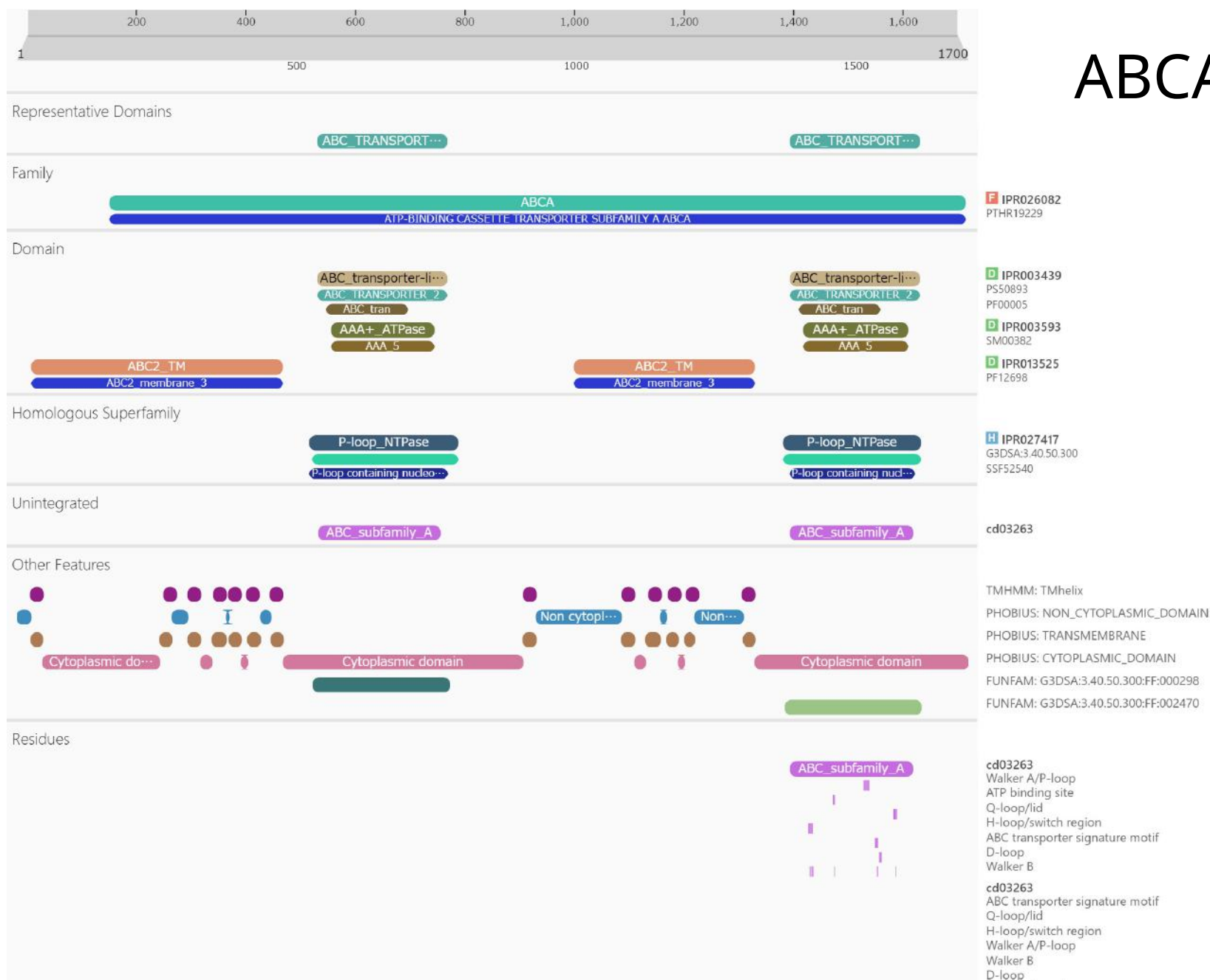
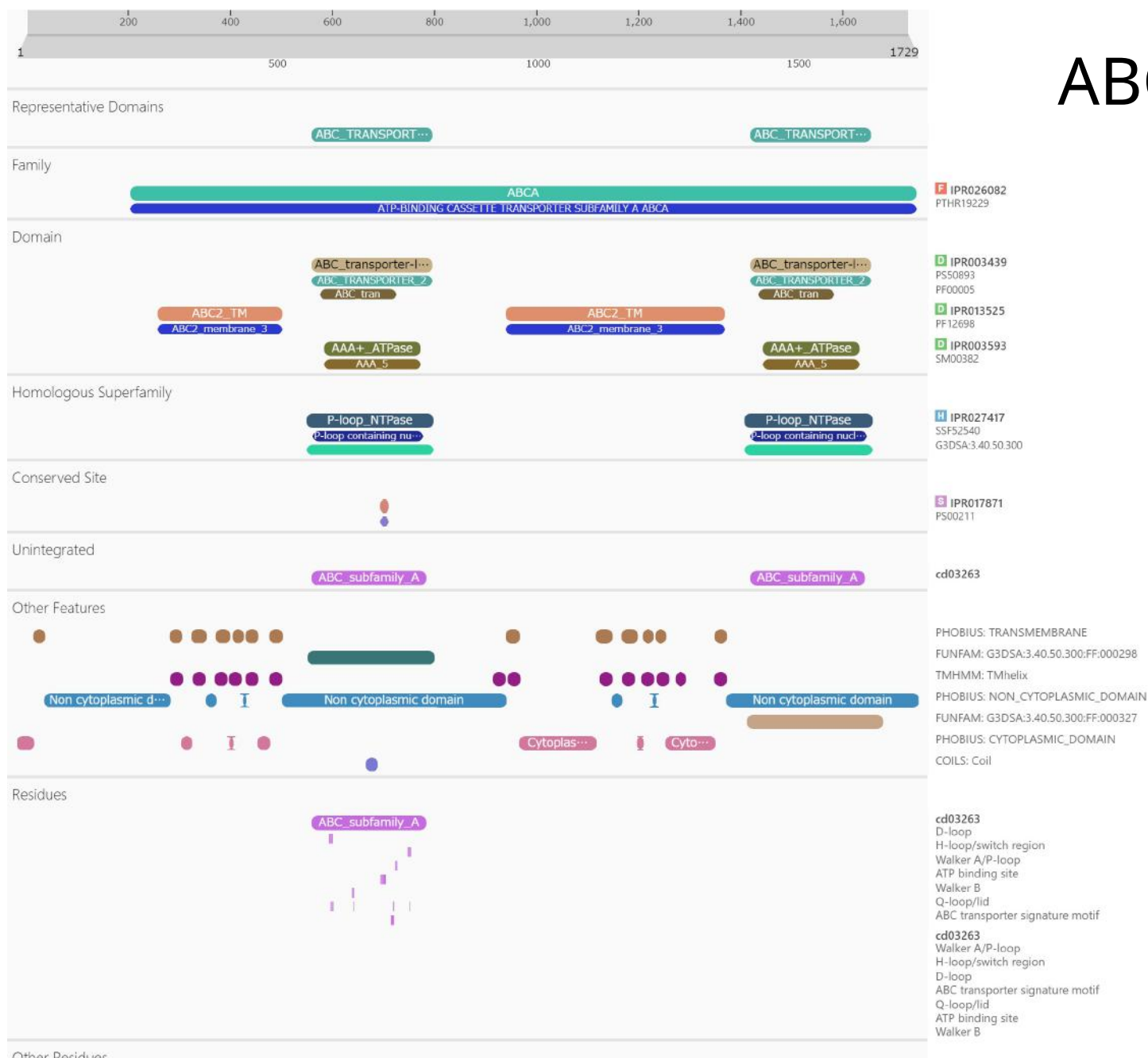


Supplementary Figure 4. Domain prediction of BmABC transporters defined in this study using InterPro.

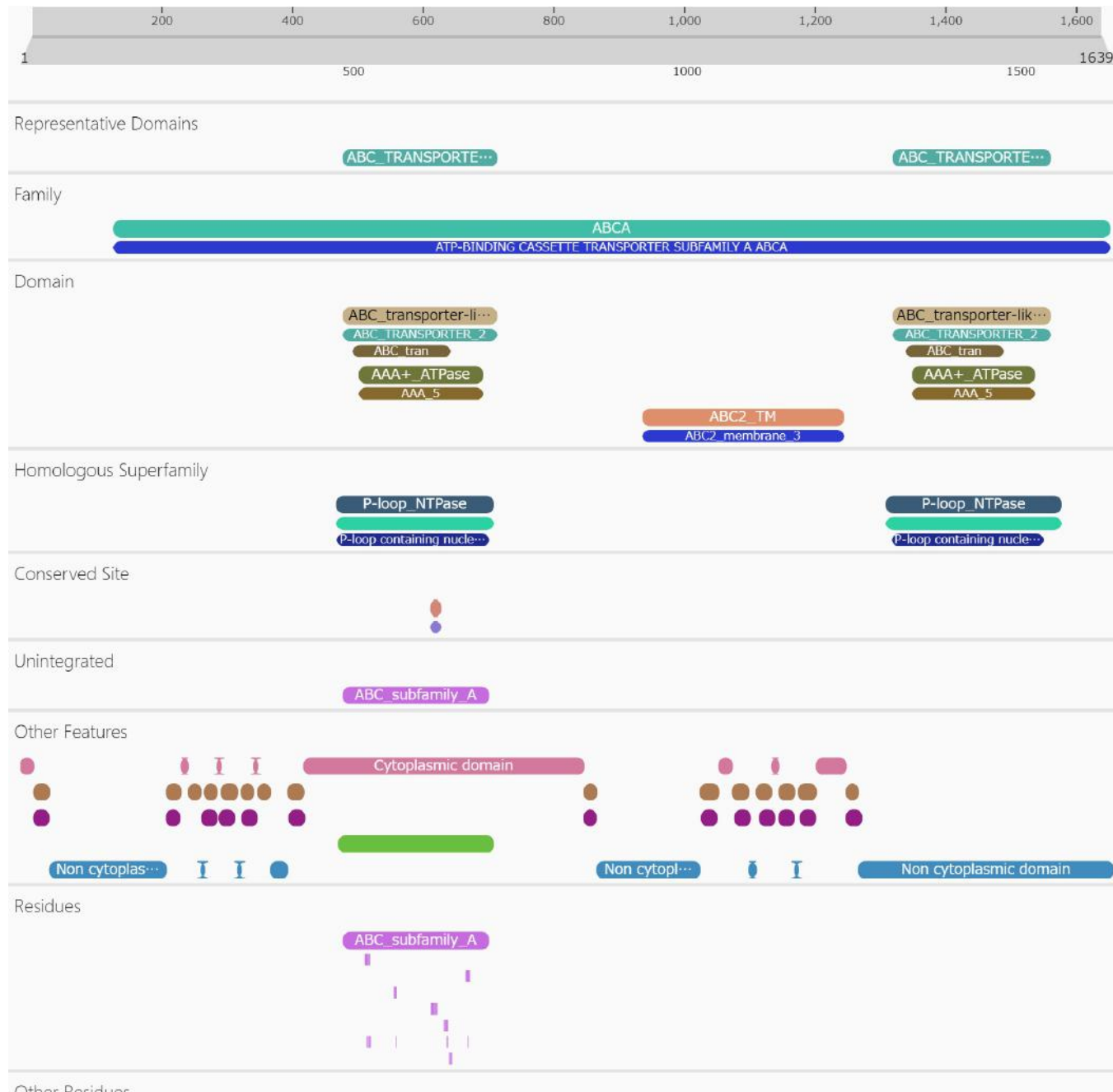
ABCA3



ABCA2



ABCA4



F IPR026082
PTHR19229

D IPR003439
PSS0893
PF00005

D IPR003593
SM00382

D IPR013525
PF12698

H IPR027417
G3DSA:3.40.50.300
SSF52540

S IPR017871
PS00211

cd03263

PHOBIUS: CYTOPLASMIC_DOMAIN

PHOBIUS: TRANSMEMBRANE

TMHMM: TMhelix

FUNFAM: G3DSA:3.40.50.300:FF:002275

PHOBIUS: NON_CYTOPLASMIC_DOMAIN

cd03263

Walker A/P-loop

H-loop/switch region

Q-loop/lid

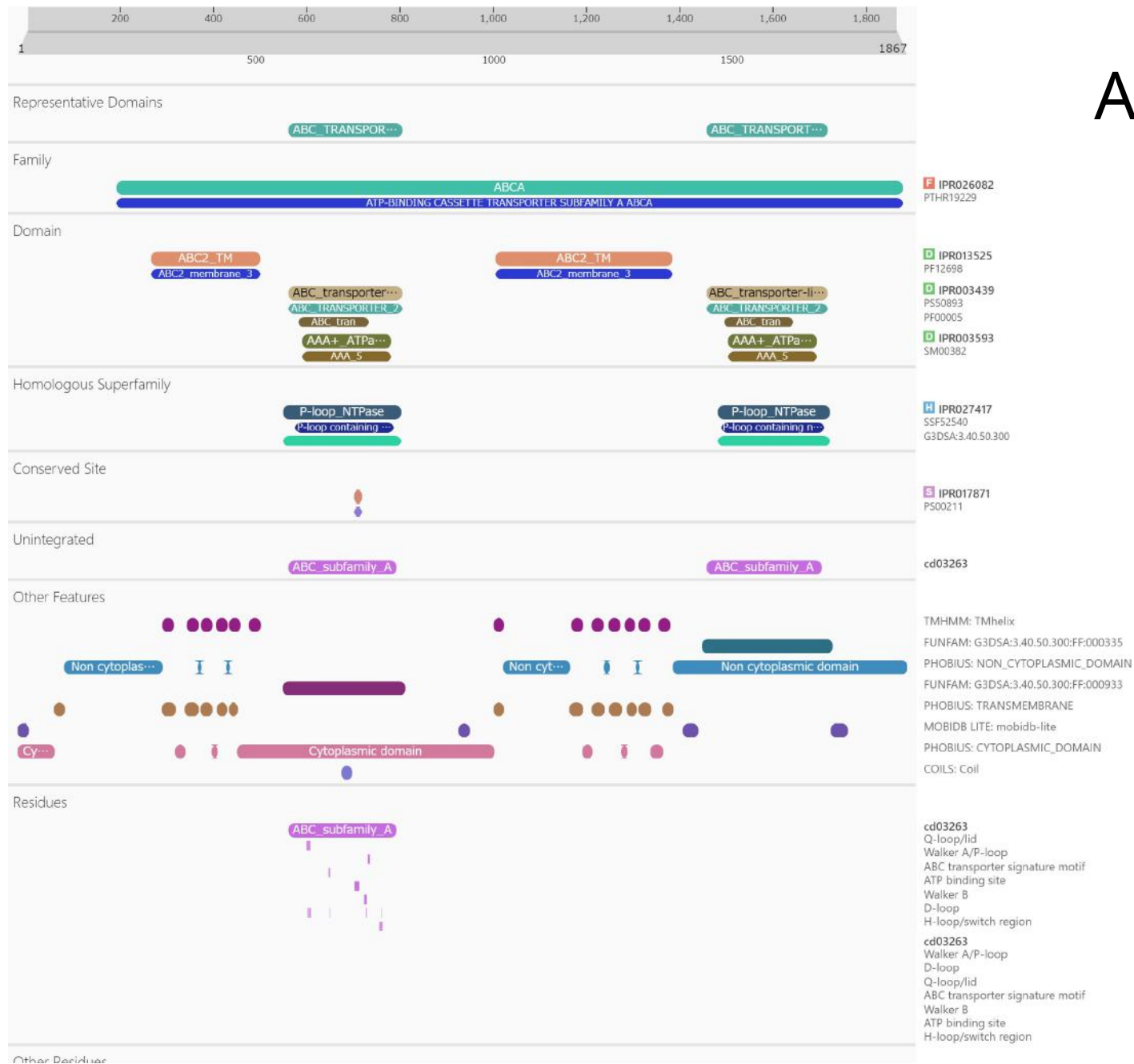
ABC transporter signature motif

Walker B

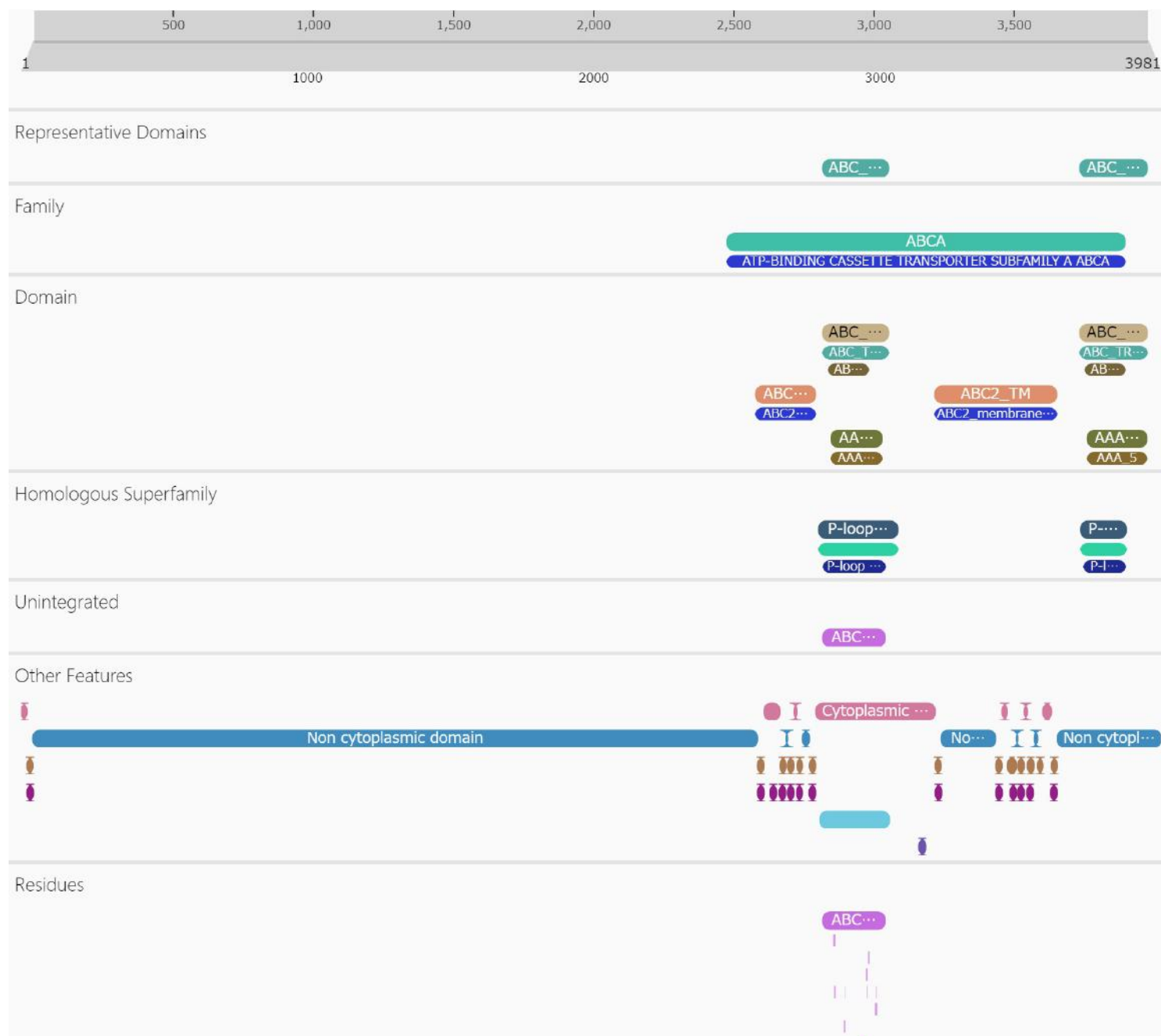
ATP binding site

D-loop

ABCA5



ABCA1



F IPR026082
PTHR19229

D IPR003439
PS50893
PF00005

D IPR013525
PF12698

D IPR003593
SM00382

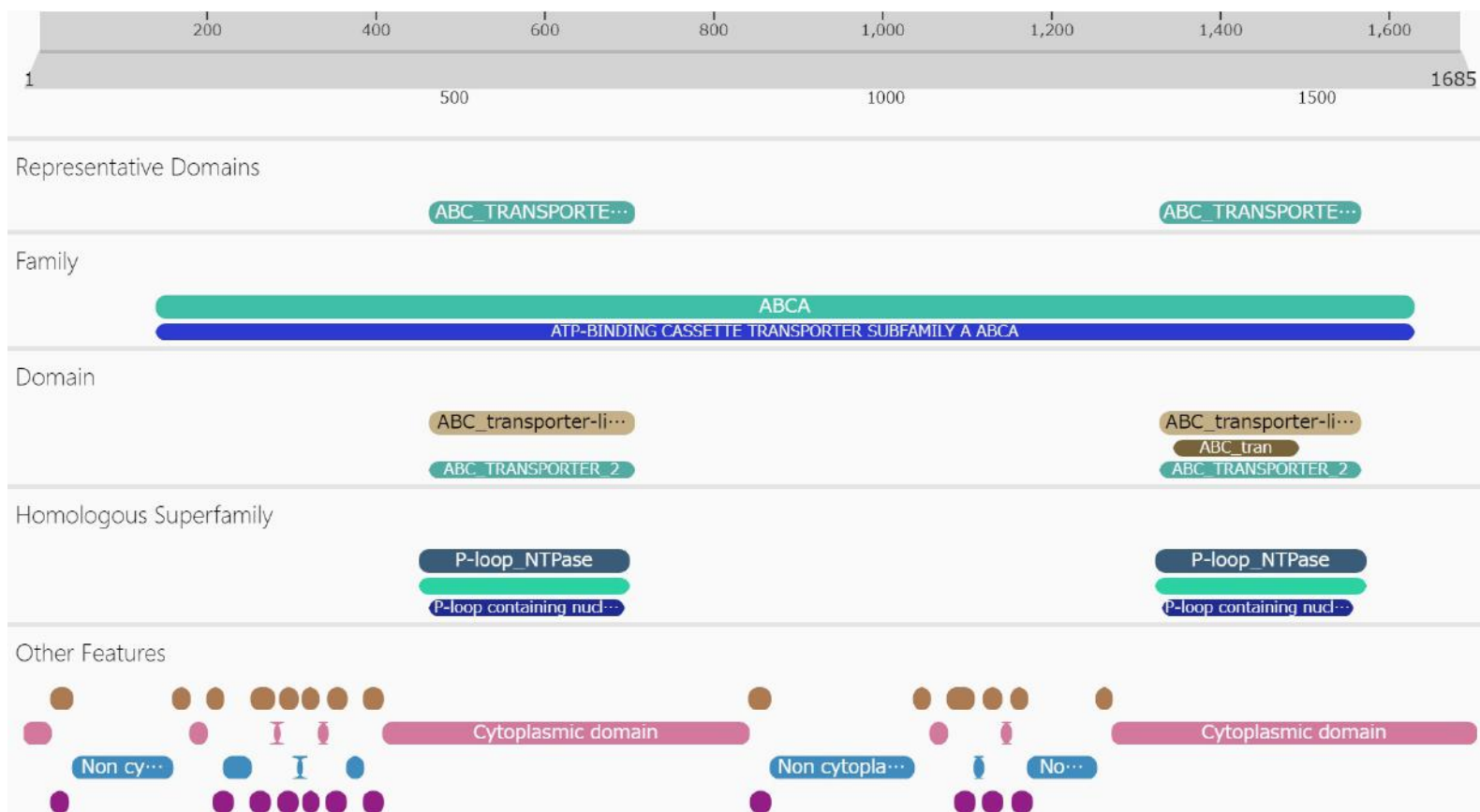
H IPR027417
G3DSA:3.40.50.300
SSF52540

cd03263

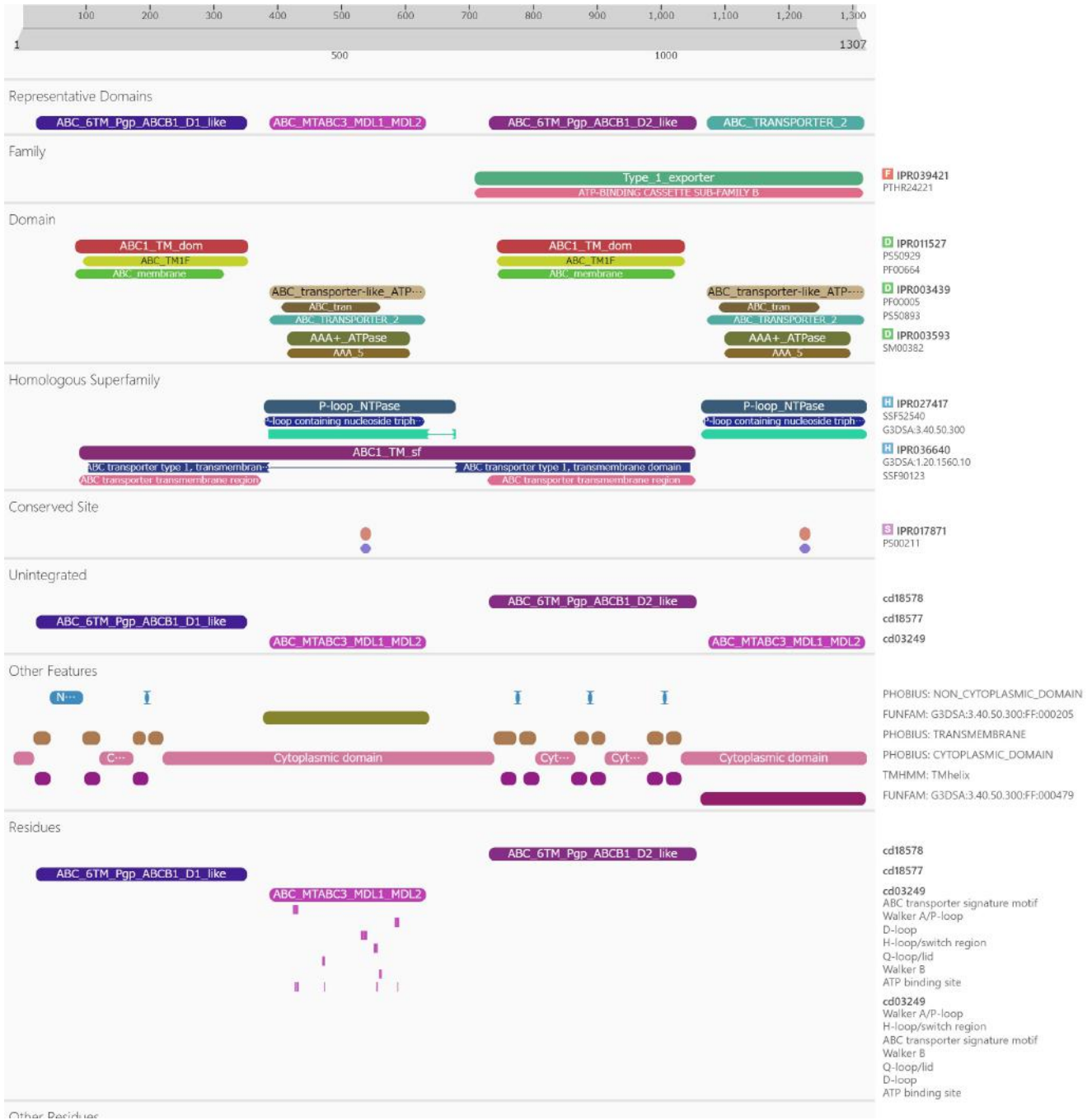
PHOBIUS: CYTOPLASMIC_DOMAIN
PHOBIUS: NON_CYTOPLASMIC_DOMAIN
PHOBIUS: TRANSMEMBRANE
TMHMM: TMhelix
FUNFAM: G3DSA:3.40.50.300:FF:001253
MOBIDB LITE: mobidb-lite

cd03263
Walker A/P-loop
D-loop
Walker B
ATP binding site
H-loop/switch region
Q-loop/lid
ABC transporter signature motif

ABCA12



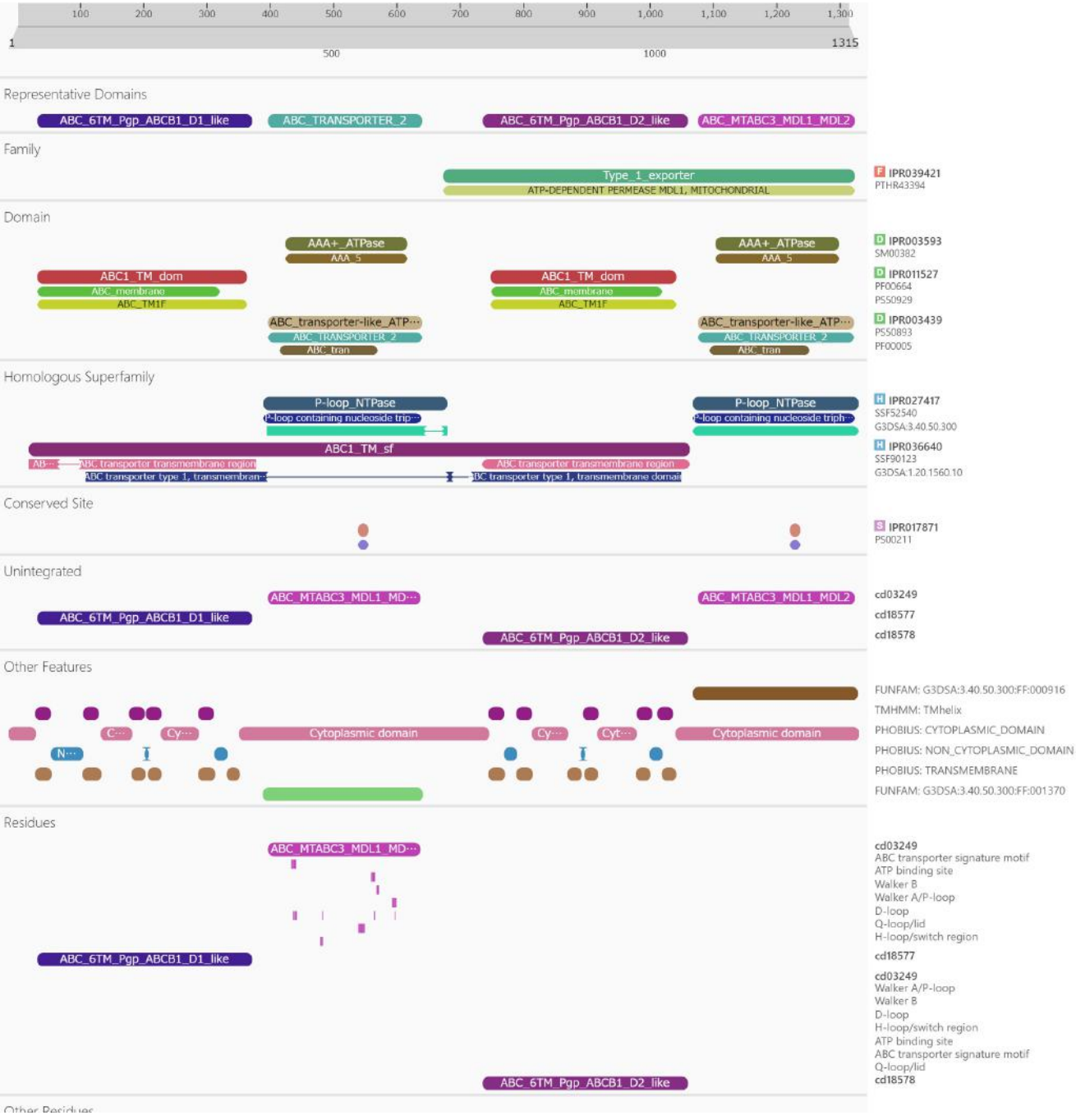
ABCB1



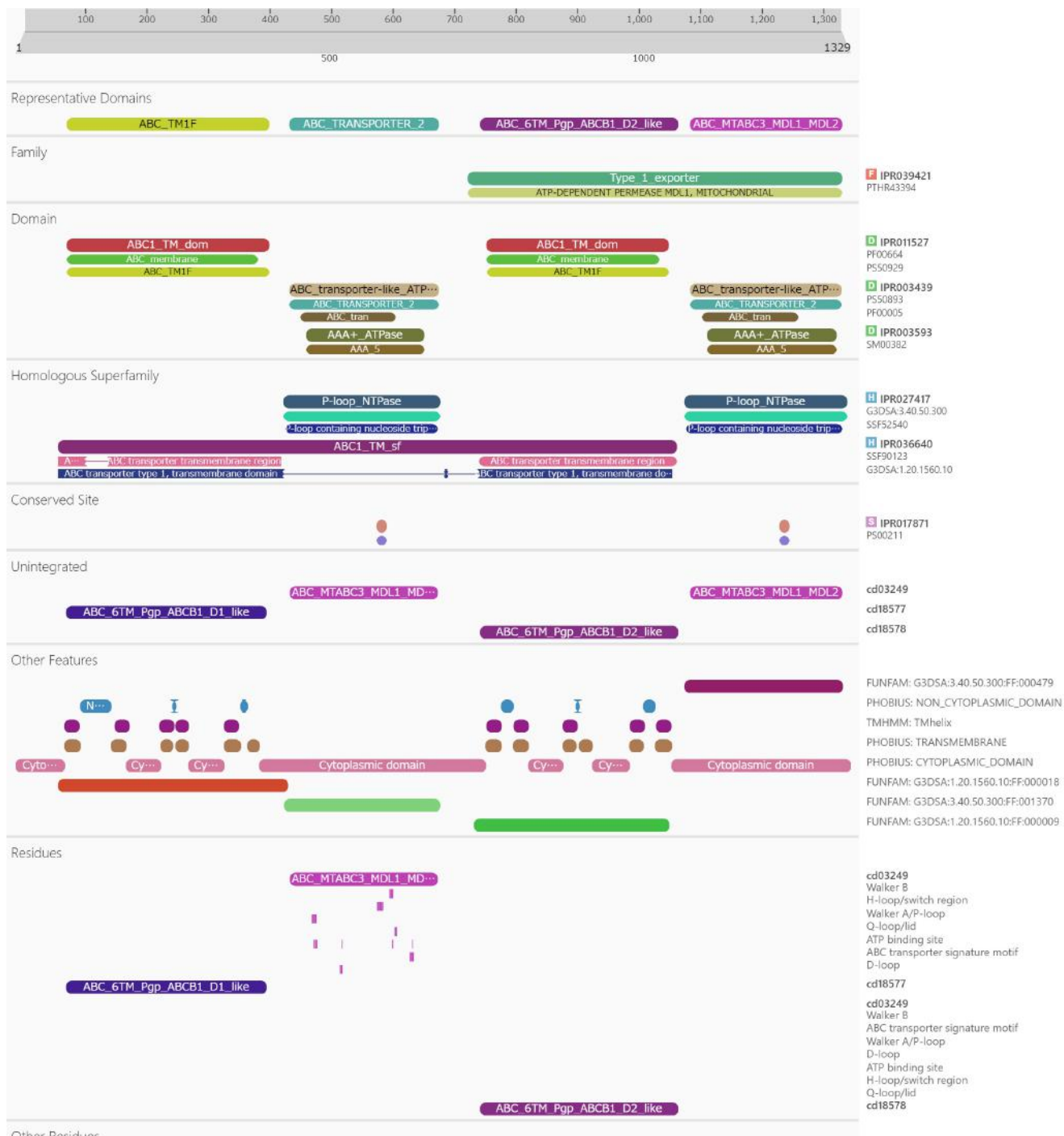
ABCB2



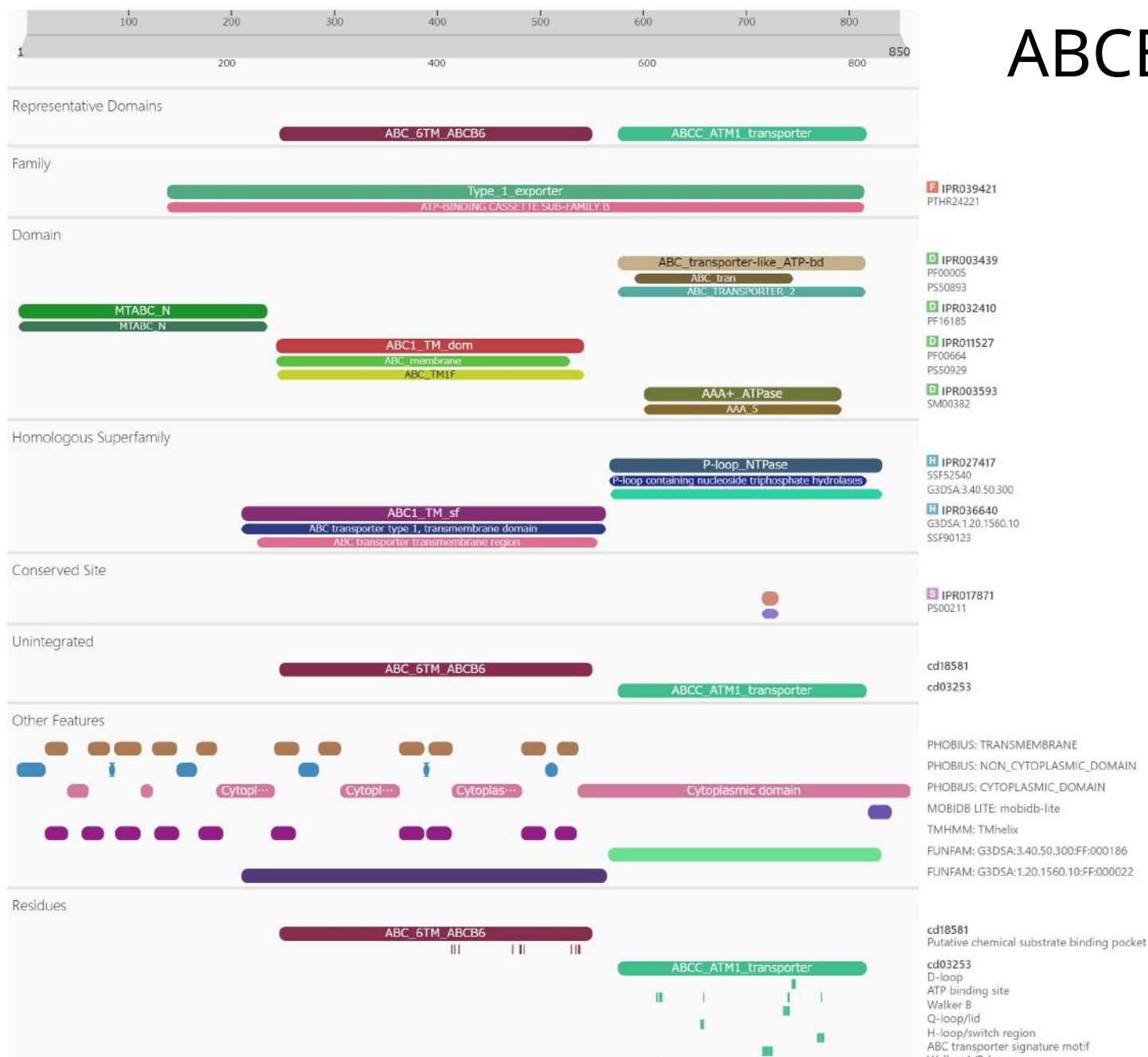
ABCB3



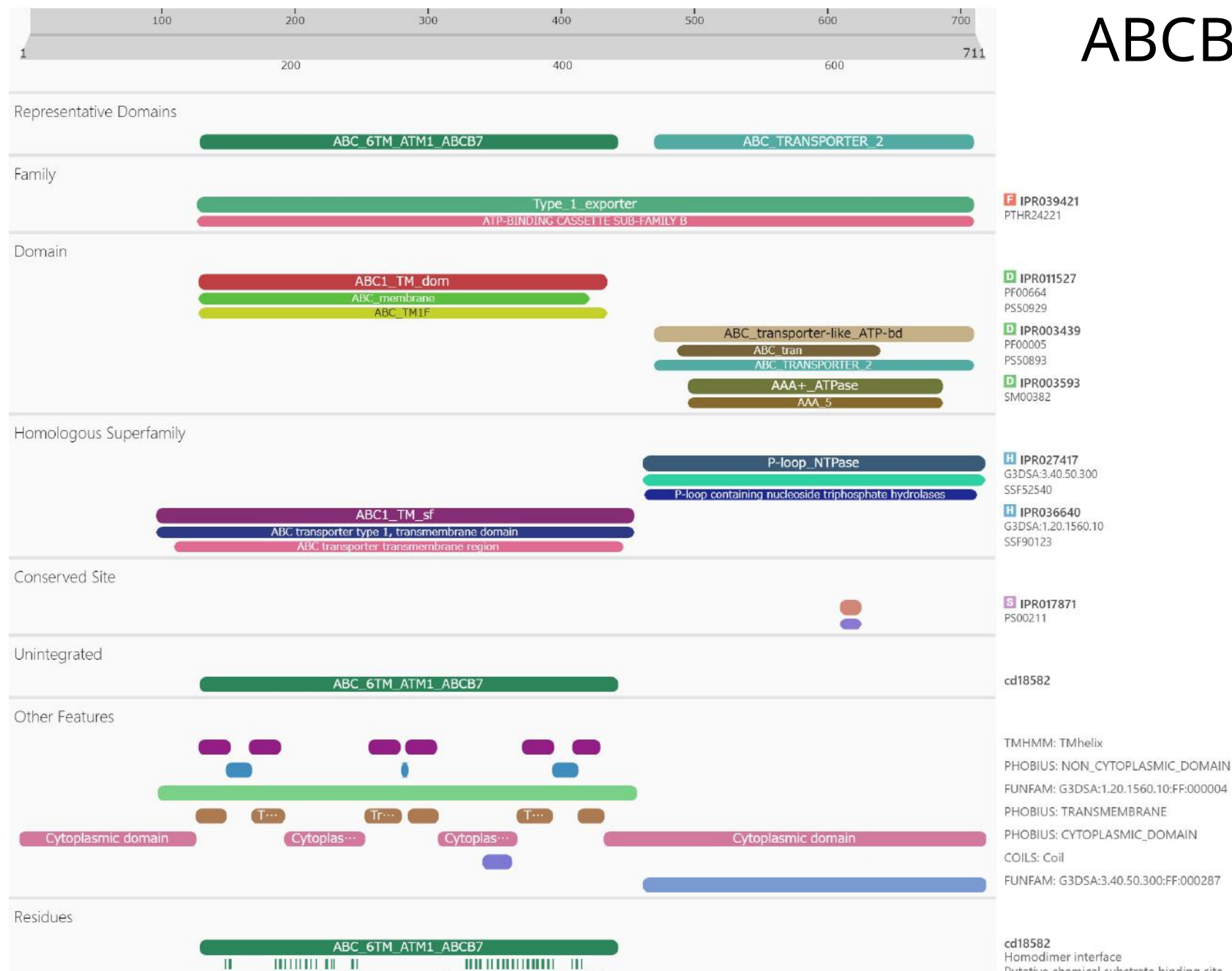
ABCB4



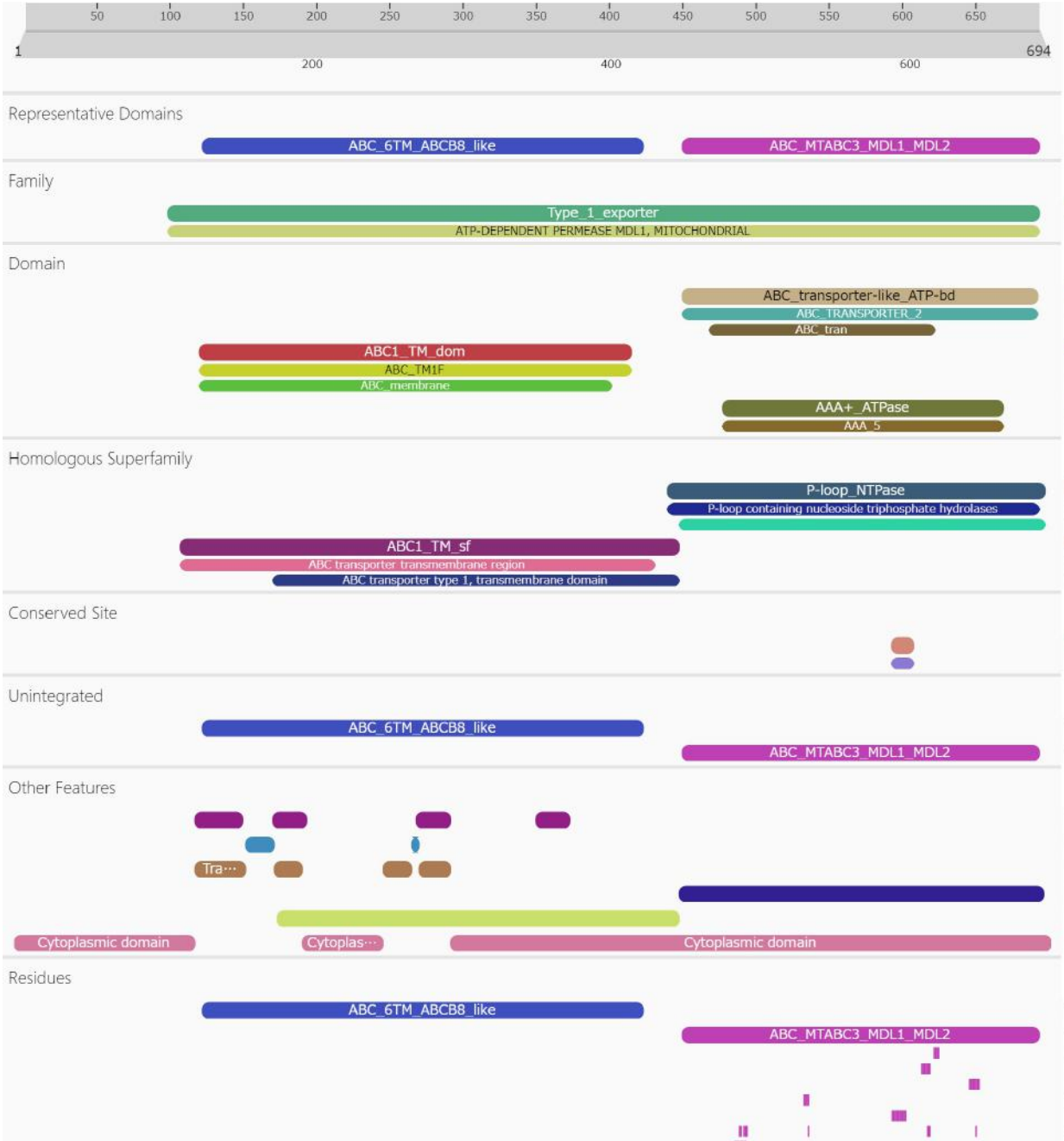
ABCB5



ABCB6



ABCB7



IPR039421
PTHR43394

IPR003439
PS50893
PF00005

IPR011527
PS50929
PF00664

IPR003593
SM00382

IPR027417
SSF52540
G3DSA:3.40.50.300

IPR036640
SSF90123
G3DSA:1.20.1560.10

IPR017871
PS00211

cd18574

cd03249

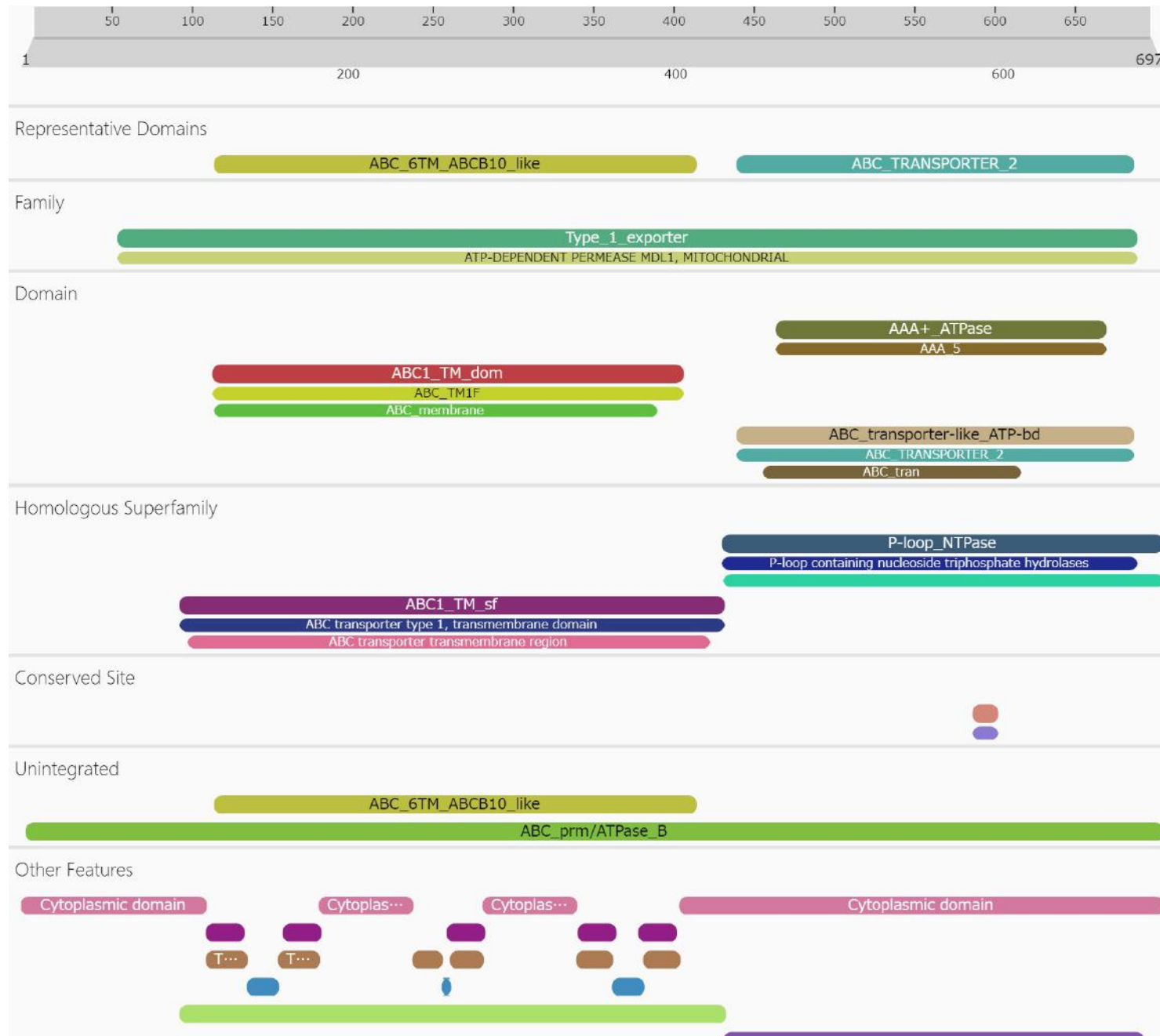
TMHMM: TMhelix
PHOBIOUS: NON_CYTOPLASMIC_DOMAIN
PHOBIOUS: TRANSMEMBRANE
FUNFAM: G3DSA:3.40.50.300:FF:000403
FUNFAM: G3DSA:1.20.1560.10:FF:000016
PHOBIOUS: CYTOPLASMIC_DOMAIN

cd18574

cd03249

D-loop
Walker B
H-loop/switch region
Q-loop/lid
ABC transporter signature motif
ATP binding site
Walker A/B loop

ABCB8



F IPR039421
PTHR43394

D IPR003593
SM00382

D IPR011527
PSS0929
PF00664

D IPR003439
PSS0893
PF00005

H IPR027417
SSF52540
G3DSA:3.40.50.300

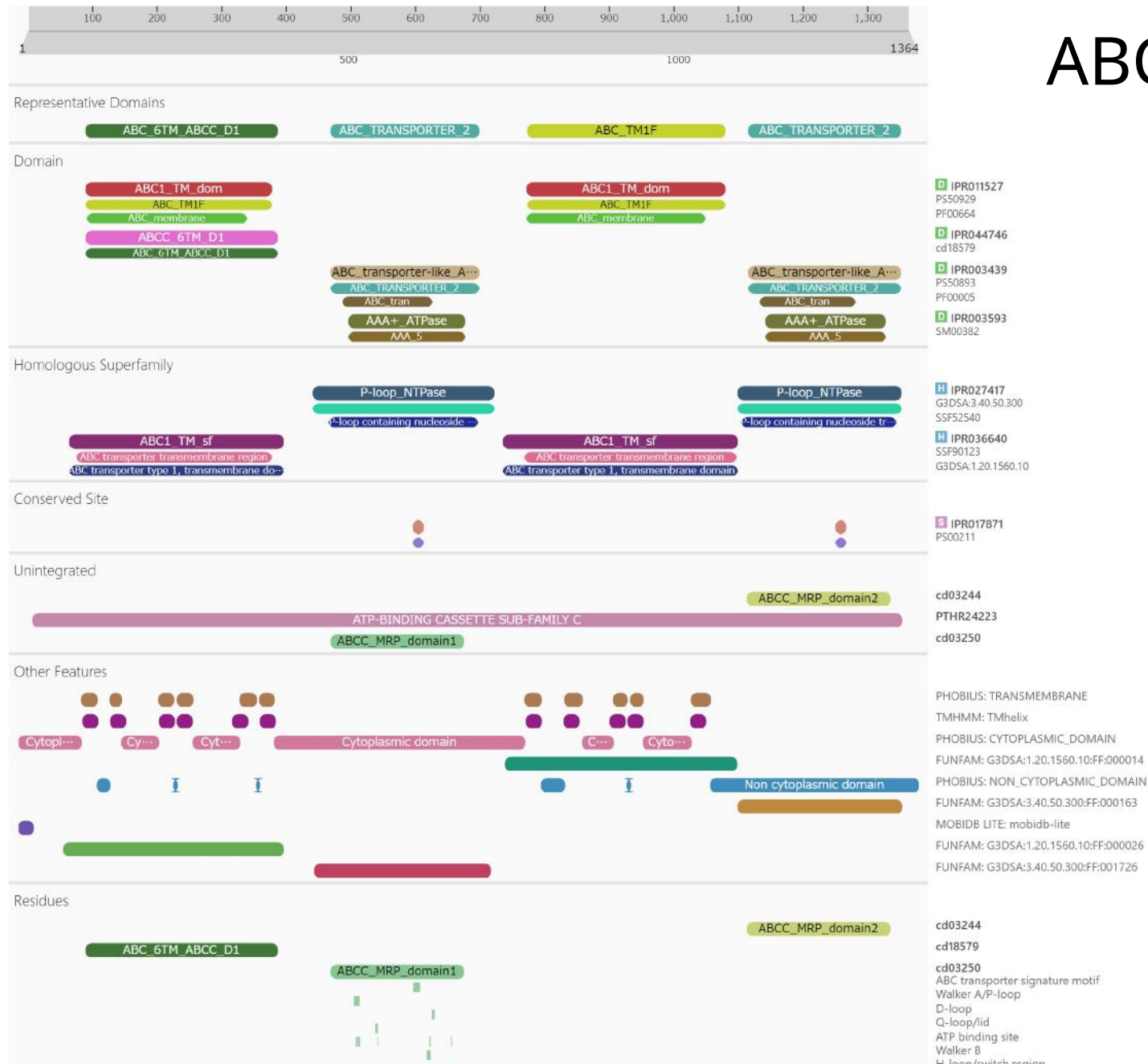
H IPR036640
G3DSA:1.20.1560.10
SSF90123

S IPR017871
PS00211

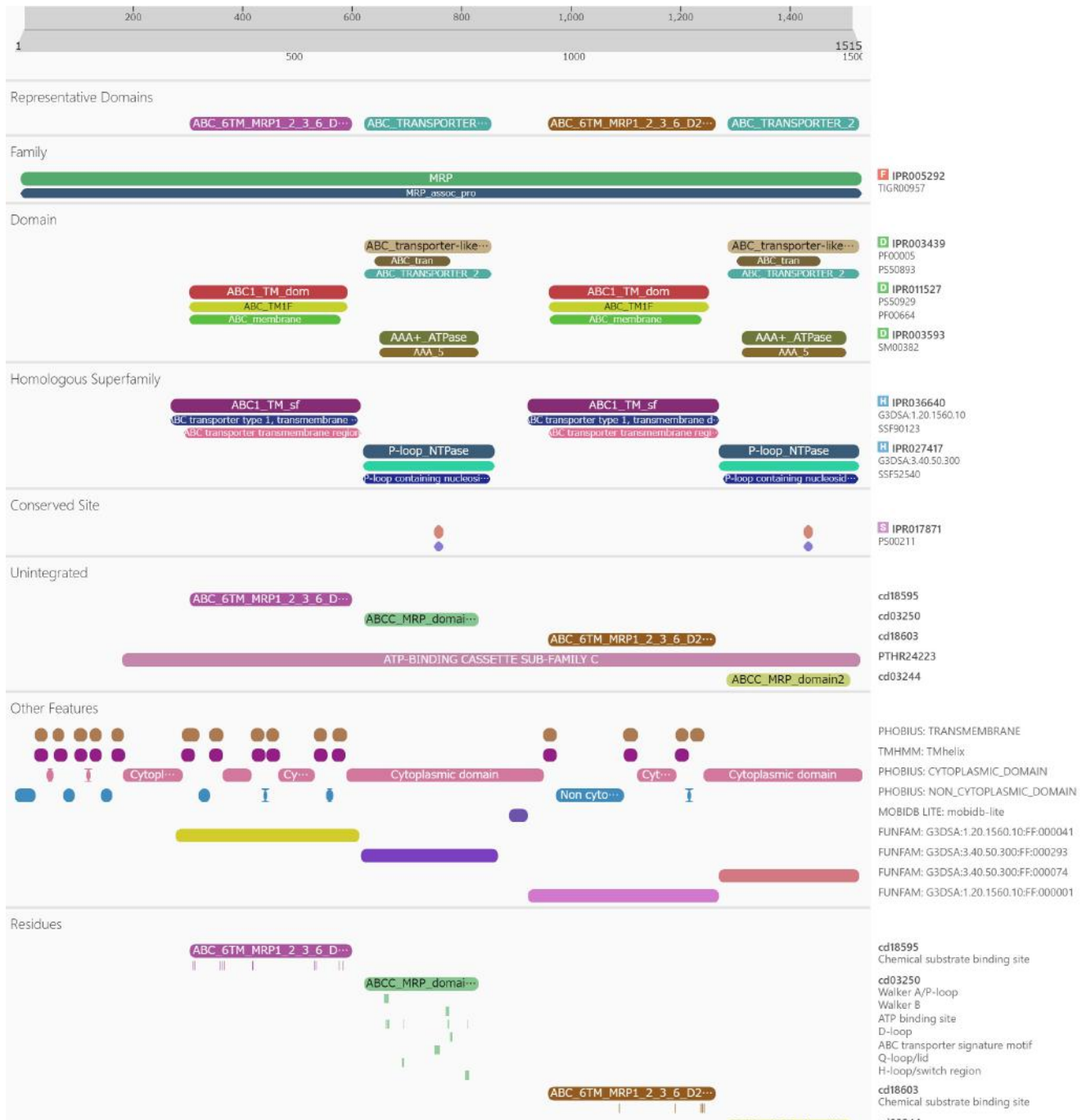
cd18573
PIRSF002773

PHOBIUS: CYTOPLASMIC_DOMAIN
TMHMM: TMhelix
PHOBIUS: TRANSMEMBRANE
PHOBIUS: NON_CYTOPLASMIC_DOMAIN
FUNFAM: G3DSA:1.20.1560.10:FF:000048
FUNFAM: G3DSA:3.40.50.300:FF:000218

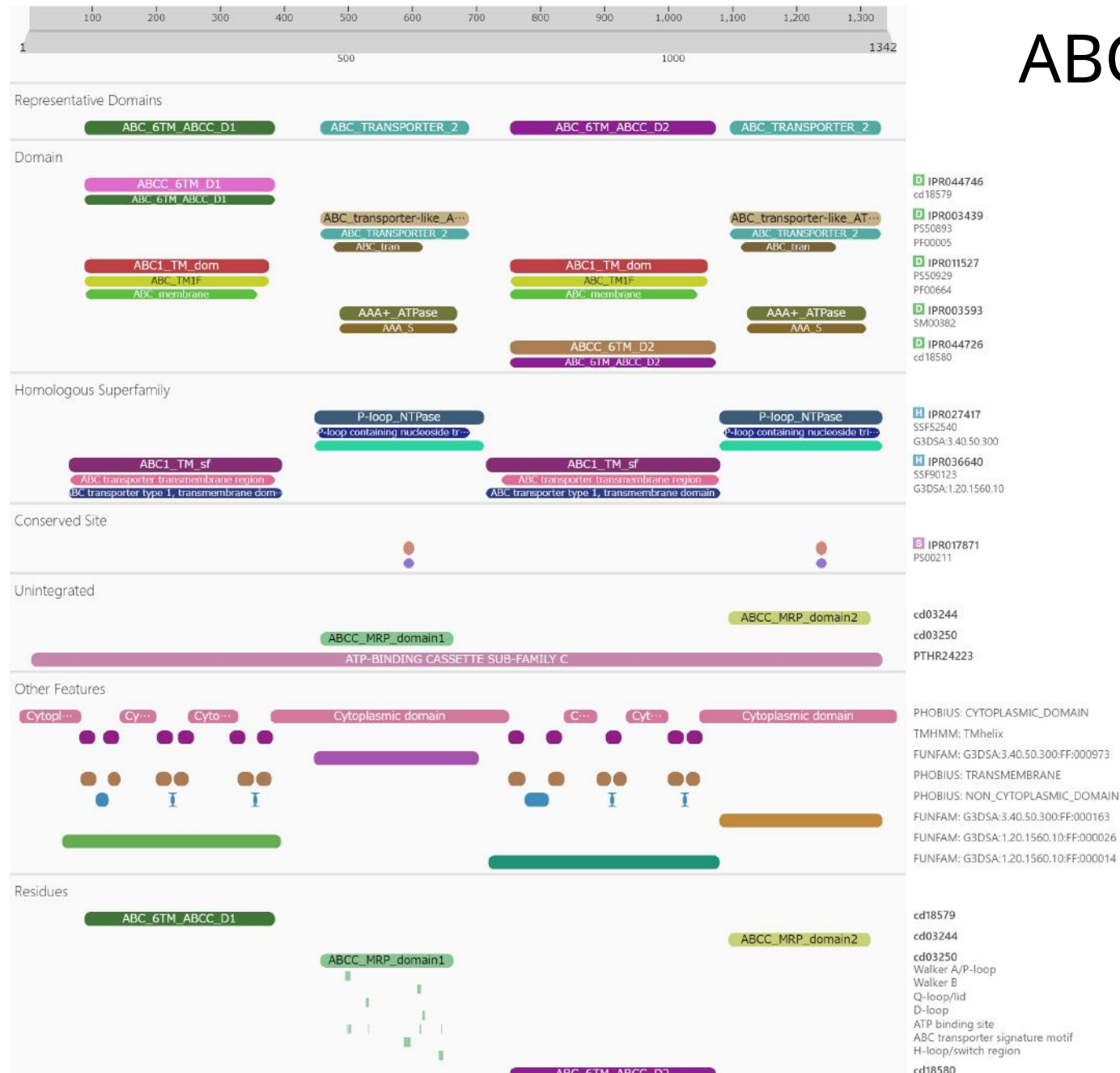
ABCB9



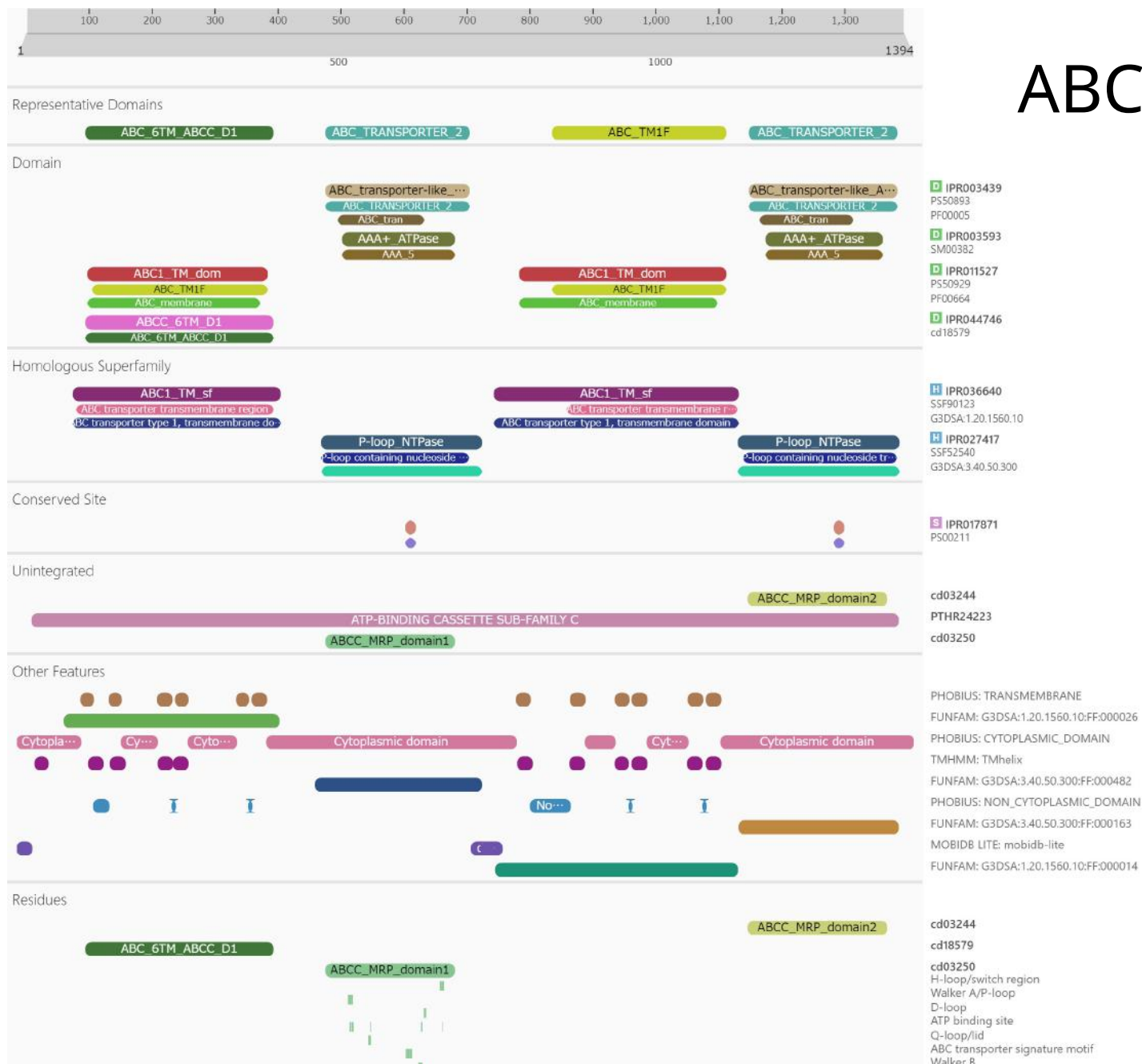
ABCC3



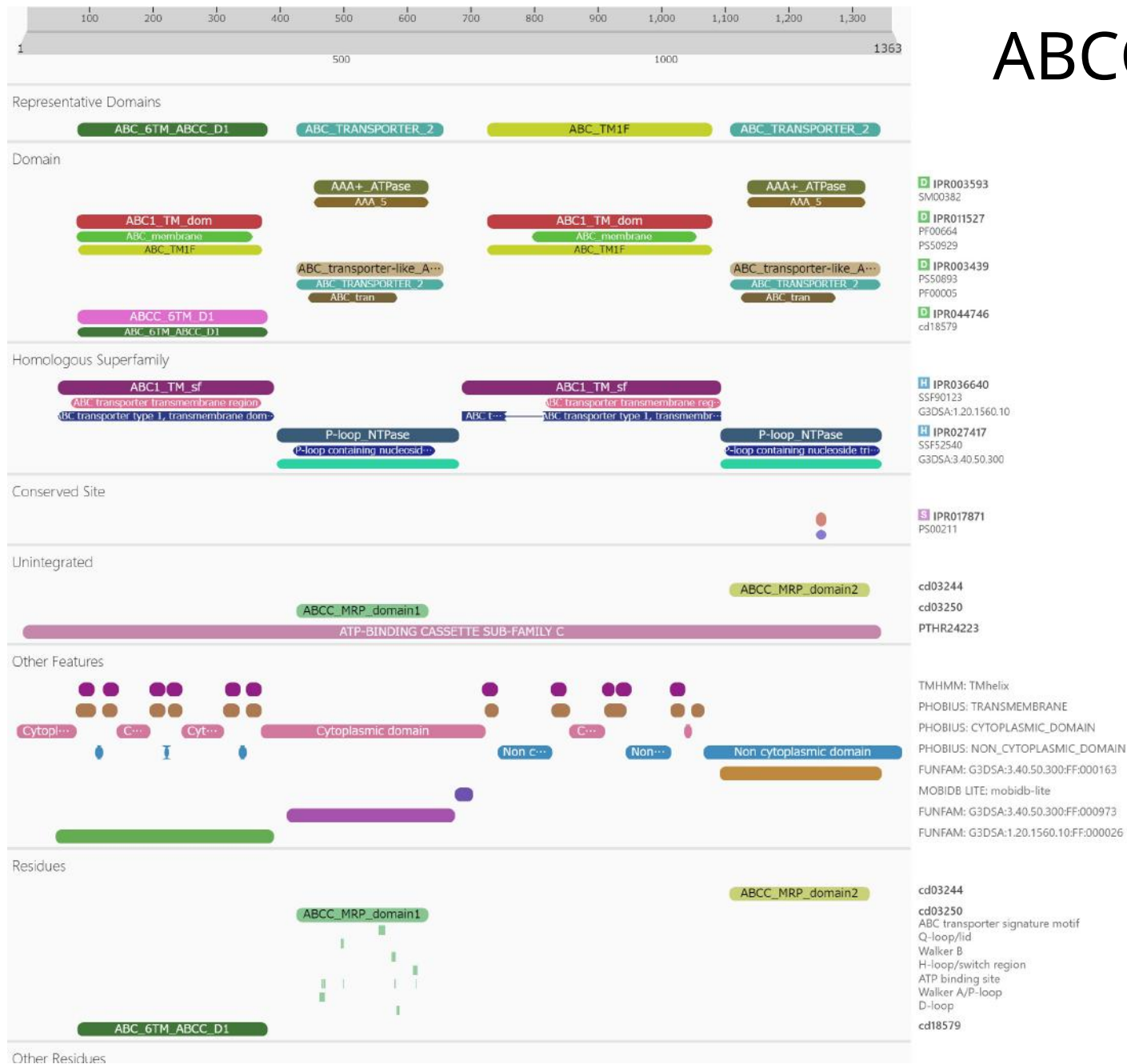
ABCC1



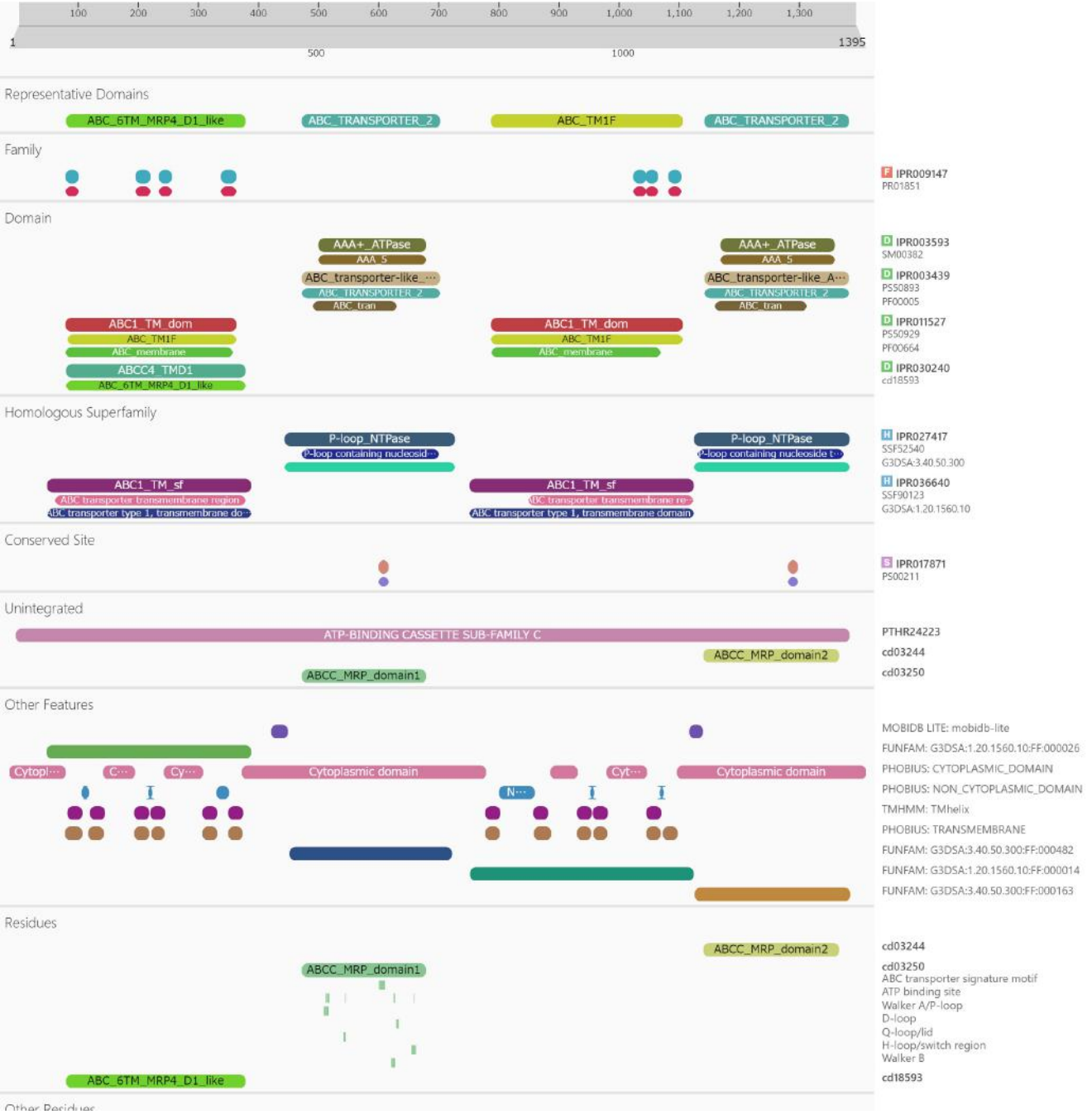
ABCC2



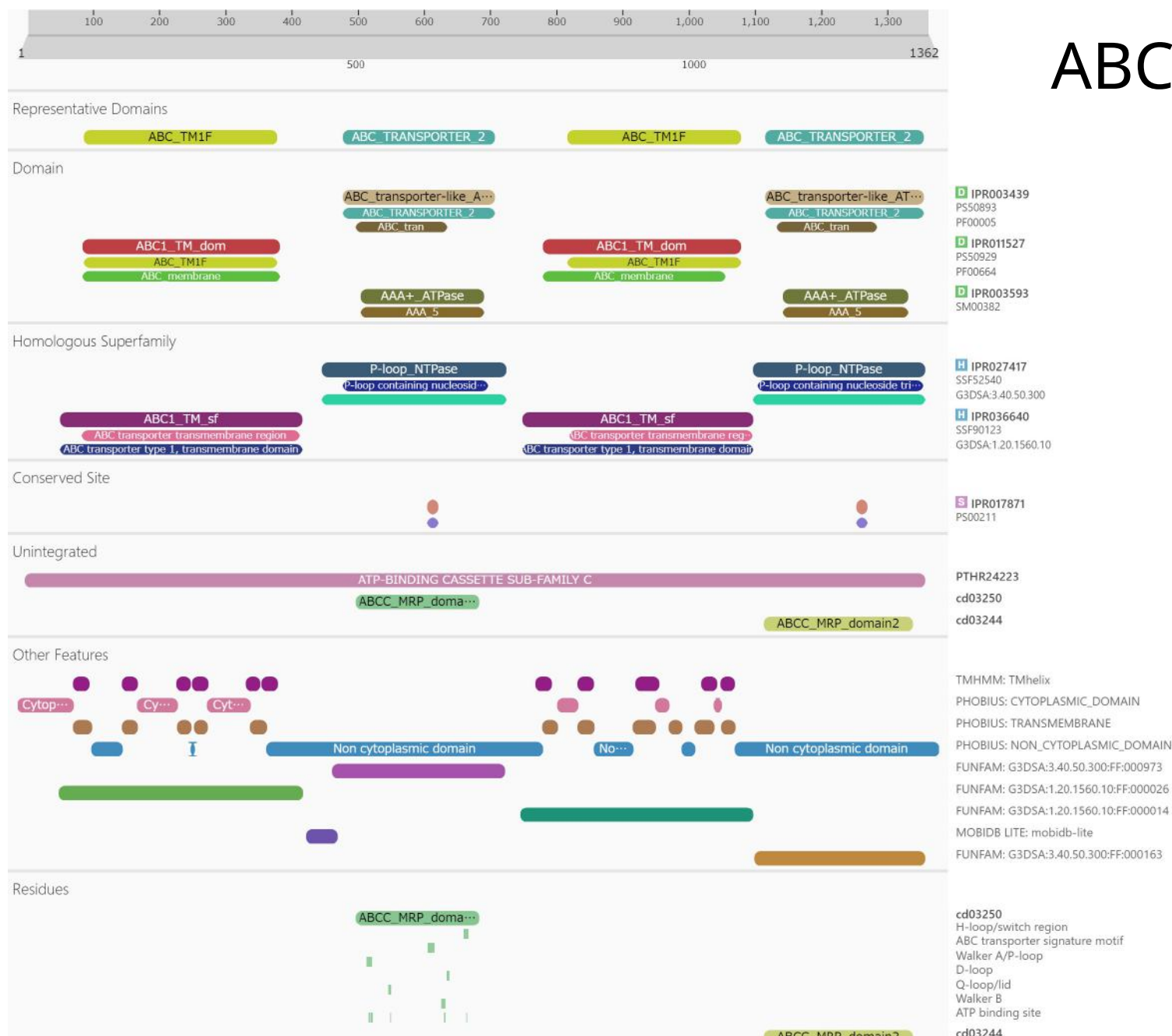
ABCC5



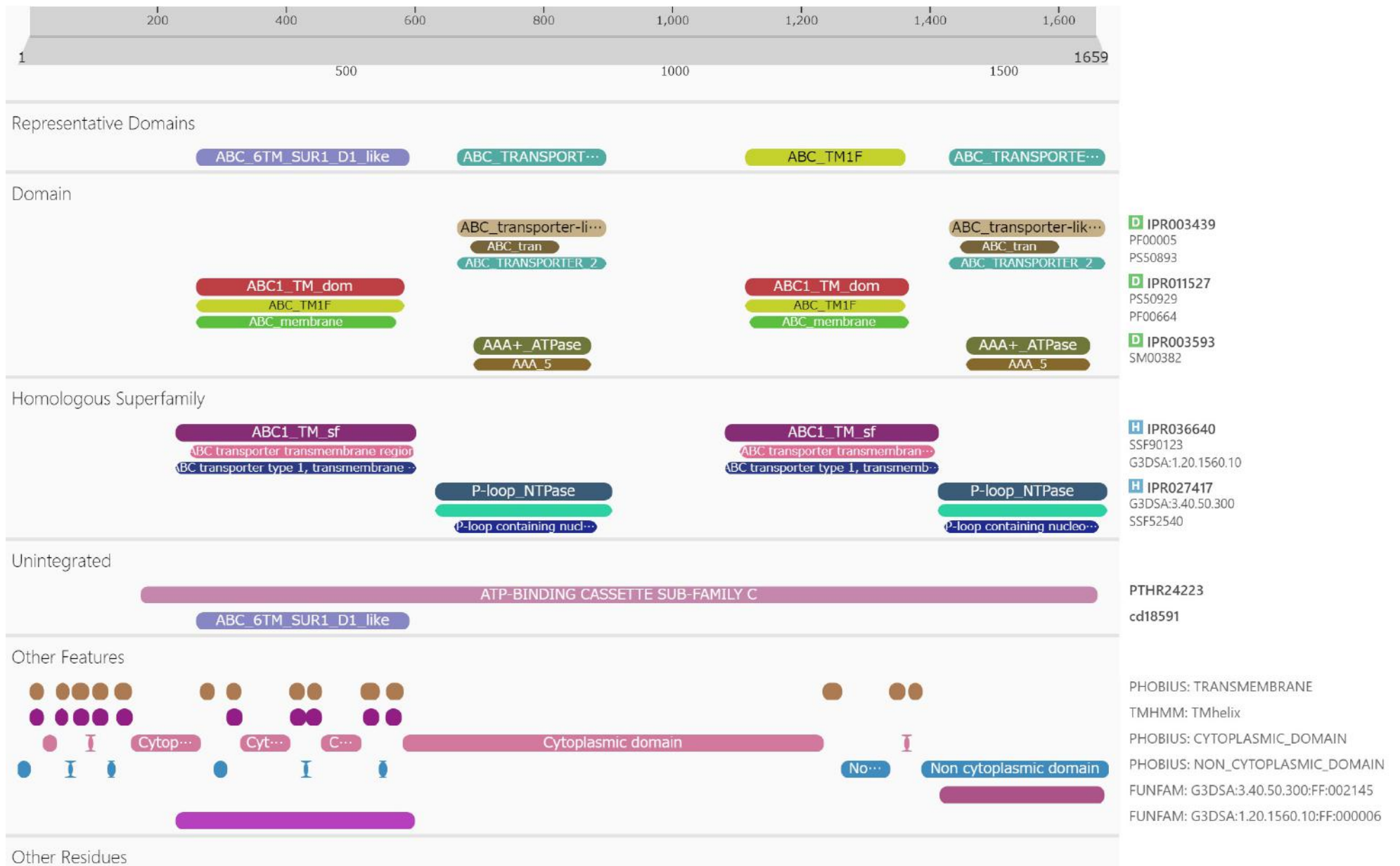
ABCC4



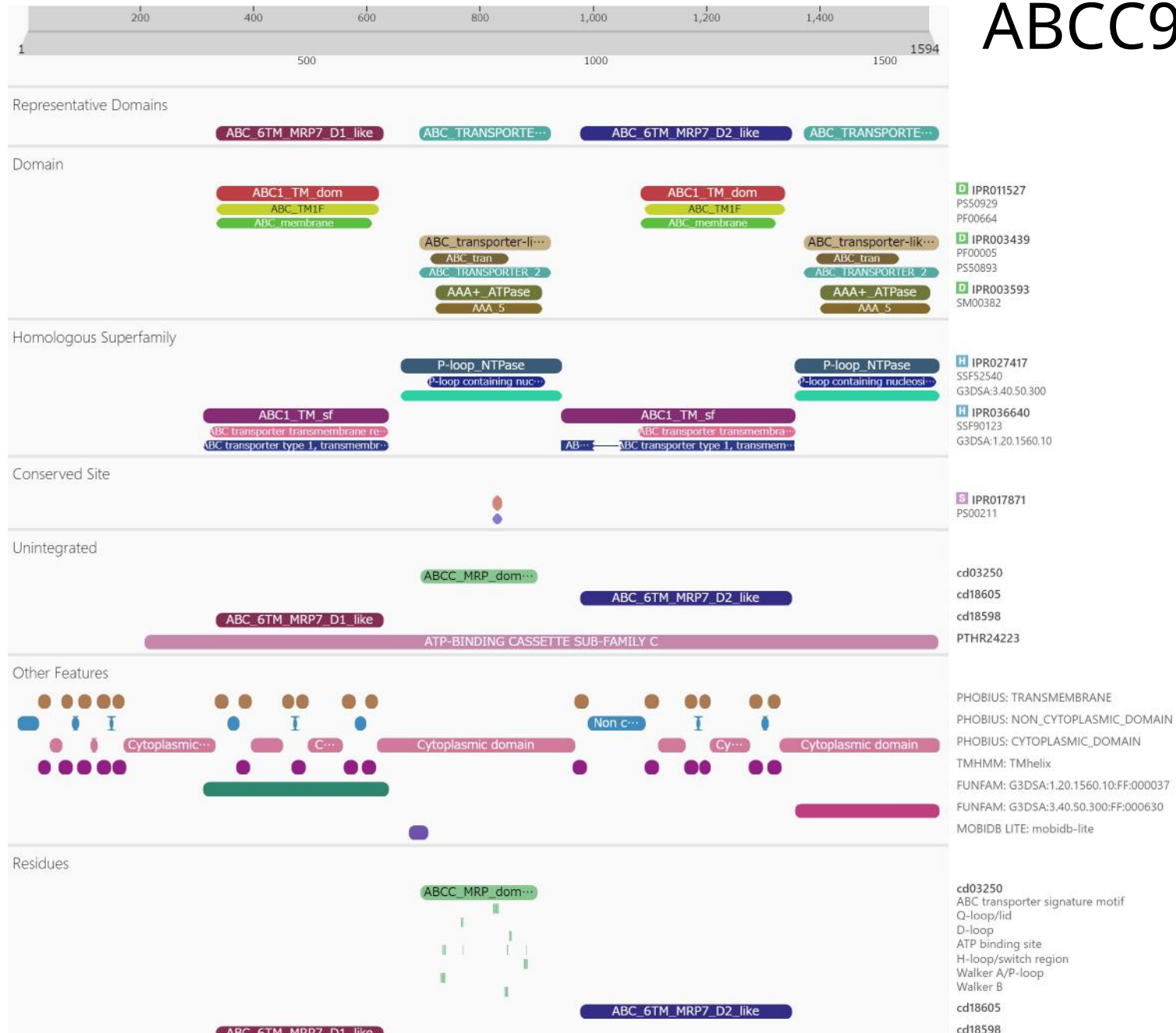
ABCC4-like1



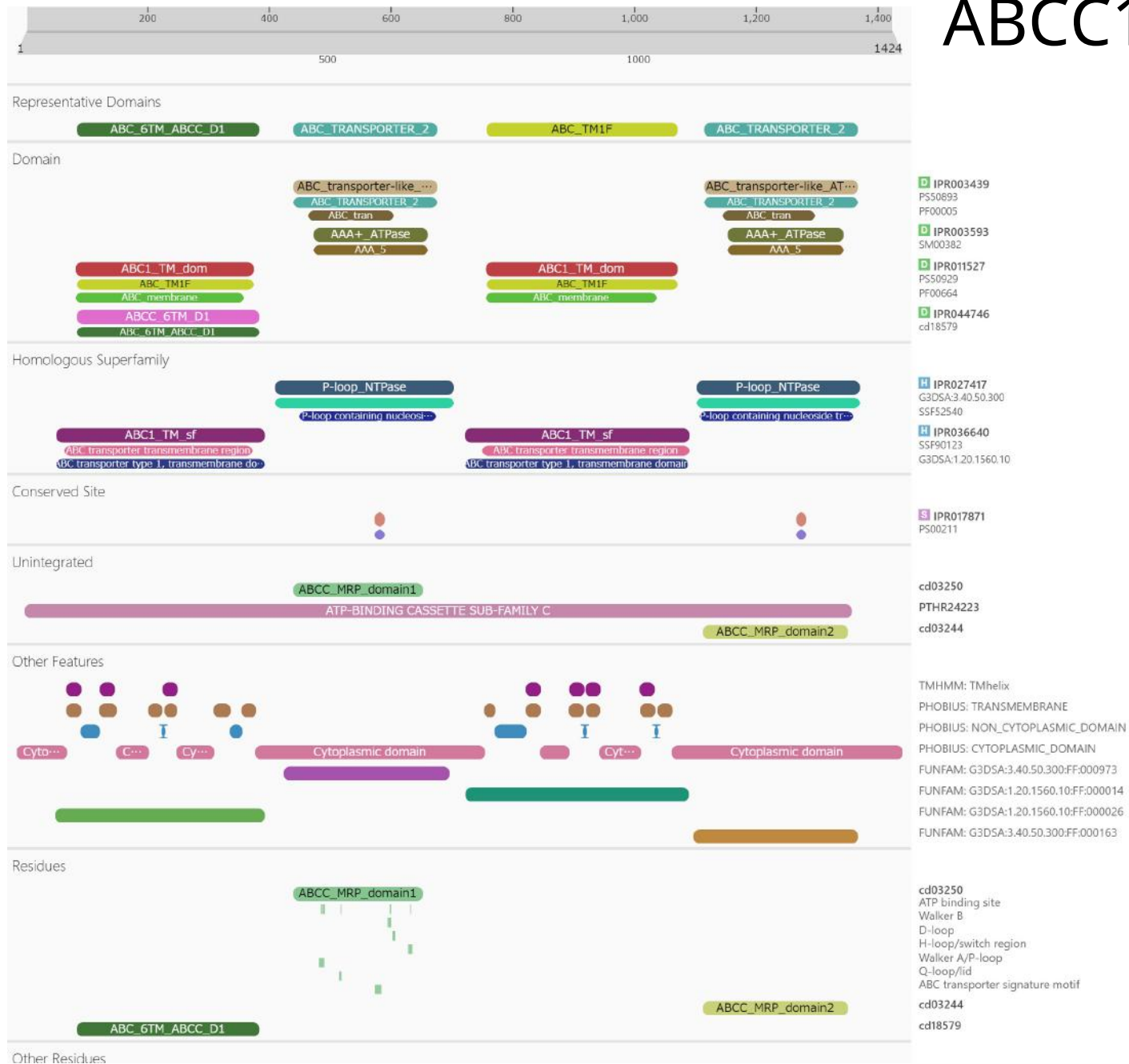
ABCC4-like2



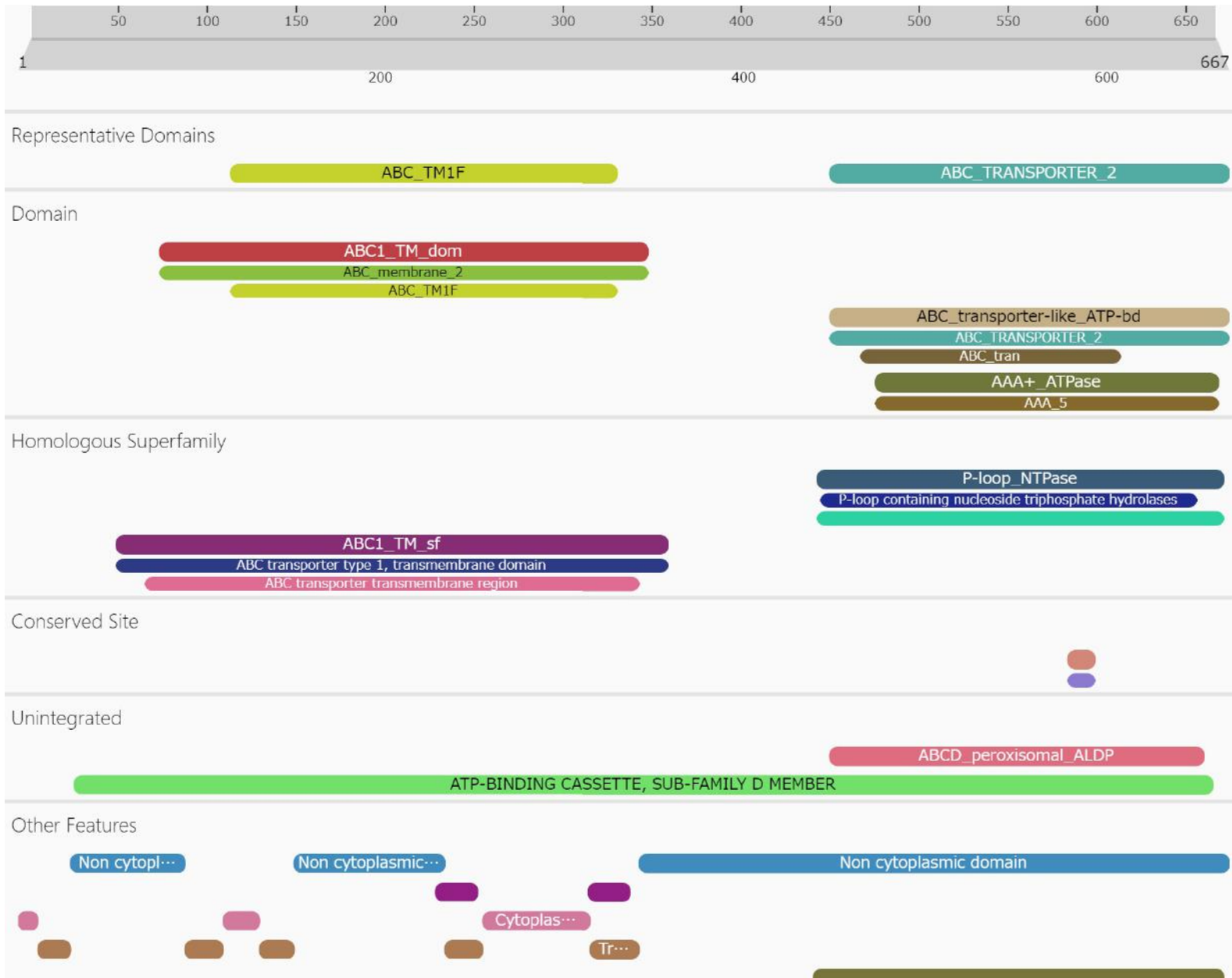
ABCC9



ABCC10



ABCC11



D IPR011527
PF06472
PS50929

D IPR003439
PS50893
PF00005

D IPR003593
SM00382

H IPR027417
SSF52540
G3DSA:3.40.50.300

H IPR036640
G3DSA:1.20.1560.10
SSF90123

S IPR017871
PS00211

cd03223
PTHR11384

PHOBIUS: NON_CYTOPLASMIC_DOMAIN
TMHMM: TMhelix
PHOBIUS: CYTOPLASMIC_DOMAIN
PHOBIUS: TRANSMEMBRANE
FUNFAM: G3DSA:3.40.50.300:FF:000636



ABCD1

Representative Domains



Domain



D IPR011527
PF06472
PS50929

D IPR003439
PS50893
PF00005

D IPR003593
SM00382

Homologous Superfamily



H IPR027417
SSF52540
G3DSA:3.40.50.300

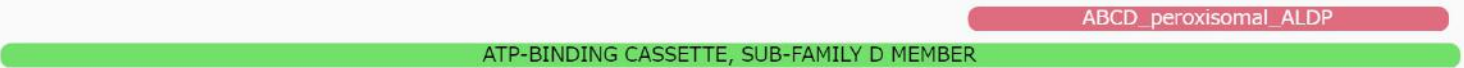
H IPR036640
G3DSA:1.20.1560.10
SSF90123

Conserved Site



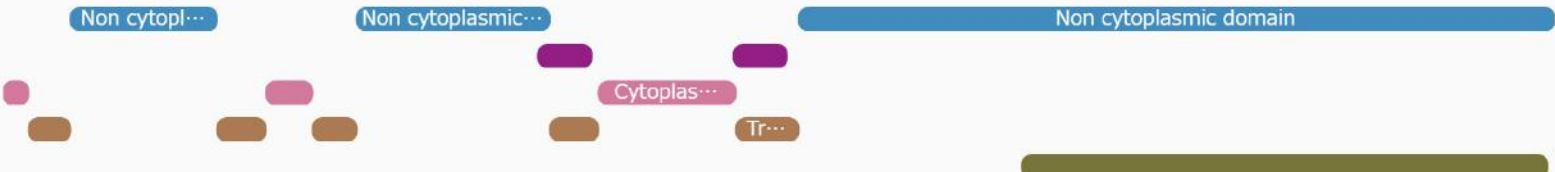
S IPR017871
PS00211

Unintegrated



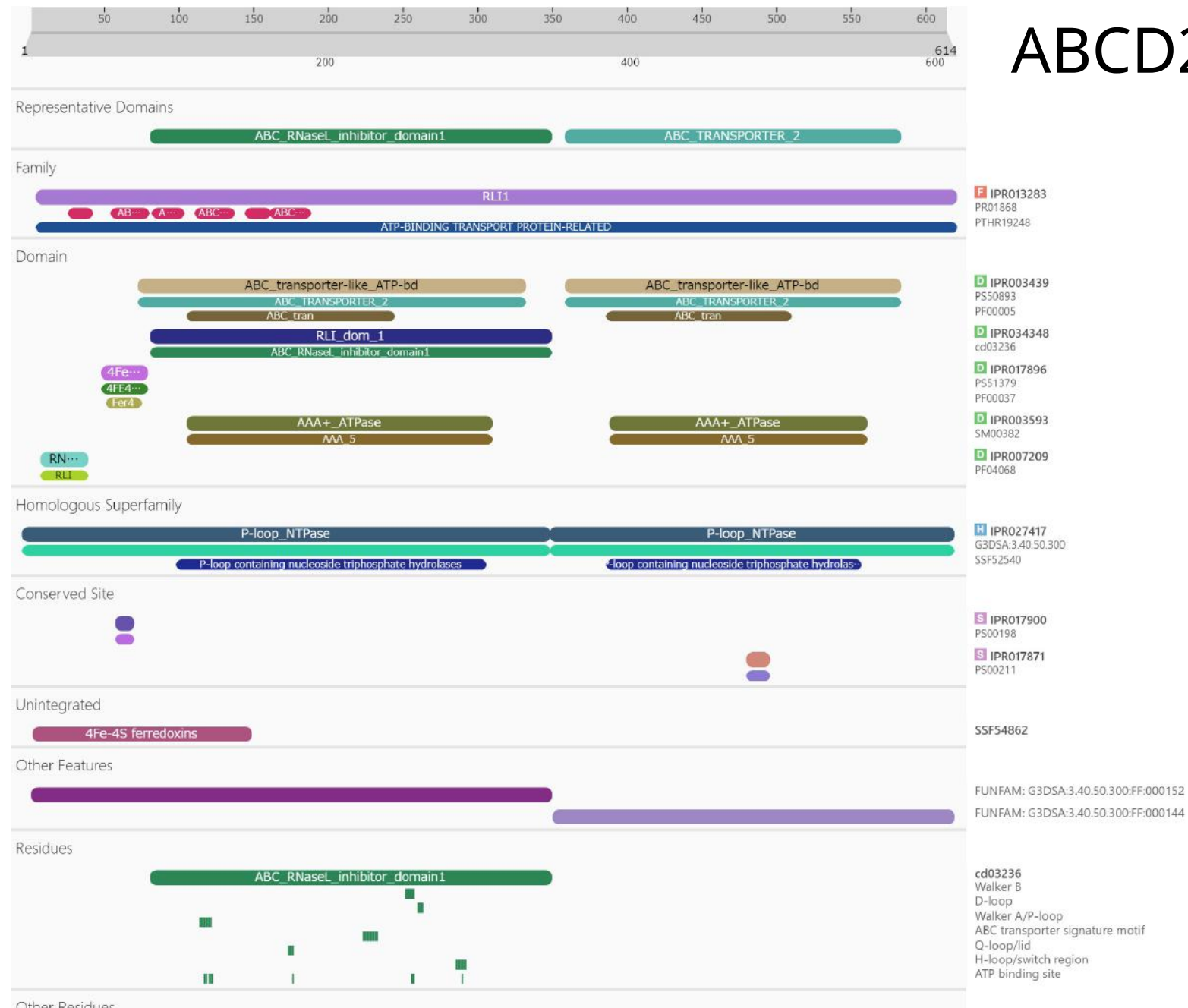
cd03223
PTHR11384

Other Features

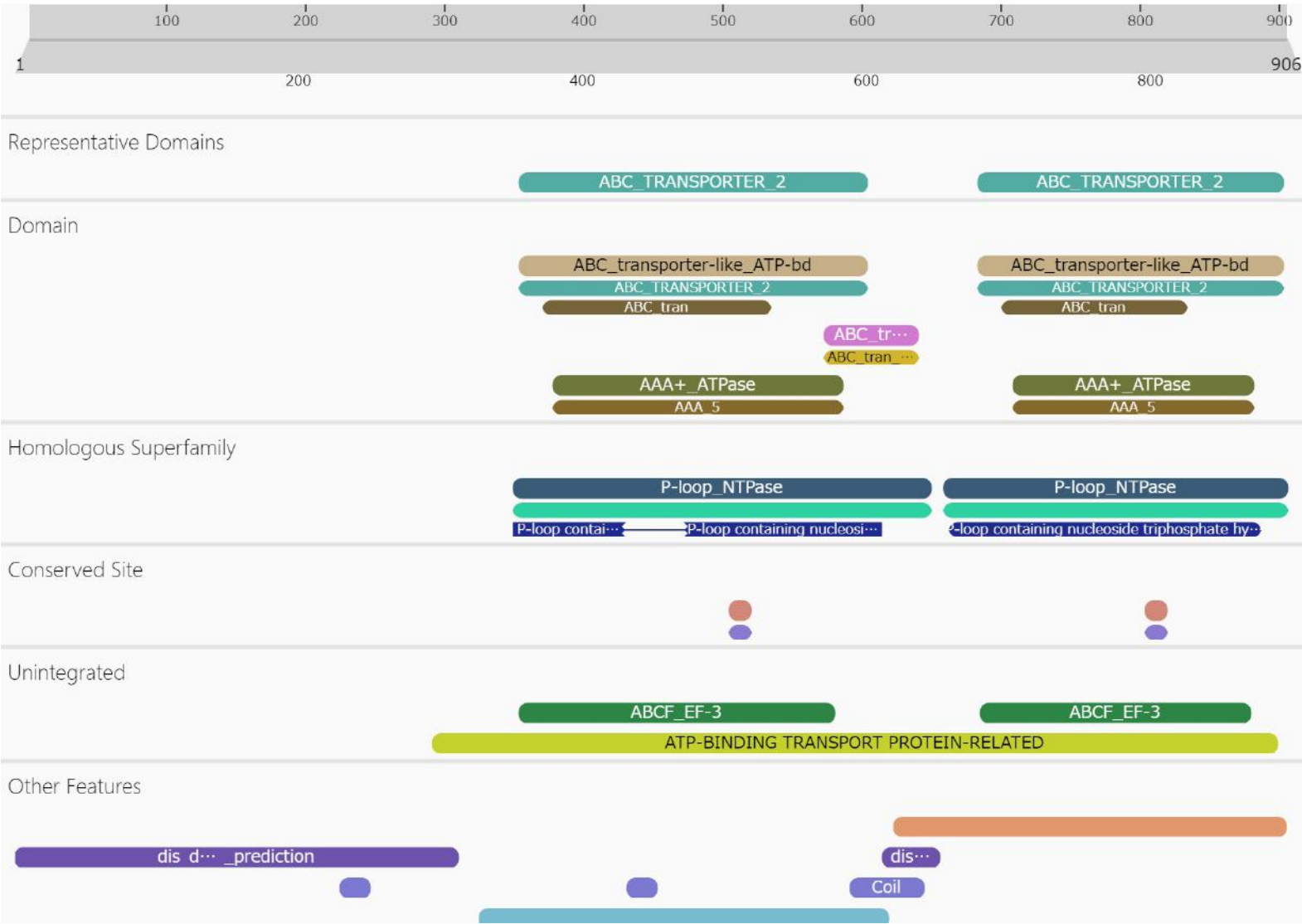


PHOBIUS: NON_CYTOPLASMIC_DOMAIN
TMHMM: TMhelix
PHOBIUS: CYTOPLASMIC_DOMAIN
PHOBIUS: TRANSMEMBRANE
FUNFAM: G3DSA:3.40.50.300:FF:000636

ABCD2



ABCE1



D IPR003439
PS50893
PF00005

D IPR032781
PF12848

D IPR003593
SM00382

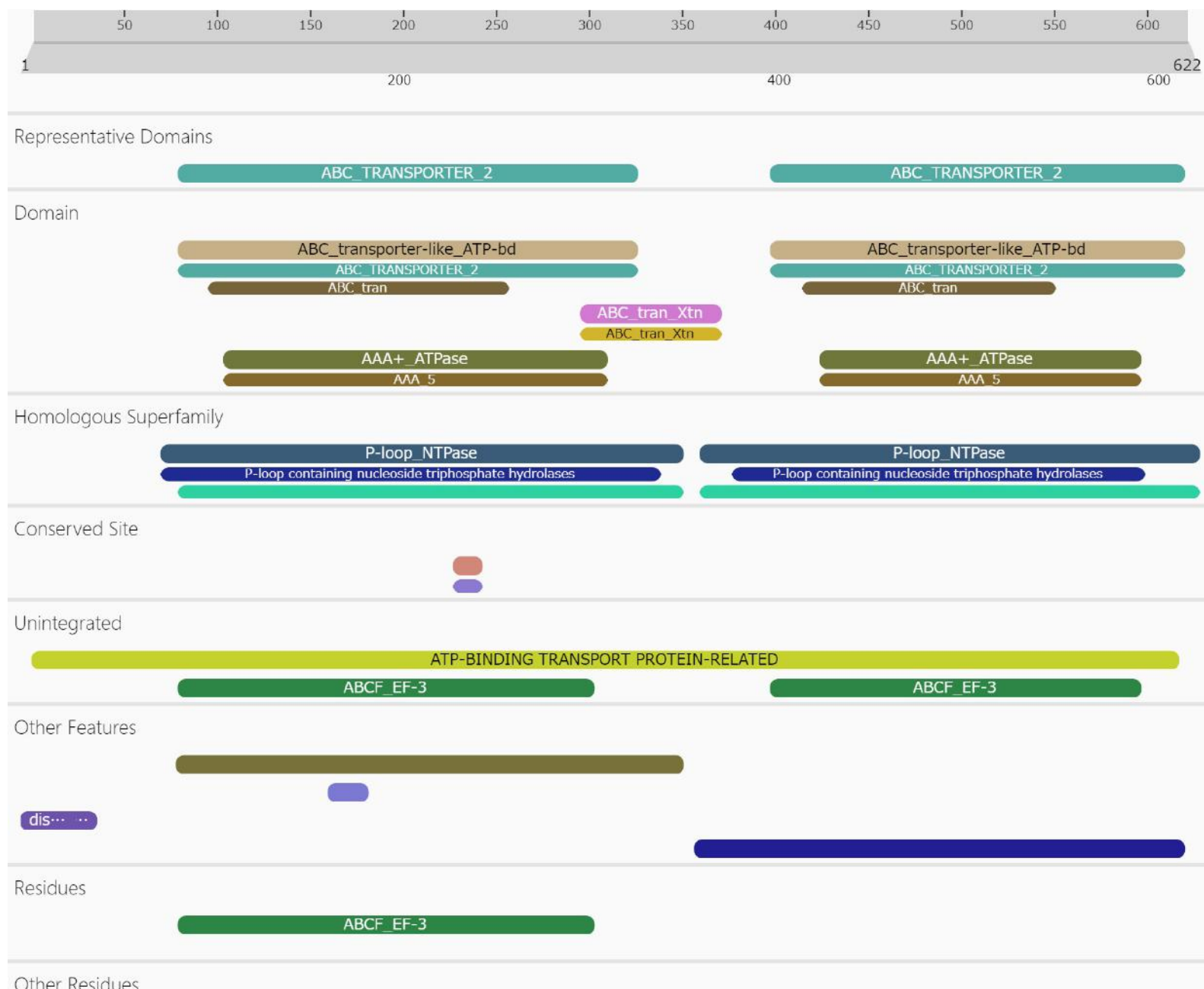
H IPR027417
G3DSA:3.40.50.300
SSF52540

S IPR017871
PS00211

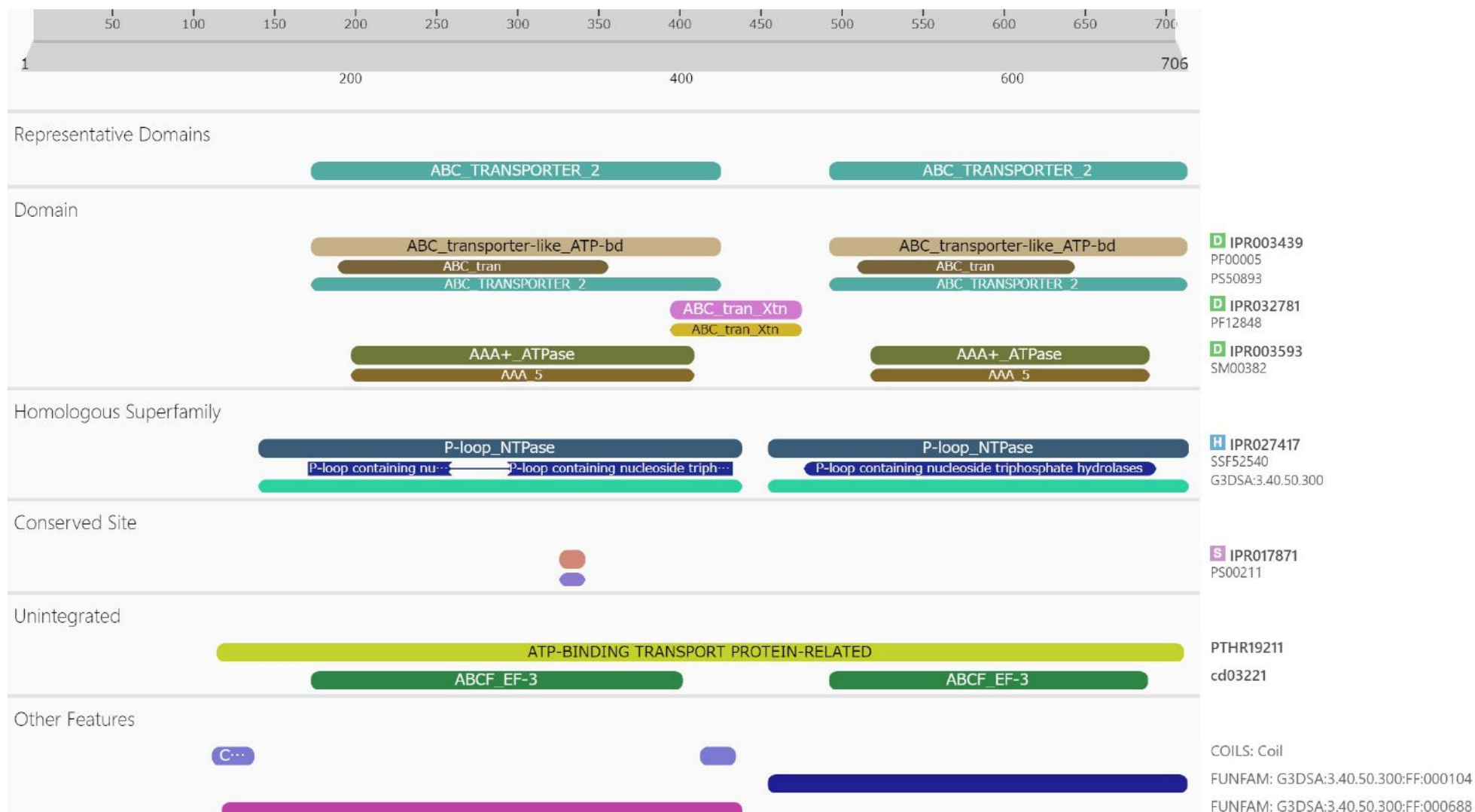
cd03221
PTHR19211

FUNFAM: G3DSA:3.40.50.300:FF:000471
MOBIDB LITE: mobidb-lite
COILS: Coil
FUNFAM: G3DSA:3.40.50.300:FF:000472

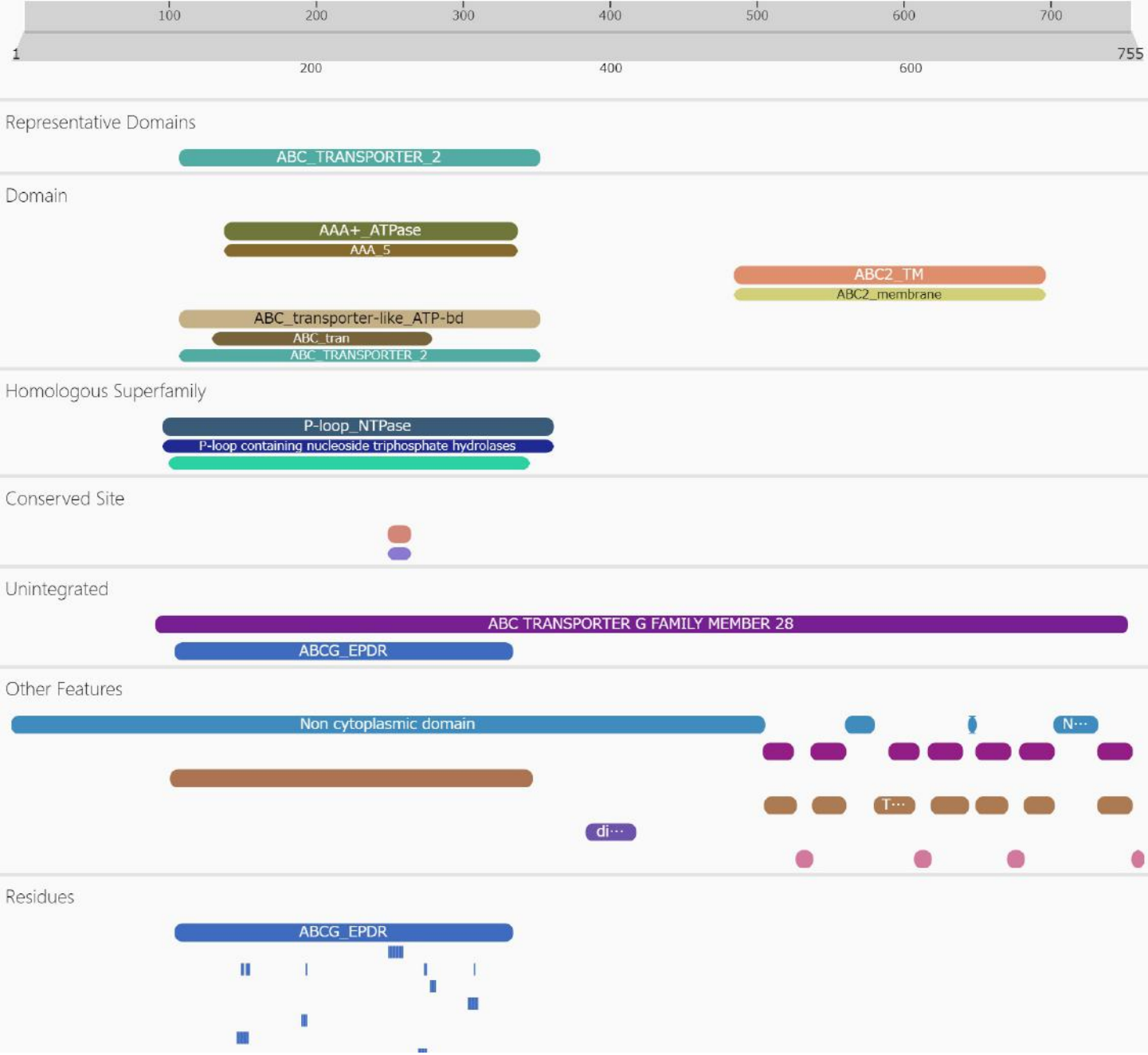
ABCF1



ABCF2



ABCF3



PS50893

D IPR003593
SM00382

D IPR013525
PF01061

D IPR003439
PF00005
PS50893

H IPR027417
SSF52540
G3DSA:3.40.50.300

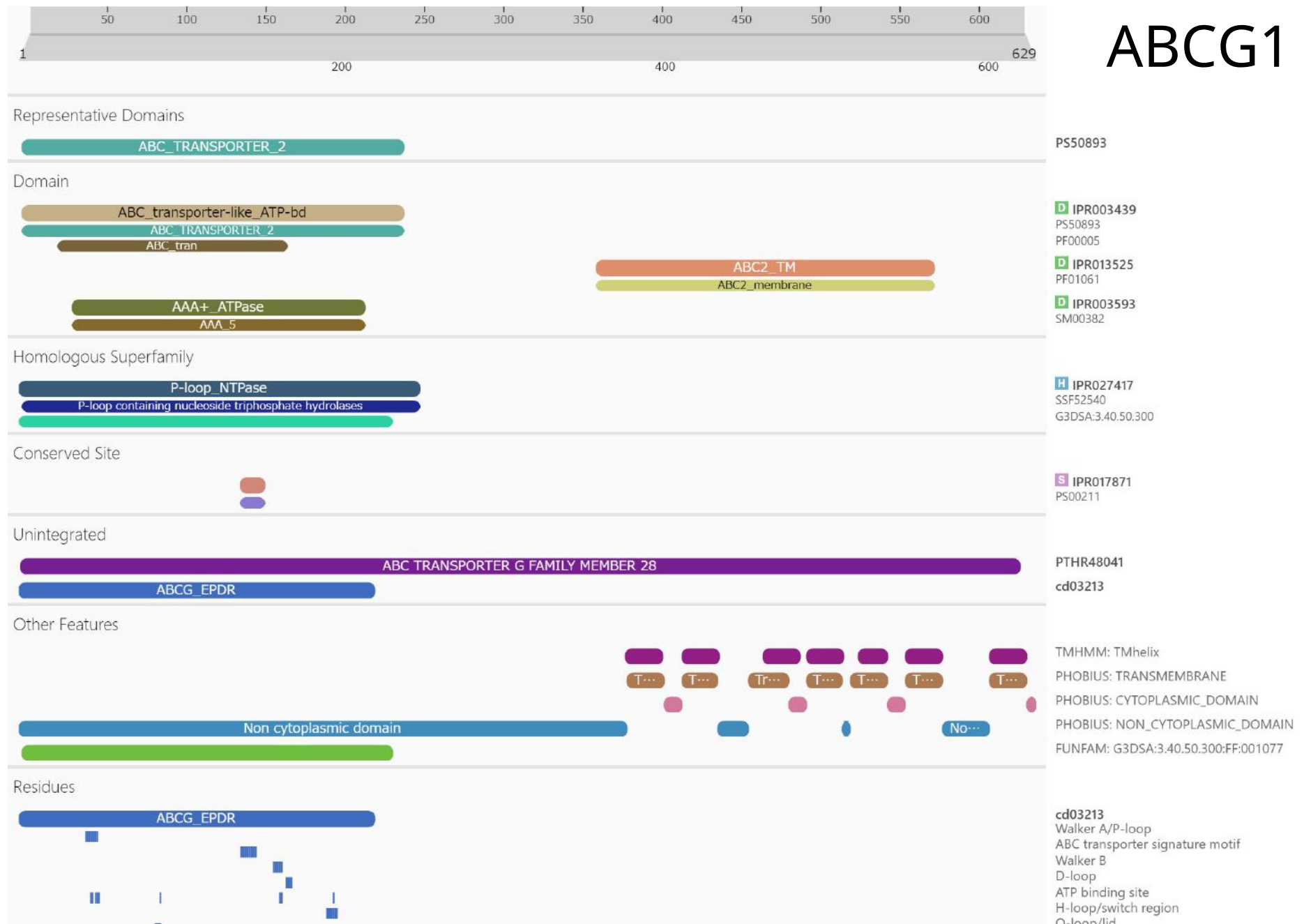
S IPR017871
PS00211

PTHR48041
cd03213

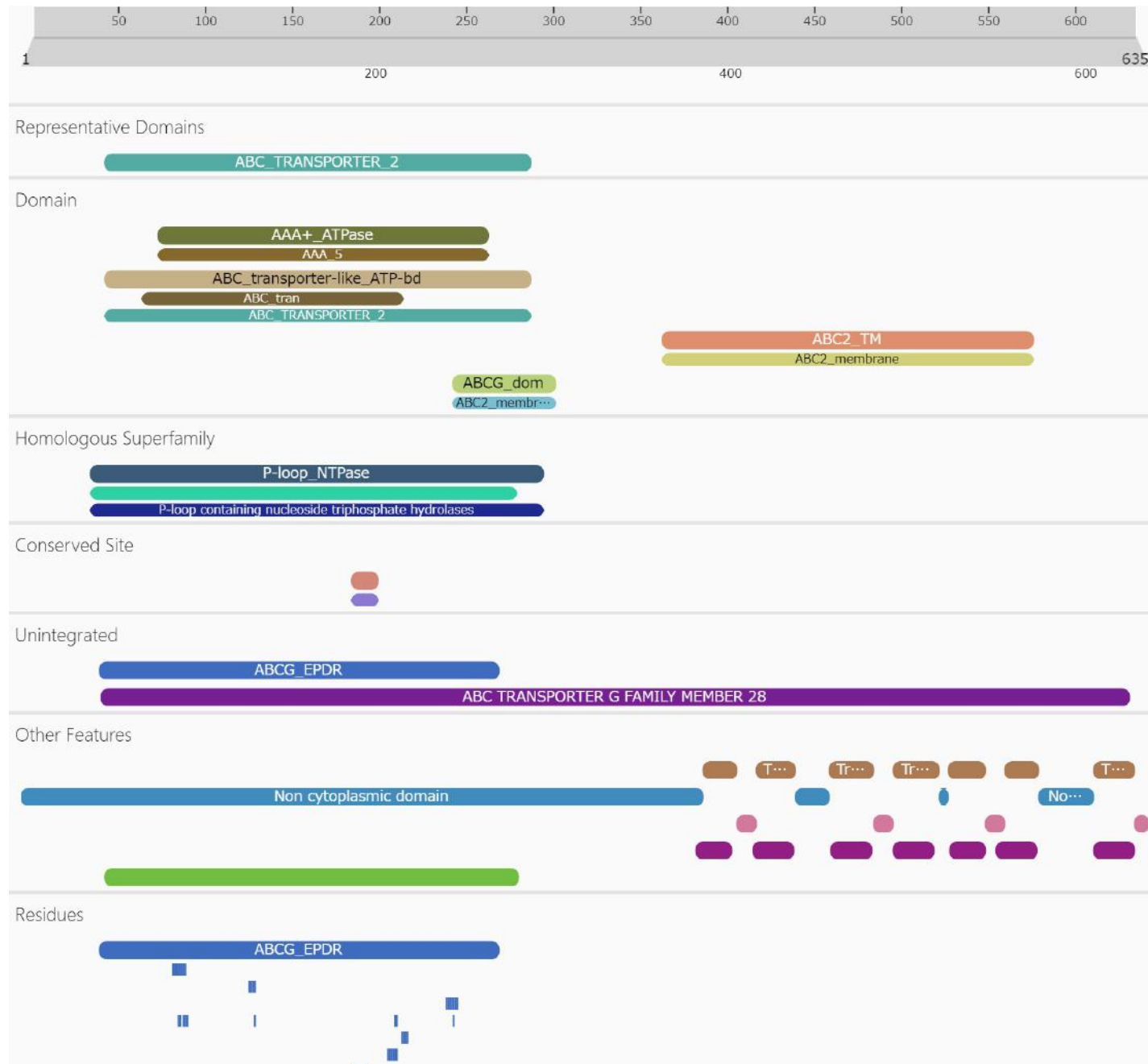
PHOBIUS: NON_CYTOPLASMIC_DOMAIN
TMHMM: TMhelix
FUNFAM: G3DSA:3.40.50.300:FF:000891
PHOBIUS: TRANSMEMBRANE
MOBIDB LITE: mobidb-lite
PHOBIUS: CYTOPLASMIC_DOMAIN

cd03213
ABC transporter signature motif
ATP binding site
D-loop
H-loop/switch region
Q-loop/lid
Walker A/P-loop
Walker B

ABCG1



ABCG2



PS50893

D IPR003593
SM00382

D IPR003439
PF00005
PS50893

D IPR013525
PF01061

D IPR043926
PF19055

H IPR027417
G3DSA:3.40.50.300
SSF52540

S IPR017871
PS00211

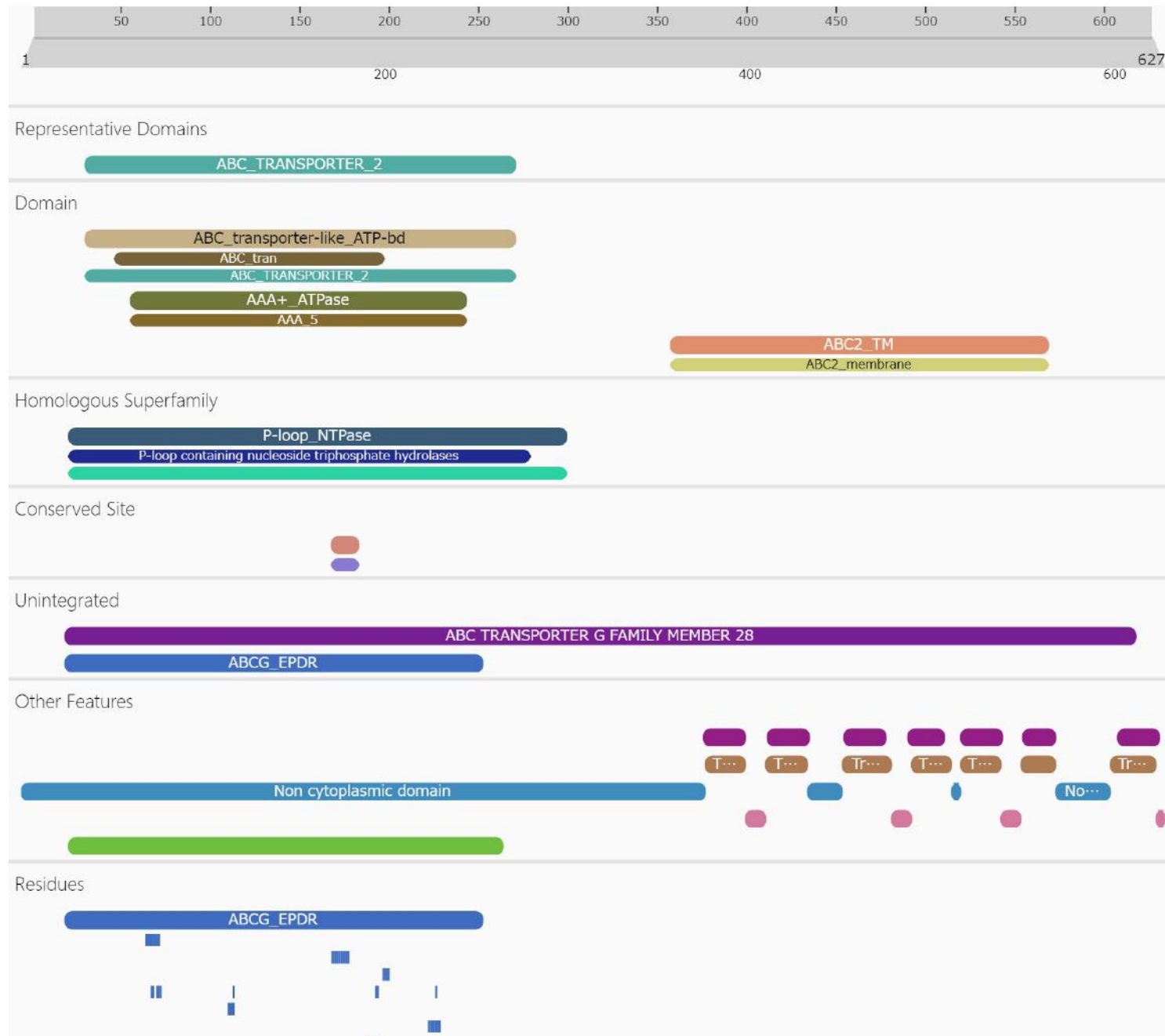
cd03213

PTHR48041

PHOBIUS: TRANSMEMBRANE
PHOBIUS: NON_CYTOPLASMIC_DOMAIN
PHOBIUS: CYTOPLASMIC_DOMAIN
TMHMM: TMhelix
FUNFAM: G3DSA:3.40.50.300:FF:001077

cd03213
Walker A/P-loop
Q-loop/lid
H-loop/switch region
ATP binding site
D-loop
Walker B
ABC transporter signature motif

ABCG3



PS50893

D IPR003439

PF00005

PS50893

D IPR003593

SM00382

D IPR013525

PF01061

H IPR027417

SSF52540

G3DSA:3.40.50.300

S IPR017871

PS00211

PTHR48041

cd03213

TMHMM: TMhelix

PHOBIUS: TRANSMEMBRANE

PHOBIUS: NON_CYTOPLASMIC_DOMAIN

PHOBIUS: CYTOPLASMIC_DOMAIN

FUNFAM: G3DSA:3.40.50.300:FF:001077

cd03213

Walker A/P-loop

ABC transporter signature motif

D-loop

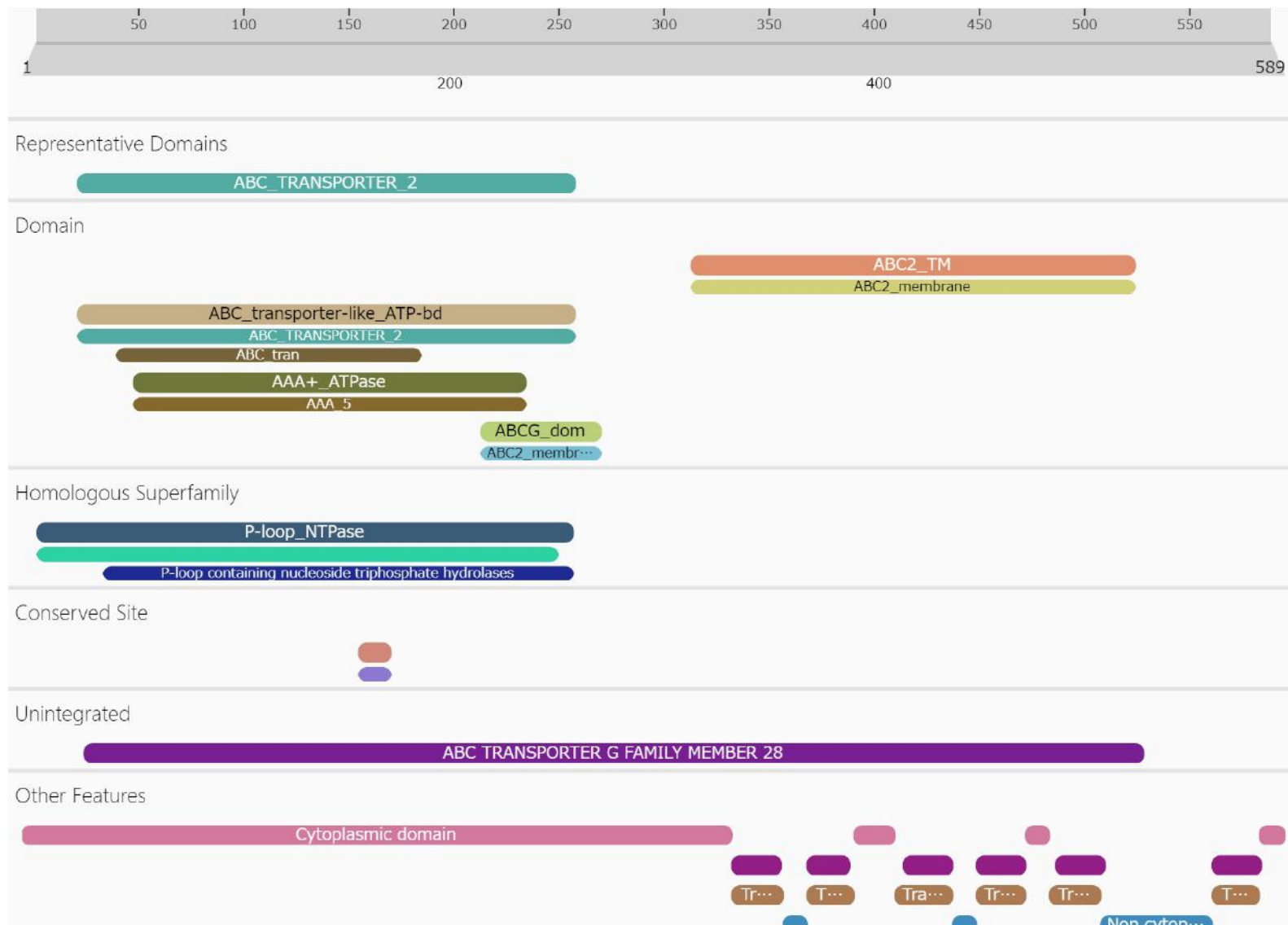
ATP binding site

Q-loop/lid

H-loop/switch region

Walker B

ABCG4



PS50893

D IPR013525
PF01061

D IPR003439
PS50893
PF00005

D IPR003593
SM00382

D IPR043926
PF19055

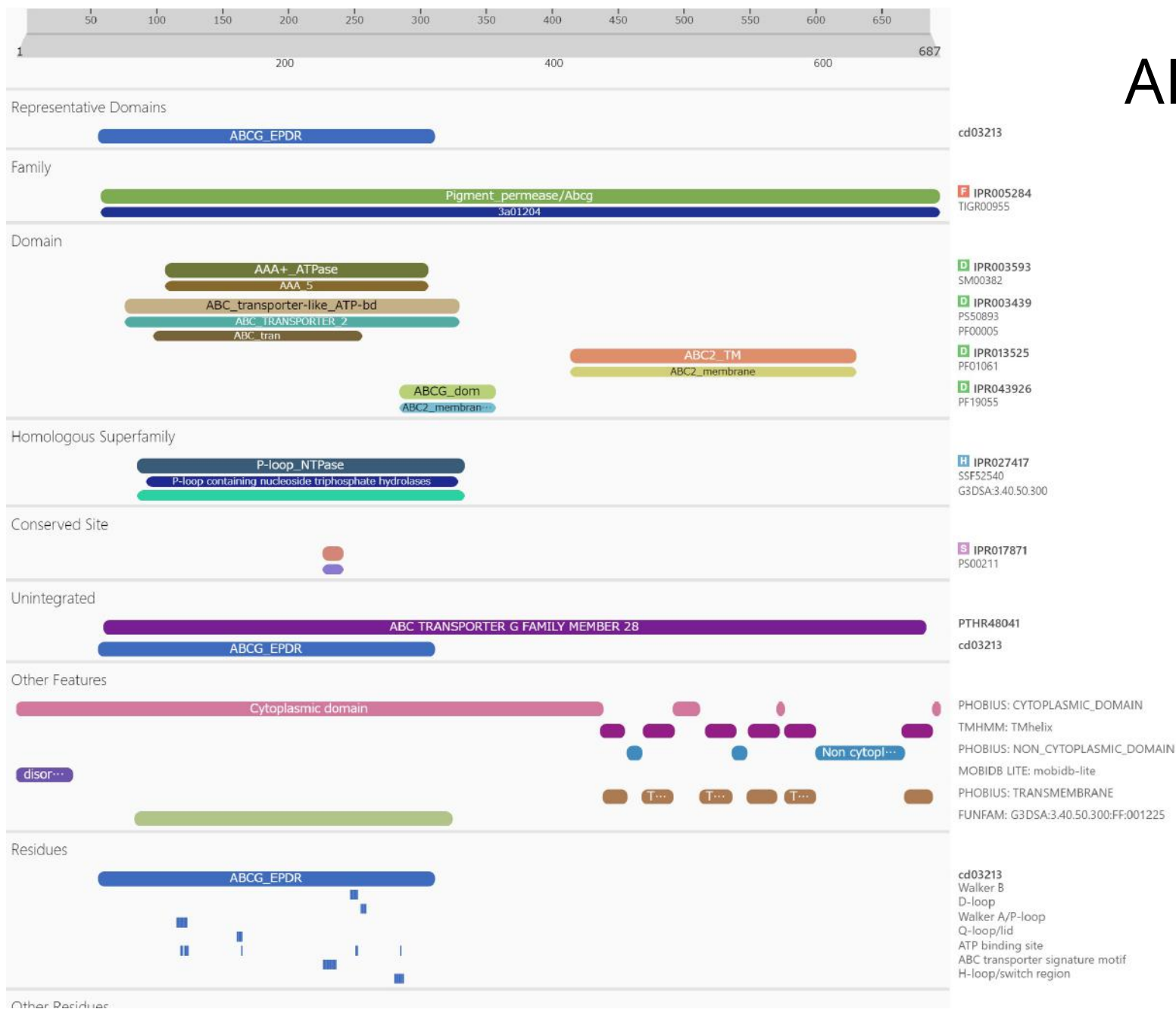
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G3DSA:3.40.50.300
SSF52540

S IPR017871
PS00211

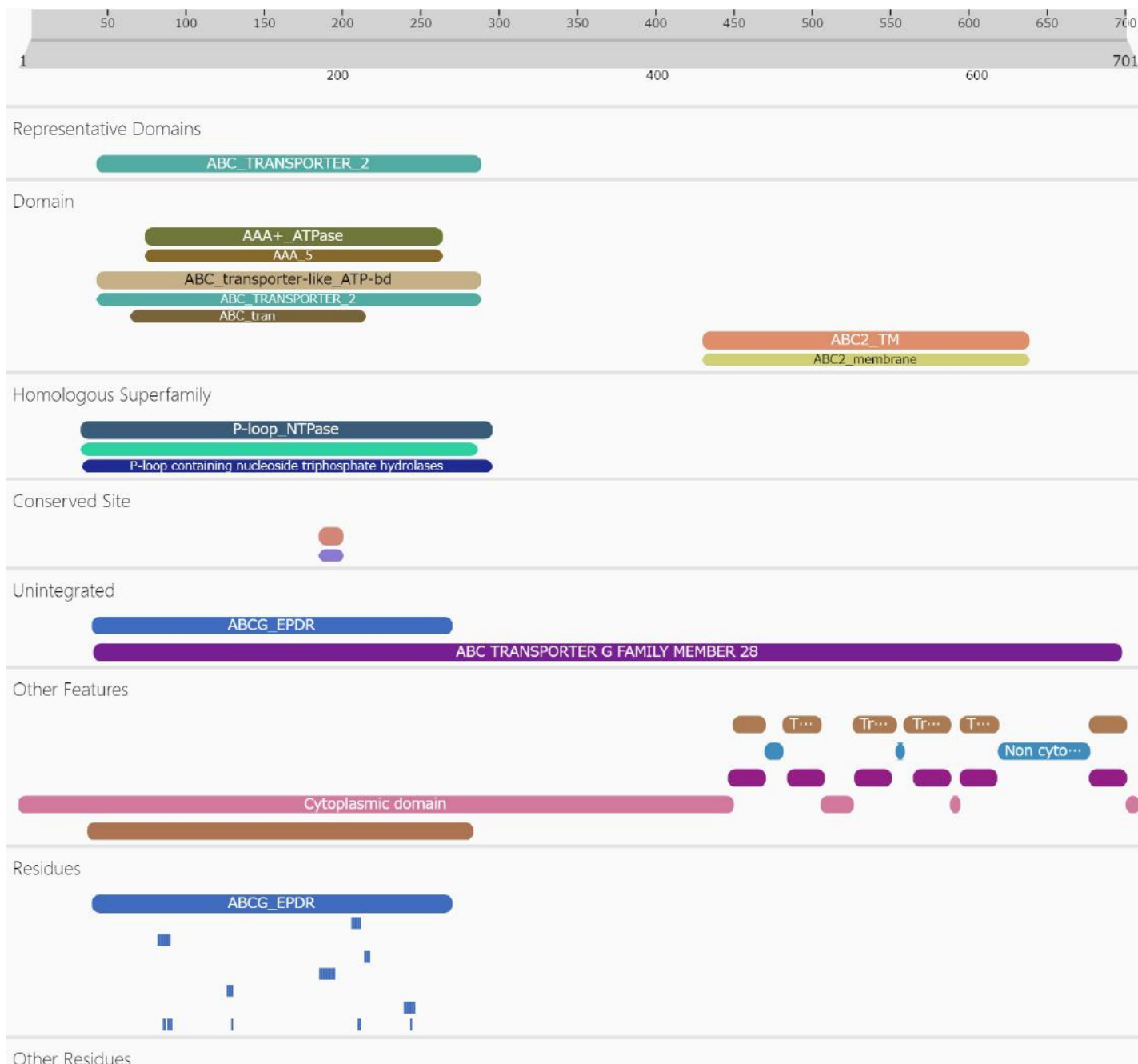
PTHR48041

PHOBIUS: CYTOPLASMIC_DOMAIN
TMHMM: TMhelix
PHOBIUS: TRANSMEMBRANE
PHOBIUS: NON_CYTOPLASMIC_DOMAIN

ABCG5



ABCG6



PS50893

D IPR003593
SM00382

D IPR003439
PS50893
PF00005

D IPR013525
PF01061

H IPR027417
G3DSA:3.40.50.300
SSF52540

S IPR017871
PS00211

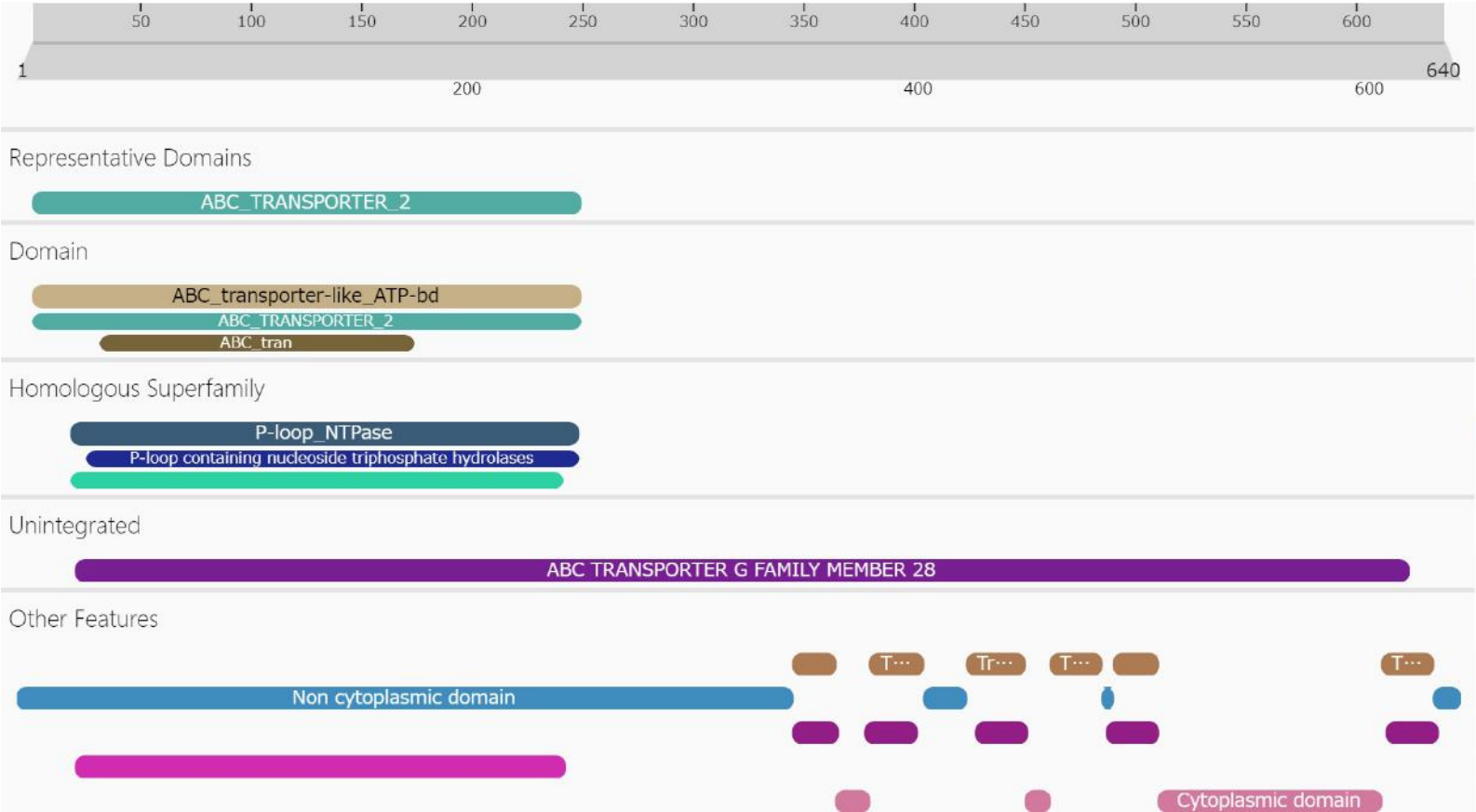
cd03213

PTHR48041

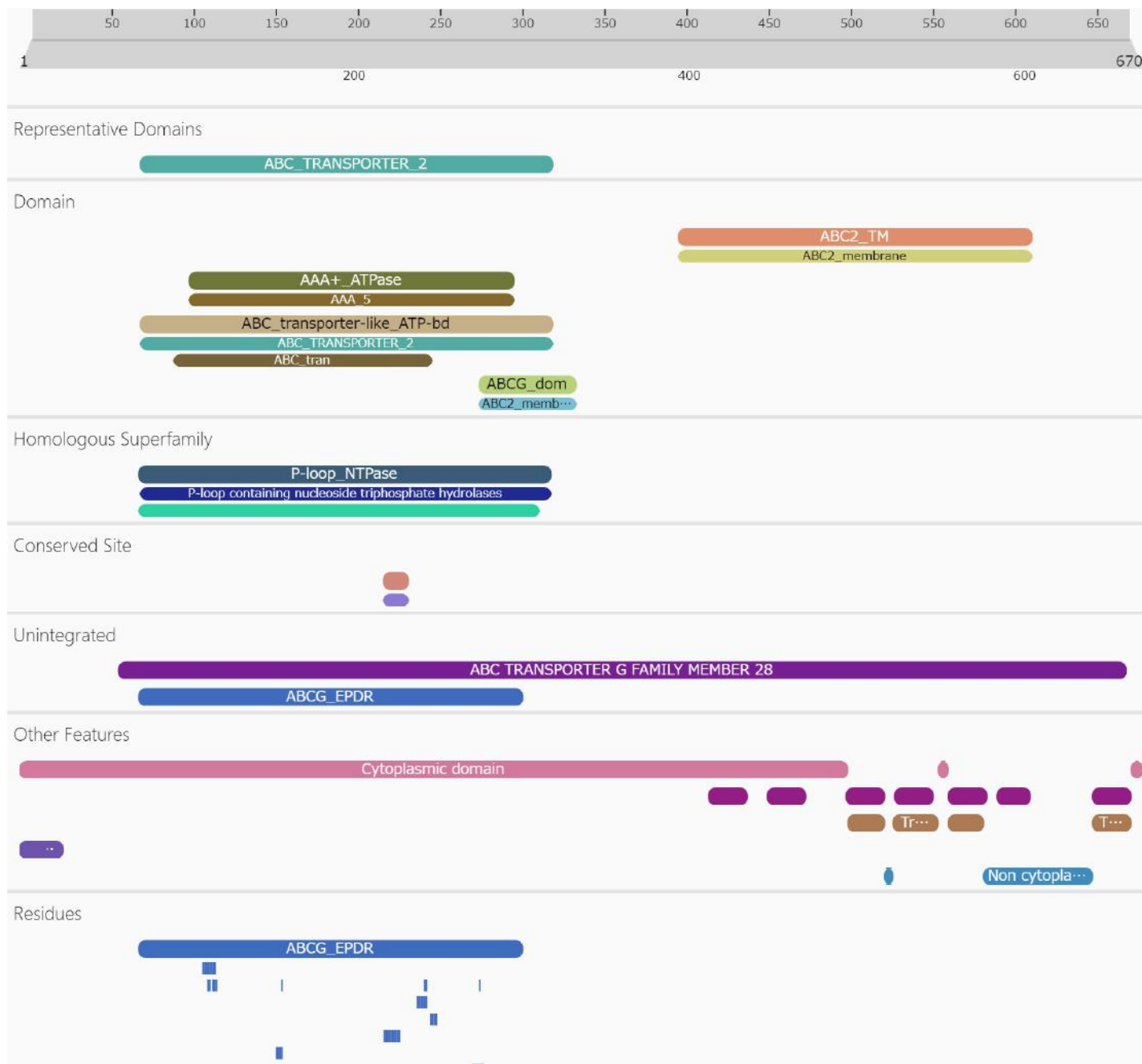
PHOBIUS: TRANSMEMBRANE
PHOBIUS: NON_CYTOPLASMIC_DOMAIN
TMHMM: TMhelix
PHOBIUS: CYTOPLASMIC_DOMAIN
FUNFAM: G3DSA:3.40.50.300:FF:000891

cd03213
Walker B
Walker A/P-loop
D-loop
ABC transporter signature motif
Q-loop/lid
H-loop/switch region
ATP binding site

ABCG7



ABCG8



PS50893

D IPR013525
PF01061

D IPR003593
SM00382

D IPR003439
PS50893
PF00005

D IPR043926
PF19055

H IPR027417
SSF52540
G3DSA:3.40.50.300

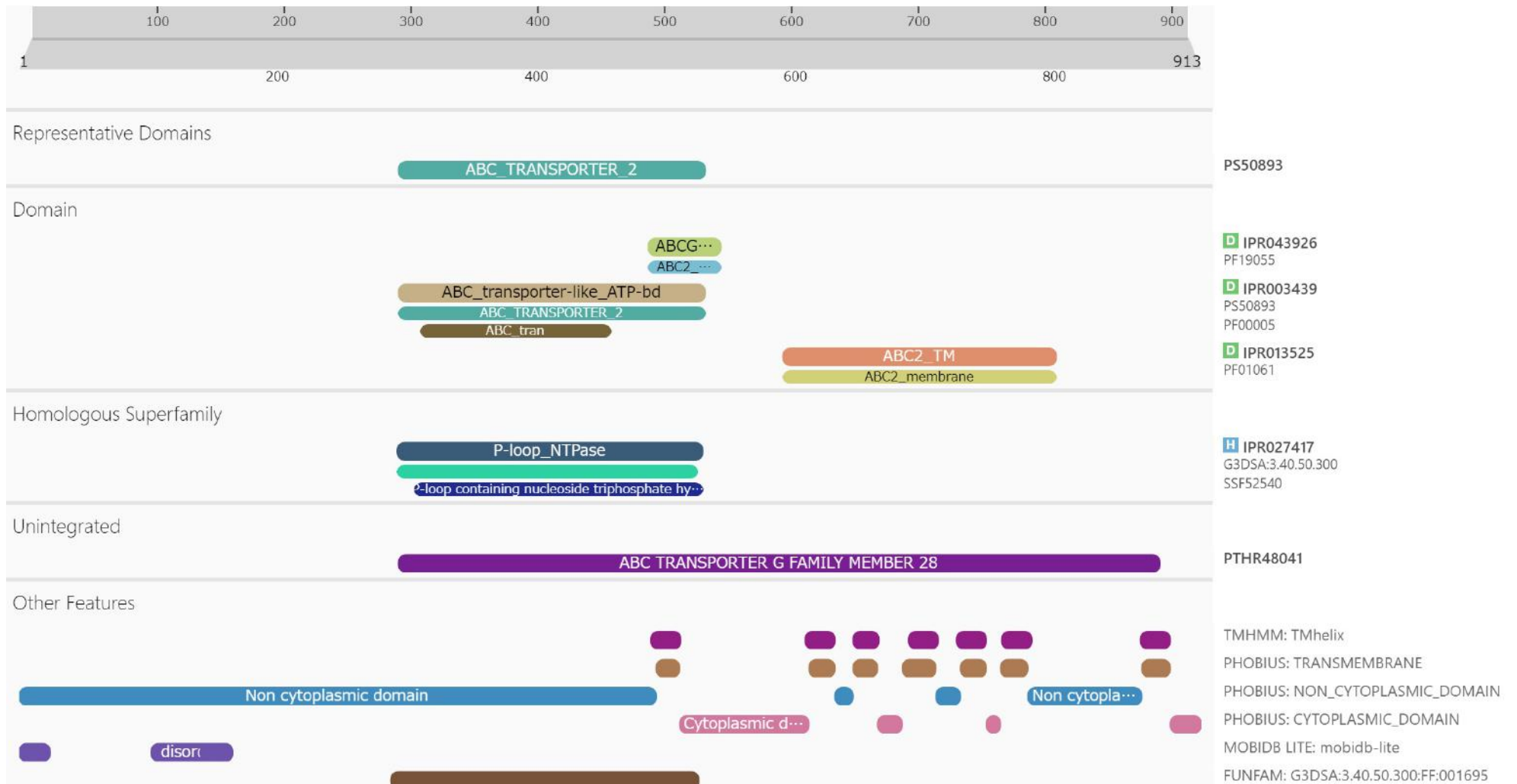
S IPR017871
PS00211

PTHR48041
cd03213

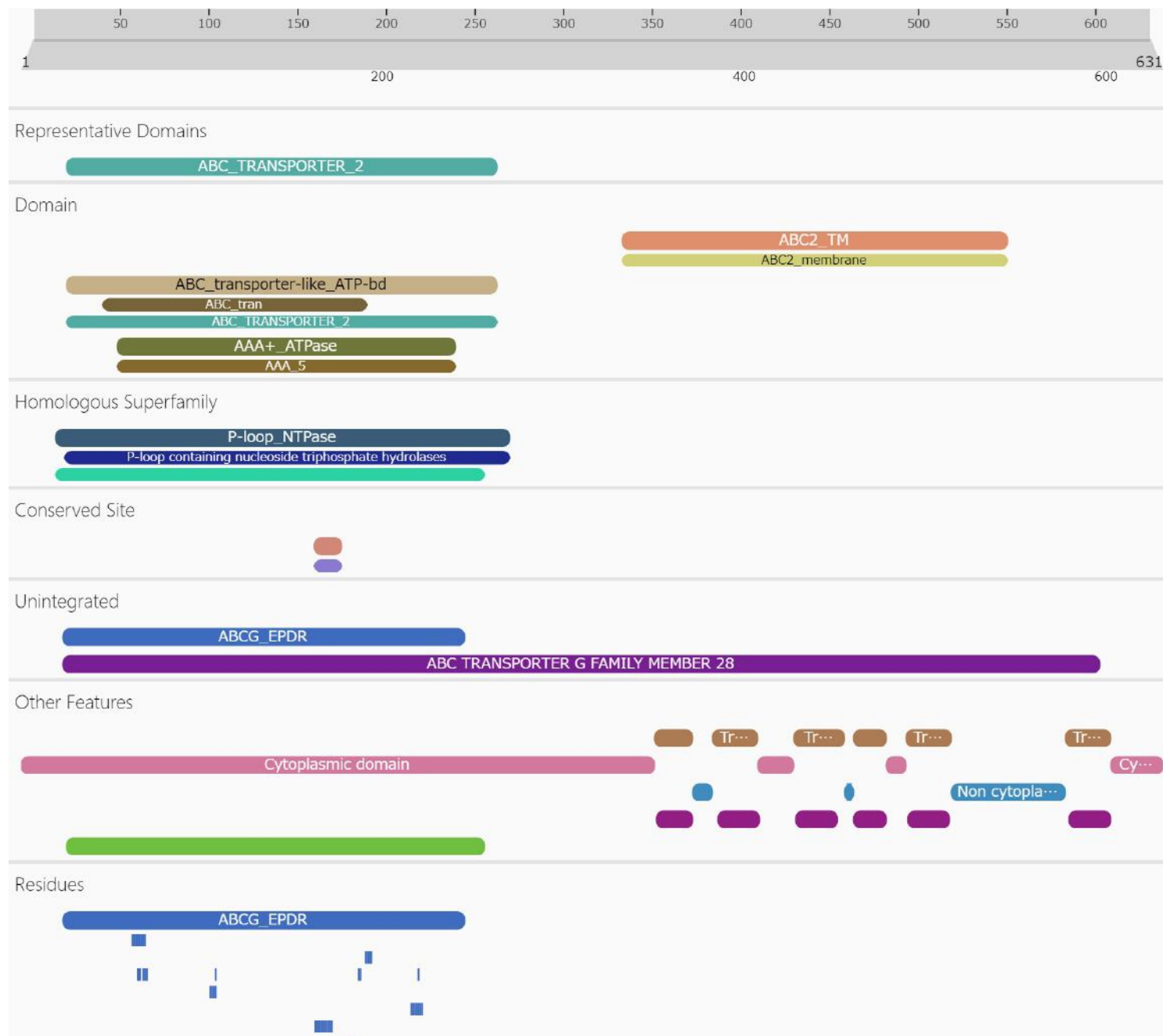
PHOBIUS: CYTOPLASMIC_DOMAIN
TMHMM: TMhelix
PHOBIUS: TRANSMEMBRANE
MOBIDB LITE: mobidb-lite
PHOBIUS: NON_CYTOPLASMIC_DOMAIN

cd03213
Walker A/P-loop
ATP binding site
Walker B
D-loop
ABC transporter signature motif
Q-loop/lid
H-loop/switch region

ABCG9



ABCG10



PS50893

D IPR013525
PF01061

D IPR003439
PF00005
PS50893

D IPR003593
SM00382

H IPR027417
SSF52540
G3DSA:3.40.50.300

S IPR017871
PS00211

cd03213

PTHR48041

PHOBIUS: TRANSMEMBRANE

PHOBIUS: CYTOPLASMIC_DOMAIN

PHOBIUS: NON_CYTOPLASMIC_DOMAIN

TMHMM: TMhelix

FUNFAM: G3DSA:3.40.50.300:FF:001077

cd03213

Walker A/P-loop

D-loop

ATP binding site

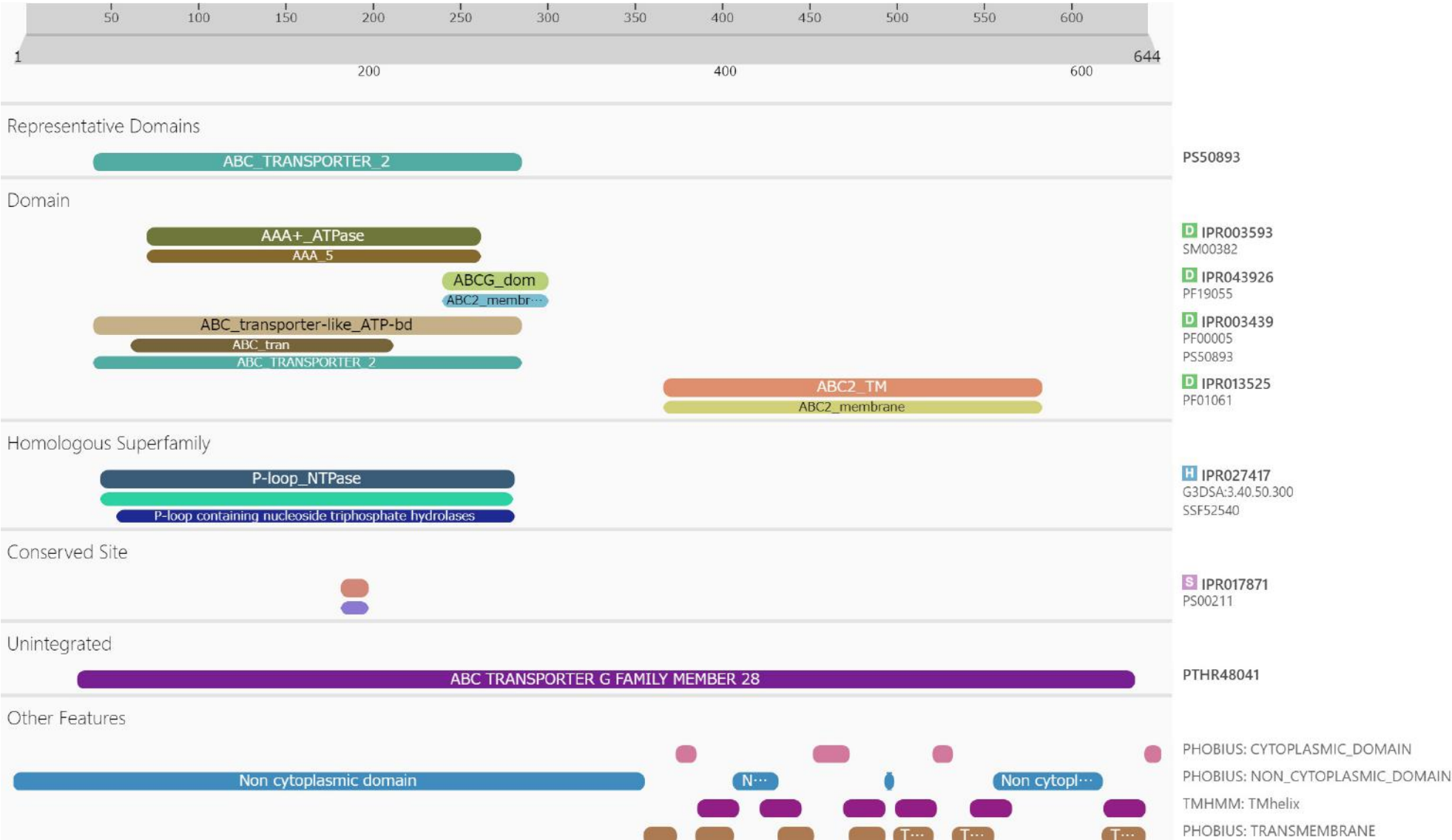
Q-loop/lid

H-loop/switch region

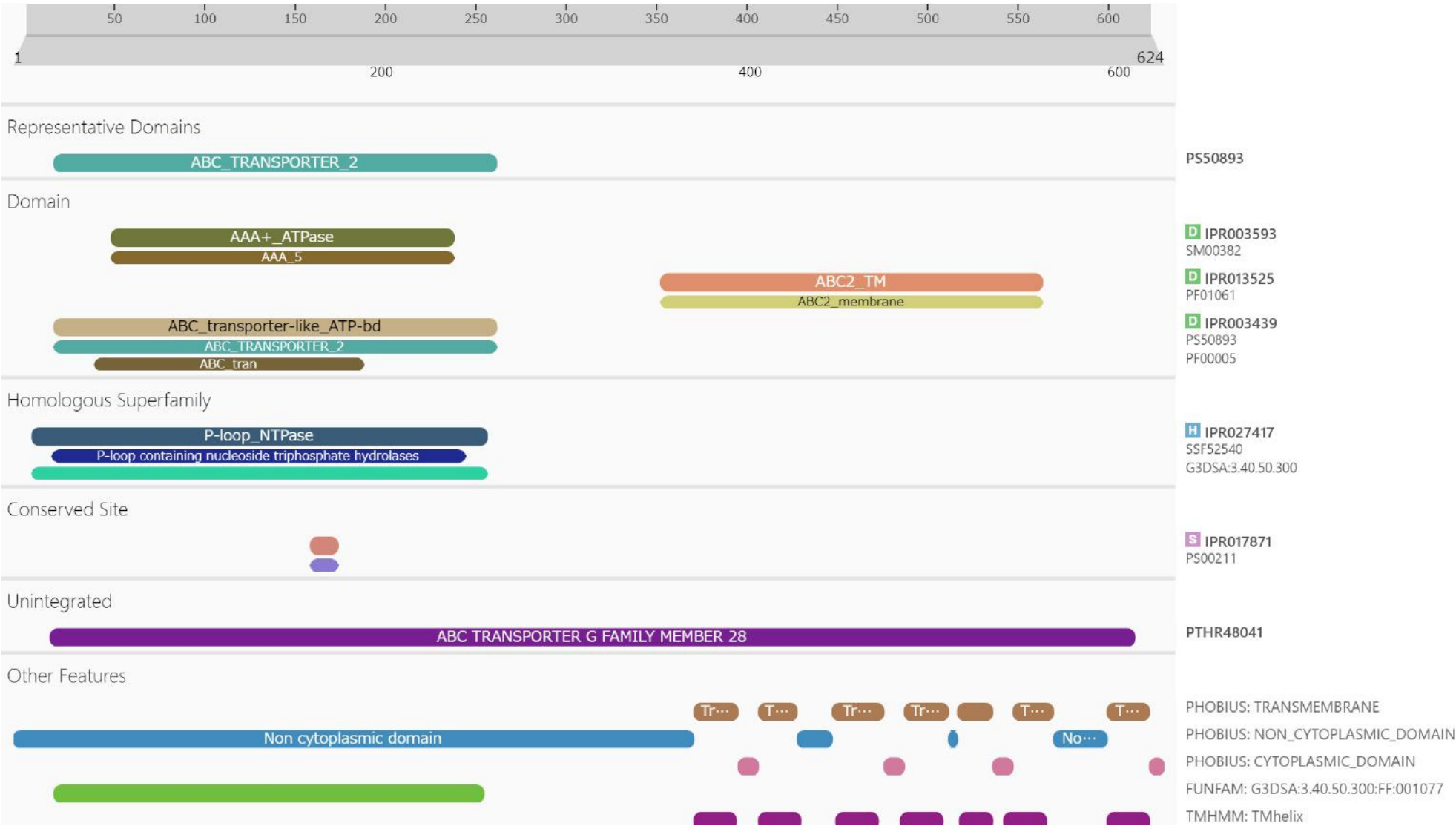
ABC transporter signature motif

Walker B

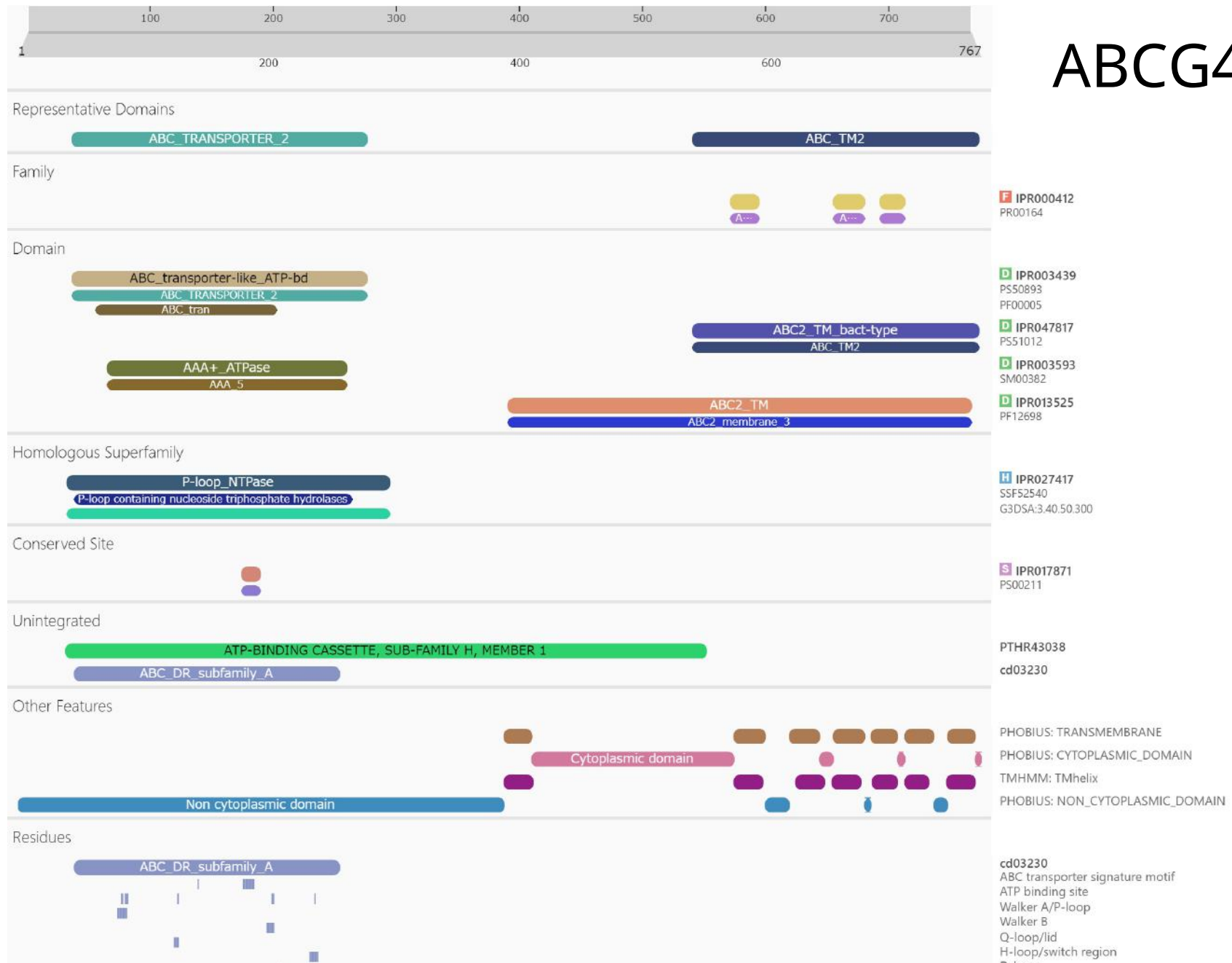
ABCG11



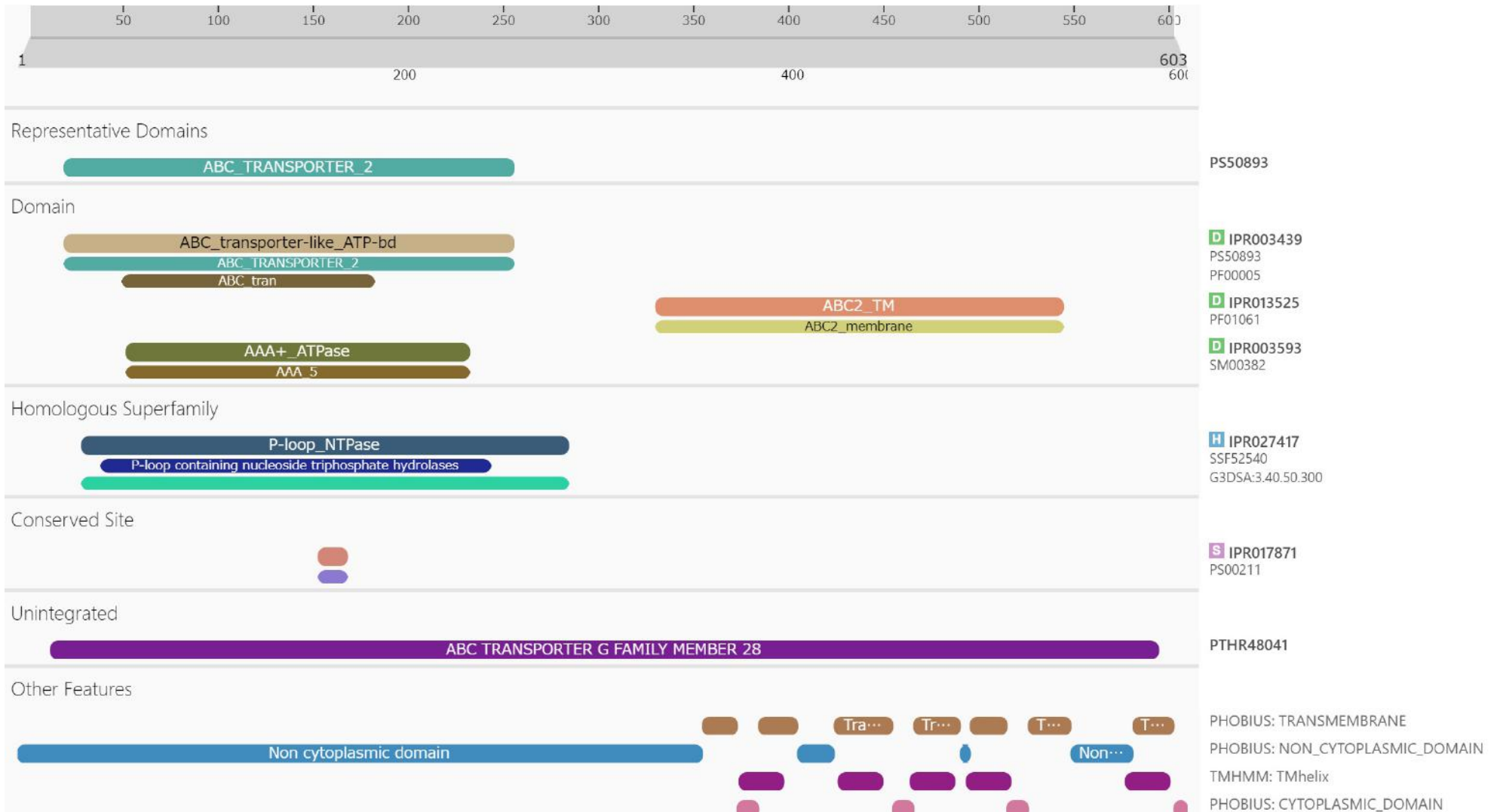
ABCG12



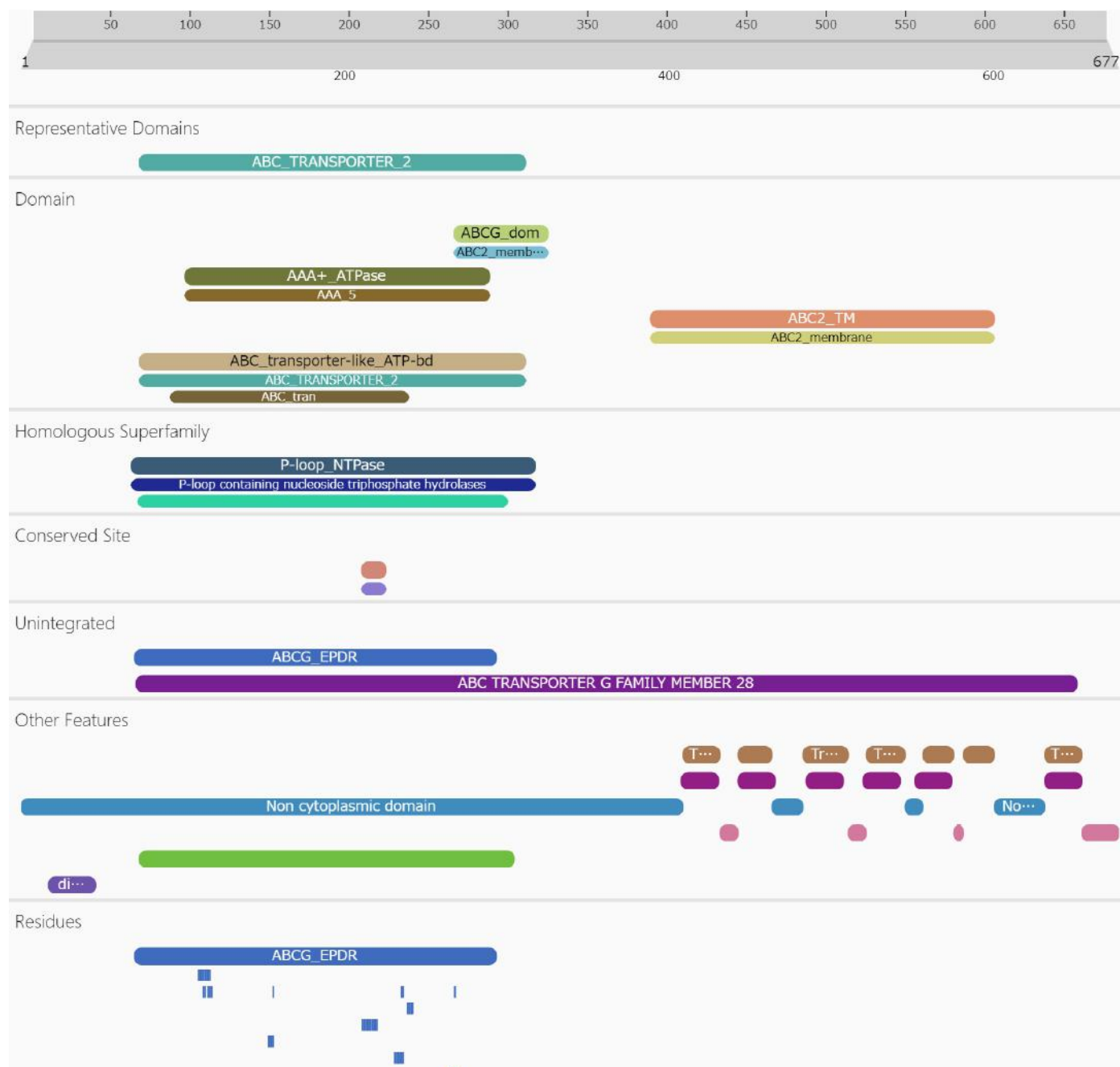
ABCG4-like1



ABCG23



ABCG4-like2



PS50893

IPR043926
PF19055

IPR003593
SM00382

IPR013525
PF01061

IPR003439
PS50893
PF00005

IPR027417
SSF52540
G3DSA:3.40.50.300

IPR017871
PS00211

cd03213

PTHR48041

PHOBIUS: TRANSMEMBRANE

TMHMM: TMhelix

PHOBIUS: NON_CYTOPLASMIC_DOMAIN

PHOBIUS: CYTOPLASMIC_DOMAIN

FUNFAM: G3DSA:3.40.50.300:FF:001077

MOBIDB LITE: mobidb-lite

cd03213

Walker A/P-loop

ATP binding site

D-loop

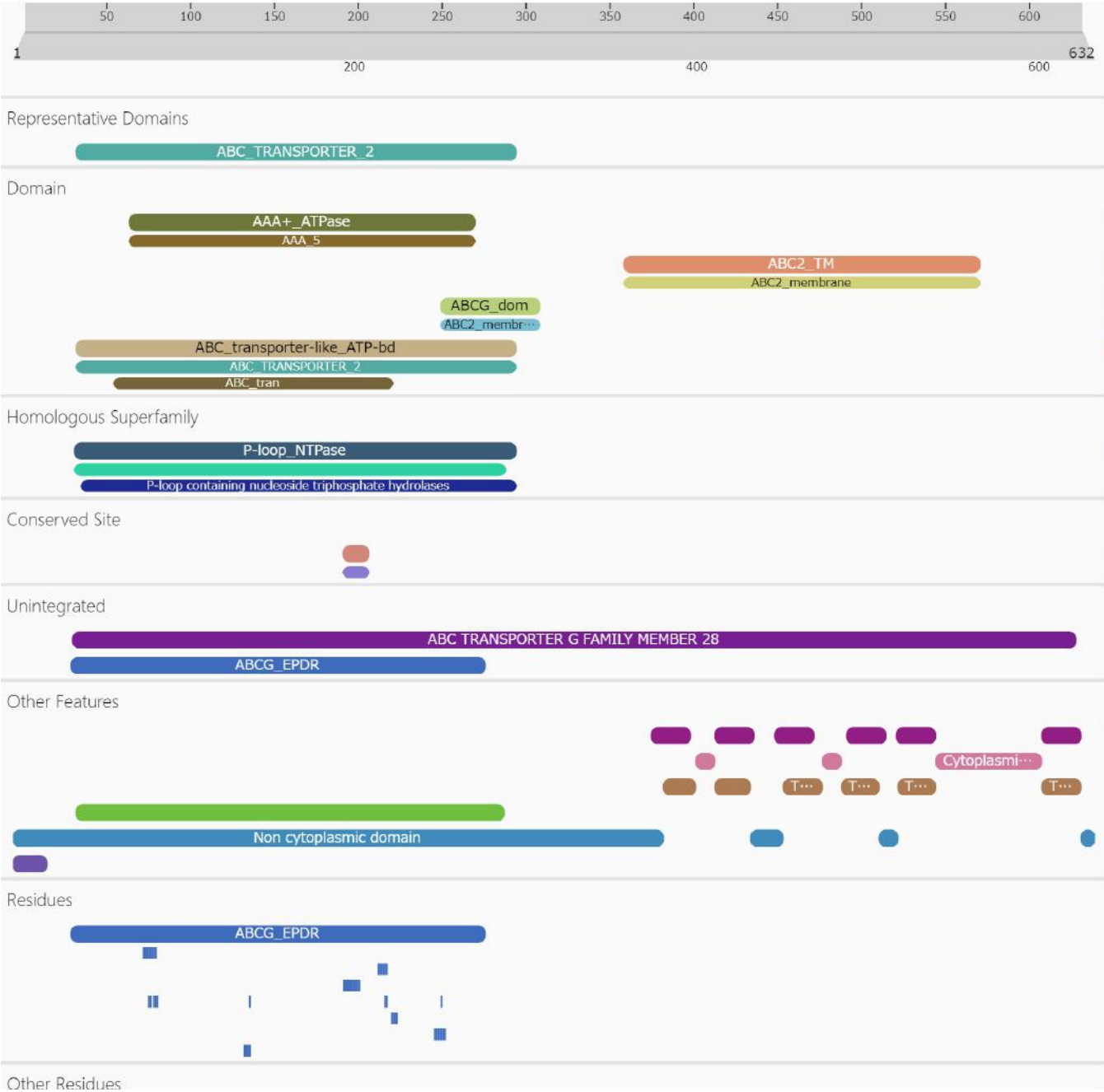
ABC transporter signature motif

Q-loop/lid

Walker B

H-loop/switch region

ABCG1-like1



PS50893

D IPR003593
SM00382

D IPR013525
PF01061

D IPR043926
PF19055

D IPR003439
PS50893
PF00005

H IPR027417
G3DSA:3.40.50.300
SSF52540

S IPR017871
PS00211

PTHR48041
cd03213

TMHMM: TMhelix
PHOBIUS: CYTOPLASMIC_DOMAIN
PHOBIUS: TRANSMEMBRANE
FUNFAM: G3DSA:3.40.50.300:FF:001077
PHOBIUS: NON_CYTOPLASMIC_DOMAIN
MOBIDB LITE: mobidb-lite

cd03213
Walker A/P-loop
Walker B
ABC transporter signature motif
ATP binding site
D-loop
H-loop/switch region
Q-loop/lid

ABCG4-like3



Representative Domains



Domain



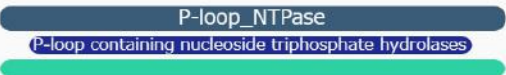
D IPR013525
PF12698

D IPR003439
PF00005
PS50893

D IPR003593
SM00382

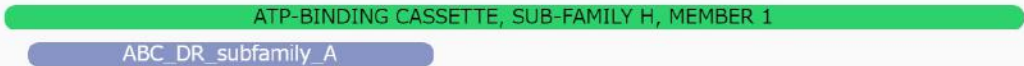
D IPR047817
PS51012

Homologous Superfamily



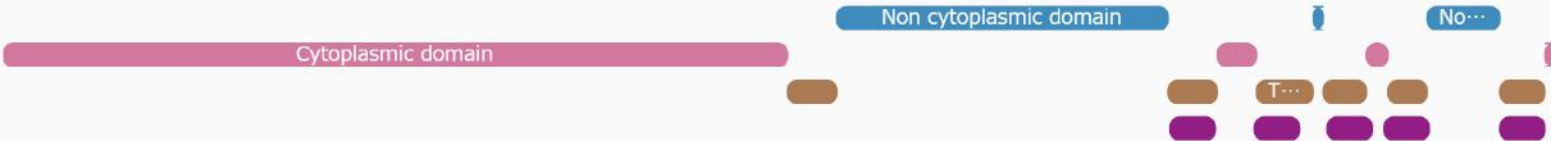
H IPR027417
SSF52540
G3DSA:3.40.50.300

Unintegrated



PTHR43038
cd03230

Other Features



PHOBIUS: NON_CYTOPLASMIC_DOMAIN
PHOBIUS: CYTOPLASMIC_DOMAIN
PHOBIUS: TRANSMEMBRANE
TMHMM: TMhelix

Residues



cd03230
H-loop/switch region
Q-loop/lid
D-loop
Walker B
ATP binding site
Walker A/P-loop
ABC transporter signature motif

ABCH1



Representative Domains

ABC_TRANSPORTER_2

PS50893

Domain

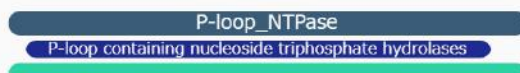


D IPR013525
PF12698

D IPR003593
SM00382

D IPR003439
PS50893
PF00005

Homologous Superfamily



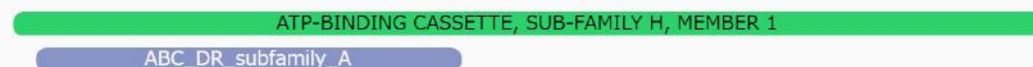
H IPR027417
SSF52540
G3DSA:3.40.50.300

Conserved Site



S IPR017871
PS00211

Unintegrated



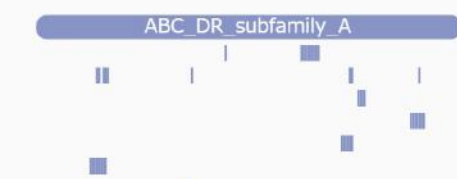
PTHR43038
cd03230

Other Features



PHOBIUS: CYTOPLASMIC_DOMAIN
TMHMM: TMhelix
PHOBIUS: TRANSMEMBRANE
PHOBIUS: NON_CYTOPLASMIC_DOMAIN

Residues



cd03230
ABC transporter signature motif
ATP binding site
D-loop
H-loop/switch region
Walker B
Walker A/P-loop
O-loop/lid

ABCH2

