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. 30, 2020, 3:34 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:

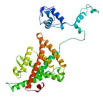
- Waterhouse, A., Bertoni, M., Bienert, S., Studer, G., Tauriello, G., Gumienny, R., Heer, F.T., de Beer, T.A.P., Rempfer, C., Bordoli, L., Lepore, R., Schwede, T. SWISS-MODEL: homology modelling of protein structures and complexes. Nucleic Acids Res. 46(W1), W296-W303 (2018). doi
- Guex, N., Peitsch, 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

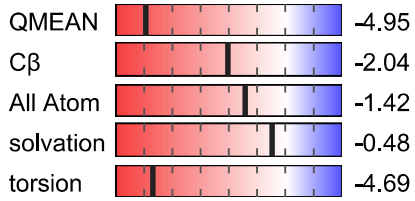
Results

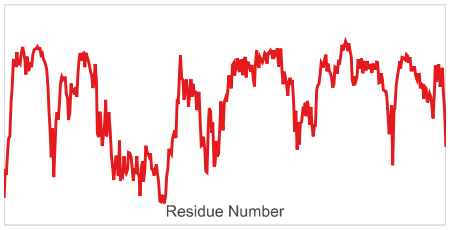
The SWISS-MODEL template library (SMTL version 2020-12-23, PDB release 2020-12-18) was searched with BLAST (Camacho et al.) and HHBlits (Steinegger et al.) for evolutionary related structures matching the target sequence in Table T1. For details on the template search, see Materials and Methods. Overall 2478 templates were found (Table T2).

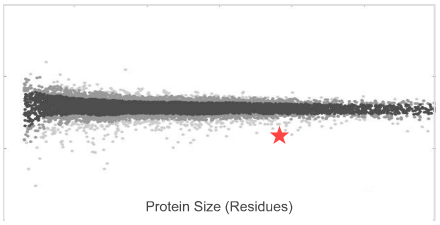
Models

The following models were built (see Materials and Methods "Model Building"):

Model #02	File	Built with	Oligo-State	Ligands	GMQE	QMEAN
	PDB	ProMod3 3.2.0	monomer	2 x ZN: ZINC ION;	0.21	-4.95







Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
4nqa.2.B	39.30	monomer	0.00	HHblits	X-ray	3.10Å	0.39	437 - 820	0.46	Liver X nuclear receptor beta

Included Ligands

Ligand	Description
2 x ZN	ZINC ION

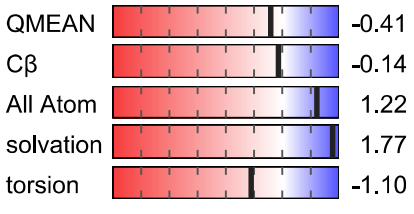
Excluded ligands

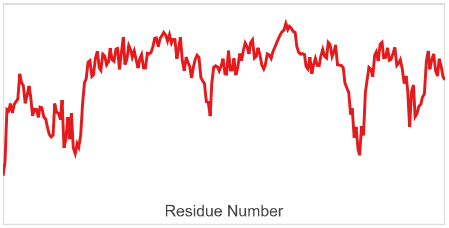
Ligand Name.Number	Reason for Exclusion	Description
965.4	Binding site not conserved.	[3-(3-{[2-CHLORO-3-(TRIFLUOROMETHYL)BENZYL](2,2-DIPHENYLETHYL)AMINO}PROPOXY)PHENYL]ACETIC ACID
9CR.1	Binding site not conserved.	(9CIS)-RETINOIC ACID
ZN.2	Binding site not conserved.	ZINC ION

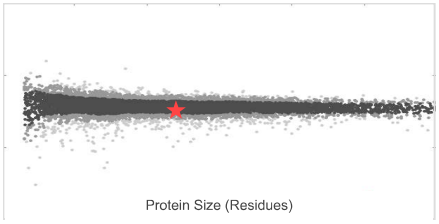
Ligand Name.Number	Reason for Exclusion	Description
ZN.3	Binding site not conserved.	ZINC ION

```
Target    MNLSPMMYRLNHAQGQKLPMAAEQQQQQSQQHPQQQQQPTTTPQTTPPTPTQSQQQQIIPSHILLQQQLDAASANTNSSN
4nqa.2.B  ------------------------------------------------------------------------------

Target    SNTTISNSHSITHHSNNEPVFLNNFTEQESNTPLALRQASNASSTSNSALLHTIHQHHSHTHQAPPTPPNHSRLIHSTAA
4nqa.2.B  ------------------------------------------------------------------------------

Target    NNLVITNAAAAAALVAASAAAAAANQVDVLSSNSSVEENLKLLKTAIKSEPLPHDLNSASNSNHNNHNNVNNLSSNKEDL
4nqa.2.B  ------------------------------------------------------------------------------

Target    ISLAACSALANVVIPASSANAVASSSTSVSSTMSSAKANVLKNVSTSALSNAITQVALAAGAGNGGSVSASGGVVSAAAG
4nqa.2.B  ------------------------------------------------------------------------------

Target    SVAGAGGSGGEALTSSNGSMVFVPSKRARMELREEWISTPSPGSVPSTAPLSPSSASQNHMYGANMSNGYASPMSAGSYD
4nqa.2.B  ------------------------------------------------------------------------------

Target    PFSPNGKTGRDDLSPSSSLNGFSTSDASDVKKIKKGPAPRLQEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKN--A
4nqa.2.B  ----------------------------------APKMLGHELCRVCGDKASGFHYNVLSCEGCKGFFRRSVVRGGAR

Target    VYCCKFGHACEMDMYMRRKCQECRLKKCLAVGMRPECVVPENQCAMKRREKKAQKEKDKIQTSVCATEIKKEILDLMTCE
4nqa.2.B  RYACRGGGTCQMDAFMRRKCQQCRLRKCKEAGMREQCVLSEEQIRKKKIRKQQQQESQSQSQSPVGPQG----SSSSASG

Target    PPSHPTCPLLPEDILAKCQARNIPPLSYNQLAVIYKLIWYQDGYEQPSEEDLKRI----MSSPDENESQHDVSFRHITEI
4nqa.2.B  PGASPG---GSEAGSQGSGEGEGVQLTAAQELMIQQLVAAQLQCNKRSFSDQPKVTPWPLGADPQSRDARQQRFAHFTEL

Target    TILTVQLIVEFAKGLPAFTKIPQEDQITLLKACSSEVMMLRMARRYDHNSDSIFFANNRSYTRDSYKMA-GMADNIEDLL
4nqa.2.B  AIISVQEIVDFAKQVPGFLQLGREDQIALLKASTIEIMLLETARRYNHETECITFLKDFTYSKDDFHRAGLQVEFINPIF

Target    HFCRQMYSMKVDNVEYALLTAIVIFS-DRPGLEEAELVEAIQSYYIDTLRIYILNRHCGDPMSLVFFAKLLSILTELRTL
4nqa.2.B  EFSRAMRRLGLDDAEYALLIAINIFSADRPNVQEPGRVEALQQPYVEALLSYTRIKRPQ---DQLRFPRMLMKLVSLRTL

Target    GNQNAEMCFSLKLKNRKLPKFLEEIWDV
4nqa.2.B  SSVHSEQVFALRLQDKKLPPLLSEIWDV
```

Model #01	File	Built with	Oligo-State	Ligands	GMQE	QMEAN
	PDB	ProMod3 3.2.0	monomer	1 x P1A: 2,3,14,20,22-PENTAHYDROXYCHOLEST-7-EN-6-ONE;	0.16	-0.41







Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
4ozt.1.A	68.49	monomer	0.00	BLAST	X-ray	2.70Å	0.50	581 - 820	0.29	Ecdysone receptor

Included Ligands

Ligand	Description
1 x P1A	2,3,14,20,22-PENTAHYDROXYCHOLEST-7-EN-6-ONE

Excluded ligands

Ligand Name.Number	Reason for Exclusion	Description
NEQ.2	Binding site not conserved.	N-ETHYLMALEIMIDE

```
Target    MNLSPMMYRLNHAQGQKLPMAAEQQQQQSQQHPQQQQQPTTTPQTTPPTPTQSQQQQIIPSHILLQQQLDAASANTNSSN
4ozt.1.A  ------------------------------------------------------------------------------

Target    SNTTISNSHSITHHSNNEPVFLNNFTEQESNTPLALRQASNASSTSNSALLHTIHQHHSHTHQAPPTPPNHSRLIHSTAA
4ozt.1.A  ------------------------------------------------------------------------------

Target    NNLVITNAAAAAALVAASAAAAAANQVDVLSSNSSVEENLKLLKTAIKSEPLPHDLNSASNSNHNNHNNVNNLSSNKEDL
4ozt.1.A  ------------------------------------------------------------------------------

Target    ISLAACSALANVVIPASSANAVASSSTSVSSTMSSAKANVLKNVSTSALSNAITQVALAAGAGNGGSVSASGGVVSAAAG
4ozt.1.A  ------------------------------------------------------------------------------

Target    SVAGAGGSGGEALTSSNGSMVFVPSKRARMELREEWISTPSPGSVPSTAPLSPSSASQNHMYGANMSNGYASPMSAGSYD
4ozt.1.A  ------------------------------------------------------------------------------

Target    PFSPNGKTGRDDLSPSSSLNGFSTSDASDVKKIKKGPAPRLQEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAVY
4ozt.1.A  ------------------------------------------------------------------------------

Target    CCKFGHACEMDMYMRRKCQECRLKKCLAVGMRPECVVPENQCAMKRREKKAQKEKDKIQTSVCATEIKKEILDLMTCEPP
4ozt.1.A  ------------------------------------------------------------------------------

Target    SHPTCPLLPEDILAKCQARNIPPLSYNQLAVIYKLIWYQDGYEQPSEEDLKRIMSSPDENESQHDVSFRHITEITILTVQ
4ozt.1.A  --------------------VKPISPEQEELIHRLVYFQNEYEQPSDEDLKRISNTPSEGEDQSDLNFRHITEITILTVQ

Target    LIVEFAKGLPAFTKIPQEDQITLLKACSSEVMMLRMARRYDHNSDSIFFANNRSYTRDSYKMAGMADNIEDLLHFCRQMY
4ozt.1.A  LIVEFAKRLPGFDKLLREDQIALLKACSSEVMMLRMARRYDVGSDSILFANNQPYTRDSYSLAGMGETVDDLLRFCRQMY

Target    SMKVDNVEYALLTAIVIFSDRPGLEEAELVEAIQSYYIDTLRIYILNRHCGDPMSLVFFAKLLSILTELRTLGNQNAEMC
4ozt.1.A  GMKVDNAEYALLTAIVIFSERPSLIEGWKVEKIQEIYLEALKVYVDNRR--KPASGTIFAKLLSVLTELRTLGNLNSEMC

Target    FSLKLKNRKLPKFLEEIWDV
4ozt.1.A  FSLKLKNKKLPPFLAEIWDV
```

Materials and Methods

Template Search

Template search with BLAST and HHBlits has been performed against the SWISS-MODEL template library (SMTL, last update: 2020-12-23, last included PDB release: 2020-12-18).

The target sequence was searched with BLAST against the primary amino acid sequence contained in the SMTL. A total of 1151 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 1360 templates were found.

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.

```
MNLSPMMYRLNHAQGQKLPMAAEQQQQQSQQHPQQQQQPTTTPQTTPPTPTQSQQQQIIPSHILLQQQLDAASANTNSSNSNTTISNSHSITHHSNNEPV
FLNNFTEQESNTPLALRQASNASSTSNSALLHTIHQHHSHTHQAPPTPPNHSRLIHSTAANNLVITNAAAAAALVAASAAAAAANQVDVLSSNSSVEENL
KLLKTAIKSEPLPHDLNSASNSNHNNHNNVNNLSSNKEDLISLAACSALANVVIPASSANAVASSSTSVSSTMSSAKANVLKNVSTSALSNAITQVALAA
GAGNGGSVSASGGVVSAAAGSVAGAGGSGGEALTSSNGSMVFVPSKRARMELREEWISTPSPGSVPSTAPLSPSSASQNHMYGANMSNGYASPMSAGSYD
PFSPNGKTGRDDLSPSSSLNGFSTSDASDVKKIKKGPAPRLQEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAVYCCKFGHACEMDMYMRRKCQE
CRLKKCLAVGMRPECVVPENQCAMKRREKKAQKEKDKIQTSVCATEIKKEILDLMTCEPPSHPTCPLLPEDILAKCQARNIPPLSYNQLAVIYKLIWYQD
GYEQPSEEDLKRIMSSPDENESQHDVSFRHITEITILTVQLIVEFAKGLPAFTKIPQEDQITLLKACSSEVMMLRMARRYDHNSDSIFFANNRSYTRDSY
KMAGMADNIEDLLHFCRQMYSMKVDNVEYALLTAIVIFSDRPGLEEAELVEAIQSYYIDTLRIYILNRHCGDPMSLVFFAKLLSILTELRTLGNQNAEMC
FSLKLKNRKLPKFLEEIWDV
```

Table T2:

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Coverage	Description
4nqa.2.B	39.30	monomer	-	HHblits	X-ray	3.10Å	0.39	0.46	Liver X nuclear receptor beta
4nqa.1.B	39.30	monomer	-	HHblits	X-ray	3.10Å	0.39	0.46	Liver X nuclear receptor beta
3dzy.1.B	27.22	monomer	-	HHblits	X-ray	3.10Å	0.34	0.44	Peroxisome proliferator-activated receptor gamma
3e00.1.B	27.22	monomer	-	HHblits	X-ray	3.10Å	0.34	0.44	Peroxisome proliferator-activated receptor gamma
3dzu.1.A	34.62	monomer	-	BLAST	X-ray	3.20Å	0.37	0.44	Retinoic acid receptor RXR-alpha
3dzu.1.B	27.22	monomer	-	HHblits	X-ray	3.20Å	0.34	0.44	Peroxisome proliferator-activated receptor gamma
3dzy.1.A	34.62	monomer	-	BLAST	X-ray	3.10Å	0.37	0.44	Retinoic acid receptor RXR-alpha
5uan.1.B	35.44	monomer	-	BLAST	X-ray	3.51Å	0.38	0.41	Retinoic acid receptor beta
4nqa.1.B	38.36	monomer	-	BLAST	X-ray	3.10Å	0.39	0.45	Liver X nuclear receptor beta
4nqa.2.B	38.36	monomer	-	BLAST	X-ray	3.10Å	0.39	0.45	Liver X nuclear receptor beta
3e00.1.A	34.62	monomer	-	BLAST	X-ray	3.10Å	0.37	0.44	Retinoic acid receptor RXR-alpha
4iqr.2.A	33.23	homo-dimer	0.05	HHblits	X-ray	2.90Å	0.36	0.39	Hepatocyte nuclear factor 4-alpha
4iqr.1.A	33.23	homo-dimer	0.03	HHblits	X-ray	2.90Å	0.36	0.39	Hepatocyte nuclear factor 4-alpha
4iqr.2.B	33.23	homo-dimer	0.05	HHblits	X-ray	2.90Å	0.36	0.39	Hepatocyte nuclear factor 4-alpha
5uan.1.A	34.91	monomer	-	BLAST	X-ray	3.51Å	0.37	0.41	Retinoic acid receptor RXR-alpha
4nqa.1.A	34.91	monomer	-	BLAST	X-ray	3.10Å	0.37	0.41	Retinoic acid receptor RXR-alpha

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Coverage	Description
4iqr.1.B	33.23	homo-dimer	0.03	HHblits	X-ray	2.90Å	0.36	0.39	Hepatocyte nuclear factor 4-alpha
3dzy.1.B	32.40	monomer	-	BLAST	X-ray	3.10Å	0.37	0.44	Peroxisome proliferator-activated receptor gamma
1z5x.1.B	62.24	monomer	-	BLAST	X-ray	3.07Å	0.48	0.36	Ecdysone receptor ligand binding domain
6fx0.1.A	33.03	monomer	-	HHblits	X-ray	1.90Å	0.37	0.40	Retinoic acid receptor gamma
3dzu.1.B	32.40	monomer	-	BLAST	X-ray	3.20Å	0.37	0.44	Peroxisome proliferator-activated receptor gamma
3e00.1.B	32.40	monomer	-	BLAST	X-ray	3.10Å	0.37	0.44	Peroxisome proliferator-activated receptor gamma
2nxx.1.B	68.09	monomer	-	BLAST	X-ray	2.75Å	0.50	0.29	Ecdysone Receptor (EcR, NRH1)
4nqa.2.A	34.91	monomer	-	BLAST	X-ray	3.10Å	0.37	0.41	Retinoic acid receptor RXR-alpha
1r1k.1.A	69.83	monomer	-	BLAST	X-ray	2.90Å	0.51	0.30	Ecdysone receptor
1r20.1.B	70.25	monomer	-	BLAST	X-ray	3.00Å	0.51	0.30	ECDYSONE RECEPTOR
4ozt.1.A	68.49	monomer	-	BLAST	X-ray	2.70Å	0.50	0.29	Ecdysone receptor
3ixp.1.D	70.25	monomer	-	BLAST	X-ray	2.85Å	0.51	0.30	Ecdysone receptor
2r40.2.C	69.83	monomer	-	BLAST	X-ray	2.40Å	0.51	0.30	Ecdysone Receptor
3ipu.1.A	40.51	homo-dimer	0.17	BLAST	X-ray	2.40Å	0.40	0.29	Oxysterols receptor LXR-alpha
1r20.1.B	74.49	monomer	-	HHblits	X-ray	3.00Å	0.52	0.24	ECDYSONE RECEPTOR
3fal.1.B	40.93	monomer	-	BLAST	X-ray	2.36Å	0.40	0.29	Oxysterols receptor LXR-alpha
3ipq.1.A	40.51	homo-dimer	0.16	BLAST	X-ray	2.00Å	0.40	0.29	Oxysterols receptor LXR-alpha
3fal.1.D	40.93	monomer	-	BLAST	X-ray	2.36Å	0.40	0.29	Oxysterols receptor LXR-alpha
2acl.2.B	41.03	monomer	-	BLAST	X-ray	2.80Å	0.40	0.29	Oxysterols receptor LXR-alpha
2acl.1.B	41.03	monomer	-	BLAST	X-ray	2.80Å	0.40	0.29	Oxysterols receptor LXR-alpha
2acl.3.B	41.03	monomer	-	BLAST	X-ray	2.80Å	0.40	0.29	Oxysterols receptor LXR-alpha
2nxx.1.B	73.20	monomer	-	HHblits	X-ray	2.75Å	0.51	0.24	Ecdysone Receptor (EcR, NRH1)
5avi.1.A	40.51	homo-dimer	0.18	BLAST	X-ray	2.70Å	0.40	0.29	Oxysterols receptor LXR-alpha
1z5x.1.B	70.47	monomer	-	HHblits	X-ray	3.07Å	0.51	0.24	Ecdysone receptor ligand binding domain
1r1k.1.A	73.98	monomer	-	HHblits	X-ray	2.90Å	0.52	0.24	Ecdysone receptor
3ixp.1.D	74.49	monomer	-	HHblits	X-ray	2.85Å	0.52	0.24	Ecdysone receptor
4iqr.2.B	36.84	homo-dimer	-	BLAST	X-ray	2.90Å	0.38	0.32	Hepatocyte nuclear factor 4-alpha
2r40.2.C	73.98	monomer	-	HHblits	X-ray	2.40Å	0.52	0.24	Ecdysone Receptor
4ozt.1.A	73.20	monomer	-	HHblits	X-ray	2.70Å	0.52	0.24	Ecdysone receptor
4iqr.2.A	36.84	homo-dimer	-	BLAST	X-ray	2.90Å	0.38	0.32	Hepatocyte nuclear factor 4-alpha
4iqr.1.B	36.84	homo-dimer	-	BLAST	X-ray	2.90Å	0.38	0.32	Hepatocyte nuclear factor 4-alpha
4iqr.1.A	36.84	homo-dimer	-	BLAST	X-ray	2.90Å	0.38	0.32	Hepatocyte nuclear factor 4-alpha
4ozr.1.A	69.90	monomer	-	BLAST	X-ray	2.70Å	0.50	0.24	Ecdysone receptor
3hzf.1.A	32.04	monomer	-	BLAST	X-ray	2.50Å	0.36	0.25	Thyroid hormone receptor, alpha isoform 1 variant

The table above shows the top 50 filtered templates. A further 1,332 templates were found which were considered to be less suitable for modelling than the filtered list.
1a28.1.A, 1a28.2.A, 1a52.1.A, 1a52.1.B, 1a6y.1.C, 1a6y.1.D, 1bsx.1.A, 1by4.1.C, 1by4.1.D, 1by4.2.C, 1by4.2.D, 1cit.1.C, 1dkf.1.A, 1dkf.1.B, 1dsz.1.C, 1dsz.1.D, 1e3g.1.A, 1ere.1.A, 1err.1.B, 1exa.1.A, 1fby.1.A, 1fcx.1.A, 1fcy.1.A, 1fm6.1.B, 1fm6.2.A, 1fm6.2.B, 1g1u.1.A, 1g1u.1.B, 1g1u.1.C, 1g1u.1.D, 1g2n.1.A, 1g50.1.A, 1g5y.1.B, 1ga5.1.D, 1gdc.1.A, 1glu.1.C, 1glu.1.D, 1gs4.1.A, 1gwq.1.A, 1gwr.1.A, 1h9u.1.A, 1hcp.1.A, 1hcq.1.C, 1hcq.2.C, 1hcq.2.D, 1hg4.1.A, 1hj1.1.A, 1hlz.1.C, 1hra.1.A, 1i37.1.A, 1i38.1.A, 1i7g.1.A, 1i7i.1.A, 1i7i.2.A, 1ilh.1.A, 1k4w.1.A, 1k74.1.A, 1k74.1.B, 1k7l.1.A, 1k7l.3.A, 1k7l.4.A, 1kb2.1.C, 1kb4.1.D, 1kb6.1.C, 1kkq.1.A, 1kkq.2.A, 1kkq.3.A, 1kkq.4.A, 1knu.1.A, 1knu.1.B, 1kv6.1.A, 1l2i.1.A, 1l2j.1.A, 1lat.1.C, 1lat.1.D, 1lo1.1.C, 1lv2.1.A, 1m13.1.A, 1m2z.1.A, 1m2z.1.C, 1m7w.1.A, 1m7w.1.B, 1m7w.2.A, 1m7w.2.B, 1mv9.1.A,

1n46.1.A, 1n46.1.B, 1n4h.1.A, 1nav.1.A, 1nax.1.A, 1nde.1.A, 1nhz.2.B, 1nq0.1.A, 1nq1.1.A, 1nq2.1.A, 1nq7.1.A, 1nuo.1.A, 1nyx.1.A, 1nyx.1.B, 1osh.1.A, 1osv.1.A, 1osv.2.A, 1ot7.1.A, 1ot7.2.A, 1ovl.1.A, 1ovl.1.B, 1ovl.1.C, 1ovl.1.D, 1p8d.1.A, 1p8d.2.A, 1p93.1.A, 1p93.4.A, 1pcg.1.A, 1pdu.1.A, 1pk5.1.A, 1pk5.2.A, 1pq6.1.B, 1pq6.3.B, 1pq6.3.C, 1pq9.2.A, 1pq9.3.B, 1pq9.3.D, 1prg.1.A, 1prg.1.B, 1pzl.1.A, 1q4x.1.A, 1qkm.1.A, 1qkn.1.A, 1qkt.1.A, 1qku.1.A, 1r0n.1.C, 1r0n.1.D, 1r0o.1.C, 1r0o.1.D, 1r1k.1.B, 1r20.1.A, 1r4i.1.C, 1r4i.1.D, 1r4o.1.C, 1r4o.1.D, 1r4r.1.C, 1r4r.1.D, 1r5k.1.A, 1r5k.1.B, 1r5k.2.A, 1r6g.1.A, 1rdt.1.A, 1rdt.1.C, 1rgd.1.A, 1rkg.1.A, 1rxr.1.A, 1s0x.1.A, 1s9p.1.A, 1s9p.1.B, 1s9p.2.A, 1s9p.2.B, 1s9q.1.A, 1s9q.1.B, 1sj0.1.A, 1skx.1.A, 1sqn.1.A, 1sqn.2.A, 1t5z.1.A, 1t7f.1.A, 1tfc.1.A, 1u3q.1.A, 1u3q.1.B, 1u3q.2.A, 1u9e.1.A, 1u9e.2.A, 1uhl.1.A, 1uhl.1.B, 1upv.1.A, 1vjb.1.A, 1vjb.1.B, 1wm0.1.A, 1x7e.1.A, 1x7j.1.A, 1x7j.1.B, 1x7r.1.A, 1xap.1.A, 1xb7.1.A, 1xdk.1.A, 1xdk.1.B, 1xiu.1.A, 1xiu.1.B, 1xls.1.A, 1xls.1.B, 1xnn.1.A, 1xnx.1.A, 1xnx.1.B, 1xq3.1.A, 1xqc.1.A, 1xqc.1.B, 1xqc.2.B, 1xv9.1.A, 1xv9.1.B, 1xzx.1.A, 1y0s.1.A, 1y9r.1.A, 1y9r.2.A, 1ya3.1.A, 1ya3.2.A, 1ya3.3.A, 1yje.1.A, 1ymt.1.A, 1ynw.1.C, 1ynw.1.D, 1yok.1.A, 1yow.1.A, 1yp0.1.A, 1yye.1.A, 1yye.1.B, 1z5x.1.A, 1z95.1.A, 1zaf.1.A, 1zaf.1.B, 1zdt.1.A, 1zdt.2.A, 1zdu.1.A, 1zeo.1.A, 1zeo.1.B, 1zgy.1.A, 1zh7.1.A, 1zky.1.A, 1zky.1.B, 1zuc.1.A, 1zuc.1.B, 2a3i.1.A, 2a66.1.C, 2aa5.1.A, 2aa6.1.A, 2abi.1.A, 2abi.2.A, 2abi.3.A, 2acl.1.A, 2acl.1.B, 2acl.2.B, 2acl.3.B, 2acl.4.A, 2acl.4.B, 2ama.1.A, 2ath.1.A, 2ath.1.B, 2awh.1.A, 2ax6.1.A, 2ax8.1.A, 2b23.1.A, 2b50.1.A, 2bj4.1.A, 2bj4.1.B, 2c7a.1.A, 2c7a.1.B, 2ebl.1.A, 2env.1.A, 2ewp.1.A, 2ewp.1.B, 2fai.1.A, 2fai.1.B, 2ff0.1.C, 2fsz.1.A, 2g0g.1.A, 2g0h.1.A, 2g0h.1.B, 2g44.1.A, 2g44.1.B, 2g5o.1.A, 2gda.1.A, 2giu.1.A, 2gl8.1.A, 2gl8.1.B, 2gpo.1.C, 2gpp.1.A, 2gpu.1.A, 2gpv.2.D, 2gwx.1.A, 2gwx.2.A, 2h77.1.A, 2h79.1.A, 2han.1.C, 2han.1.D, 2hfp.1.A, 2hvc.1.A, 2i0j.1.A, 2i4p.1.A, 2iog.1.A, 2iok.1.A, 2j14.1.A, 2j4a.1.A, 2j7x.1.A, 2jf9.1.C, 2jfa.1.B, 2lbd.1.A, 2lze.1.A, 2nll.1.C, 2nll.1.D, 2npa.1.A, 2nv7.1.A, 2nv7.1.B, 2nxx.1.A, 2o9i.1.A, 2o9i.2.A, 2oax.1.A, 2oax.3.A, 2oax.4.A, 2oax.5.A, 2oax.6.A, 2ocf.1.A, 2om9.2.A, 2ouz.1.A, 2ovh.2.A, 2oz7.1.A, 2p4y.1.A, 2p4y.1.B, 2p54.1.A, 2p7z.1.A, 2pin.1.A, 2pin.1.B, 2pjl.1.A, 2pob.1.A, 2prg.1.A, 2prg.2.A, 2pv0.1.A, 2pv0.2.A, 2pv0.3.A, 2pvc.1.A, 2pvc.3.A, 2q1h.1.A, 2q3y.1.A, 2q59.1.A, 2q59.1.B, 2q5g.1.A, 2q5g.2.A, 2q5p.1.A, 2q5p.1.B, 2q5s.1.A, 2q5s.1.B, 2q60.1.A, 2q60.1.B, 2q60.1.C, 2q60.1.D, 2q6j.1.A, 2q6j.1.B, 2q6r.1.A, 2q70.1.A, 2q7i.1.A, 2q7k.1.A, 2q8s.1.A, 2q8s.1.B, 2qa6.1.B, 2qa8.1.A, 2qa8.1.B, 2qh6.1.A, 2qmv.1.A, 2qpy.1.A, 2qr9.1.A, 2qw4.1.A, 2qw4.3.A, 2qw4.4.A, 2qxs.1.A, 2qxs.1.B, 2qzo.1.A, 2r40.2.B, 2r6w.1.A, 2r6w.1.B, 2rew.1.A, 2v0v.1.A, 2v0v.2.A, 2v0v.3.A, 2v0v.4.A, 2v7c.1.A, 2v7c.2.A, 2vst.1.A, 2vst.2.A, 2vv0.2.A, 2vv1.2.A, 2vv2.2.A, 2vv4.2.A, 2xhs.1.A, 2xkw.1.A, 2xkw.2.A, 2xyj.2.A, 2xyw.1.A, 2yat.1.A, 2yfe.1.A, 2yfe.2.A, 2yja.1.B, 2yjd.1.A, 2ylo.1.A, 2ylq.1.A, 2yly.1.A, 2yly.1.B, 2z4b.1.A, 2z4j.1.A, 2zbs.1.A, 2zk0.2.A, 2zk0.2.B, 2zk1.2.A, 2zk1.2.B, 2zk3.2.A, 2zk3.2.B, 2zk6.2.A, 2znn.1.A, 2znp.1.A, 2znp.1.B, 2zvt.1.A, 2zvt.1.B, 2zxm.1.A, 3a1a.1.A, 3a2h.1.A, 3a2i.1.A, 3a2j.1.A, 3a9e.1.A, 3a9e.1.B, 3ads.2.A, 3adt.1.A, 3adt.1.B, 3adu.1.B, 3adv.1.B, 3adw.1.B, 3an3.1.A, 3an3.1.B, 3b0q.1.A, 3b0q.1.B, 3b0t.1.A, 3b0w.1.A, 3b1m.1.A, 3bej.1.A, 3bej.2.A, 3bqd.1.A, 3cbb.1.C, 3cbb.1.D, 3cjw.1.A, 3cld.1.A, 3cqv.1.A, 3cs6.1.A, 3cs8.1.A, 3ctb.1.A, 3ctb.2.A, 3cwd.1.A, 3cwd.2.A, 3d24.1.A, 3d24.1.C, 3d57.1.A, 3d5f.2.A, 3d5f.3.A, 3d90.1.A, 3d90.2.A, 3dct.1.A, 3dr1.1.A, 3dt3.1.A, 3dt3.1.B, 3dy6.2.B, 3dzu.1.A, 3dzy.1.A, 3e00.1.A, 3e7c.1.A, 3e94.1.A, 3ert.1.A, 3et0.2.A, 3et1.1.A, 3et1.2.A, 3et2.1.A, 3et2.2.A, 3et3.1.A, 3eyb.1.A, 3f5c.1.A, 3f5c.1.B, 3f5c.1.C, 3f7d.1.A, 3fal.1.A, 3fal.1.B, 3fal.1.C, 3fal.1.D, 3fc6.1.A, 3fei.1.A, 3fli.1.A, 3fs1.1.A, 3fur.1.A, 3fxv.1.A, 3g0w.1.A, 3g6p.1.C, 3g6p.1.D, 3g6q.2.A, 3g6r.1.D, 3g6t.1.A, 3g6t.1.B, 3g8i.1.A, 3g8n.1.A, 3g8n.1.B, 3g8o.1.A, 3g8u.1.A, 3g8x.1.B, 3g9e.1.A, 3g9i.2.A, 3g9m.1.A, 3g9m.1.B, 3g9o.1.B, 3gd2.1.A, 3gn8.1.A, 3gws.1.A, 3gwx.1.A, 3gwx.1.B, 3gyt.1.A, 3gz9.1.A, 3h0a.1.A, 3h0a.1.B, 3h52.1.A, 3h52.1.B, 3h52.2.A, 3h52.2.B, 3hc6.1.A, 3hlv.1.A, 3hlv.1.B, 3hm1.1.A, 3hm1.1.B, 3hod.1.A, 3hod.1.B, 3hq5.1.A, 3hzf.1.A, 3ilz.1.A, 3imy.1.A, 3ipq.1.A, 3ipu.1.A, 3ixp.1.A, 3jzb.1.A, 3jzc.1.A, 3k23.1.A, 3k23.2.A, 3k23.3.A, 3k6p.1.A, 3k8s.1.A, 3k8s.1.B, 3kba.1.A, 3kba.2.A, 3kdt.1.A, 3kfc.1.A, 3kfc.1.B, 3kfc.2.B, 3kmg.1.A, 3kmg.2.A, 3kmr.1.A, 3kmz.1.A, 3kyt.1.A, 3l03.1.A, 3l03.1.B, 3l0e.1.A, 3l0j.1.A, 3l0l.1.A, 3l1b.1.A, 3l3x.1.A, 3m7r.1.A, 3m9e.1.A, 3m9e.1.B, 3m9e.2.A, 3m9e.2.B, 3mne.1.A, 3mno.1.A, 3mnp.1.A, 3n00.1.A, 3noa.1.B, 3nsq.1.A, 3nsq.1.B, 3okh.1.A, 3oki.1.A, 3oki.2.A, 3omp.1.A, 3os8.1.A, 3osi.1.A, 3osi.2.A, 3oz0.1.A, 3ozj.1.A, 3p0u.1.A, 3p0u.1.B, 3p88.1.A, 3p89.1.A, 3p8x.1.A, 3pba.1.A, 3pba.2.A, 3pcu.1.A, 3plz.1.A, 3prg.1.A, 3q95.1.A, 3q95.2.A, 3qt0.1.A, 3r29.1.A, 3r29.1.B, 3r2a.1.A, 3r2a.1.B, 3r2a.1.C, 3r2a.1.D, 3r5n.1.A, 3r8a.1.A, 3r8a.2.A, 3r8i.1.A, 3rlj.1.A, 3rll.1.A, 3rut.1.A, 3rvf.1.A, 3ry9.1.A, 3ry9.2.A, 3s9s.1.A, 3sp6.1.A, 3sp9.1.A, 3sz1.1.A, 3sz1.2.A, 3t03.1.A, 3t03.2.A, 3t9k.1.A, 3t9k.2.A, 3tx7.1.B, 3ty0.1.A, 3up0.1.A, 3up3.1.A, 3uuc.1.A, 3uuc.1.B, 3uud.1.A, 3uud.1.B, 3uvv.1.A, 3uvv.1.B, 3v3e.1.A, 3v3e.1.B, 3v3q.1.B, 3v4a.1.A, 3v9y.1.A, 3vhu.1.A, 3vhv.1.A, 3vji.1.A, 3vji.1.B, 3vn2.1.A, 3vt3.1.A, 3vt7.1.A, 3vtc.1.A, 3w0g.1.A, 3w0h.1.A, 3wff.1.A, 3wfg.1.A, 3wgp.1.A, 3wj4.1.A, 3wj4.1.B, 3wt6.1.A, 3wwr.1.A, 3x1i.2.A, 3zra.1.A, 3zra.2.A, 4aa6.1.A, 4aa6.1.B, 4aa6.2.A, 4aa6.2.B, 4b7w.1.A, 4b7w.1.B, 4bcr.1.A, 4ci4.1.A, 4ci5.1.A, 4ci5.2.A, 4cn2.1.C, 4cn2.1.D, 4cn3.1.A, 4cn3.1.B, 4cn3.2.A, 4cn3.2.B, 4cn5.1.A, 4cn5.1.B, 4cn7.1.A, 4cn7.1.B, 4cn7.2.A, 4csj.1.A, 4dk8.1.A, 4dk8.1.C, 4dm6.1.A, 4dm6.2.A, 4dma.1.A, 4dma.1.B, 4dor.1.A, 4dor.1.B, 4dos.1.A, 4dqm.1.A, 4e2j.1.A, 4e4q.1.B, 4em9.1.A, 4em9.2.A, 4ema.1.A, 4ema.2.A, 4f9m.1.A, 4fgy.1.A, 4fhh.1.A, 4fn9.1.B, 4fne.1.A, 4g2i.1.A, 4hee.1.A, 4hn5.1.A, 4hn5.1.D, 4hn6.1.A, 4hn6.1.D, 4is8.1.A, 4is8.2.A, 4iu7.1.A, 4iu7.2.A, 4iui.1.C, 4iwc.1.A, 4j26.1.A, 4j5w.1.A, 4j5w.1.B, 4j5w.1.C, 4j5w.1.D, 4j5x.1.A, 4j5x.1.C, 4j5x.1.D, 4jaz.1.A, 4jgv.1.A, 4jgv.1.B, 4jyg.1.A, 4jyg.1.B, 4k7a.1.A, 4kzj.1.A, 4kzj.2.A, 4kzm.1.A, 4kzm.2.A, 4l96.1.A, 4l98.1.A, 4log.1.A, 4log.1.B, 4lsj.1.A, 4ltw.1.A, 4m8h.1.A, 4mdd.1.A, 4mg5.1.A, 4mg5.1.B, 4n1y.1.A, 4n5g.1.A, 4n5g.1.C, 4n73.1.A, 4nb6.1.A, 4nie.1.A, 4nqa.1.A, 4nqa.2.A, 4nuf.1.A, 4ny9.1.A, 4o8f.1.A, 4o8f.1.B, 4oar.1.A, 4oc7.1.A, 4oea.1.A, 4ogh.1.A, 4oiv.1.A, 4oiv.1.B, 4oj4.1.A, 4ojb.1.A, 4oln.1.A, 4oln.1.B, 4ond.1.A, 4ond.2.B, 4oni.1.A, 4oni.2.A, 4oor.1.A, 4oor.2.A, 4ozr.1.A, 4ozr.1.B, 4ozt.1.B, 4p6w.1.A, 4p6x.1.A, 4p6x.2.A, 4p6x.3.A, 4p6x.5.A, 4pld.1.A, 4ple.4.A, 4pp6.1.A, 4prg.1.A, 4prg.1.B, 4prg.1.D, 4pvu.1.A, 4pvu.1.B, 4pwl.1.A, 4pwl.1.B, 4pxm.1.A, 4q0a.1.A, 4q13.1.A, 4q13.1.B, 4q50.1.A, 4q50.1.B, 4q50.3.A, 4q50.4.B, 4qbq.1.A, 4qbq.1.B, 4qbr.1.A, 4qbs.1.A, 4qe6.1.A, 4qe8.1.A, 4qe8.2.A, 4qjr.1.A, 4ql8.1.A, 4qm0.3.B, 4r06.1.A, 4r06.1.B, 4r2u.1.A, 4r2u.1.B, 4r6s.1.A, 4r6s.1.B, 4rak.1.A, 4rak.1.B, 4ref.1.A, 4ref.2.A, 4rmd.1.A, 4ruj.1.A, 4rwv.1.A, 4rze.1.A, 4rze.1.B, 4rzf.1.A, 4rzf.1.B, 4rzg.1.A, 4rzg.1.B, 4s0s.1.A, 4s14.1.A, 4s15.1.A, 4s15.2.A, 4tnt.1.A, 4tnt.1.B, 4u7p.1.A, 4u7t.1.A, 4uda.1.A, 4udb.1.A, 4udc.1.A, 4udd.1.A, 4umm.1.A, 4umm.1.D, 4umm.1.E, 4wlb.1.A, 4wpf.1.A, 4wqp.1.A, 4wvd.1.B, 4wvd.2.B, 4xai.1.A, 4xai.1.C, 4xaj.1.A, 4xaj.1.B, 4xaj.2.A, 4xaj.2.B, 4xhd.2.B, 4xi3.1.A, 4xld.1.A, 4xuh.2.A, 4y29.1.A, 4ymq.1.A, 4ynk.1.A, 4ypq.1.A, 4zi1.1.A, 4zjr.1.A, 4zjw.1.A, 4zjw.2.A, 4zn7.1.A, 4zn7.1.B, 4zn9.1.A, 4znh.1.A, 4znv.1.A, 4zo1.1.A, 4zo1.1.B, 4zom.1.A, 5a86.1.A, 5a86.1.B, 5aau.1.A, 5aav.1.A, 5aav.1.B, 5acc.1.A, 5ak2.1.A, 5apk.1.A, 5avi.1.A, 5ayg.1.A, 5azt.1.A, 5azt.2.A, 5b5b.1.A, 5c4o.1.A, 5c4t.1.A, 5cbx.1.A, 5cbx.1.B, 5cbx.2.B, 5cby.1.A, 5cby.1.B, 5cbz.1.A, 5cbz.1.B, 5cbz.2.A, 5cbz.2.B, 5cc0.1.A, 5cc0.1.D, 5cc1.1.A, 5cc1.1.B, 5cj6.1.A, 5dks.1.A, 5dlr.1.B, 5dsh.1.A, 5duh.1.A, 5dv8.1.A, 5dvc.1.A, 5dwl.1.A, 5dx3.1.A, 5dx3.1.B, 5dxp.1.A, 5dxp.1.B, 5dyb.1.A, 5e0w.1.B, 5e0x.1.B, 5e15.1.A, 5e15.1.B, 5e1c.1.A, 5e1c.1.B, 5e69.1.A, 5e69.1.D, 5e6a.1.D, 5e6b.1.A, 5e6c.1.B, 5e6d.1.D, 5ec9.1.A, 5ejv.1.A, 5emp.1.A, 5emp.1.B, 5eth.1.A, 5f9b.1.A, 5f9b.1.B, 5fqs.1.A, 5g43.1.A, 5gic.1.A, 5gid.1.A, 5gie.1.A, 5gtn.1.A, 5gto.1.A, 5gtr.1.A, 5hcv.1.A, 5hjp.1.A, 5hjp.1.B, 5hjp.2.A, 5hjp.2.B, 5hyk.1.A, 5hyr.1.A, 5hzc.1.B, 5i4v.1.A, 5i4v.1.B, 5iaw.1.A, 5iaw.2.A, 5ick.1.A, 5ick.2.A, 5ixk.1.A, 5iz0.1.A, 5iz0.2.A, 5ji0.1.A, 5ji0.1.B, 5jjm.1.A, 5jy3.2.A, 5jy3.2.B, 5k13.1.A, 5k38.1.A, 5k3l.1.A, 5k3l.2.A, 5k3m.1.A, 5k3n.1.A, 5k3n.2.A, 5k6e.1.A, 5k6e.2.A, 5k74.2.A, 5kce.1.B, 5kcu.1.B, 5krb.1.B, 5krb.1.D, 5kya.1.A, 5kya.1.B, 5l0m.1.A, 5l11.1.A, 5l7g.1.A, 5lga.1.A, 5lsg.1.A, 5lsg.2.A, 5lwp.1.A, 5m24.1.A, 5m96.1.A, 5m96.2.A, 5mj5.1.A, 5mk4.1.A, 5mku.1.A, 5mwp.1.A, 5nft.1.A, 5ni5.1.A, 5nma.1.C, 5nti.1.A, 5ntk.1.A, 5ntk.2.A,

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