SWISS-MODEL   Homology Modelling Report

Model Building Report

This document lists the results for the homology modelling project "HRTV RdRp" submitted to SWISS-MODEL workspace on April 10, 2025, 12:33 a.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 FT, de Beer TAP, Rempfer C, Bordoli L, Lepore R, Schwede T
  SWISS-MODEL: homology modelling of protein structures and complexes.
  Nucleic Acids Res 46, W296-W303. (2018) 🔎 29788355 🔗 10.1093/nar/gky427

- Bienert S, Waterhouse A, de Beer TAP, Tauriello G, Studer G, Bordoli L, Schwede T
  The SWISS-MODEL Repository - new features and functionality.
  Nucleic Acids Res 45, D313-D319. (2017) 🔎 27899672 🔗 10.1093/nar/gkw1132

- Studer G, Tauriello G, Bienert S, Biasini M, Johner N, Schwede T
  ProMod3 - A versatile homology modelling toolbox.
  PLOS Comp Biol 17(1), e1008667. (2021) 🔎 33507980 🔗 10.1371/journal.pcbi.1008667

- Studer G, Rempfer C, Waterhouse AM, Gumienny R, Haas J, Schwede T
  QMEANDisCo - distance constraints applied on model quality estimation.
  Bioinformatics 36, 1765-1771. (2020) 🔎 31697312 🔗 10.1093/bioinformatics/btz828

- 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) 🔎 28874689 🔗 10.1038/s41598-017-09654-8

Results

The SWISS-MODEL template library (SMTL version 2025-04-02, PDB release 2025-03-28) 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 189 templates were found (Table T2).

Models

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

Model #02	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.4.1	monomer	None	0.68	0.70 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
7alp.1.A	73.32	monomer	0.00	BLAST	EM	-	0.53	1 - 2069	1.00	Replicase

Excluded ligands

Ligand Name.Number	Reason for Exclusion	Description
MG.1	Not in contact with model.	MAGNESIUM ION
MG.2	Not in contact with model.	MAGNESIUM ION

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Target     MNLEALCSRVLSERGLSTGEPGVYDQIFERPGLPNLEVTVDSTGVVVDVGAIPDSASQLGSSINAGVLTIPLSEAYKINH
7alp.1.A   MNLEVLCGRINVENGLSLGEPGLYDQIYDRPGLPDLDVTVDATGVTVDIGAVPDSASQLGSSINAGLITIQLSEAYKINH

Target     DFTFSGLTKTTDRKLSEVFPLVHDGSDSMTPDVIHTRLDGTVVVIEFTTTRSTNMGGLEAAYRSKLEKYRDPLNRRSDIM
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7alp.1.A    DFTFSGLSKTTDRRLSEVFPITHDGSDGMTPDVIHTRLDGTIVVVEFTTTRSHNIGGLEAAYRTKIEKYRDPISRRVDIM


Target      PDASIYFGIIVVSASGVLTNMPLTQDEAEELMFRFCVANEIYSQARAMDAEVELQKSEEEYEAISRARAFFTLFDYDDGK
7alp.1.A    ENPRVFFGVIVVSSGGVLSNMPLTQDEAEELMYRFCIANEIYTKARSMDADIELQKSEEELEAISRALSFFSLFEPNIER


Target      LSEAFPNSDIEMLRRFLSQPVDTSFVTTTLKEKEQEAYKRMCEEHYLKSGMSTKERLEANRNDAIDKTRALMERLHNMSS
7alp.1.A    VEGTFPNSEIEMLEQFLSTPADVDFITKTLKAKEVEAYADLCDSHYLKPEKTIQERLEINRCEAIDKTQDLLAGLHARSN


Target      KELHSNKSTVKLPPWVVKPSDRTLDVKTDTGSGELLNHGPYGELWSRCFLEIVLGNVEGVISSPEKELEIAISDDPEADT
7alp.1.A    KQTSLNRGTVKLPPWLPKPSSESIDIKTDSGFGSLMDHGAYGELWAKCLLDVSLGNVEGVVSDPAKELDIAISDDPEKDT


Target      PKAAKIKYHRFRPELSLESKHEFSLQGIEGKRWKHSARNVLKDEMSHKTMSPFVDVSNIEEFLIMNNLLNDTSFNREGLQ
7alp.1.A    PKEAKITYRRFKPALSSSARQEFSLQGVEGKKWKRMAANQKKEKESHDALSPFLDVEDIGDFLTFNNLLADSRYGDESVQ


Target      ETINLLLEKATEMHQNGLSTALNDSFKRNFNTNVVQWSMWVSCLAQELASALKQHCKPGEFIIKKLMHWPIFAIIKPTKS
7alp.1.A    RAVSILLEKASAMQDTELTHALNDSFKRNLSSNVVQWSLWVSCLAQELASALKQHCRAGEFIIKKLKFWPIYVIIKPTKS


Target      SSHIFYSLAIKKANIKRRLIGDVFTDTIDAGEWEFSEFKSLKTCKLTNLINLPCTMLNSIAFWREKMGVAPWISRKACSE
7alp.1.A    SSHIFYSLGIRKADVTRRLTGRVFSETIDAGEWELTEFKSLKTCKLTNLVNLPCTMLNSIAFWREKLGVAPWLVRKPCSE


Target      LREQVAITFLMSLEDKSTTEELVTLTRYSQMEGFVSPPLLPKPQKMVEKLEVPLRTKLQVFLFRRHLDAIVRVAASPFPI
7alp.1.A    LREQVGLTFLISLEDKSKTEEIITLTRYTQMEGFVSPPMLPKPQKMLGKLDGPLRTKLQVYLLRKHLDCMVRIASQPFSL


Target      VARDGRVEWTGTFNAITGRSTGLENMVNNWYIGYYKNKEESTELNALGEMYKKIVEIEAEKPASSEYLGWGDTSSPKRHE
7alp.1.A    IPREGRVEWGGTFHAISGRSTNLENMVNSWYIGYYKNKEESTELNALGEMYKKIVEMEEDKPSSPEFLGWGDTDSPKKHE


Target      FSRSFLKSACISLEKEIEMRHGKSWKQSLEERVLKELGSKNLLDLATMKATSNFSKEWEAFSEVRTKEYHRSKLLEKMAE
7alp.1.A    FSRSFLRAACSSLEREIAQRHGRQWKQNLEERVLREIGTKNILDLASMKATSNFSKDWELYSEVQTKEYHRSKLLEKMAT


Target      LIEHGLMWYVDAAGHAWKAVLDDKCMRICLFKKNQHGGLREIYVTNANARLVQFGVETMARCVCELSPHETIANPRLKSS
7alp.1.A    LIEKGVMWYIDAVGQAWKAVLDDGCMRICLFKKNQHGGLREIYVMDANARLVQFGVETMARCVCELSPHETVANPRLKNS


Target      IIENHGLKSARQLGQGTINVNSSNDAKKWSQGHYTTKLAMVLCWFMPAKFHRFIWAGISMFRCKKMMMDLRFLEKLSTKA
7alp.1.A    IIENHGLKSARSLGPGSININSSNDAKKWNQGHYTTKLALVLCWFMPAKFHRFIWAAISMFRRKKMMVDLRFLAHLSSKS


Target      NQKTDDDFRKDLAGAFHGNVEVPWMTQGATYLQTETGMMQGILHFTSSLLHSCVQSFYKAYFLSRLKEGIAGRTIKAAID
7alp.1.A    ESRSSDPFREAMTDAFHGNREVSWMDKGRTYIKTETGMMQGILHFTSSLLHSCVQSFYKSYFVSKLKEGYMGESISGVVD


Target      VLEGSDDSAIMISLKPASDNEEAMARFLTANLLYSVRVINPLFGIYSSEKSTVNTLFCVEYNSEFHFHKHLVRPTIRWVA
7alp.1.A    VIEGSDDSAIMISIRPKSDMDEVRSRFFVANLLHSVKFLNPLFGIYSSEKSTVNTVYCVEYNSEFHFHRHLVRPTLRWIA


Target      ASHQISESEALASRQEDYANLLTQCLEGGSSFSLTYLIQCAQLVHHYMLLGLCLHPLFGTFVGMLIEDPDPALGFFIMDN
7alp.1.A    ASHQISETEALASRQEDYSNLLTQCLEGGASFSLTYLIQCAQLLHHYMLLGLCLHPLFGTFMGMLISDPDPALGFFLMDN


Target      PAFAGGAGFRFNLWRSCKFTNLGKKYAFFFNEIQGKTKGDADYRALDATTGGTLSHSVMIYWGDRRKYQHLLDRMGLPKD
7alp.1.A    PAFAGGAGFRFNLWRACKTTDLGRKYAYYFNEIQGKTKGDEDYRALDATSGGTLSHSVMVYWGDRKKYQALLNRMGLPED


Target      WVERIDENPSVLYRRPENKQELILRLAEKVHSPGVTSSFSKGHVVPRVVAAGVYLLSRHCFRYTASIHGRGASQKASLIK
7alp.1.A    WVEQIDENPGVLYRRAANKKELLLKLAEKVHSPGVTSSLSKGHVVPRVVAAGVYLLSRHCFRFSSSIHGRGSTQKASLIK


Target      LLVMSSTSAERNQGRLNPNQERMLFPQVQEYERVLTLLDEVTALTGKFVVRERNIVKSRVELFQEPVDLRCKAENLIAEM
7alp.1.A    LLMMSSISAMKHGGSLNPNQERMLFPQAQEYDRVCTLLEEVEHLTGKFVVRERNIVRSRIDLFQEPVDLRCKAEDLVSEV


Target      WFGLKRTKLGPRLLKEEWDKLRASFSWLSTDHKETLDVGPFLSHVQFRNFIAHVDAKSRSVRLLGAPVKKSGGVTTVSQV
7alp.1.A    WFGLKRTKLGPRLLKEEWDKLRASFAWLSTDPSETLRDGPFLSHVQFRNFIAHVDAKSRSVRLLGAPVKKSGGVTTISQV


Target      VKSNFFPGFILDSSESLDDQERVEGVSILKHILFMTLNGPYTDEQKKAMVLEAFQYFALPHAAEVVKRSRSLTLCLMKNF
7alp.1.A    VRMNFFPGFSLEAEKSLDNQERLESISILKHVLFMVLNGPYTEEYKLEMIIEAFSTLVIPQPSEVIRKSRTMTLCLLSNY


Target      IEQRGGSILDQIEKAQSGTVGGFSKPQKPYRKQSGGIGYKGKGVWSGIMENTNVQILIDGDGSSNWIEEIRLSSESRLFD
7alp.1.A    LSSRGGSILDQIERAQSGTLGGFSKPQKTFIRPGGGVGYKGKGVWTGVMEDTHVQILIDGDGTSNWLEEIRLSSDARLYD


Target      VIESVRRLCDDINVNNRVTSSFRGHCMVRLSNFKVKPASRVEGCPVRLMPSSFRIKELQNPDEVFLRVRGDILNLSILLQ
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7alp.1.A   VIESIRRLCDDLGINNRVASAYRGHCMVRLSGFKIKPASRTDGCPVRIMERGFRIRELQNPDEVKMRVRGDILNLSVTIQ

Target     EDRVMNLLSYRARDTDISESAASYLWMNRTDFSFGKKEPSCSWMCLKTLDSWAWNQAARVLERNIKTPGIDNTAMGNIFK
7alp.1.A   EGRVMNILSYRPRDTDISESAAAYLWSNRDLFSFGKKEPSCSWICLKTLDNWAWSHASVLLANDRKTQGIDNRAMGNIFR

Target     DCLESSLRKQGLLRSRIAEMVERHVIPLTSQELVDILEEDVDFSEMMQSDIMEGDLDIDILMEGSPMLWAAEVEEMGEAM
7alp.1.A   DCLEGSLRKQGLMRSKLTEMVEKNVVPLTTQELVDILEEDIDFSDVIAVELSEGSLDIESIFDGAPILWSAEVEEFGEGV

Target     VILSQSGKYYHLKLMDQAATTLSTILGKDGCRLLLGERTCGSNLREQVKPYLTLLQIREGDVNWVSEYKDDTRGLDEDSA
7alp.1.A   VAVSYSSKYYHLTLMDQAAITMCAIMGKEGCRGLLTEKRCMAAIREQVRPFLIFLQIPEDSISWVSDQFCDSRGLDEEST

Target     EMWG
7alp.1.A   IMWG
```

Materials and Methods

Template Search

Template search with BLAST and HHblits has been performed against the SWISS-MODEL template library (SMTL, last update: 2025-04-02, last included PDB release: 2025-03-28).

The target sequence was searched with BLAST against the primary amino acid sequence contained in the SMTL. A total of 23 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 167 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 (Studer et al.). 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.

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

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- Steinegger M, Meier M, Mirdita M, Vöhringer H, Haunsberger SJ, Söding J
  HH-suite3 for fast remote homology detection and deep protein annotation.
  BMC Bioinformatics 20, 473. (2019) 📖 31521110 🔶 10.1186/s12859-019-3019-7

- Mirdita M, von den Driesch L, Galiez C, Martin MJ, Söding J, Steinegger M
  Uniclust databases of clustered and deeply annotated protein sequences and alignments.
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Table T1:

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

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MNLEALCSRVLSERGLSTGEPGVYDQIFERPGLPNLEVTVDSTGVVVDVGAIPDSASQLGSSINAGVLTIPLSEAYKINHDFTFSGLTKTTDRKLSEVFP
LVHDGSDSMTPDVIHTRLDGTVVVIEFTTTRSTNMGGLEAAYRSKLEKYRDPLNRRSDIMPDASIYFGIIVVSASGVLTNMPLTQDEAEELMFRFCVANE
IYSQARAMDAEVELQKSEEEYEAISRARAFFTLFDYDDGKLSEAFPNSDIEMLRRFLSQPVDTSFVTTTLKEKEQEAYKRMCEEHYLKSGMSTKERLEAN
RNDAIDKTRALMERLHNMSSKELHSNKSTVKLPPWVVKPSDRTLDVKTDTGSGELLNHGPYGELWSRCFLEIVLGNVEGVISSPEKELEIAISDDPEADT
PKAAKIKYHRFRPELSLESKHEFSLQGIEGKRWKHSARNVLKDEMSHKTMSPFVDVSNIEEFLIMNNLLNDTSFNREGLQETINLLLEKATEMHQNGLST
ALNDSFKRNFNTNVVQWSMWVSCLAQELASALKQHCKPGEFIIKKLMHWPIFAIIKPTKSSSHIFYSLAIKKANIKRRLIGDVFTDTIDAGEWEFSEFKS
LKTCKLTNLINLPCTMLNSIAFWREKMGVAPWISRKACSELREQVAITFLMSLEDKSTTEELVTLTRYSQMEGFVSPPLLPKPQKMVEKLEVPLRTKLQV
FLFRRHLDAIVRVAASPFPIVARDGRVEWTGTFNAITGRSTGLENMVNNWYIGYYKNKEESTELNALGEMYKKIVEIEAEKPASSEYLGWGDTSSPKRHE
FSRSFLKSACISLEKEIEMRHGKSWKQSLEERVLKELGSKNLLDLATMKATSNFSKEWEAFSEVRTKEYHRSKLLEKMAELIEHGLMWYVDAAGHAWKAV
LDDKCMRICLFKKNQHGGLREIYVTNANARLVQFGVETMARCVCELSPHETIANPRLKSSIIENHGLKSARQLGQGTINVNSSNDAKKWSQGHYTTKLAM
VLCWFMPAKFHRFIWAGISMFRCKKMMMDLRFLEKLSTKANQKTDDDFRKDLAGAFHGNVEVPWMTQGATYLQTETGMMQGILHFTSSLLHSCVQSFYKA
YFLSRLKEGIAGRTIKAAIDVLEGSDDSAIMISLKPASDNEEAMARFLTANLLYSVRVINPLFGIYSSEKSTVNTLFCVEYNSEFHFHKHLVRPTIRWVA
ASHQISESEALASRQEDYANLLTQCLEGGSSFSLTYLIQCAQLVHHYMLLGLCLHPLFGTFVGMLIEDPDPALGFFIMDNPAFAGGAGFRFNLWRSCKFT
NLGKKYAFFFNEIQGKTKGDADYRALDATTGGTLSHSVMIYWGDRRKYQHLLDRMGLPKDWVERIDENPSVLYRRPENKQELILRLAEKVHSPGVTSSFS
KGHVVPRVVAAGVYLLSRHCFRYTASIHGRGASQKASLIKLLVMSSTSAERNQGRLNPNQERMLFPQVQEYERVLTLLDEVTALTGKFVVRERNIVKSRV
ELFQEPVDLRCKAENLIAEMWFGLKRTKLGPRLLKEEWDKLRASFSWLSTDHKETLDVGPFLSHVQFRNFIAHVDAKSRSVRLLGAPVKKSGGVTTVSQV
VKSNFFPGFILDSSESLDDQERVEGVSILKHILFMTLNGPYTDEQKKAMVLEAFQYFALPHAAEVVKRSRSLTLCLMKNFIEQRGGSILDQIEKAQSGTV
GGFSKPQKPYRKQSGGIGYKGKGVWSGIMENTNVQILIDGDGSSNWIEEIRLSSESRLFDVIESVRRLCDDINVNNRVTSSFRGHCMVRLSNFKVKPASR
VEGCPVRLMPSSFRIKELQNPDEVFLRVRGDILNLSILLQEDRVMNLLSYRARDTDISESAASYLWMNRTDFSFGKKEPSCSWMCLKTLDSWAWNQAARV
LERNIKTPGIDNTAMGNIFKDCLESSLRKQGLLRSRIAEMVERHVIPLTSQELVDILEEDVDFSEMMQSDIMEGDLDIDILMEGSPMLWAAEVEEMGEAM
VILSQSGKYYHLKLMDQAATTLSTILGKDGCRLLLGERTCGSNLREQVKPYLTLLQIREGDVNWVSEYKDDTRGLDEDSAEMWG
```

Table T2:

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Coverage	Description
8r6y.1.A	73.22	monomer	-	BLAST	EM	NA	0.53	1.00	RNA-directed RNA polymerase L
8r6w.1.A	73.22	monomer	-	BLAST	EM	NA	0.53	1.00	RNA-directed RNA polymerase L
7alp.1.A	73.32	monomer	-	BLAST	EM	NA	0.53	1.00	Replicase
8asd.1.A	73.22	monomer	-	BLAST	EM	NA	0.53	1.00	RNA-directed RNA polymerase
6l42.1.A	73.27	monomer	-	BLAST	EM	NA	0.53	1.00	RNA polymerase
8r6u.1.A	73.22	monomer	-	BLAST	EM	NA	0.53	1.00	RNA-directed RNA polymerase L
8as7.1.A	73.22	monomer	-	BLAST	EM	NA	0.53	1.00	RNA-dependent RNA-polymerase L protein
6y6k.1.A	73.27	monomer	-	BLAST	EM	NA	0.53	1.00	RNA-dependent RNA polymerase
7qtl.1.B	14.20	monomer	-	HHblits	EM	NA	0.28	0.15	RNA-directed RNA polymerase catalytic subunit
7r0e.1.B	14.20	monomer	-	HHblits	EM	NA	0.28	0.15	RNA-directed RNA polymerase catalytic subunit
7zpl.1.F	14.20	monomer	-	HHblits	EM	NA	0.28	0.15	RNA-directed RNA polymerase catalytic subunit
8poh.1.G	14.20	monomer	-	HHblits	EM	NA	0.28	0.15	RNA-directed RNA polymerase catalytic subunit
7z4o.2.B	14.20	monomer	-	HHblits	X-ray	3.41Å	0.28	0.15	RNA-directed RNA polymerase catalytic subunit

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Coverage	Description
7zpm.1.B	14.20	monomer	-	HHblits	EM	NA	0.28	0.15	RNA-directed RNA polymerase catalytic subunit
6tu5.1.B	14.20	monomer	-	HHblits	X-ray	3.33Å	0.28	0.15	RNA-directed RNA polymerase catalytic subunit
6tu5.1.E	14.20	monomer	-	HHblits	X-ray	3.33Å	0.28	0.15	RNA-directed RNA polymerase catalytic subunit

The table above shows the top 16 filtered templates. A further 158 templates were found which were considered to be less suitable for modelling than the filtered list.

4wrt.1.D, 4wsb.1.B, 5amq.1.A, 5amr.1.A, 5epi.3.B, 5msg.1.B, 6evj.1.B, 6f5o.1.B, 6f5p.1.C, 6klc.1.A, 6kld.1.A, 6kle.1.A, 6kuj.1.B, 6kut.1.B, 6l42.1.A, 6ntv.1.A, 6qcs.1.B, 6qct.1.B, 6qcv.1.B, 6qhg.1.A, 6qhg.2.A, 6qnw.2.B, 6qnw.4.B, 6qpf.1.B, 6qpg.3.B, 6qpg.4.B, 6qvv.1.A, 6qw5.1.A, 6qwl.1.B, 6qx3.1.D, 6qx8.1.B, 6rr7.1.B, 6szu.1.B, 6t0n.1.B, 6t0r.1.B, 6t0v.1.B, 6t0w.1.B, 6t2c.1.B, 6ueb.1.A, 6xya.1.A, 6xzd.1.C, 6xzd.1.F, 6xzq.1.F, 6y0c.1.B, 6y6k.1.A, 6z6b.1.C, 6z6g.1.C, 6z8k.1.E, 7alp.1.A, 7ckl.1.A, 7eei.1.A, 7eju.1.A, 7el9.1.A, 7ela.1.C, 7elb.1.C, 7elc.1.A, 7nhc.1.B, 7nhx.1.B, 7ni0.1.B, 7nk8.1.C, 7och.1.A, 7oe3.1.A, 7oe7.1.A, 7oea.1.A, 7ojj.1.A, 7ojk.1.A, 7ojl.1.A, 7ojn.1.A, 7ori.1.D, 7orj.1.A, 7ork.1.A, 7orl.1.B, 7orm.1.D, 7orn.1.A, 7vgq.1.A, 7vh2.1.A, 7vh3.1.A, 7x6s.1.A, 7yes.1.A, 7yet.1.A, 7z42.1.B, 8as6.1.A, 8as7.1.A, 8asb.1.A, 8asd.1.A, 8asg.1.A, 8bf5.1.B, 8c4s.1.A, 8c4t.1.A, 8c4u.1.A, 8c4v.1.A, 8ci5.1.A, 8gh6.1.A, 8h69.1.D, 8jsm.1.A, 8ki6.1.A, 8ki7.1.A, 8ki8.1.A, 8ki9.1.A, 8kia.1.A, 8p0b.1.B, 8p0g.1.B, 8p1k.1.A, 8p1l.1.A, 8p1m.1.A, 8p1n.1.A, 8pm0.1.B, 8pnq.1.B, 8psn.1.B, 8pso.1.B, 8pss.1.B, 8psx.1.B, 8pt2.1.B, 8pth.1.B, 8ptj.1.B, 8qe5.1.A, 8qgt.1.A, 8qgu.1.A, 8qh3.1.A, 8qhd.1.A, 8qhd.1.B, 8qhd.1.C, 8qz8.1.B, 8r1j.1.B, 8r1j.1.E, 8r1l.1.C, 8r3l.1.B, 8r60.1.F, 8r6u.1.A, 8r6w.1.A, 8r6y.1.A, 8rmp.1.B, 8rmq.1.B, 8rms.1.B, 8rn0.1.C, 8rn1.1.B, 8rn2.1.B, 8rn3.1.B, 8rn5.1.B, 8rn6.1.B, 8rn7.1.B, 8rn9.1.B, 8rn9.1.D, 8rna.1.I, 8rnc.1.G, 8xpo.1.A, 8y7m.1.B, 8y7o.1.D, 8z85.1.B, 8z8j.1.B, 8z8n.1.B, 8z8x.1.B, 8z97.1.B, 8z98.1.B, 8z9h.1.H, 8z9r.1.B, 8z9r.1.I, 9f2r.1.B