BIOZENTRUM
University of Basel
The Center for Molecular Life Sciences

SWISS-MODEL Homology Modelling Report

Model Building Report

This document lists the results for the homology modelling project "Untitled Project" submitted to SWISS-MODEL workspace on Dec. 22, 2020, 9:58 p.m..The submitted primary amino acid sequence is given in Table T1.

If you use any results in your research, please cite the relevant publications:

- Waterhouse, A., Bertoni, M., Bienert, S., Studer, G., Tauriello, G., Gumienny, R., Heer, F.T., de Beer, T.A.P., Rempfer, C., Bordoli, L., Lepore, R., Schwede, T. SWISS-MODEL: homology modelling of protein structures and complexes. Nucleic Acids Res. 46(W1), W296-W303 (2018). doi
- Guex, N., Peitsch, M.C., Schwede, T. Automated comparative protein structure modeling with SWISS-MODEL and Swiss-PdbViewer: A historical perspective. Electrophoresis 30, S162-S173 (2009). doi
- Bienert, S., Waterhouse, A., de Beer, T.A.P., Tauriello, G., Studer, G., Bordoli, L., Schwede, T. The SWISS-MODEL Repository - new features and functionality. Nucleic Acids Res. 45, D313-D319 (2017). doi
- Studer, G., Rempfer, C., Waterhouse, A.M., Gumienny, G., Haas, J., Schwede, T. QMEANDisCo - distance constraints applied on model quality estimation. Bioinformatics 36, 1765-1771 (2020). doi
- Bertoni, M., Kiefer, F., Biasini, M., Bordoli, L., Schwede, T. Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. Scientific Reports 7 (2017). doi

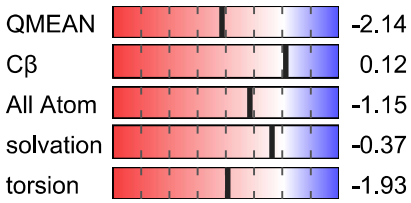
Results

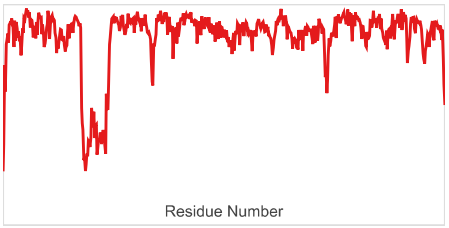
The SWISS-MODEL template library (SMTL version 2020-12-16, PDB release 2020-12-11) was searched with BLAST (Camacho et al.) and HHBlits (Steinegger et al.) for evolutionary related structures matching the target sequence in Table T1. For details on the template search, see Materials and Methods. Overall 1630 templates were found (Table T2).

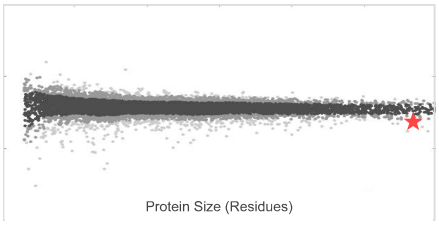
Models

The following model was built (see Materials and Methods "Model Building"):

Model #01	File	Built with	Oligo-State	Ligands	GMQE	QMEAN
	PDB	ProMod3 3.2.0	monomer	1 x SO4: SULFATE ION;	0.60	-2.14







Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
1qon.1.A	89.70	monomer	0.00	BLAST	X-ray	2.72Å	0.60	140 - 709	0.77	ACETYLCHOLINESTERASE

Included Ligands

Ligand	Description
1 x SO4	SULFATE ION

Excluded ligands

Ligand Name.Number	Reason for Exclusion	Description
I40.3	Not biologically relevant.	9-(3-IODOBENZYLAMINO)-1,2,3,4-TETRAHYDROACRIDINE
NAG-NAG-BMA-BMA-BMA.1	Not biologically relevant.	beta-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

```
Target    MARFITSSSLSPSTTPSFASATASPAIASSLPRSKSTKATKARKTILSANSFKTSSLSSLSSSASSPSLSSSPSFFKSSS
1qon.1.A  ------------------------------------------------------------------------------

Target    SSKSRYSSSHLFNAFASLIPSSLAFSSLSFSSLTSTNDLYRGFFATLVILLRMSSVAYGITDRLIVQTTSGPVRGRAVTV
1qon.1.A  ------------------------------------------------------------VIDRLVVQTSSGPVRGRSVTV

Target    QGREVHVFTGIPYAKPPVDDLRFRKPVPAEPWHGVLDATRLPATCVQERYEYFPGFSGEEIWNPNTNVSEDCLYMNIWAP
1qon.1.A  QGREVHVYTGIPYAKPPVEDLRFRKPVPAEPWHGVLDATGLSATCVQERYEYFPGFSGEEIWNPNTNVSEDCLYINVWAP

Target    SKARLRHGRGANGVEH--AAKTDPDHLIHSATPQNTTNGLPILIWIYGGGFMTGSATLDIYNADIMSAVGNVIVASFQYR
1qon.1.A  AKARLRHGRGANGGEHPNGKQADTDHLIHNGNPQNTTNGLPILIWIYGGGFMTGSATLDIYNADIMAAVGNVIVASFQYR

Target    VGAFGFLHLSPVMPG-FEEEAPGNVGLWDQALALRWLKENARAFGGNPEWMTLFGESAGSSSVNAQLVSPVTRGLVKRGM
1qon.1.A  VGAFGFLHLAPEMPSEFAEEAPGNVGLWDQALAIRWLKDNAHAFGGNPEWMTLFGESAGSSSVNAQLMSPVTRGLVKRGM

Target    MQSGTMNAPWSHMTSEKAVEIGKALINDCNCNASLLSENPQSVMACMRSVDAKTISVQQWNSYSGILSFPSAPTIDGAFF
1qon.1.A  MQSGTMNAPWSHMTSEKAVEIGKALINDCNCNASMLKTNPAHVMSCMRSVDAKTISVQQWNSYSGILSFPSAPTIDGAFL

Target    TADPMTLMKTADMTGYDIMIGNVKDEGTYFLLYDFIDYFDKDEATSLPRDKYLEIMNNIFNKATQAEREAIIFQYTSWEG
1qon.1.A  PADPMTLMKTADLKDYDILMGNVRDEGTYFLLYDFIDYFDKDDATALPRDKYLEIMNNIFGKATQAEREAIIFQYTSWEG

Target    NPGYQNQQQIGRAVGDHFFTCPTNEYAQALAERGAQVHYYYFTHRTSTSLWGEWMGVLHGDEIEYFFGQPLNTSLQYRPV
1qon.1.A  NPGYQNQQQIGRAVGDHFFTCPTNEYAQALAERGASVHYYYFTHRTSTSLWGEWMGVLHGDEIEYFFGQPLNNSLQYRPV

Target    ERELGKRMLNSVIEFAKTGNPAVDGEEWPNFSKEDPVYYVFSTDEKTEKLQRGPLAKRCSFWNDYLPKVRSWVGSECENN
1qon.1.A  ERELGKRMLSAVIEFAKTGNPAQDGEEWPNFSKEDPVYYIFSTDDKIEKLARGPLAARCSFWNDYLPKVRSWAGT-----

Target    NAASAAVNNINGQQYLLKWVIMLTIMVTCIFQ
1qon.1.A  --------------------------------
```

Materials and Methods

Template Search

Template search with BLAST and HHBlits has been performed against the SWISS-MODEL template library (SMTL, last update: 2020-12-16, last included PDB release: 2020-12-11).

The target sequence was searched with BLAST against the primary amino acid sequence contained in the SMTL. A total of 163 templates were found.

An initial HHblits profile has been built using the procedure outlined in (Steinegger et al.), followed by 1 iteration of HHblits against Uniclust30 (Mirdita, von den Driesch et al.). The obtained profile has then be searched against all profiles of the SMTL. A total of 1475 templates were found.

Template Selection

For each identified template, the template's quality has been predicted from features of the target-template alignment. The templates with the highest quality have then been selected for model building.

Model Building

Models are built based on the target-template alignment using ProMod3. Coordinates which are conserved between the target and the template are copied from the template to the model. Insertions and deletions are remodelled using a fragment library. Side chains are then rebuilt. Finally, the geometry of the resulting model is regularized by using a force field. In case loop modelling with ProMod3 fails, an alternative model is built with PROMOD-II (Guex et al.).

Model Quality Estimation

The global and per-residue model quality has been assessed using the QMEAN scoring function (Studer et al.).

Ligand Modelling

Ligands present in the template structure are transferred by homology to the model when the following criteria are met: (a) The ligands are annotated as biologically relevant in the template library, (b) the ligand is in contact with the model, (c) the ligand is not clashing with the protein, (d) the residues in contact with the ligand are conserved between the target and the template. If any of these four criteria is not satisfied, a certain ligand will not be included in the model. The model summary includes information on why and which ligand has not been included.

Oligomeric State Conservation

The quaternary structure annotation of the template is used to model the target sequence in its oligomeric form. The method (Bertoni et al.) is based on a supervised machine learning algorithm, Support Vector Machines (SVM), which combines interface conservation, structural clustering, and other template features to provide a quaternary structure quality estimate (QSQE). The QSQE score is a number between 0 and 1, reflecting the expected accuracy of the interchain contacts for a model built based a given alignment and template. Higher numbers indicate higher reliability. This complements the GMQE score which estimates the accuracy of the tertiary structure of the resulting model.

References

- **BLAST**
  Camacho, C., Coulouris, G., Avagyan, V., Ma, N., Papadopoulos, J., Bealer, K., Madden, T.L. BLAST+: architecture and applications. BMC Bioinformatics 10, 421-430 (2009). doi>
- **HHblits**
  Steinegger, M., Meier, M., Mirdita, M., Vöhringer, H., Haunsberger, S. J., Söding, J. HH-suite3 for fast remote homology detection and deep protein annotation. BMC Bioinformatics 20, 473 (2019). doi>
- **Uniclust30**
  Mirdita, M., von den Driesch, L., Galiez, C., Martin, M.J., Söding, J., Steinegger, M. Uniclust databases of clustered and deeply annotated protein sequences and alignments. Nucleic Acids Research 45, D170–D176 (2016). doi>

Table T1:

Primary amino acid sequence for which templates were searched and models were built.

```
MARFITSSSLSPSTTPSFASATASPAIASSLPRSKSTKATKARKTILSANSFKTSSLSSLSSSASSPSLSSSPSFFKSSSSSKSRYSSSHLFNAFASLIP
SSLAFSSLSFSSLTSTNDLYRGFFATLVILLRMSSVAYGITDRLIVQTTSGPVRGRAVTVQGREVHVFTGIPYAKPPVDDLRFRKPVPAEPWHGVLDATR
LPATCVQERYEYFPGFSGEEIWNPNTNVSEDCLYMNIWAPSKARLRHGRGANGVEHAAKTDPDHLIHSATPQNTTNGLPILIWIYGGGFMTGSATLDIYN
ADIMSAVGNVIVASFQYRVGAFGFLHLSPVMPGFEEEAPGNVGLWDQALALRWLKENARAFGGNPEWMTLFGESAGSSSVNAQLVSPVTRGLVKRGMMQS
GTMNAPWSHMTSEKAVEIGKALINDCNCNASLLSENPQSVMACMRSVDAKTISVQQWNSYSGILSFPSAPTIDGAFFTADPMTLMKTADMTGYDIMIGNV
KDEGTYFLLYDFIDYFDKDEATSLPRDKYLEIMNNIFNKATQAEREAIIFQYTSWEGNPGYQNQQQIGRAVGDHFFTCPTNEYAQALAERGAQVHYYYFT
HRTSTSLWGEWMGVLHGDEIEYFFGQPLNTSLQYRPVERELGKRMLNSVIEFAKTGNPAVDGEEWPNFSKEDPVYYVFSTDEKTEKLQRGPLAKRCSFWN
DYLPKVRSWVGSECENNNAASAAVNNINGQQYLLKWVIMLTIMVTCIFQ
```

Table T2:

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Coverage	Description
1qon.1.A	89.70	monomer	-	BLAST	X-ray	2.72Å	0.60	0.77	ACETYLCHOLINESTERASE
1qon.1.A	89.72	monomer	-	HHblits	X-ray	2.72Å	0.59	0.77	ACETYLCHOLINESTERASE
6xyy.1.A	89.55	monomer	-	HHblits	X-ray	2.70Å	0.59	0.77	Acetylcholinesterase
6xyy.1.A	89.70	monomer	-	BLAST	X-ray	2.70Å	0.60	0.77	Acetylcholinesterase
6xys.1.A	89.55	monomer	-	HHblits	X-ray	2.46Å	0.59	0.77	Acetylcholinesterase
6xys.1.A	89.70	monomer	-	BLAST	X-ray	2.46Å	0.60	0.77	Acetylcholinesterase
1qo9.1.A	89.72	monomer	-	HHblits	X-ray	2.70Å	0.59	0.77	ACETYLCHOLINESTERASE
1qo9.1.A	89.70	monomer	-	BLAST	X-ray	2.70Å	0.60	0.77	ACETYLCHOLINESTERASE
2whp.2.A	39.89	monomer	-	HHblits	X-ray	2.20Å	0.40	0.71	ACETYLCHOLINESTERASE
1q83.1.A	39.63	homo-dimer	0.50	HHblits	X-ray	2.65Å	0.40	0.71	Acetylcholinesterase
2c0p.2.A	39.89	monomer	-	HHblits	X-ray	2.50Å	0.40	0.71	ACETYLCHOLINESTERASE
5ydh.1.A	40.08	homo-dimer	0.30	HHblits	X-ray	3.21Å	0.41	0.71	Acetylcholinesterase
5ydj.1.A	39.92	homo-dimer	0.36	HHblits	X-ray	3.04Å	0.41	0.71	Acetylcholinesterase
6h14.1.A	39.16	homo-dimer	0.43	HHblits	X-ray	1.86Å	0.41	0.70	Acetylcholinesterase
5x61.1.A	39.85	homo-dimer	0.34	HHblits	X-ray	3.40Å	0.41	0.71	Acetylcholinesterase
2w6c.1.A	39.09	monomer	-	HHblits	X-ray	2.69Å	0.41	0.70	ACETYLCHOLINESTERASE
6o5s.1.A	38.91	homo-dimer	0.22	HHblits	X-ray	2.80Å	0.40	0.71	Acetylcholinesterase
6qaa.1.A	41.30	monomer	-	BLAST	X-ray	1.90Å	0.41	0.72	Cholinesterase
1f8u.1.A	38.65	monomer	-	HHblits	X-ray	2.90Å	0.40	0.71	ACETYLCHOLINESTERASE
5ydi.1.A	39.85	homo-dimer	0.48	HHblits	X-ray	3.45Å	0.41	0.71	Acetylcholinesterase
6tt0.1.A	39.09	monomer	-	HHblits	X-ray	2.80Å	0.41	0.70	Acetylcholinesterase
2c0p.2.A	41.28	monomer	-	BLAST	X-ray	2.50Å	0.41	0.71	ACETYLCHOLINESTERASE
2whp.2.A	41.28	monomer	-	BLAST	X-ray	2.20Å	0.41	0.71	ACETYLCHOLINESTERASE

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Coverage	Description
5fpq.2.B	40.30	homo-dimer	0.52	BLAST	X-ray	2.40Å	0.41	0.70	ACETYLCHOLINESTERASE
5hf5.1.A	40.30	homo-dimer	0.44	BLAST	X-ray	2.15Å	0.41	0.70	Acetylcholinesterase
5hf8.1.B	40.30	homo-dimer	0.46	BLAST	X-ray	2.80Å	0.41	0.70	Acetylcholinesterase
6f25.1.A	40.30	homo-dimer	0.49	BLAST	X-ray	3.05Å	0.41	0.70	Acetylcholinesterase
4bdt.2.E	38.84	homo-dimer	0.39	HHblits	X-ray	3.10Å	0.40	0.71	ACETYLCHOLINESTERASE
2jge.2.A	41.09	monomer	-	BLAST	X-ray	2.60Å	0.41	0.71	ACETYLCHOLINESTERASE
4b84.1.A	41.40	homo-dimer	0.48	BLAST	X-ray	2.60Å	0.41	0.71	ACETYLCHOLINESTERASE
4a16.1.A	41.40	homo-dimer	0.49	BLAST	X-ray	2.65Å	0.41	0.71	ACETYLCHOLINESTERASE
4tpk.1.A	40.84	monomer	-	BLAST	X-ray	2.70Å	0.41	0.73	Cholinesterase
5lkr.2.A	41.48	monomer	-	BLAST	X-ray	2.52Å	0.41	0.70	Cholinesterase
4xii.1.A	41.48	homo-dimer	0.41	BLAST	X-ray	2.70Å	0.41	0.70	Cholinesterase
3o9m.1.A	41.48	homo-tetramer	0.21	BLAST	X-ray	2.98Å	0.41	0.70	Cholinesterase
6arx.1.A	42.07	homo-dimer	0.66	BLAST	X-ray	2.30Å	0.42	0.70	Acetylcholinesterase
5ydh.1.A	42.42	homo-dimer	0.27	BLAST	X-ray	3.21Å	0.42	0.70	Acetylcholinesterase
3lii.1.A	40.30	homo-dimer	0.52	BLAST	X-ray	3.20Å	0.41	0.70	Acetylcholinesterase
5x61.1.A	42.42	homo-dimer	0.31	BLAST	X-ray	3.40Å	0.42	0.70	Acetylcholinesterase
2cek.1.A	41.39	monomer	-	BLAST	X-ray	2.20Å	0.42	0.69	ACETYLCHOLINESTERASE
5ydi.1.A	42.42	homo-dimer	0.50	BLAST	X-ray	3.45Å	0.42	0.70	Acetylcholinesterase
2pm8.1.A	41.67	homo-octamer	0.13	BLAST	X-ray	2.80Å	0.41	0.70	Cholinesterase
5ehx.1.A	41.39	monomer	-	BLAST	X-ray	2.10Å	0.42	0.69	Acetylcholinesterase
6eue.1.A	41.39	homo-dimer	0.46	BLAST	X-ray	2.00Å	0.42	0.69	Acetylcholinesterase
6fqn.1.A	41.39	homo-dimer	0.42	BLAST	X-ray	2.30Å	0.42	0.69	Acetylcholinesterase
1amn.1.A	41.39	monomer	-	BLAST	X-ray	2.80Å	0.42	0.69	ACETYLCHOLINESTERASE
6i2t.1.A	41.48	homo-tetramer	0.27	BLAST	EM	NA	0.41	0.70	Cholinesterase
6i2t.1.B	41.48	homo-tetramer	0.27	BLAST	EM	NA	0.41	0.70	Cholinesterase
4qwm.1.A	34.28	monomer	-	BLAST	X-ray	2.17Å	0.38	0.66	E3
5tym.1.A	34.48	monomer	-	BLAST	X-ray	1.84Å	0.38	0.66	Carboxylic ester hydrolase

The table above shows the top 50 filtered templates. A further 1,456 templates were found which were considered to be less suitable for modelling than the filtered list.
1a7u.1.A, 1a88.1.A, 1a8q.1.A, 1a8s.1.A, 1ac5.1.A, 1acj.1.A, 1akn.1.A, 1amn.1.A, 1aql.1.A, 1auo.1.A, 1auo.1.B, 1azw.1.A, 1b6g.1.A, 1bcr.1.A, 1bee.1.A, 1bn6.1.A, 1bro.1.A, 1brt.1.A, 1bu8.1.A, 1c2b.1.A, 1c2o.1.A, 1c4x.1.A, 1c7i.1.A, 1c7j.1.A, 1cex.1.A, 1cle.1.A, 1cpy.1.A, 1cqw.1.A, 1cqz.1.A, 1crl.1.A, 1cub.1.A, 1cud.1.A, 1cud.2.A, 1cud.3.A, 1cue.1.A, 1cuf.1.A, 1cug.1.A, 1cuj.1.A, 1cus.1.A, 1cuu.1.A, 1cuv.1.A, 1cux.1.A, 1cuy.1.A, 1cuz.1.A, 1cvl.1.A, 1din.1.A, 1dqy.1.A, 1dqz.1.A, 1dqz.1.B, 1dwo.1.A, 1e5t.1.A, 1e89.1.A, 1eb8.1.A, 1eea.1.A, 1eh5.1.A, 1ehy.1.A, 1ek1.1.B, 1ek2.1.B, 1eth.1.A, 1evq.1.A, 1ex9.1.A, 1f0n.1.A, 1f6w.1.A, 1f8u.1.A, 1ffa.1.A, 1ffb.1.A, 1ffd.1.A, 1ffe.1.A, 1fj2.1.A, 1fss.3.A, 1g4h.1.A, 1ggv.1.A, 1gkk.1.A, 1gpl.1.A, 1gz7.1.A, 1h2y.1.A, 1hde.1.A, 1hkh.1.A, 1hlg.1.A, 1hpl.1.A, 1i6w.1.A, 1i6w.1.B, 1imj.1.A, 1isp.1.A, 1ivy.1.A, 1ivy.1.B, 1j1i.1.A, 1jfr.1.A, 1ji3.1.A, 1jjf.1.A, 1jji.1.A, 1jji.3.A, 1jkm.1.A, 1jmy.1.A, 1jt2.1.A, 1ju3.1.A, 1k4y.1.A, 1k6e.1.A, 1k8q.1.A, 1kez.1.A, 1kez.1.B, 1kez.2.B, 1ku0.1.A, 1ku0.2.A, 1ku6.1.A, 1l7a.1.A, 1l7q.1.A, 1l7r.1.A, 1lbs.4.A, 1llf.1.A, 1lpb.1.B, 1lpm.1.A, 1lzk.1.A, 1m33.1.A, 1maa.1.A, 1mah.1.C, 1mj5.1.A, 1mn6.1.B, 1mna.1.A, 1mnq.1.A, 1mnq.1.B, 1mo2.1.A, 1mpx.1.A, 1mtz.1.A, 1mu0.1.A, 1mx1.1.A, 1n5m.1.A, 1n8s.1.A, 1nx9.1.A, 1o6f.1.A, 1o6g.1.A, 1ods.1.A, 1odt.1.A, 1pfq.1.A, 1pfq.1.B, 1pja.1.A, 1pv1.1.A, 1q0r.1.A, 1q83.1.A, 1qe3.1.A, 1qge.1.A, 1qlw.1.A, 1qo7.1.A, 1qz3.1.A, 1r1d.1.A, 1r3d.1.A, 1r88.1.A, 1r9m.1.A, 1r9n.1.A, 1rp1.1.A, 1ryy.1.A, 1sci.1.A, 1sfr.1.A, 1t2n.1.A, 1t4m.1.A, 1tah.1.A, 1thg.1.A, 1tht.1.A, 1tqh.1.A, 1trh.1.A, 1u2e.1.A, 1u4n.1.A, 1u8e.1.A, 1u8e.1.B, 1ufo.1.A, 1ufo.1.B, 1ufo.2.B, 1uk6.1.A, 1ukc.1.A, 1uoq.1.A, 1uxo.1.A, 1va4.1.A,

1va5.1.A, 1ve7.1.A, 1vkh.1.A, 1vz2.1.A, 1vz3.1.A, 1w52.1.A, 1wb4.1.A, 1wcy.1.A, 1whs.1.A, 1wht.1.A, 1wom.1.A, 1wpr.1.A, 1wpr.2.A, 1wpx.1.A, 1x2e.1.A, 1xfd.1.A, 1xkl.1.A, 1xkl.1.C, 1xqv.1.A, 1xqx.1.A, 1xqy.1.A, 1xrl.1.A, 1xro.1.A, 1xrq.1.A, 1xzd.1.A, 1xzf.1.A, 1xzg.1.A, 1xzi.1.A, 1xzj.1.A, 1y37.1.A, 1y7h.2.A, 1y7i.1.A, 1yaj.4.B, 1yas.1.A, 1yb6.1.A, 1ycd.1.A, 1yr2.1.A, 1ys2.1.A, 1ysc.1.A, 1z68.1.A, 1z68.1.B, 1zd3.1.A, 1zi8.1.A, 1zi9.1.A, 1zic.1.A, 1zix.1.A, 1zj4.1.A, 1zj5.1.A, 1zoi.1.A, 2ajc.3.C, 2b20.1.A, 2b4k.1.A, 2b61.1.A, 2bce.1.A, 2bgr.1.A, 2bkl.1.A, 2bub.1.A, 2buc.2.B, 2c7b.1.A, 2cek.1.A, 2cjp.1.A, 2cmf.1.B, 2cut.1.A, 2d0d.1.A, 2d80.1.A, 2d81.1.A, 2dcm.1.A, 2dsn.1.A, 2dst.1.A, 2dst.1.B, 2e3j.1.A, 2ecf.1.A, 2eep.1.A, 2es4.1.A, 2fj0.1.A, 2fuk.1.A, 2fx5.1.A, 2g5p.1.A, 2gbg.1.A, 2gyv.1.A, 2gzr.1.A, 2gzs.1.A, 2h1i.1.A, 2h1i.2.A, 2h7c.1.E, 2h7x.1.A, 2ha2.1.B, 2ha6.1.A, 2hdw.1.A, 2hfk.1.A, 2hih.1.A, 2hm7.1.A, 2hrq.2.A, 2hu5.1.B, 2hu8.1.A, 2i3d.1.A, 2j3q.1.A, 2j4c.1.A, 2j4f.1.A, 2jbw.1.A, 2jbw.2.A, 2jge.2.A, 2jid.1.A, 2k2q.1.B, 2nw6.1.A, 2o2g.1.A, 2o2i.1.A, 2o7r.1.A, 2ocg.1.A, 2ock.1.A, 2ocl.1.A, 2og1.1.A, 2ogs.1.A, 2ogt.1.A, 2ogz.1.B, 2ole.1.A, 2onc.1.A, 2oxe.1.A, 2pbl.1.A, 2pl5.1.A, 2pm8.1.A, 2ppl.1.A, 2pse.1.A, 2psf.1.A, 2psf.2.A, 2psh.1.A, 2psj.1.A, 2pu7.1.A, 2puh.1.A, 2pvs.1.A, 2pvs.2.A, 2q0x.1.A, 2qjr.1.A, 2qjw.1.A, 2qjw.1.B, 2qky.1.B, 2qm0.1.A, 2qm0.1.B, 2qmq.1.A, 2qr5.1.A, 2qru.1.A, 2qs9.1.A, 2qt9.1.A, 2qub.1.A, 2qvb.1.A, 2qxt.1.A, 2qzp.1.A, 2qzp.2.A, 2r11.1.A, 2r8b.1.A, 2rau.1.A, 2rht.1.A, 2rip.1.A, 2ron.1.A, 2uz0.1.A, 2v9z.1.A, 2vax.1.A, 2veo.1.A, 2vf2.1.A, 2w22.1.A, 2w6c.1.A, 2wfl.1.A, 2wfm.1.A, 2wid.1.A, 2wil.1.A, 2wj3.1.A, 2wm2.1.A, 2wqz.1.A, 2wqz.2.A, 2wtm.1.A, 2wtm.1.B, 2wtm.2.B, 2wug.1.A, 2x5x.1.A, 2xb6.1.A, 2xe4.1.A, 2xlc.1.A, 2xmb.1.A, 2xmq.1.A, 2xmr.1.A, 2xms.1.A, 2xmz.1.A, 2xqf.1.A, 2xt0.1.A, 2xua.1.A, 2xug.1.A, 2xuk.1.A, 2y6v.1.B, 2yij.1.A, 2yxp.1.A, 2yys.1.A, 2yys.2.A, 2z3z.1.A, 2z5g.1.A, 2z8x.1.A, 2z8z.1.A, 2zj6.1.A, 2zjf.1.A, 2zsh.1.A, 2zyh.1.A, 2zyh.2.A, 2zyi.1.A, 2zyi.2.A, 2zyr.1.A, 2zyr.2.A, 2zys.1.A, 3a2l.1.A, 3a2n.1.A, 3a70.1.A, 3afi.1.A, 3afi.1.B, 3afi.2.B, 3aik.1.A, 3aim.1.A, 3ain.1.A, 3aio.1.A, 3ans.1.A, 3auk.1.A, 3azo.1.A, 3azq.1.A, 3b12.1.A, 3b3q.1.A, 3b5e.1.A, 3bdi.1.A, 3bdv.1.A, 3be8.1.A, 3be8.1.B, 3bf8.1.A, 3biw.1.B, 3bjr.1.A, 3bl8.1.A, 3bl8.1.B, 3bl8.2.A, 3bl8.2.B, 3bwx.1.A, 3bxp.1.A, 3bxp.1.B, 3c5v.1.A, 3c5w.1.C, 3c87.1.A, 3c87.2.A, 3c8d.1.A, 3c8h.2.A, 3ccc.2.A, 3cn7.1.A, 3cxu.1.A, 3d0k.1.A, 3d2a.1.A, 3d2b.1.A, 3d2c.1.A, 3d3n.1.A, 3d7r.1.A, 3ddu.1.A, 3dnm.1.A, 3dnm.3.A, 3doh.1.A, 3dqz.1.A, 3ds8.1.A, 3e0x.1.A, 3e1g.1.A, 3e4d.1.A, 3ebl.1.A, 3f67.1.A, 3f9c.1.A, 3fbw.1.A, 3fcx.1.A, 3fcx.1.B, 3fcy.1.A, 3flb.1.A, 3fle.1.A, 3fnb.1.A, 3fob.1.A, 3fob.1.B, 3fsg.1.A, 3fsg.1.C, 3fsg.2.B, 3fvr.1.A, 3fwh.1.A, 3fyt.1.A, 3fyu.1.B, 3g02.1.A, 3g8y.1.A, 3g9x.1.A, 3ga7.1.A, 3gel.1.A, 3gff.1.A, 3gro.1.A, 3guu.1.A, 3gzj.1.A, 3h04.1.A, 3h1b.1.A, 3h2h.1.A, 3h2i.1.A, 3h2j.1.A, 3hea.1.A, 3hi4.1.A, 3hju.1.A, 3hju.1.B, 3hlk.1.A, 3hrh.1.A, 3hxk.1.A, 3hys.1.A, 3hys.1.B, 3i1i.1.A, 3i2f.1.A, 3i2g.1.A, 3i2h.1.A, 3i2j.1.A, 3ia2.1.A, 3ib3.1.A, 3ibt.1.A, 3icv.1.A, 3ida.1.A, 3iuj.1.A, 3ium.1.A, 3iun.1.A, 3iuq.1.A, 3iur.1.A, 3ivm.1.A, 3jwe.1.A, 3k2i.1.A, 3k6k.1.A, 3k6k.2.A, 3k9b.1.A, 3kd2.1.A, 3kda.1.A, 3koo.1.A, 3ksr.1.A, 3kxp.1.A, 3lii.1.A, 3llc.1.A, 3lp5.1.A, 3ls2.1.A, 3mga.1.A, 3mga.2.A, 3mun.1.A, 3mve.1.A, 3mve.1.B, 3n0t.2.A, 3n2z.1.A, 3nox.1.A, 3nuz.1.A, 3nwo.1.A, 3o0d.1.A, 3o0d.7.A, 3o4g.1.B, 3o4h.2.A, 3o4i.1.A, 3o4j.1.A, 3o4j.1.B, 3o9m.1.A, 3oc0.1.B, 3og9.1.A, 3og9.2.A, 3oos.1.A, 3our.1.A, 3our.2.A, 3p2m.1.A, 3pdc.1.A, 3pe6.1.A, 3pf8.1.A, 3pi6.1.A, 3pic.1.A, 3puh.1.B, 3q8w.1.A, 3qbj.1.A, 3qh4.1.A, 3qit.1.A, 3qit.1.B, 3qit.2.A, 3qit.2.B, 3qm1.1.A, 3qmm.1.A, 3qmv.1.A, 3qmv.1.B, 3qmv.2.B, 3qpc.1.A, 3qvm.1.A, 3qyj.1.A, 3qzu.1.A, 3r3u.1.B, 3r3w.1.A, 3r3y.1.A, 3r3z.1.A, 3rk4.1.A, 3rks.1.A, 3rli.1.A, 3s2z.1.A, 3s8y.1.A, 3sc2.1.A, 3sk0.1.A, 3stu.1.A, 3stu.1.B, 3stx.1.A, 3stx.1.B, 3sty.1.A, 3sty.1.B, 3t4u.1.A, 3trd.1.A, 3u0v.1.A, 3u1t.1.A, 3umj.1.A, 3v1k.1.A, 3v1l.1.A, 3v48.1.A, 3v9a.1.A, 3vdx.1.A, 3vdx.1.B, 3vdx.1.C, 3vis.1.A, 3vis.2.A, 3vkf.1.A, 3vvl.1.A, 3vvm.1.A, 3w05.1.A, 3w05.2.A, 3w06.1.A, 3w9b.1.A, 3w9u.1.A, 3wa6.1.A, 3wi7.1.A, 3wib.1.A, 3wio.1.A, 3wj1.1.A, 3wj2.1.A, 3wk4.1.A, 3wl5.1.A, 3wl6.1.A, 3wl8.1.A, 3wla.1.A, 3wmr.1.A, 3wqh.1.A, 3wqh.1.B, 3wwo.1.A, 3wwp.3.B, 3wyd.1.A, 3wzl.1.A, 3wzm.1.A, 3x3h.1.A, 3zpx.1.A, 3zwq.1.A, 4a16.1.A, 4a5s.1.B, 4amy.1.A, 4ao6.1.A, 4ao7.1.A, 4aqd.1.A, 4aqd.1.B, 4ax4.1.A, 4axb.1.A, 4az0.1.A, 4b0p.1.A, 4b6g.1.A, 4b84.1.A, 4b9a.1.A, 4bat.1.A, 4baz.1.A, 4bdt.2.E, 4be4.1.A, 4be9.1.A, 4bp8.1.A, 4bp9.1.A, 4brs.1.A, 4brs.2.A, 4brz.1.A, 4btv.1.A, 4bvj.1.A, 4bvk.1.A, 4bvl.1.A, 4bym.1.A, 4bzw.1.A, 4c4z.1.A, 4c6h.1.A, 4c87.1.A, 4c89.1.A, 4ccy.1.A, 4cfs.1.A, 4cg1.1.A, 4cg3.1.A, 4cib.1.B, 4d9j.1.A, 4d9j.1.B, 4d9j.1.C, 4d9j.1.D, 4d9j.1.E, 4d9j.2.D, 4d9j.2.F, 4dgq.1.A, 4diu.1.A, 4dm7.1.A, 4dmf.1.A, 4dmh.1.A, 4dmk.1.A, 4dnp.1.A, 4dnq.1.A, 4dtc.1.B, 4e14.1.A, 4e15.1.A, 4e46.1.A, 4eb0.1.A, 4ebb.1.A, 4etw.1.A, 4ezi.1.A, 4f0j.1.A, 4f21.1.A, 4f21.5.A, 4f5z.1.A, 4f60.1.A, 4fbl.1.A, 4fbm.1.A, 4fdm.1.A, 4ffv.1.A, 4fhz.1.A, 4fkb.1.A, 4fle.1.A, 4flm.1.A, 4flm.1.B, 4fmp.1.A, 4fnm.1.A, 4fol.1.A, 4ftw.1.A, 4g4g.1.A, 4g4i.1.A, 4g5x.1.A, 4g8b.1.A, 4g8c.1.A, 4gdm.1.A, 4gdm.2.A, 4gec.1.A, 4geg.1.A, 4gw3.1.A, 4h0c.1.A, 4h18.1.A, 4h18.3.A, 4h77.1.A, 4h7d.1.A, 4h7e.1.A, 4h7f.1.A, 4h7h.1.A, 4h7i.1.A, 4h7j.1.A, 4h7k.1.A, 4hrx.1.A, 4hs9.1.A, 4hvt.1.A, 4hxf.1.F, 4hxg.1.A, 4hzg.1.A, 4i3f.1.A, 4i4c.2.A, 4ih4.1.A, 4ih9.1.A, 4ih9.2.A, 4inz.1.A, 4io0.1.A, 4iq4.1.A, 4iq4.1.B, 4iq4.1.C, 4iq4.1.D, 4iq4.1.F, 4itv.1.A, 4itv.1.C, 4itv.1.D, 4itv.1.F, 4itv.1.G, 4itv.1.H, 4itv.1.J, 4itv.1.L, 4ivj.1.A, 4ivj.1.B, 4ivj.1.C, 4j0c.1.A, 4j0g.1.A, 4j0g.2.A, 4j0h.2.A, 4j0k.2.A, 4j7a.1.A, 4jei.1.A, 4jnc.1.A, 4jui.1.A, 4jui.2.A, 4jyp.2.A, 4k2a.1.A, 4k5q.1.A, 4k6g.1.A, 4k6h.1.A, 4k6h.1.B, 4k6k.1.A, 4kaa.1.A, 4kaf.1.A, 4ke6.6.A, 4ke9.1.A, 4ke9.3.A, 4kr0.1.A, 4krx.1.A, 4kyv.1.A, 4kyv.2.A, 4l0c.1.A, 4l72.3.B, 4l9a.1.A, 4l9a.2.A, 4lhe.1.A, 4lxg.1.A, 4lxh.1.A, 4lxi.1.A, 4m0m.1.A, 4mea.1.A, 4meb.1.A, 4mj3.1.A, 4mql.1.A, 4mqm.1.A, 4mws.1.A, 4mxd.1.A, 4myd.1.A, 4n5h.1.D, 4nmw.1.A, 4ns4.1.A, 4nvr.1.A, 4nvr.1.B, 4nzz.1.A, 4o08.1.A, 4ob6.1.A, 4ob7.1.A, 4ob8.1.A, 4opm.1.A, 4ose.1.A, 4ou4.1.A, 4ou5.1.A, 4p08.1.A, 4p92.1.A, 4p93.1.A, 4p9n.1.A, 4pf1.1.A, 4po3.1.A, 4pqe.1.A, 4psu.1.A, 4pv7.1.A, 4pw0.1.A, 4q05.1.A, 4q1v.1.A, 4q34.1.A, 4q3k.1.A, 4q3l.1.A, 4q3o.1.A, 4q82.1.A, 4qdt.1.A, 4qdu.1.A, 4qdx.1.A, 4qdz.1.A, 4qe3.1.A, 4qek.1.A, 4qes.1.A, 4qes.1.B, 4qf0.1.A, 4qf0.1.E, 4qff.1.B, 4qff.1.C, 4qff.1.D, 4qff.1.E, 4qff.1.F, 4qff.1.G, 4qff.1.H, 4qff.1.I, 4qff.1.J, 4qff.1.L, 4qla.1.A, 4qlo.1.A, 4qnn.1.A, 4qwm.1.A, 4qww.1.A, 4qzv.1.A, 4qzv.2.A, 4r1d.1.A, 4rgy.1.A, 4rnc.1.A, 4rot.1.A, 4tpk.1.A, 4u2b.1.A, 4u2c.1.A, 4u2d.1.A, 4u2e.1.A, 4u2f.1.A, 4u2g.1.A, 4ufn.1.A, 4ufo.1.A, 4ufp.1.A, 4uhb.1.A, 4uhc.1.A, 4uhd.1.A, 4uhh.1.A, 4upd.1.A, 4uyw.1.A, 4uyw.2.A, 4uyz.1.A, 4uyz.3.A, 4uz1.1.A, 4uz5.1.A, 4uz6.2.A, 4uz7.1.A, 4uza.1.A, 4uzj.1.A, 4uzk.1.A, 4uzl.1.A, 4uzq.1.A, 4v2i.1.A, 4w63.1.A, 4w9r.1.A, 4wbh.1.A, 4wbh.1.B, 4wcv.1.A, 4wdq.1.A, 4wdr.1.A, 4wfi.1.A, 4wfj.1.A, 4wjl.1.A, 4wy5.1.A, 4wy8.1.A, 4wy8.1.B, 4x00.1.A, 4x6u.1.A, 4x7b.1.A, 4x85.1.A, 4x90.3.A, 4x92.1.A, 4x93.1.A, 4x93.2.A, 4x94.1.A, 4x95.1.A, 4x96.1.A, 4xii.1.A, 4xjv.1.A, 4xvc.1.A, 4xwg.1.C, 4xx1.1.C, 4xx1.2.C, 4xx1.3.C, 4y7d.1.A, 4y9s.1.A, 4yk7.1.A, 4ypv.1.A, 4ywf.1.A, 4z8z.1.A, 4zi5.1.A, 4zrs.1.A, 4zrs.1.B, 4zv9.1.A, 4zv9.4.A, 4zwn.1.A, 4zxf.1.A, 4zxh.1.A, 5a2g.1.A, 5a62.1.A, 5a7g.1.A, 5a7h.1.A, 5ai0.1.A, 5ajh.1.A, 5ajh.2.A, 5als.1.A, 5ao9.1.A, 5bov.1.A, 5bv7.1.A, 5c7y.1.A, 5c8v.1.A, 5cbk.1.A, 5ce5.1.A, 5ch5.1.A, 5cml.1.A, 5cml.2.A, 5ct4.1.A, 5ct4.2.A, 5ct6.1.A, 5ct6.2.A, 5ct8.1.A, 5cur.1.A, 5cw2.1.A, 5cw2.3.A, 5cxu.1.A, 5cxx.1.A, 5d6o.1.A, 5d8m.1.A, 5dnw.1.A, 5dti.1.A, 5dti.1.B, 5dwd.1.A, 5dyt.1.A, 5e4y.1.A, 5egn.1.A, 5ehx.1.A, 5eih.1.B, 5esr.1.A, 5f2h.1.A, 5f2h.1.B, 5f4z.1.A, 5fdf.1.F, 5flk.1.A, 5fpq.2.B, 5frd.1.A, 5fv4.1.A, 5g59.1.A, 5g5c.1.A, 5g5m.1.A, 5g5m.1.B, 5gma.1.A, 5gmr.1.A, 5gms.1.A, 5gng.1.A, 5gv5.5.A, 5h3h.1.A, 5h6b.1.A, 5h6g.1.A, 5hc0.1.A, 5hc2.1.A, 5hc3.1.A, 5hcu.1.A, 5hdf.1.A, 5hdp.1.A, 5hf5.1.A, 5hf8.1.B, 5hfn.1.A, 5hk8.1.A, 5hq3.1.A, 5hq3.1.B, 5hz2.1.A, 5hzg.2.A, 5i9i.1.A, 5ie4.1.A, 5ie4.2.A, 5ie5.1.A, 5ie5.2.A, 5ie6.2.A, 5ie7.2.A, 5ih7.1.A, 5ikk.1.A, 5ikx.1.A, 5iq0.1.A, 5iq2.1.A, 5iq3.1.A, 5ivh.1.A, 5ivk.1.A, 5j3j.1.A, 5j8j.1.A, 5ja1.1.A, 5jad.1.A, 5jd4.1.A, 5jd5.1.A, 5jd6.1.A, 5jkf.1.A, 5jkj.1.A, 5jrk.1.B, 5jrl.1.A, 5jrl.1.B, 5jyc.2.B, 5jz9.1.A, 5jzb.1.A, 5k3d.1.A, 5k5e.1.A, 5k5e.1.B, 5kwj.2.A, 5l2p.1.A, 5l8s.1.A, 5lcn.1.A, 5lcn.1.B, 5lcn.2.A, 5lcn.2.B, 5lk6.1.A, 5lka.1.A, 5lkr.2.A, 5lls.1.A, 5lui.1.A, 5luj.1.A, 5luk.1.A, 5lul.1.A, 5mif.1.A, 5mlx.1.A, 5mly.1.A, 5mxp.1.A, 5mxp.1.B, 5n4b.1.A, 5n4c.1.A, 5n4d.1.A, 5n4e.1.A, 5n4f.1.A, 5nfq.1.A, 5ng7.1.A, 5ng7.1.B, 5nn0.1.A, 5no5.1.A, 5o3u.3.A, 5o3v.1.A, 5o3w.4.A, 5o3x.1.A, 5o7g.1.A, 5oj6.1.A, 5ojk.1.A, 5olj.1.A, 5olu.1.A, 5swn.1.A, 5sym.1.A, 5syn.1.A, 5t6o.1.A, 5t88.1.A, 5t88.2.A, 5tdx.1.A, 5tdx.2.A, 5thm.1.A, 5tns.1.B, 5txc.1.A, 5txe.1.A,

5txf.1.A, 5tyj.1.A, 5tyk.1.A, 5tym.1.A, 5ugz.1.A, 5ugz.2.A, 5uw3.1.A, 5uw5.1.A, 5uw7.1.A, 5uzw.1.A, 5v5v.1.A, 5v7o.1.A, 5vns.1.A, 5vol.1.A, 5vta.1.A, 5w15.1.A, 5w1u.1.A, 5w8o.1.A, 5w8p.1.A, 5x6s.1.A, 5x88.1.A, 5xav.1.A, 5xb6.1.A, 5xeq.1.A, 5xfy.1.A, 5xfz.1.A, 5xg0.1.A, 5xh3.1.A, 5xjh.1.A, 5xks.1.A, 5xks.5.A, 5xm6.1.A, 5xmd.1.A, 5xmd.2.A, 5xo6.1.A, 5xpx.1.A, 5xwz.1.A, 5y51.1.A, 5y57.1.A, 5y57.6.A, 5y5d.1.A, 5y5v.1.A, 5y5v.6.A, 5y6y.1.A, 5y7h.1.B, 5yae.1.A, 5ydj.1.A, 5yfe.1.A, 5yhp.1.A, 5yns.1.A, 5yp1.1.A, 5yp1.1.B, 5yp1.2.A, 5yp1.2.B, 5yp4.2.A, 5yzm.1.A, 5yzn.1.A, 5yzo.1.A, 5z5j.1.A, 5z7w.1.A, 5z7x.1.A, 5z7y.1.A, 5z82.1.A, 5z89.1.A, 5z8p.1.A, 5z97.1.A, 5z97.2.B, 5zhs.1.A, 5zno.1.A, 5zoa.1.A, 5zrr.1.A, 5zun.1.A, 6a6o.1.A, 6a9d.1.A, 6a9d.1.B, 6aae.1.A, 6aae.1.B, 6agq.1.A, 6aid.1.A, 6ane.1.A, 6ap8.1.A, 6arx.1.A, 6ary.1.A, 6atx.1.A, 6avv.1.A, 6avw.1.A, 6avx.1.A, 6avy.1.A, 6ax1.1.A, 6azb.1.A, 6azc.1.A, 6azd.1.A, 6ba8.1.A, 6ba9.1.A, 6bje.1.A, 6brt.1.A, 6brt.3.B, 6can.1.A, 6can.2.A, 6cl4.1.A, 6cob.1.B, 6cod.1.A, 6e7k.1.A, 6eb3.1.A, 6eb3.2.A, 6ecb.1.A, 6ecc.1.A, 6ehn.1.A, 6eic.1.A, 6elx.1.A, 6elx.2.A, 6emi.1.A, 6eoo.1.A, 6eor.1.A, 6eos.1.B, 6eqd.1.A, 6eqq.1.A, 6esj.1.A, 6esj.1.B, 6eue.1.A, 6eul.1.A, 6eyf.1.A, 6ez2.1.A, 6f25.1.A, 6f7q.1.B, 6f9o.1.A, 6fj4.1.A, 6fkx.1.A, 6fkx.1.B, 6fkx.1.D, 6fqn.1.A, 6fr2.1.A, 6fsd.1.A, 6fvj.1.A, 6fvj.3.A, 6fvj.4.A, 6fvj.5.A, 6fvj.6.A, 6fvj.7.A, 6fw5.1.A, 6fw5.2.A, 6fw5.3.A, 6fw5.4.A, 6fz1.1.A, 6fz8.1.A, 6fz9.1.A, 6fzc.1.A, 6fzd.1.A, 6g4o.1.A, 6g4p.1.B, 6g75.1.A, 6gi0.1.A, 6gi1.1.A, 6gi1.2.A, 6gi5.1.A, 6goc.1.A, 6grw.1.A, 6gu8.1.A, 6gud.1.A, 6gug.1.A, 6gui.1.A, 6gul.1.A, 6gun.1.A, 6gun.2.B, 6guo.1.A, 6guo.1.B, 6gup.1.A, 6gup.1.B, 6gxl.1.B, 6h0t.1.A, 6h0v.1.A, 6h14.1.A, 6h18.1.A, 6hiv.105.A, 6hsw.1.A, 6hsw.3.A, 6hxa.1.A, 6i0c.1.A, 6i2t.1.A, 6i2t.1.B, 6i5e.1.A, 6i8d.1.A, 6i8d.1.B, 6i8f.1.A, 6i8f.1.B, 6i8w.1.A, 6i8w.2.A, 6idy.1.A, 6iey.1.A, 6iey.1.B, 6igr.1.A, 6ii2.1.A, 6ii2.2.A, 6ii2.3.A, 6ii2.4.A, 6ij3.1.A, 6ij4.1.A, 6ij5.1.A, 6ij6.1.A, 6ilw.1.A, 6ilx.1.A, 6imp.1.A, 6imp.2.A, 6iog.1.A, 6ioh.1.A, 6isp.1.A, 6isq.1.A, 6ix2.1.A, 6ix4.1.A, 6j1p.1.A, 6j1p.2.A, 6j1q.1.A, 6j1q.2.A, 6j1r.1.A, 6j1r.2.A, 6j1s.1.A, 6j1s.2.A, 6j2r.1.A, 6jci.1.A, 6jd9.1.A, 6jqz.1.A, 6jr9.1.A, 6jzl.1.A, 6k1t.1.A, 6k34.1.A, 6k3c.1.A, 6k3c.1.B, 6k5e.1.A, 6k5e.1.B, 6k5e.1.C, 6k5e.2.A, 6k5e.2.C, 6kd0.1.A, 6keu.1.A, 6kf1.1.A, 6kf1.1.D, 6kf5.1.A, 6kf7.1.A, 6khk.1.A, 6kmo.1.A, 6ksi.1.A, 6kuo.1.A, 6kuq.1.A, 6kus.1.A, 6kxh.1.A, 6kxr.1.A, 6ky5.1.A, 6l4b.1.A, 6l4b.1.B, 6l4g.1.A, 6l4h.1.A, 6l4h.1.B, 6l4h.2.A, 6l7m.1.A, 6l7m.1.B, 6l7m.1.C, 6l8q.1.A, 6lzh.1.A, 6mlk.1.A, 6mly.1.A, 6mly.3.A, 6mot.1.A, 6mou.1.A, 6mvd.2.A, 6n5g.1.A, 6n8e.1.A, 6ne9.1.A, 6nff.1.A, 6nkc.1.A, 6nkf.1.A, 6nkf.2.B, 6nkg.1.A, 6ny9.1.A, 6o5j.1.A, 6o5s.1.A, 6o69.1.A, 6oau.1.A, 6ob0.1.A, 6oyc.2.A, 6pux.1.A, 6qaa.1.A, 6qe2.1.A, 6qgc.1.A, 6qgn.1.A, 6qgo.1.A, 6qgq.2.A, 6qgq.3.A, 6qgs.1.A, 6qgs.2.A, 6qgs.5.A, 6qin.1.A, 6qks.1.A, 6qku.1.A, 6qla.1.A, 6qzv.1.A, 6r6v.1.A, 6r8r.1.A, 6ra2.1.A, 6ra2.2.A, 6ra2.3.A, 6rb3.1.A, 6rj8.1.A, 6rky.1.A, 6rs4.1.A, 6rt8.1.A, 6ru1.1.A, 6ru2.1.A, 6rv8.1.A, 6rzn.1.A, 6rzo.1.A, 6rzo.1.B, 6s06.1.A, 6s3g.1.A, 6s3j.1.A, 6s42.1.A, 6s97.1.A, 6sbn.1.A, 6scd.1.A, 6scj.1.A, 6sp5.1.A, 6sx4.1.A, 6syr.1.A, 6syu.1.A, 6syv.1.A, 6sz0.1.A, 6szo.1.A, 6t0e.1.A, 6t0e.2.A, 6t0i.1.A, 6t6h.1.A, 6tf5.1.A, 6ths.1.A, 6tht.1.A, 6tj2.1.A, 6tkx.1.A, 6tt0.1.A, 6u2m.1.A, 6u7m.1.A, 6uh8.1.A, 6uh9.1.A, 6unw.1.A, 6v7n.1.A, 6vap.1.A, 6vap.2.A, 6ve6.1.A, 6vh9.1.A, 6wia.1.A, 6xfo.1.A, 6y9e.1.A, 6y9f.1.A, 6y9g.1.A, 6y9g.2.A, 6y9k.1.A, 6ynx.1.e, 6ysk.1.A, 6yuo.1.A, 6yus.1.A, 6yuy.1.A, 6yv0.1.A, 6yv4.1.A, 6yxi.1.A, 6z1p.81.A, 6zl7.1.A, 7al5.1.B, 7al5.1.C, 7al5.1.D, 7al6.1.A, 7al6.1.B, 7al6.1.C, 7al6.1.D, 7cef.1.A, 7cef.2.A, 7ceh.1.A, 7clz.1.A, 7cof.1.A, 7cog.3.A