase-conjugated secondary antibodies (Dako) and developed using a Pierce enhanced chemiluminescence detection system (Thermo Fisher Scientific). All densitometric quantifications were done with ImageJ software.

For the IP-on-IP approach, a polyclonal population of HEK293 cells stably expressing EGFP-TEV-B56δ was used (selected with 2 μg/mL puromycin). The EGFP-TEV expression vector was a gift of E. Heroes (KU Leuven, Leuven, Belgium). Forty-eight hours after transfection with HA-Au (pMB001) or HA-mutant Au (pMB001), EGFP trapping was performed, and the trapped complexes were incubated overnight at 4°C with 0.2 μg/μL of recombinant TEV protease in TEV cleavage buffer (TBS, 1 mM DTT, 0.5 mM EDTA). Following addition of EDTA (1 mM), PMSF (1 mM), and TLCK (1 mM), the TEV eluates were subjected to HA immunoprecipitation with HA-agarose beads and the washed immunoprecipitates were analyzed by immunoblotting with anti-HA, anti-PP2A-C, and anti-B56δ antibodies (20, 21).

For PP2A activity measurements, the HA-agarose beads were washed once more with 20 mM Tris-HCl pH 7.4 plus 1 mM DTT, and finally resuspended in 60 μL enzyme dilution buffer (catalog 20-169, Millipore). All assays were performed with 20 μL of this phosphatase suspension and 4.5 μL of 2 mM stock of K-R-pT-I-R-R phosphopeptide (catalog 12-219, Millipore) for 10–60 minutes at 30°C (still in the linear range of the assay). The released free phosphate was determined by the addition of malachite green solution (10/1 mix of solution A and B; [catalog 20-105, Millipore] and solution B [catalog 20-104, Millipore]). After 15 min incubation at room temperature, absorbance at 630 nm was measured in a multi-channel spectrophotometer. Picomolar amounts of phosphate released were calculated by comparison with a standard curve of known KH₂PO₄ concentrations, as outlined in the manufacturer’s instructions (Ser/Thr Phosphatase Assay Kit 1, Millipore). Specific phosphatase activity was obtained by correcting for Pwo polymerase (Roche Applied Science) and complementary DNA oligonucleotide primers (Sigma-Aldrich) containing the desired point mutations (primer sequences in Supplemental Table 2). All mutations were confirmed by sequencing (LGC Limited). Thereafter, HEK293 cells (ATCC) were transfected with PEI transfection reagents according to standard protocol. Forty-eight hours after transfection, cells were rinsed with PBS, lysed in 200 μL NET buffer (50 mM Tris pH 7.4, 150 mM NaCl, 15 mM EDTA, and 1% Nonidet P-40) containing protease and phosphatase inhibitor cocktail (Roche Applied Science), and centrifuged for 15 minutes at 13,000 g. In case phosphatase activity needed to be measured, phosphatase inhibitors were omitted from the lysis buffer.

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these absolute values for amount of C present in the samples, as determined by immunoblotting with anti-C antibodies and quantification of the signals by ImageJ software.

For protein-stability analysis, HEK293 cells were transfected with EGFP-B56 (WT); with EGFP-B56-P53S or EGFP-B56-E198K mutants (pEGFP-C1); or with HA-Aα (WT), HA-Aα-R182W, or HA-Aα-P179L mutants (pMB001), one 10 cm plate per plasmid. Twenty-four hours after transfection, each 10-cm plate was split over 6 wells on a 6-well plate, in which eventually 50 μM cycloheximide (CHX, Sigma-Aldrich) was added per well to block translation. Following incubation with CHX for different time points (0, 10, and 24 hours), whole-cell lysates were prepared in NET lysis buffer and further analyzed by immunoblotting with anti-vinculin mouse monoclonals (Sigma-Aldrich), anti-HA, or anti-GFP antibodies. Band intensities were quantified using ImageJ software.

Statistics. Statistical analysis of biochemical data was done with 1-way multiple-comparisons ANOVA, and P < 0.05 was considered to be significant.

The calculation of the chance likelihood for finding 10 de novo mutations in the same 9-amino acid stretch of B56 was based on the following assumptions: The target size is <10−6 of the total ORF size, the number of random missense changes per generation is on average about 2,000 ID cases were tested. In that case, the phenotype should also be random, and this was not the case.

Study approval. The DDD study has UK Research Ethics Committee (REC) approval (10/H0305/83, granted by the Cambridge South REC, and GEN/284/12 granted by the Republic of Ireland REC). In other cases, ascertainment of patients was part of the clinical routine. All patients’ families have consented to publication of clinical findings. Written informed consent was also obtained for publication of all facial photographs presented in Figure 1.

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