Supplementary Information: A new class of synthetic beta-solenoid proteins with the fragment-free computational design of a beta-hairpin extension

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1 Methods

1.1 Cloning

The SynRFR24.1 gene sequence was codon optimised, synthesised and cloned into the pET11a expression plasmid by GeneArt (Table S3). Turns were added and deleted by PCR followed by recircularisation using Gibson assembly or restriction enzyme digestion and ligation. The turn deletion, synRFR20.1, was created by using the synRFR_del120_139_gib_FOR and synRFR_del120_139_gib_REV PCR primers (Table S4) and the plasmid was religated using Gibson assembly [1]. The single turn insertion, synRFR28.1, was created using the synRFR_ins20_restrict_FOR and synRFR_ins20_restrict_REV PCR primers followed by digestion with the restriction enzymes PsiI and PmeI (New England Biolabs) to create compatible overhangs and recircularisation using T4 ligase (New England Biolabs).

Variable loop regions were ordered as linear DNA gBlocks from IDT (Table S5), the original SynRFR24.1 plasmid (including the non-variable parts of the coding sequence) was linearised using the synRFR_loop_prep_FOR and synRFR_loop_prep_REV PCR primers and the final construct formed using In-Fusion HD (Clontech Laboratories, Inc.).

The SynRFR24.t1428_sfGFP variant was created by linearising the SynRFR24.t1428 plasmid with the t1428_GFP_FOR and t1428_GFP_REV primers and the coding sequence for sfGFP coding sequence was amplified from a plasmid using the sfGFP_FOR and sfGFP_REV primers with appropriate overhangs using PCR. The two PCR products were then joined using Gibson assembly to create the final construct. The SynRFR24.t1428_sfGFP_mut variant was similarly created using the t1428_W113A_GFP_FOR, t1428_GFP_REV, sfGFP_FOR and sfGFP_W113A_REV primers.

1.2 Crystallisation and Structure Solution

Crystallisation conditions for the structures solved are shown in Table S1, as well as data collection and refinement statistics. Diffraction data were collected at Diamond Light Source with the exception of SynRFR24.2 which was collected on an in-house rotating-anode source, and processed with xia2 [2] and XDS [3]. The SynRFR24.1 structure was solved by molecular replacement [4] with a composite model constructed from the source models, N-terminus of 3DU1 [5] and C-terminus of 2BM4 [6]. Molecular replacement models for SynRFR24 variants were derived from the 1.8 Å SynRFR24.1 structure. Loop variant structures were solved with the theoretically predicted structures, and rebuilt.

Structures were built and rebuilt with COOT [7] and refined with Refmac5 [8] or Phenix [9]. Validation was performed with Molprobity [10]. Coordinates and structure factors were deposited in the Protein Data Bank [11].

The correctness of the loop structures was verified with molecular replacement using a model with the loop excised, and then a cycle of refinement in Refmac, and maps calculated from this no-loop model. As shown in Fig. S1. The t1555 loop is consistent with the electron density, although at 4.4Å the detailed

conformation is unknown. The t1428 loop is visible in nearly the predicted conformation, t801 is clearly different, and t3284 is not resolved over its entire length.

1.3 Size exclusion chromatography-multi-angle light scattering (SEC-MALS)

An Agilent 1260 system (Agilent Technologies) with a miniDAWN TREOS (Wyatt Technologies) light scattering detector and an Optilab T-rEX (Wyatt Technologies) refractive index detector were used together with a Superdex 200 Increase 10/300 GL column (GE Healthcare). The column was prequilibrated with bicine buffer (100 mM bicine and 150 mM NaCl buffer titrated to pH 9.0 with NaOH). 100 μl of approximately 5 mg/ml protein was injected for each of the different designs. Data was analysed using the ASTRA software (Wyatt Technologies) in order to estimate the molar mass of the protein. The length variant SynRFR proteins eluted in the order expected from the size exclusion column and their MALS estimated molar masses were consistent with being homodimeric (Fig. S2). The loop insertion variant proteins all eluted at similar volumes except for SynRFR24.t1428 (Fig. S3). The MALS molar masses were estimated to be $\sim$50 kDa for all loop variant proteins, including SynRFR24.t1428, corresponding to homodimers.

The elution time of SynRFR24.t1428 in the SEC is later than the other loop-extension variants, suggesting a smaller hydrodynamic radius or that the hydrophobic residues on the loop are interacting with the column matrix. Using PISA [12], the C-terminal dimer-dimer interface was calculated to have a surface area of 684 Å^2 and an energy of -14.2 kcal mol^{-1}, and is predicted to be involved in complex formation. The loop dimer interface observed in the crystal has an area of 467 Å^2 and -5.3 kcal mol^{-1} and is not predicted to be involved in complex formation. Therefore we think it unlikely that this dimer is being formed in solution, as it would require the breaking of a strong interface and the formation of a weaker one, despite the anomalous SEC result.

The GFP domain insertion variant (SynRFR24.t1428_sfGFP and SynRFR24.t1428_sfGFP_mut) molar masses, estimated to be around 100 KDa, were also consistent with being homodimeric as expected (Fig. S4).

1.4 Thermofluor assay for protein stability

To measure the thermal stability of each of the SynRFR proteins, melting experiments were performed in the presence of 10X final concentration of SYPRO Orange dye (Life Technologies) and a final protein concentration of approximately 0.75 mg/ml in 100 mM bicine and 150 mM NaCl buffer titrated to pH 9.0 with NaOH. The samples were heated from 25 °C to 99 °C at rate of 1 °C/minute in a StepOnePlus Real-Time PCR system (Applied Biosystems) with fluorescence measured at standard excitation/emission wavelengths. The protein melting temperature, T_m, was estimated using the R statistical package [13] by fitting a smoothing cubic spline and finding the maximum of the first derivative. The SynRFR length variant proteins showed T_m values ranging from 65 to 73 °C (Fig. S5), while the loop insertion variants had lower T_m values ranging from 54 to 60 °C (Fig. S6).

1.5 Synthetic RFR scaffold design

An alignment of 5-mer sequences corresponding to a single pentapeptide RFR repeat was created from the sequences of the repeat region taken from the PDB structures 2J8K and 3DU1 giving an alignment of 65 5-mers. The frequency table generated using these sequences was then edited to exclude known problematic residues such as proline, and to ensure an alanine at position 1 and a leucine at position 3 giving the final residue frequency table used in this work (Table S2) with a consensus sequence of ADLSG.

1.6 Computational protein design methods

We used our in-house developed software, PD2 [14,15], and Rosetta3 [16] to design free-form loop embellishments. PD2 can be downloaded from http://www.sbg.bio.ic.ac.uk/~phyre2/PD2/. PD2 was used to generate *de novo* backbone loops while Rosetta was used for sequence design and full-atom energy minimisation. The full protocol is described in detail in the following sections.

1.6.1 PD2 C_α potential energy function and Monte Carlo move set

The C_α potential energy function has been previously described and used for generating *de novo* backbone scaffolds and for sampling backbone conformations for loop prediction [14,17]. The potential energy function was composed of 5 terms (equation (1)).

$$E_{ca} = E_{local} + E_{bond} + E_{bump} + E_{radgyr} + E_{hbond} \quad (1)$$

Where E_{local} was composed of harmonic pseudo C_α-C_α-C_α bond angle, C_α-C_α-C_α-C_α dihedral terms and reference energies with parameters that vary depending on the local structural alphabet classification, E_{bond} was a pseudo C_α-C_α bond term, E_{bump} was a soft steric repulsive term, and E_{hbond} was a pseudo hydrogen bonding statistical potential term using pseudo N and O atoms. The E_{local} reference energy terms were parameterised such that the equilibrium distributions of each local structural alphabet "letter" and each pair of consecutive "letters" reproduced the observed distributions in a training set of high resolution protein structures [17].

The potential energy function did not include any sequence-dependent terms and was only intended to reproduce the average properties of polypeptide chain. Despite being sequence-independent, it was found to be comparable to fragment-based methods and capable of sub-Ångstrom loop predictions [14] when combined with other methods as part of a hierarchical approach.

Loop conformations were sampled from the C_α potential energy function using a Markov chain Monte Carlo based method. For sampling loop conformations, only local moves were used that do not propagate to the rest of the chain. These consisted of a crankshaft move, a bond length move, and a bond angle move as described previously [14].

1.6.2 PD2_ca2main backbone reconstruction method

C_α models were converted into full backbone models using our recently developed algorithm [15]. This algorithm uses a 528 letter structural alphabet determined by fitting Gaussian mixture models to a high resolution training set. Each letter in the alphabet consists of 6 C_α atoms centred around an idealised trans- or cis-peptide bond built using CHARMM residue definitions [18]. Backbones are reconstructed by finding the best fitting letter to each 6 C_α fragment in order to position the idealised peptide bond. C_β and backbone amide hydrogen atoms were then added using CHARMM residue definitions. During loop ensemble generation 8 C_α atoms are permitted to move resulting the in the reconstruction of 9 intervening peptide bonds. This means that 10 residues had variable phi/psi dihedral angles.

1.6.3 PD2 backbone potential energy function

A simple backbone potential energy function was used to regularise backbone geometry using gradient minimisation after backbone reconstruction as described above. This simple potential energy function (equation (2)) has been previously described previously [14, 17] and contains terms taken from the OPLS-US force field [19] and a reimplementation of the Rosetta backbone hydrogen bonding statistical potential [20].

$$E_{bb} = E_{ang} + E_{bond} + E_{tor} + E_{impr\_tor} + E_{LJ_{1-4}} + E_{LJ_{1-5}} + E_{bump} + E_{bb\_hb} \quad (2)$$

1.6.4 Loop backbone ensemble generation

The methods described above have been used for sampling backbone loop conformational space in a sequence-independent way [14] in order to predict loop structures. When side-chains were repacked and the loop structure gradient minimised in the full-atom Rosetta potential energy function [16], we showed that picking the lowest energy loop frequently gave sub-Å RMSD loop structure predictions despite the fact that sequence information was not used to guide initial backbone conformational sampling [14]. This result suggests that designable backbone loop conformations can be sampled without using backbone fragments from known protein structures.

An ensemble of loop conformations was generated using this sampling method [14]. Briefly, C_α residue insertions were created by linear interpolation between fixed anchor end points follow by gradient minimisation to remove clashes and regularise bond lengths. This is followed by successive short C_α coarse-grained Monte

Carlo simulated annealing runs to generate an ensemble. After each C_α simulated annealing run, backbone atoms are reconstructed using the PD2_ca2main method described above and gradient minimised in the PD2 backbone potential energy function. During ensemble generation only atoms in the loop region are moved and loop sampling is not biased by any explicit or implicit sequence information (e.g. by the use of backbone fragments from known protein structures or the use of potential energy functions with sequence-dependent terms).

1.7 Detailed *de novo* loop design protocol

Waters were removed from the initial high resolution structure for beta1, PDB code 4YC5, and the amino acid identities at positions D129 and K128 were changed to glycine. The resulting structure was gradient minimised using the Rosetta FastRelax protocol with coordinate restraints to the crystal structure with the command line:

```
relax -relax:constrain_relax_to_start_coords -relax:coord_constrain_sidechains -relax:
    ramp_constraints false -ex1 -ex2 -use_input_sc -flip_HNQ -no_optH false -s 4
    YC5_nowat_K128G_D129G.pdb
```

Due to the rough nature of full-atom potential energy landscapes, small changes in coordinates can result in large changes in potential energy. The purpose of this procedure is to minimise the potential energy while remaining very close to the initial crystal structure coordinates.

An 8 residue insertion was created between residues 128 and 129 using the PD2 software package [14,15,17] and the command line:

```
pd2_loop_model --insert_chain A --insert_resnum 109 --insert_seq GAAAAAAG -i 4
    YC5_nowat_K128G_D129G_relaxed.pdb -o beta1_8res_109_insert.pdb --ca_insert --renumber
```

4000 loop conformations were then sampled from a sequence independent coarse-grained potential energy function and loop backbone atoms reconstructed using the command (the algorithms used are previously described [14, 15]):

```
pd2_loop_model --loop_model:fiser_test_protocol_corrected -i beta1_8res_109_insert.pdb -o
    beta1_8res_insert_108_samples.pdb --loop_model:insert_resnum 108 --loop_model:insert_overwrite
    10 --loop_model:num_structs 4000 --loop_model:insert_chain A
```

Note that the phi/psi angles of the residues flanking the 8 residue insertion were also permitted degrees of freedom during loop sampling making this equivalent to a 10 residue loop prediction.

A sequence was designed for each loop conformation samples using RosettaScripts [21]. The amino acid identities of residues immediately adjacent (residues 68-69, 85-86, 88-90, 106-108, 117-119) to the loop were also allowed to vary in addition to the loop region itself (residues 109-116). The permitted degrees of freedom during the design process were the side-chain and backbone of residues 66-71, 85-90, 105-120, 133-138, 154-159. Sequences were designed with the command:

```
rosetta_scripts -database rosettadb -s input.pdb -nstruct 1 -parser:protocol rosetta_script.xml -
    parser:view -no_optH false
```

where the contents of rosetta_script.xml was:

```
<ROSETTASCRIPTS>
       <SCOREFXNS>
              <SFXN_relax weights=talaris2013>
              </SFXN_relax>
       </SCOREFXNS>
       <TASKOPERATIONS>
              <ReadResfile name=rrf filename=resfile/>
              <ReadResfile name=rrf_hp filename=resfile_hp/>
       </TASKOPERATIONS>
       <FILTERS>
       </FILTERS>
       <MOVERS>
```

```
            <FlxbbDesign name=des ncycles=3 sfxn_design=SFXN_relax sfxn_relax=SFXN_relax
                task_operations=rrf>
                   <MoveMap>
                          <Chain number=1 chi=0 bb=0 /> Turns off all degrees of freedom for
                              chain A
                          <Span begin=66 end=71 chi=1 bb=0/> This line turns the side-chain (chi
                              ) and backbone (bb) freedoms back on
                          <Span begin=85 end=90 chi=1 bb=1/> This line turns the side-chain (chi
                              ) and backbone (bb) freedoms back on
                          <Span begin=105 end=106 chi=1 bb=1/> This line turns the side-chain (
                              chi) and backbone (bb) freedoms back on
                          <Span begin=107 end=118 chi=1 bb=1/> This line turns the side-chain (
                              chi) and backbone (bb) freedoms back on
                          <Span begin=119 end=120 chi=1 bb=1/> This line turns the side-chain (
                              chi) and backbone (bb) freedoms back on
                          <Span begin=133 end=138 chi=1 bb=1/> This line turns the side-chain (
                              chi) and backbone (bb) freedoms back on
                          <Span begin=154 end=159 chi=1 bb=0/> This line turns the side-chain (
                              chi) and backbone (bb) freedoms back on
                   </MoveMap>
            </FlxbbDesign>
            <FlxbbDesign name=des_hp ncycles=3 sfxn_design=SFXN_relax sfxn_relax=SFXN_relax
                task_operations=rrf_hp>
                   <MoveMap>
                          <Chain number=1 chi=0 bb=0 /> Turns off all degrees of freedom for
                              chain A
                          <Span begin=66 end=71 chi=1 bb=0/> This line turns the side-chain (chi
                              ) and backbone (bb) freedoms back on
                          <Span begin=85 end=90 chi=1 bb=1/> This line turns the side-chain (chi
                              ) and backbone (bb) freedoms back on
                          <Span begin=105 end=106 chi=1 bb=1/> This line turns the side-chain (
                              chi) and backbone (bb) freedoms back on
                          <Span begin=107 end=118 chi=1 bb=1/> This line turns the side-chain (
                              chi) and backbone (bb) freedoms back on
                          <Span begin=119 end=120 chi=1 bb=1/> This line turns the side-chain (
                              chi) and backbone (bb) freedoms back on
                          <Span begin=133 end=138 chi=1 bb=1/> This line turns the side-chain (
                              chi) and backbone (bb) freedoms back on
                          <Span begin=154 end=159 chi=1 bb=0/> This line turns the side-chain (
                              chi) and backbone (bb) freedoms back on
                   </MoveMap>
            </FlxbbDesign>

      </MOVERS>
      <APPLY_TO_POSE>
      </APPLY_TO_POSE>
      <PROTOCOLS>
            <Add mover=des_hp/>
            <Add mover=des/>
      </PROTOCOLS>
</ROSETTASCRIPTS>
```

The contents of resfile_hp was:

```
NATRO
start
66 A NATAA     #ASN
68 A PIKAA GAVILWYFMP #SER
69 A PIKAA GAVILWYFMP #GLY
71 A NATAA     #ASN
```

```
85 A PIKAA GAVILWYFMP #ALA
86 A PIKAA GAVILWYFMP #ASP
87 A NATRO    #LEU
88 A PIKAA GAVILWYFMP #HIS
89 A PIKAA GAVILWYFMP #GLU
90 A PIKAA GAVILWYFMP #ALA
106 A PIKAA GAVILWYFMP
107 A PIKAA GAVILWYFMP
108 A PIKAA GAVILWYFMP
109 A PIKAA GAVILWYFMP
110 A PIKAA GAVILWYFMP
111 A PIKAA GAVILWYFMP
112 A PIKAA GAVILWYFMP
113 A PIKAA GAVILWYFMP
114 A PIKAA GAVILWYFMP
115 A PIKAA GAVILWYFMP
116 A PIKAA GAVILWYFMP
117 A PIKAA GAVILWYFMP
118 A PIKAA GAVILWYFMP
119 A PIKAA GAVILWYFMP
133 A PIKAA GAVILWYFMP #ALA
134 A PIKAA GAVILWYFMP #ASP
135 A NATRO   #LEU
136 A PIKAA GAVILWYFMP #GLN
137 A PIKAA GAVILWYFMP #GLY
138 A PIKAA GAVILWYFMP #ALA
154 A NATAA   #ASN
156 A PIKAA GAVILWYFMP #SER
157 A PIKAA GAVILWYFMP #GLU
159 A NATAA   #MET
```

and the contents of resfile was:

```
NATRO
start
66 A NATAA    #ASN
68 A NOTAA C  #SER
69 A NOTAA C  #GLY
71 A NATAA    #ASN
85 A NOTAA C  #ALA
86 A NOTAA C  #ASP
87 A NATRO    #LEU
88 A NOTAA C  #HIS
89 A NOTAA C  #GLU
90 A NOTAA C  #ALA
106 A NOTAA CFYILV
107 A NOTAA C
108 A NOTAA C
109 A NOTAA C
110 A NOTAA C
111 A NOTAA C
112 A NOTAA C
113 A NOTAA C
114 A NOTAA C
115 A NOTAA C
116 A NOTAA C
117 A NOTAA C
118 A NOTAA C
119 A NOTAA C
133 A NOTAA C #ALA
```

```
134 A NOTAA CFYILV    #ASP
135 A NATRO    #LEU
136 A NOTAA C  #GLN
137 A NOTAA C  #GLY
138 A NOTAA C  #ALA
154 A NATAA    #ASN
156 A NOTAA C  #SER
157 A NOTAA C  #GLU
159 A NATAA    #MET
```

This resulted in 4000 sequence designs for each of the 4000 loop conformations. Each of these designed sequences, seq_i, was threaded onto each of the 4000 conformations, $conf_j$. Each of the resulting 16,000,000 sequence-conformation combinations, $seq_i conf_j$, was energy minimised using the Rosetta FastRelax protocol with the permitted degrees of freedom being the side-chain and backbone of residues 66-71, 85-90, 105-120, 133-138, 154-159. The command line used was:

```
rosetta_scripts -database rosettadb -s input.pdb -use_input_sc -nstruct 1 -parser:protocol
    rosetta_script_relax.xml -parser:view -no_optH false
```

where the file rosetta_script_relax.xml contained :

```
<ROSETTASCRIPTS>
       <SCOREFXNS>
              <SFXN_relax weights=talaris2013>
              </SFXN_relax>
       </SCOREFXNS>
       <TASKOPERATIONS>
       </TASKOPERATIONS>
       <FILTERS>
       </FILTERS>
       <MOVERS>
              <FastRelax name=frel scorefxn=SFXN_relax repeats=8 >
                     <MoveMap>
                            <Chain number=1 chi=0 bb=0 /> Turns off all degrees of freedom for
                                chain A
                            <Span begin=66 end=71 chi=1 bb=0/> This line turns the side-chain (chi
                                ) and backbone (bb) freedoms back on
                            <Span begin=85 end=90 chi=1 bb=1/> This line turns the side-chain (chi
                                ) and backbone (bb) freedoms back on
                            <Span begin=105 end=106 chi=1 bb=1/> This line turns the side-chain (
                                chi) and backbone (bb) freedoms back on
                            <Span begin=107 end=118 chi=1 bb=1/> This line turns the side-chain (
                                chi) and backbone (bb) freedoms back on
                            <Span begin=119 end=120 chi=1 bb=1/> This line turns the side-chain (
                                chi) and backbone (bb) freedoms back on
                            <Span begin=133 end=138 chi=1 bb=1/> This line turns the side-chain (
                                chi) and backbone (bb) freedoms back on
                            <Span begin=154 end=159 chi=1 bb=0/> This line turns the side-chain (
                                chi) and backbone (bb) freedoms back on
                     </MoveMap>
              </FastRelax>
       </MOVERS>
       <APPLY_TO_POSE>
       </APPLY_TO_POSE>
       <PROTOCOLS>
              <Add mover=frel/>
       </PROTOCOLS>
</ROSETTASCRIPTS>
```

For each design, the full-atom RMSD between the designed structure, $seq_i conf_i$, and each of the threaded sequence-conformation combinations, $seq_i conf_j$ was recorded together with the corresponding minimised po-

tential energies, $E_i(j)$. This resulted in 4000×4000 RMSD/energy pairs (Fig. S7). The full-atom RMSD was calculated for residues 105-120 without superposition. Assuming the loops follow the Boltzmann distribution, these calculations permitted the ranking of each design by explicitly considering alternative low energy conformational states using equation (3).

$$P_i = \frac{\sum\limits_{j \in F} e^{-\frac{E_i(j)}{k_B T}}}{\sum\limits_{j=1}^{N} e^{-\frac{E_i(j)}{k_B T}}} \tag{3}$$

where P_i was the probability of the designed loop, i, being in the desired folded conformation, $E_i(j)$ was the gradient minimised energy of sequence i on structure j, F was the set of correctly folded loops (defined as less than 1 Å RMSD from the designed structure), N was 4000 (i.e. all 4000 conformations) and k_BT was set to 0.8 [22].

A list of 10 designs (t754, t801, t1117, t1166, t1428, t1555, t1916, t2570, t3280 and t3284) was selected for experimental characterisation by picking structures with $P_i > 0.9$, the lowest folded loop energy less than the mean lowest folded loop energy (< -324.8) Rosetta Energy Units (REU), the energy gap lowest energy 1 Å RMSD and the lowest energy 2 Å RMSD loop < -2 REU, RosettaHoles score < 2.3 [23,24], and structures with no residues in forbidden regions of the Ramachandran plot.

1.8 Production of figures

The logo plot in Fig. 1 was produced using WebLogo [25]. All molecular images were produced using PyMOL [26]. Other figures were produced using R [13].

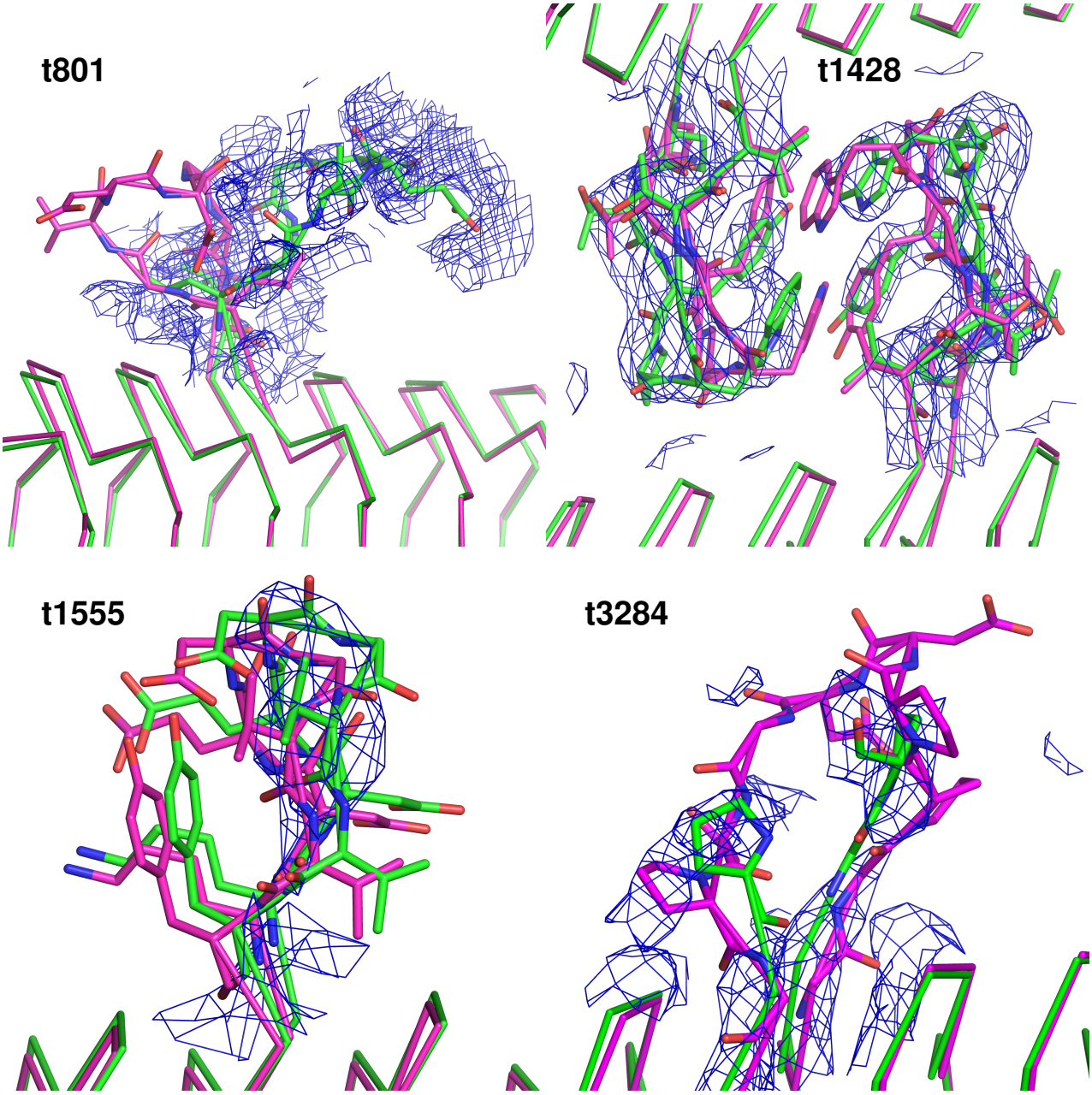

Figure S1: 2mFo-dFc maps contoured at 1σ after molecular replacement with the predicted models with the loop removed, and shown with the full predicted model in magenta and in green the final refined model.

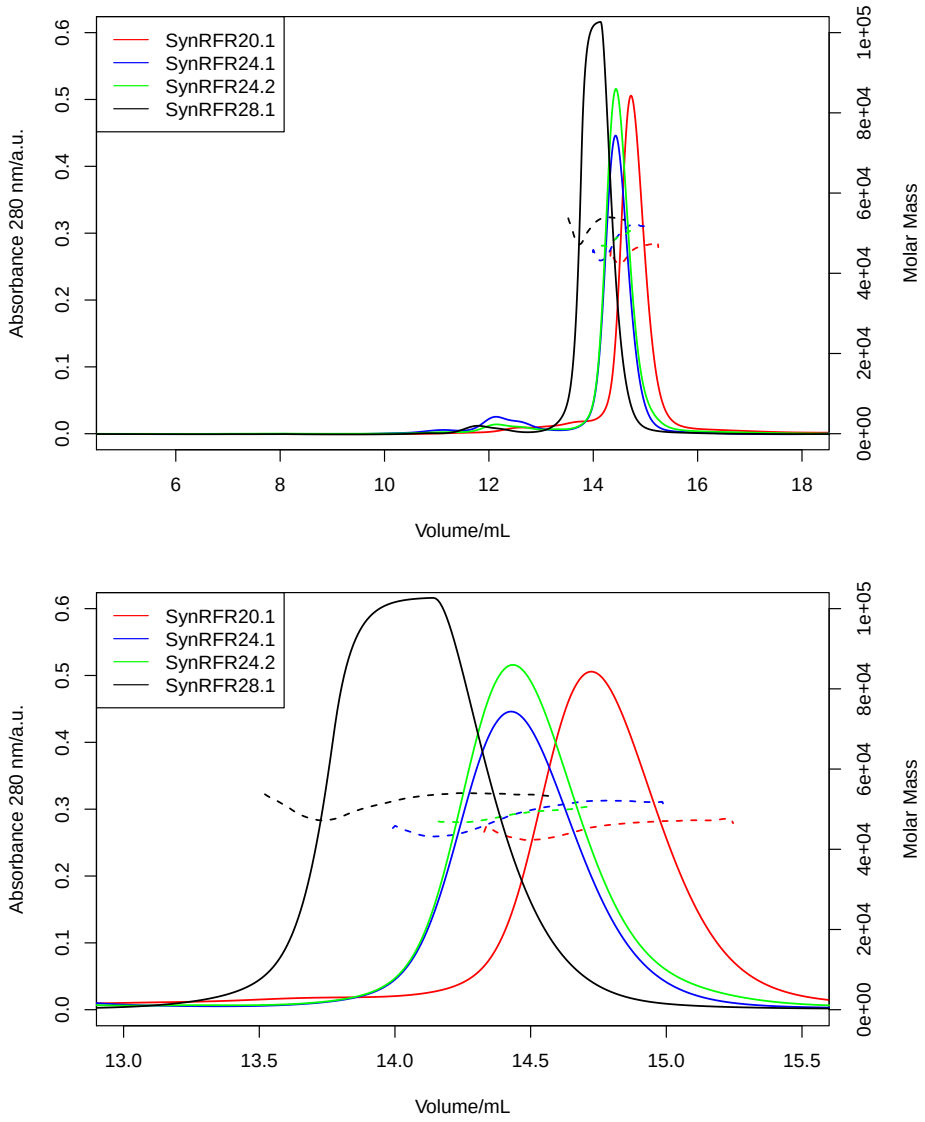

Figure S2: SynRFR length variant SEC-MALS. The lower plot is a zoomed-in plot of the same data shown in the upper plot. The dotted lines show MALS estimated molar masses, the solid lines show UV absorbance.

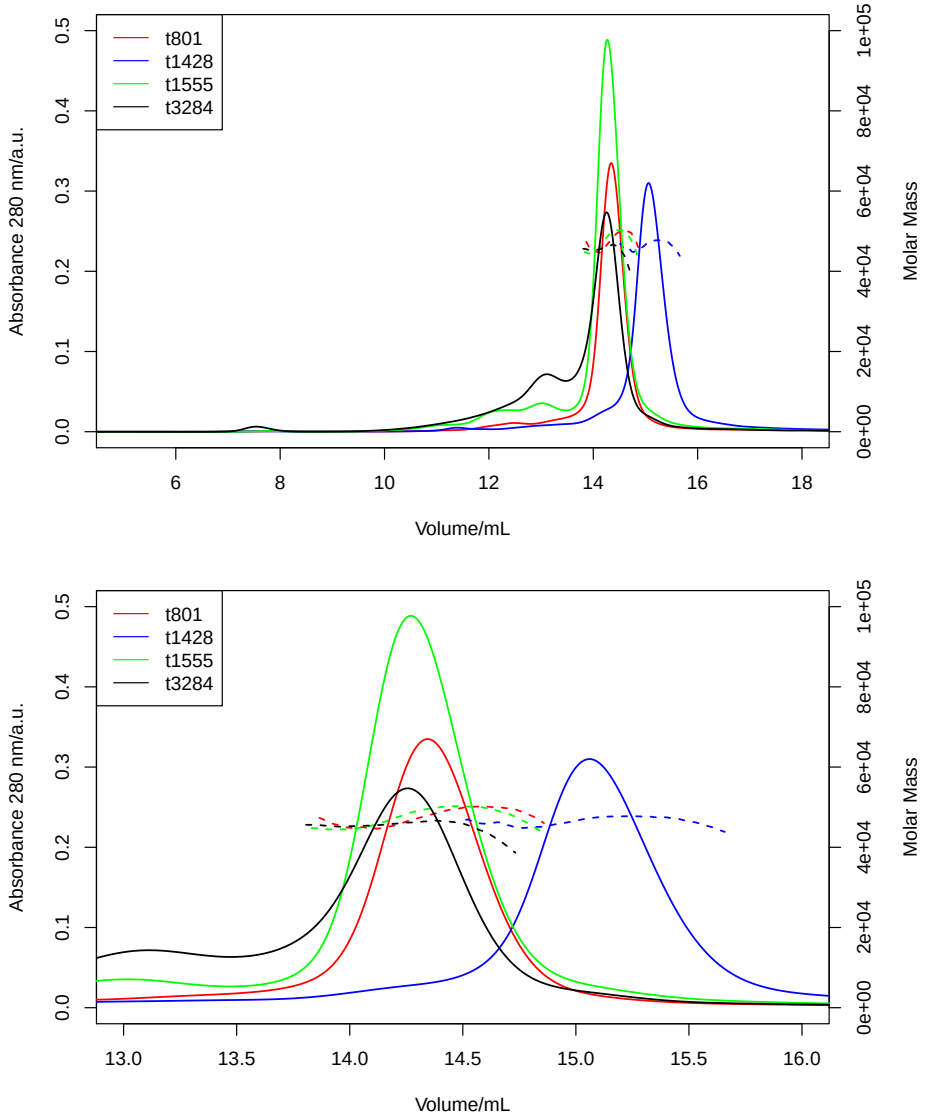

Figure S3: SynRFR loop variant SEC-MALS. The lower plot is a zoomed-in plot of the same data shown in the upper plot. The dotted lines show MALS estimated molar masses, the solid lines show UV absorbance.

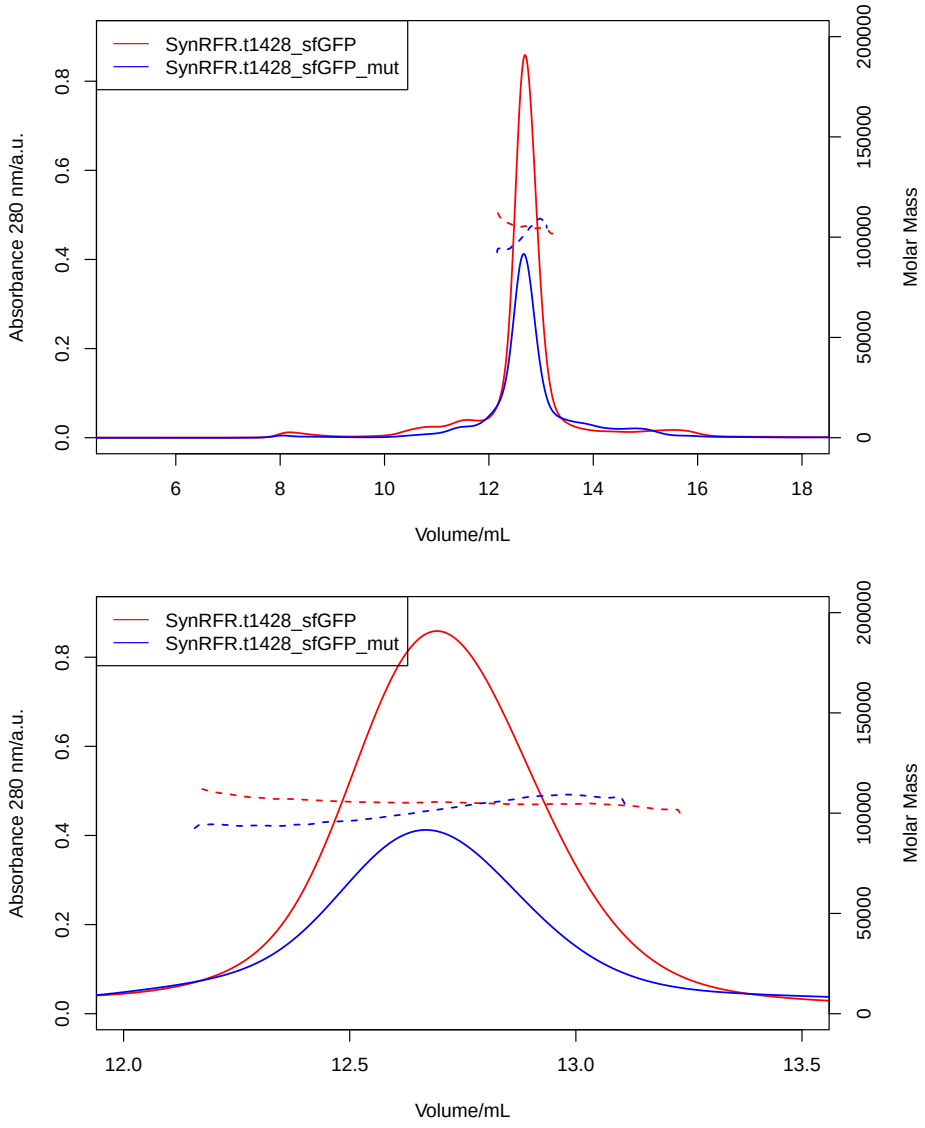

Figure S4: SynRFR sfGFP variant SEC-MALS. The lower plot is a zoomed-in plot of the same data shown in the upper plot. The dotted lines show MALS estimated molar masses, the solid lines show UV absorbance.

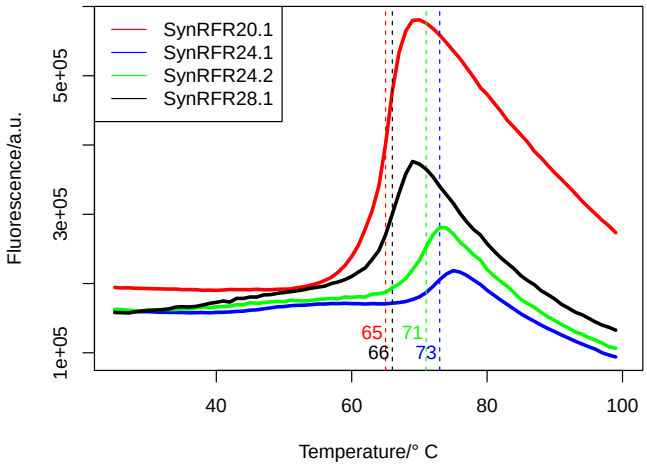

Figure S5: SynRFR length variant thermofluor melting curves. Dotted vertical lines show estimated melting temperatures.

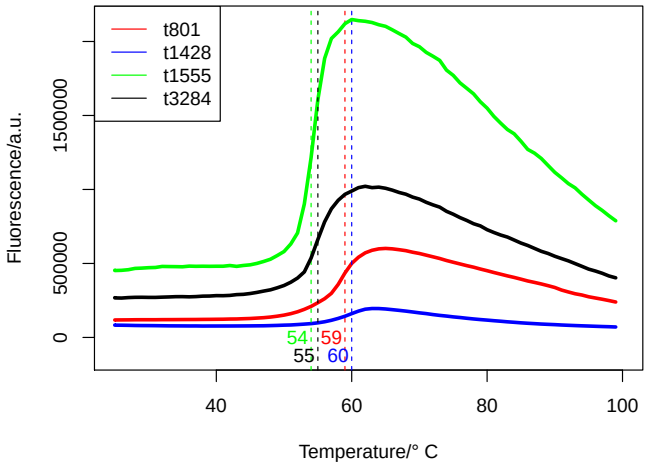

Figure S6: SynRFR loop variant thermofluor melting curves. Dotted vertical lines show estimated melting temperatures.

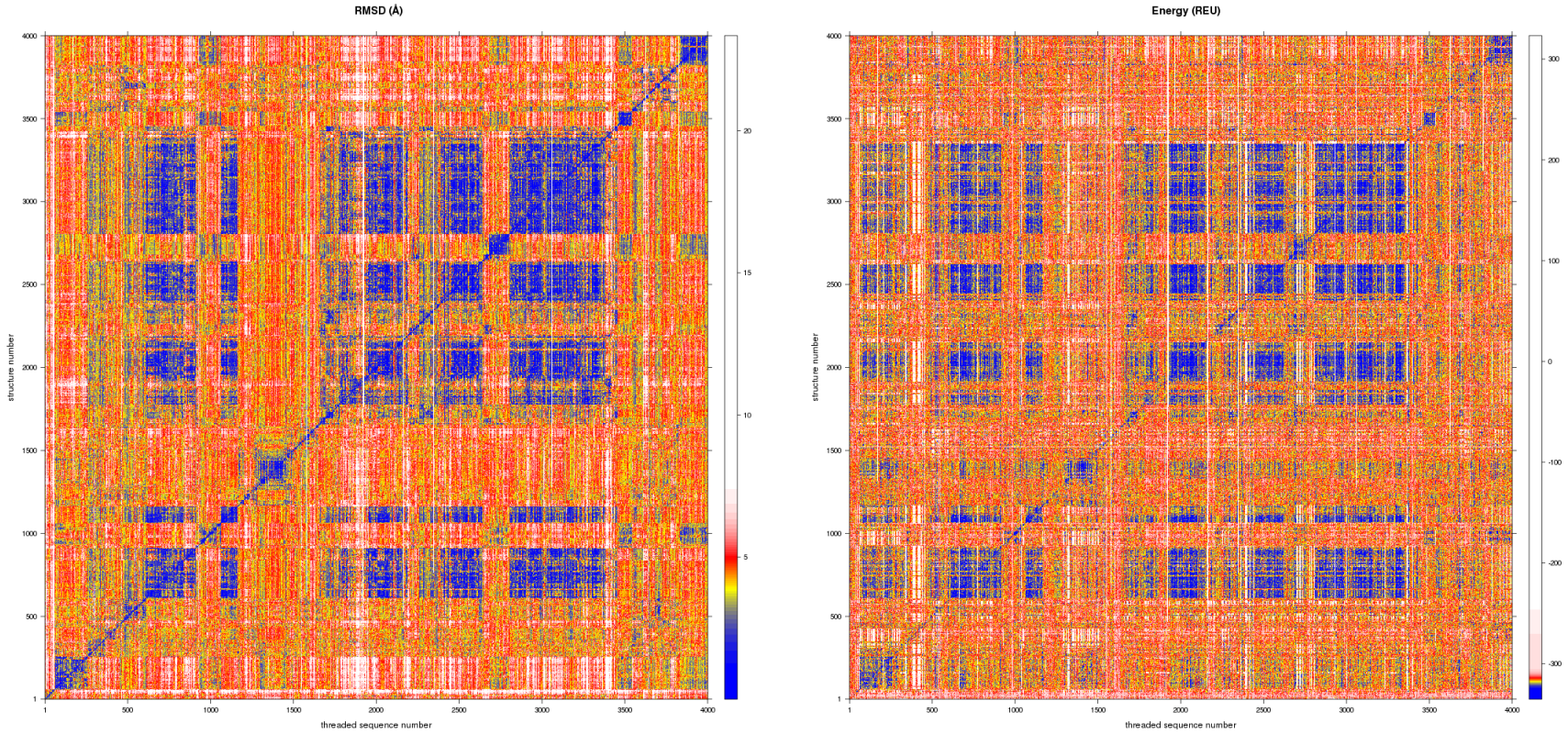

Figure S7: The designed sequence for each loop conformation was threaded onto all 4000 sampled loop structures and energy minimised. The resulting energies and all-atom loop RMSDs (to the designed loop structure) values were recorded giving the two 4000×4000 matrices shown here (a subset of these matrices is shown in Fig. 2b). These values were used to select designs using equation 3. Good designs have low RMSD values and low energy values (i.e. blue coloured elements on both matrices) producing funnel shaped plots as in Fig. 2c.

PDB code	4YC5	4YDT	4YCQ	4YEI	4YFO	5DZB	5DRA	5DN0	5DNS	5DQA	5DI5
Protein	SynRFR24.1	SynRFR24.1	SynRFR24.1	SynRFR24.2	SynRFR28.1	SynRFR28.1	SysRFR20.1	syn-RFR24.t1555	syn-RFR24.t1428	syn-RFR24.t3284	syn-RFR24.t801
Crystallization condition	0.1M Bis Tris pH 5.5, 3.0 M sodium chloride	160mM MgCl2, 80mM sodium cacodylate pH 6.5, 40% v/v PEG200	0.1 M CAPS pH 10.5, 40% (v/v) MPD	80 mM MES pH 6.5, 128 mM magnesium sulfate	90 mM Bis Tris pH 5.5, 2.7M sodium chloride	20% v/v 1,4 butanediol, HEPES pH 7.5, 0.2 M sodium chloride	1.1 M sodium acetate pH 4.6	30% v/v glycerol, 1.26 M ammonium dihydrogen phosphate pH 7	0.2 M sodium bromide, 20% w/v PEG 3350	0.1M MES pH 6.5, 1.6 M magnesium sulfate	0.2 M ammonium acetate, 0.1 M Bis Tris pH 5.5, 45% v/v MPD
Beamline	I02 Diamond Light Source	I02 Diamond Light Source	I02 Diamond Light Source	Rotating anode Rigaku Micromax-007 HF	I04-1 Diamond Light Source	I03 Diamond Light Source	I04-1 Diamond Light Source	I03 Diamond Light Source	I03 Diamond Light Source	I04 Diamond Light Source	I02 Diamond Light Source
Data set											
Wavelength	1.0403	1.0403	1.0403	1.54187	0.92	0.97625	0.92	0.97625	0.98	0.9184	0.97949
Space group	P 41 22	H 3 2	P 32 2 1	I 2 2 2	H 3 2	P 21 21 21	P 43 21 2	I 41 2 2	P 32 2 1	I 2 2 2	P 32 2 1
a,b,c (Å)	64.57, 64.57, 160.40	102.37, 102.37, 290.43	125.42, 125,42, 47.920	110.360, 115.960, 164.120	105.180, 105.180, 323.500	56.960, 86.530, 362.320	48.340, 48.340, 221.390	108.270, 108.270, 151.090	104.570, 104.570, 87.480	106.060, 115.710, 167.890	123.460, 123.460, 47.830
alpha beta gamma (°)	90, 90, 90	90, 90, 120	90, 90, 120	90, 90, 90	90, 90, 120	90.00, 90.00, 90.00	90.00, 90.00, 90.00	90.00, 90.00, 90.00	90.000, 90.000, 120.000	90.00, 90.00, 90.00	90.00, 90.00, 120.00
Resolution range	1.75-64.57 (1.75-1.80)	3.31-75.67 (3.31-40)	2.40-41.05 (2.40-2.47)	3.55-37.43 (3.55-3.65)	3.39-107.83 (3.39-3.48)	3.33-90.58 (3.33-3.42)	3.00-48.45 (3.00-3.08)	4.4-88.01 (4.4-51)	3.56-90.56 (3.56-3.65)	3.27-53.03 (3.27-3.35)	2.28-106.92 (2.28-2.34)
Total No. of reflections	484386 (35936)	66355 (5031)	180900 (14236)	59261 (4311)	94918 (6336)	355691 (26271)	71035 (10024)	25067 (1789)	135484 (10480)	108278 (8156)	214194 (15798)
No. of unique reflections	34852 (2523)	8605 (635)	16977 (1250)	12716 (920)	9607 (695)	27106 (1928)	5854 (413)	3058 (226)	6918 (520)	16280 (1180)	19284 (1374)
Completeness (%)	99.7 (99.9)	94.8 (96.9)	99.19 (99.02)	98.0 (98.0)	96.8 (98.9)	99.2 (99.4)	98.8 (98.8)	99.3 (99.3)	99.9 (100)	99.6 (99.9)	99.5 (98.6)
Multiplicity	13.9 (14.2)	7.71 (7.9)	10.66 (11.39)	4.7 (4.7)	9.9 (9.1)	13.1 (13.6)	7.1 (6.8)	8.2 (7.9)	19.6 (20.2)	6.7 (6.9)	11.1 (11.5)
<I/sigma(I)>	22.4 (3.9)	5.23 (1.08)	5.79 (3.01)	10.6 (2.1)	14.3 (4.3)	15.7 (4.0)	14.06	10.65 (3.6)	28.0 (5.0)	19.0 (2.7)	15.2 (1.8)
Rmerge	0.099 (0.777)	0.16 (0.95)	0.087 (0.91)	0.144 (0.921)	0.123 (0.55)	0.11 (0.628)	0.038 (0.106)	0.088 (0.551)	0.101 (0.863)	0.062 (0.670)	0.107 (1.449)
Wilson B (Å**2)	15.7	74.7	47.2	60.4	89.8	64.6	53.6	145.2	91.1	91.9	45
Refinement											
% test set	5.03	4.7	5.06	4.9	4.8	5.03	4.38	5.17	4.92	5.22	4.77
No. of reflections, test set	1750	405	857	623	478	1350	250	150	327	807	919
Final R cryst	0.158	0.255	0.171	0.218	0.196	0.197	0.25	0.254	0.183	0.183	0.178
Final R free	0.184	0.303	0.208	0.245	0.233	0.265	0.306	0.33	0.285	0.211	0.1875
No. of non-H atoms	1874	3186	1363	4770	1702	20212	1416	1615	3085	4709	1388
Protein	1599	3186	1333	4770	1702	10212	1416	1615	3085	4709	1369
Water	273	0	30	0	0	0	0	0	0	0	19
Ion	2	0	0	0	0	0	0	0	0	0	0
Ligand	0	0	0	0	0	0	0	0	0	0	0
R.m.s. deviations											
Bonds (Å)	0.006	0.014	0.007	0.016	0.022	0.009	0.011	0.014	0.002	0.019	0.007
Angles (°)	0.981	1.564	0.963	1.617	2.522	1.425	1.446	1.564	0.547	1.972	1.408
Average B factor, all atoms (Å **2)	20	91.9	55	106	113	98	70	206	103	118	56
Ramachandran plot											
Most favoured (%)	100	100	98.35	99.69	94.81	98	95.74	98.17	94.03	94.1	98.41
Outliers(%)	0	0	0	0	1.73	0	0	0	1	0.63	0

Table S1: Crystallization, Data Collection and Refinement information for structures determined in this study

Residue	Position 1	Position 2	Position 3	Position 4	Position 5
A	1.0000	0.0154	0.0000	0.0154	0.0462
C	0.0000	0.0154	0.0000	0.0308	0.0000
D	0.0000	0.2923	0.0000	0.0615	0.0462
E	0.0000	0.0308	0.0000	0.1231	0.1538
F	0.0000	0.0000	0.0000	0.0154	0.0000
G	0.0000	0.0000	0.0000	0.0154	0.3077
H	0.0000	0.0000	0.0000	0.0615	0.0462
I	0.0000	0.1385	0.0000	0.0154	0.0154
K	0.0000	0.0308	0.0000	0.0462	0.0769
L	0.0000	0.0308	1.0000	0.0000	0.0000
M	0.0000	0.0154	0.0000	0.0000	0.0000
N	0.0000	0.2923	0.0000	0.0462	0.0462
P	0.0000	0.0000	0.0000	0.0000	0.0000
Q	0.0000	0.0000	0.0000	0.0615	0.1077
R	0.0000	0.0308	0.0000	0.1231	0.0769
S	0.0000	0.0615	0.0000	0.2462	0.0308
T	0.0000	0.0154	0.0000	0.0923	0.0000
V	0.0000	0.0308	0.0000	0.0154	0.0000
W	0.0000	0.0000	0.0000	0.0154	0.0000
Y	0.0000	0.0000	0.0000	0.0154	0.0462

Table S2: RFR residue frequency table derived from 65 RFR 5-residue repeats

Protein name	**Amino acid sequence**	**ORF sequence**
synRFR24.1 (beta1)	MGSSHHHHHHSS GLVPRGSHMNV GEILRHYAAGKR NFQHINLQEIELT NASLTGADLSYA NLHHANLSRANL RSADLRNANLSH ANLSGANLEEAN LEAANLRGADL HEANLSGADLQE ANLTQANLKDA NLSDANLEQADL AGADLQGAVLD GANLHGANLNN ANLSEAMLTRA NLEQADLSGART TGARLDDADLR GATVDPVLWRT ASLVGARVDVD QAVAFAAAHGL CLAGGSGC	ATGGGTAGCAGCCATCATCATCATCACCATAGCA GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA CGCAATTTTCAGCATATTAACCTGCAAGAAATTG AACTGACCAATGCAAGCCTGACCGGTGCCGATCT GAGCTATGCAAATCTGCATCATGCAAATCTGAGC CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG CCAATCTGTCACATGCGAATCTGTCAGGTGCAAA TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG CGTGGTGCGGATCTGCATGAAGCGAATCTGAGTG GCGCTGATCTGCAAGAGGCAAATCTGACCCAGGC GAACCTGAAAGATGCTAATCTGTCTGATGCCAAC CTGGAACAGGCAGATCTGGCAGGGGCTGATCTGC AGGGTGCAGTTCTGGACGGTGCTAATCTGCATGG CGCAAATCTGAATAATGCGAACCTGAGCGAAGCA ATGCTGACCCGTGCGAATCTGGAGCAGGCCGACC TGAGCGGTGCACGTACCACCGGTGCACGTCTGGA TGATGCCGACCTGCGTGGTGCAACCGTTGATCCG GTTCTGTGGCGTACCGCAAGCCTGGTTGGTGCAC GTGTTGATGTTGATCAGGCAGTTGCATTTGCAGC AGCACATGGTCTGTGTCTGGCAGGTGGATCCGGC TGCTAA
synRFR24.2 (beta1mut)	MGSSHHHHHHSS GLVPRGSHMNV GEILRHYAAGKR NFQHINLQEIELT NASLTGADLSYA NLHHANLSRANL RSADLRNANLSH ANLSGANLEEAN LEAANLRGADL HEANLSGADLQE ANLTQANLKDA NLSDANLEQADL AGADLQGAVLD GANLHGANLNN ANLSEAMLTRA NLEQADLSGART TGARLDDASLH GATVDPVLWRT ASLVGARVDVD QAVAFAAAHGL CLAGGSGC	ATGGGTAGCAGCCATCATCATCATCACCATAGCA GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA CGCAATTTTCAGCATATTAACCTGCAAGAAATTG AACTGACCAATGCAAGCCTGACCGGTGCCGATCT GAGCTATGCAAATCTGCATCATGCAAATCTGAGC CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG CCAATCTGTCACATGCGAATCTGTCAGGTGCAAA TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG CGTGGTGCGGATCTGCATGAAGCGAATCTGAGTG GCGCTGATCTGCAAGAGGCAAATCTGACCCAGGC GAACCTGAAAGATGCTAATCTGTCTGATGCCAAC CTGGAACAGGCAGATCTGGCAGGGGCTGATCTGC AGGGTGCAGTTCTGGACGGTGCTAATCTGCATGG CGCAAATCTGAATAATGCGAACCTGAGCGAAGCA ATGCTGACCCGTGCGAATCTGGAGCAGGCCGACC TGAGCGGTGCACGTACCACCGGTGCACGTCTGGA TGATGCTAGCCTCCATGGTGCAACCGTTGATCCG GTTCTGTGGCGTACCGCAAGCCTGGTTGGTGCAC GTGTTGATGTTGATCAGGCAGTTGCATTTGCAGC AGCACATGGTCTGTGTCTGGCAGGTGGATCCGGC TGCTAA

synRFR20.1	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
(3beta1)	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIELT	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	NASLTGADLSYA	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	NLHHANLSRANL	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	RSADLRNANLSH	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	ANLSGANLEEAN	CCAATCTGTCACATGCGAATCTGTCAGGTGCAAA
	LEAANLRGADL	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	HEANLSGADLQE	CGTGGTGCGGATCTGCATGAAGCGAATCTGAGTG
	ANLTQANLKDA	GCGCTGATCTGCAAGAGGCAAATCTGACCCAGGC
	NLSDANLEQANL	GAACCTGAAAGATGCTAATCTGTCTGATGCCAAC
	NNANLSEAMLT	CTGGAACAGGCAAATCTGAATAATGCGAACCTGA
	RANLEQADLSG	GCGAAGCAATGCTGACCCGTGCGAATCTGGAGCA
	ARTTGARLDDA	GGCCGACCTGAGCGGTGCACGTACCACCGGTGCA
	DLRGATVDPVL	CGTCTGGATGATGCCGACCTGCGTGGTGCAACCG
	WRTASLVGARV	TTGATCCGGTTCTGTGGCGTACCGCAAGCCTGGT
	DVDQAVAFAAA	TGGTGCACGTGTTGATGTTGATCAGGCAGTTGCA
	HGLCLAGGSGC	TTTGCAGCAGCACATGGTCTGTGTCTGGCAGGTG
		GATCCGGCTGCTAA
synRFR28.1	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
(6beta1)	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIELT	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	NASLTGADLSYA	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	NLHHANLSRANL	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	RSADLRNANLSH	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	ANLSGANLEEAN	CCAATCTGTCACATGCGAATCTGTCAGGTGCAAA
	LEAANLRGADL	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	HEANLSGADLQE	CGTGGTGCGGATCTGCATGAAGCGAATCTGAGTG
	ANLTQANLKDA	GCGCTGATCTGCAAGAGGCAAATCTGACCCAGGC
	NLSDANLEQADL	GAACCTGAAAGATGCTAATCTGTCTGATGCCAAC
	AGADLQGAVLD	CTGGAACAGGCAGATCTGGCAGGGGCTGATCTGC
	GANLHGADLNG	AGGGTGCAGTTCTGGACGGTGCTAATCTGCATGG
	ADLKQADLSGA	CGCGGACCTCAACGGTGCCGATTTAAAACAGGCT
	DLGGANLNNAN	GATTTATCTGGAGCAGATTTAGGTGGCGCAAATC
	LSEAMLTRANLE	TGAATAATGCGAACCTGAGCGAAGCAATGCTGAC
	QADLSGARTTG	CCGTGCGAATCTGGAGCAGGCCGACCTGAGCGGT
	ARLDDADLRGA	GCACGTACCACCGGTGCACGTCTGGATGATGCCG
	TVDPVLWRTAS	ACCTGCGTGGTGCAACCGTTGATCCGGTTCTGTG
	LVGARVDVDQA	GCGTACCGCAAGCCTGGTTGGTGCACGTGTTGAT
	VAFAAAHGLCL	GTTGATCAGGCAGTTGCATTTGCAGCAGCACATG
	AGGSGC	GTCTGTGTCTGGCAGGTGGATCCGGCTGCTAA

synRFR24.t754	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIELT	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	NASLTGADLSYA	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	NLHHANLSRAN	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	LRSADLRNANLS	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	HANLKGANLEE	CCAATCTGTCACATGCGAATCTGAAAGGTGCAAA
	ANLEAANLRGA	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	NLAGANLSGADL	CGTGGTGCGAACCTGGCGGGCGCGAATCTGAGT
	QEANLTQAQLG	GGCGCTGATCTGCAAGAGGCAAATCTGACCCAGG
	GWSDNGETGAD	CGCAGCTGGGCGGCTGGAGCGATAACGGCGAAA
	LSDANLEQADLA	CCGGCGCTGATCTGTCTGATGCCAACCTGGAACA
	GADLYGAVLDG	GGCAGATCTGGCAGGGGCTGATCTGTATGGTGCA
	ANLHGANLNNA	GTTCTGGACGGTGCTAATCTGCATGGCGCAAATC
	NLDNAMLTRAN	TGAATAATGCGAACCTGGATAACGCAATGCTGAC
	LEQADLSGARTT	CCGTGCGAATCTGGAGCAGGCCGACCTGAGCGGT
	GARLDDADLRG	GCACGTACCACCGGTGCACGTCTGGATGATGCCG
	ATVDPVLWRTA	ACCTGCGTGGTGCAACCGTTGATCCGGTTCTGTG
	SLVGARVDVDQ	GCGTACCGCAAGCCTGGTTGGTGCACGTGTTGAT
	AVAFAAAHGLC	GTTGATCAGGCAGTTGCATTTGCAGCAGCACATG
	LAGGSGC	GTCTGTGTCTGGCAGGTGGATCCGGCTGCTAA
synRFR24.t801	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIELT	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	NASLTGADLSYA	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	NLHHANLSRAN	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	LRSADLRNANLS	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	HANLRGANLEE	CCAATCTGTCACATGCGAATCTGCGCGGTGCAAA
	ANLEAANLRGA	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	DLIGANLSGADL	CGTGGTGCGGATCTGATTGGCGCGAATCTGAGTG
	QEANLTQAQLG	GCGCTGATCTGCAAGAGGCAAATCTGACCCAGGC
	LGVEDGGLGAD	GCAGCTGGGCCTGGGCGTGGAAGATGGCGGCCT
	LSDANLEQADLA	GGGCGCTGATCTGTCTGATGCCAACCTGGAACAG
	GANLAGAVLDG	GCAGATCTGGCAGGGGCTAACCTGGCGGGTGCA
	ANLHGANLNNA	GTTCTGGACGGTGCTAATCTGCATGGCGCAAATC
	NLDYAMLTRAN	TGAATAATGCGAACCTGGATTATGCAATGCTGAC
	LEQADLSGARTT	CCGTGCGAATCTGGAGCAGGCCGACCTGAGCGGT
	GARLDDADLRG	GCACGTACCACCGGTGCACGTCTGGATGATGCCG
	ATVDPVLWRTA	ACCTGCGTGGTGCAACCGTTGATCCGGTTCTGTG
	SLVGARVDVDQ	GCGTACCGCAAGCCTGGTTGGTGCACGTGTTGAT
	AVAFAAAHGLC	GTTGATCAGGCAGTTGCATTTGCAGCAGCACATG
	LAGGSGC	GTCTGTGTCTGGCAGGTGGATCCGGCTGCTAA

synRFR24.	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
t1117	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIELT	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	NASLTGADLSYA	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	NLHHANLSRAN	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	LRSADLRNANLS	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	HANLRGANLEE	CCAATCTGTCACATGCGAATCTGCGCGGTGCAAA
	ANLEAANLRGA	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	DLVGANLSGADL	CGTGGTGCGGATCTGGTGGGCGCGAATCTGAGT
	QEANLTQAQLG	GGCGCTGATCTGCAAGAGGCAAATCTGACCCAGG
	GVYRLGEPGAD	CGCAGCTGGGCGGCGTGTATCGCCTGGGCGAACC
	LSDANLEQADLA	GGGCGCTGATCTGTCTGATGCCAACCTGGAACAG
	GANLMGAVLDG	GCAGATCTGGCAGGGGCTAACCTGATGGGTGCA
	ANLHGANLNNA	GTTCTGGACGGTGCTAATCTGCATGGCGCAAATC
	NLDYAMLTRAN	TGAATAATGCGAACCTGGATTATGCAATGCTGAC
	LEQADLSGARTT	CCGTGCGAATCTGGAGCAGGCCGACCTGAGCGGT
	GARLDDADLRG	GCACGTACCACCGGTGCACGTCTGGATGATGCCG
	ATVDPVLWRTA	ACCTGCGTGGTGCAACCGTTGATCCGGTTCTGTG
	SLVGARVDVDQ	GCGTACCGCAAGCCTGGTTGGTGCACGTGTTGAT
	AVAFAAAHGLC	GTTGATCAGGCAGTTGCATTTGCAGCAGCACATG
	LAGGSGC	GTCTGTGTCTGGCAGGTGGATCCGGCTGCTAA
synRFR24.	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
t1166	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIELT	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	NASLTGADLSYA	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	NLHHANLSRANL	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	RSADLRNANLSH	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	ANLSGANLEEAN	CCAATCTGTCACATGCGAATCTGTCAGGTGCAAA
	LEAANLRGADL	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	RGANLSGADLQ	CGTGGTGCGGATCTGCGCGGCGCGAATCTGAGTG
	EANLTQAKLGT	GCGCTGATCTGCAAGAGGCAAATCTGACCCAGGC
	WSSSGLTGADLS	GAAACTGGGCACCTGGAGCAGCAGCGGCCTGACC
	DANLEQADLAG	GGCGCTGATCTGTCTGATGCCAACCTGGAACAGG
	ADLKGAVLDGA	CAGATCTGGCAGGGGCTGATCTGAAAGGTGCAGT
	NLHGANLNNAN	TCTGGACGGTGCTAATCTGCATGGCGCAAATCTG
	LDYAMLTRANL	AATAATGCGAACCTGGATTATGCAATGCTGACCC
	EQADLSGARTT	GTGCGAATCTGGAGCAGGCCGACCTGAGCGGTGC
	GARLDDADLRG	ACGTACCACCGGTGCACGTCTGGATGATGCCGAC
	ATVDPVLWRTA	CTGCGTGGTGCAACCGTTGATCCGGTTCTGTGGC
	SLVGARVDVDQ	GTACCGCAAGCCTGGTTGGTGCACGTGTTGATGT
	AVAFAAAHGLC	TGATCAGGCAGTTGCATTTGCAGCAGCACATGGT
	LAGGSGC	CTGTGTCTGGCAGGTGGATCCGGCTGCTAA

synRFR24.	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
t1428	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIEL	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	TNASLTGADLSY	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	ANLHHANLSRA	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	NLRSADLRNANL	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	SHANLSGANLEE	CCAATCTGTCACATGCGAATCTGTCAGGTGCAAA
	ANLEAANLRGA	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	NLVGANLSGADL	CGTGGTGCGAACCTGGTGGGCGCGAATCTGAGT
	QEANLTQAMLG	GGCGCTGATCTGCAAGAGGCAAATCTGACCCAGG
	QTYPWGTVGAD	CGATGCTGGGCCAGACCTATCCGTGGGGCACCGT
	LSDANLEQADLA	GGGCGCTGATCTGTCTGATGCCAACCTGGAACAG
	GAQLVGAVLDG	GCAGATCTGGCAGGGGCTCAGCTGGTGGGTGCA
	ANLHGANLNNA	GTTCTGGACGGTGCTAATCTGCATGGCGCAAATC
	NLDNAMLTRAN	TGAATAATGCGAACCTGGATAACGCAATGCTGAC
	LEQADLSGARTT	CCGTGCGAATCTGGAGCAGGCCGACCTGAGCGGT
	GARLDDADLRG	GCACGTACCACCGGTGCACGTCTGGATGATGCCG
	ATVDPVLWRTA	ACCTGCGTGGTGCAACCGTTGATCCGGTTCTGTG
	SLVGARVDVDQ	GCGTACCGCAAGCCTGGTTGGTGCACGTGTTGAT
	AVAFAAAHGLC	GTTGATCAGGCAGTTGCATTTGCAGCAGCACATG
	LAGGSGC	GTCTGTGTCTGGCAGGTGGATCCGGCTGCTAA
synRFR24.	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
t1555	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIEL	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	TNASLTGADLSY	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	ANLHHANLSRA	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	NLRSADLRNANL	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	SHANLSGANLEE	CCAATCTGTCACATGCGAATCTGTCAGGTGCAAA
	ANLEAANLRGA	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	DLAGANLSGADL	CGTGGTGCGGATCTGGCGGGCGCGAATCTGAGT
	QEANLTQAMLG	GGCGCTGATCTGCAAGAGGCAAATCTGACCCAGG
	KDEDGVVYGAD	CGATGCTGGGCAAAGATGAAGATGGCGTGGTGT
	LSDANLEQADLA	ATGGCGCTGATCTGTCTGATGCCAACCTGGAACA
	GAQLVGAVLDG	GGCAGATCTGGCAGGGGCTCAGCTGGTGGGTGC
	ANLHGANLNNA	AGTTCTGGACGGTGCTAATCTGCATGGCGCAAAT
	NLDNAMLTRAN	CTGAATAATGCGAACCTGGATAACGCAATGCTGA
	LEQADLSGARTT	CCCGTGCGAATCTGGAGCAGGCCGACCTGAGCGG
	GARLDDADLRG	TGCACGTACCACCGGTGCACGTCTGGATGATGCC
	ATVDPVLWRTA	GACCTGCGTGGTGCAACCGTTGATCCGGTTCTGT
	SLVGARVDVDQ	GGCGTACCGCAAGCCTGGTTGGTGCACGTGTTGA
	AVAFAAAHGLC	TGTTGATCAGGCAGTTGCATTTGCAGCAGCACAT
	LAGGSGC	GGTCTGTGTCTGGCAGGTGGATCCGGCTGCTAA

synRFR24.	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
t1916	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIELT	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	NASLTGADLSYA	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	NLHHANLSRANL	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	RSADLRNANLSH	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	ANLSGANLEEAN	CCAATCTGTCACATGCGAATCTGTCAGGTGCAAA
	LEAANLRGALLT	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	GANLSGADLQE	CGTGGTGCGCTGCTGACCGGCGCGAATCTGAGTG
	ANLTQAWLGRD	GCGCTGATCTGCAAGAGGCAAATCTGACCCAGGC
	PRLGLSGADLSD	GTGGCTGGGCCGCGATCCGCGCCTGGGCCTGAGC
	ANLEQADLAGA	GGCGCTGATCTGTCTGATGCCAACCTGGAACAGG
	QLKGAVLDGAN	CAGATCTGGCAGGGGCTCAGCTGAAAGGTGCAGT
	LHGANLNNANL	TCTGGACGGTGCTAATCTGCATGGCGCAAATCTG
	DNAMLTRANLE	AATAATGCGAACCTGGATAACGCAATGCTGACCC
	QADLSGARTTG	GTGCGAATCTGGAGCAGGCCGACCTGAGCGGTGC
	ARLDDADLRGA	ACGTACCACCGGTGCACGTCTGGATGATGCCGAC
	TVDPVLWRTAS	CTGCGTGGTGCAACCGTTGATCCGGTTCTGTGGC
	LVGARVDVDQA	GTACCGCAAGCCTGGTTGGTGCACGTGTTGATGT
	VAFAAAHGLCL	TGATCAGGCAGTTGCATTTGCAGCAGCACATGGT
	AGGSGC	CTGTGTCTGGCAGGTGGATCCGGCTGCTAA
synRFR24.	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
t2570	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIELT	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	NASLTGADLSYA	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	NLHHANLSRAN	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	LRSADLRNANLS	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	HANLKGANLEE	CCAATCTGTCACATGCGAATCTGAAAGGTGCAAA
	ANLEAANLRGA	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	NLAGANLSGADL	CGTGGTGCGAACCTGGCGGGCGCGAATCTGAGT
	QEANLTQADLG	GGCGCTGATCTGCAAGAGGCAAATCTGACCCAGG
	GPPDEGKTGAD	CGGATCTGGGCGGCCCGCCGGATGAAGGCAAAAC
	LSDANLEQADLA	CGGCGCTGATCTGTCTGATGCCAACCTGGAACAG
	GAQLYGAVLDG	GCAGATCTGGCAGGGGCTCAGCTGTATGGTGCAG
	ANLHGANLNNA	TTCTGGACGGTGCTAATCTGCATGGCGCAAATCT
	NLDYAMLTRAN	GAATAATGCGAACCTGGATTATGCAATGCTGACC
	LEQADLSGARTT	CGTGCGAATCTGGAGCAGGCCGACCTGAGCGGTG
	GARLDDADLRG	CACGTACCACCGGTGCACGTCTGGATGATGCCGA
	ATVDPVLWRTA	CCTGCGTGGTGCAACCGTTGATCCGGTTCTGTGG
	SLVGARVDVDQ	CGTACCGCAAGCCTGGTTGGTGCACGTGTTGATG
	AVAFAAAHGLC	TTGATCAGGCAGTTGCATTTGCAGCAGCACATGG
	LAGGSGC	TCTGTGTCTGGCAGGTGGATCCGGCTGCTAA

synRFR24.t3280	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIEL	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	TNASLTGADLSY	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	ANLHHANLSRA	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	NLRSADLRNANL	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	SHANLSGANLEE	CCAATCTGTCACATGCGAATCTGAGCGGTGCAAA
	ANLEAANLRGA	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	DLRGANLSGADL	CGTGGTGCGGATCTGCGCGGCGCGAATCTGAGTG
	QEANLTQAKLG	GCGCTGATCTGCAAGAGGCAAATCTGACCCAGGC
	GYDDEGLGGAD	GAAACTGGGCGGCTATGATGATGAAGGCCTGGG
	LSDANLEQADLA	CGGCGCTGATCTGTCTGATGCCAACCTGGAACAG
	GAELFGAVLDG	GCAGATCTGGCAGGGGCTGAACTGTTTGGTGCAG
	ANLHGANLNNA	TTCTGGACGGTGCTAATCTGCATGGCGCAAATCT
	NLDKAMLTRAN	GAATAATGCGAACCTGGATAAAGCAATGCTGACC
	LEQADLSGARTT	CGTGCGAATCTGGAGCAGGCCGACCTGAGCGGTG
	GARLDDADLRG	CACGTACCACCGGTGCACGTCTGGATGATGCCGA
	ATVDPVLWRTA	CCTGCGTGGTGCAACCGTTGATCCGGTTCTGTGG
	SLVGARVDVDQ	CGTACCGCAAGCCTGGTTGGTGCACGTGTTGATG
	AVAFAAAHGLC	TTGATCAGGCAGTTGCATTTGCAGCAGCACATGG
	LAGGSGC	TCTGTGTCTGGCAGGTGGATCCGGCTGCTAA
synRFR24.t3284	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIEL	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	TNASLTGADLSY	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	ANLHHANLSRA	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	NLRSADLRNANL	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	SHANLEGANLEE	CCAATCTGTCACATGCGAATCTGGAAGGTGCAAA
	ANLEAANLRGA	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	RLAGANLSGADL	CGTGGTGCGCGCCTGGCGGGCGCGAATCTGAGT
	QEANLTQANLG	GGCGCTGATCTGCAAGAGGCAAATCTGACCCAGG
	GPPDDGDPGAD	CGAACCTGGGCGGCCCGCCGGATGATGGCGATCC
	LSDANLEQADLA	GGGCGCTGATCTGTCTGATGCCAACCTGGAACAG
	GANLAGAVLDG	GCAGATCTGGCAGGGGCTAACCTGGCGGGTGCA
	ANLHGANLNNA	GTTCTGGACGGTGCTAATCTGCATGGCGCAAATC
	NLDNAMLTRAN	TGAATAATGCGAACCTGGATAACGCAATGCTGAC
	LEQADLSGARTT	CCGTGCGAATCTGGAGCAGGCCGACCTGAGCGGT
	GARLDDADLRG	GCACGTACCACCGGTGCACGTCTGGATGATGCCG
	ATVDPVLWRTA	ACCTGCGTGGTGCAACCGTTGATCCGGTTCTGTG
	SLVGARVDVDQ	GCGTACCGCAAGCCTGGTTGGTGCACGTGTTGAT
	AVAFAAAHGLC	GTTGATCAGGCAGTTGCATTTGCAGCAGCACATG
	LAGGSGC	GTCTGTGTCTGGCAGGTGGATCCGGCTGCTAA

synRFR24.	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
t1428_sfGFP	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIELT	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	NASLTGADLSYA	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	NLHHANLSRANL	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	RSADLRNANLSH	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	ANLSGANLEEAN	CCAATCTGTCACATGCGAATCTGTCAGGTGCAAA
	LEAANLRGANL	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	VGANLSGADLQ	CGTGGTGCGAACCTGGTGGGCGCGAATCTGAGT
	EANLTQAMLGQ	GGCGCTGATCTGCAAGAGGCAAATCTGACCCAGG
	TYPGGGGSMRK	CGATGCTGGGCCAGACCTATCCGGGAGGTGGAG
	GEELFTGVVPIL	GCTCAATGCGTAAAGGCGAAGAGCTGTTCACTGG
	VELDGDVNGHK	TGTCGTCCCTATTCTGGTGGAACTGGATGGTGAT
	FSVRGEGEGDA	GTCAACGGTCATAAGTTTTCCGTGCGTGGCGAGG
	TNGKLTLKFICT	GTGAAGGTGACGCAACTAATGGTAAACTGACGCT
	TGKLPVPWPTL	GAAGTTCATCTGTACTACTGGTAAACTGCCGGTA
	VTTLTYGVQCF	CCTTGGCCGACTCTGGTAACGACGCTGACTTATG
	ARYPDHMKQHD	GTGTTCAGTGCTTTGCTCGTTATCCGGACCATAT
	FFKSAMPEGYV	GAAGCAGCATGACTTCTTCAAGTCCGCCATGCCG
	QERTISFKDDGT	GAAGGCTATGTGCAGGAACGCACGATTTCCTTTA
	YKTRAEVKFEG	AGGATGACGGCACGTACAAAACGCGTGCGGAAG
	DTLVNRIELKGI	TGAAATTTGAAGGCGATACCCTGGTAAACCGCAT
	DFKEDGNILGHK	TGAGCTGAAAGGCATTGACTTTAAAGAAGACGGC
	LEYNFNSHNVYI	AATATCCTGGGCCATAAGCTGGAATACAATTTTA
	TADKQKNGIKA	ACAGCCACAATGTTTACATCACCGCCGATAAACA
	NFKIRHNVEDG	AAAAAATGGCATTAAAGCGAATTTTAAAATTCGC
	SVQLADHYQQN	CACAACGTGGAGGATGGCAGCGTGCAGCTGGCT
	TPIGDGPVLLPD	GATCACTACCAGCAAAACACTCCAATCGGTGATG
	NHYLSTQSVLSK	GTCCTGTTCTGCTGCCAGACAATCACTATCTGAG
	DPNEKRDHMVL	CACGCAAAGCGTTCTGTCTAAAGATCCGAACGAG
	LEFVTAAGITHG	AAACGCGATCATATGGTTCTGCTGGAGTTCGTAA
	MDELSGGGGWG	CCGCAGCGGGCATCACGCATGGTATGGATGAACT
	TVGADLSDANLE	GTCTGGAGGCGGTGGATGGGGCACCGTGGGCGC
	QADLAGAQLVG	TGATCTGTCTGATGCCAACCTGGAACAGGCAGAT
	AVLDGANLHGA	CTGGCAGGGGCTCAGCTGGTGGGTGCAGTTCTG
	NLNNANLDNAM	GACGGTGCTAATCTGCATGGCGCAAATCTGAATA
	LTRANLEQADLS	ATGCGAACCTGGATAACGCAATGCTGACCCGTGC
	GARTTGARLDD	GAATCTGGAGCAGGCCGACCTGAGCGGTGCACGT
	ADLRGATVDPV	ACCACCGGTGCACGTCTGGATGATGCCGACCTGC
	LWRTASLVGAR	GTGGTGCAACCGTTGATCCGGTTCTGTGGCGTAC
	VDVDQAVAFAA	CGCAAGCCTGGTTGGTGCACGTGTTGATGTTGAT
	AHGLCLAGGSG	CAGGCAGTTGCATTTGCAGCAGCACATGGTCTGT
	C	GTCTGGCAGGTGGATCCGGCTGCTAA

synRFR24.	MGSSHHHHHHSS	ATGGGTAGCAGCCATCATCATCATCACCATAGCA
t1428_sfGFP	GLVPRGSHMNV	GCGGTCTGGTTCCGCGTGGTAGCCACATGAATGT
_mut	GEILRHYAAGKR	TGGTGAAATTCTGCGTCATTATGCAGCAGGTAAA
	NFQHINLQEIELT	CGCAATTTTCAGCATATTAACCTGCAAGAAATTG
	NASLTGADLSYA	AACTGACCAATGCAAGCCTGACCGGTGCCGATCT
	NLHHANLSRANL	GAGCTATGCAAATCTGCATCATGCAAATCTGAGC
	RSADLRNANLSH	CGTGCCAATCTGCGTTCTGCAGACCTGCGTAATG
	ANLSGANLEEAN	CCAATCTGTCACATGCGAATCTGTCAGGTGCAAA
	LEAANLRGANL	TCTGGAAGAAGCCAATCTGGAAGCCGCTAATCTG
	VGANLSGADLQ	CGTGGTGCGAACCTGGTGGGCGCGAATCTGAGT
	EANLTQAMLGQ	GGCGCTGATCTGCAAGAGGCAAATCTGACCCAGG
	TYPGGGGSMRK	CGATGCTGGGCCAGACCTATCCGGGAGGTGGAG
	GEELFTGVVPIL	GCTCAATGCGTAAAGGCGAAGAGCTGTTCACTGG
	VELDGDVNGHK	TGTCGTCCCTATTCTGGTGGAACTGGATGGTGAT
	FSVRGEGEGDA	GTCAACGGTCATAAGTTTTCCGTGCGTGGCGAGG
	TNGKLTLKFICT	GTGAAGGTGACGCAACTAATGGTAAACTGACGCT
	TGKLPVPWPTL	GAAGTTCATCTGTACTACTGGTAAACTGCCGGTA
	VTTLTYGVQCF	CCTTGGCCGACTCTGGTAACGACGCTGACTTATG
	ARYPDHMKQHD	GTGTTCAGTGCTTTGCTCGTTATCCGGACCATAT
	FFKSAMPEGYV	GAAGCAGCATGACTTCTTCAAGTCCGCCATGCCG
	QERTISFKDDGT	GAAGGCTATGTGCAGGAACGCACGATTTCCTTTA
	YKTRAEVKFEG	AGGATGACGGCACGTACAAAACGCGTGCGGAAG
	DTLVNRIELKGI	TGAAATTTGAAGGCGATACCCTGGTAAACCGCAT
	DFKEDGNILGHK	TGAGCTGAAAGGCATTGACTTTAAAGAAGACGGC
	LEYNFNSHNVYI	AATATCCTGGGCCATAAGCTGGAATACAATTTTA
	TADKQKNGIKA	ACAGCCACAATGTTTACATCACCGCCGATAAACA
	NFKIRHNVEDG	AAAAAATGGCATTAAAGCGAATTTTAAAATTCGC
	SVQLADHYQQN	CACAACGTGGAGGATGGCAGCGTGCAGCTGGCT
	TPIGDGPVLLPD	GATCACTACCAGCAAAACACTCCAATCGGTGATG
	NHYLSTQSVLSK	GTCCTGTTCTGCTGCCAGACAATCACTATCTGAG
	DPNEKRDHMVL	CACGCAAAGCGTTCTGTCTAAAGATCCGAACGAG
	LEFVTAAGITHG	AAACGCGATCATATGGTTCTGCTGGAGTTCGTAA
	MDELSGGGGAG	CCGCAGCGGGCATCACGCATGGTATGGATGAACT
	TVGADLSDANLE	GTCTGGAGGCGGTGGAGCTGGCACCGTGGGCGC
	QADLAGAQLVG	TGATCTGTCTGATGCCAACCTGGAACAGGCAGAT
	AVLDGANLHGA	CTGGCAGGGGCTCAGCTGGTGGGTGCAGTTCTG
	NLNNANLDNAM	GACGGTGCTAATCTGCATGGCGCAAATCTGAATA
	LTRANLEQADLS	ATGCGAACCTGGATAACGCAATGCTGACCCGTGC
	GARTTGARLDD	GAATCTGGAGCAGGCCGACCTGAGCGGTGCACGT
	ADLRGATVDPV	ACCACCGGTGCACGTCTGGATGATGCCGACCTGC
	LWRTASLVGAR	GTGGTGCAACCGTTGATCCGGTTCTGTGGCGTAC
	VDVDQAVAFAA	CGCAAGCCTGGTTGGTGCACGTGTTGATGTTGAT
	AHGLCLAGGSG	CAGGCAGTTGCATTTGCAGCAGCACATGGTCTGT
	C	GTCTGGCAGGTGGATCCGGCTGCTAA

Table S3: Open reading frame and corresponding primary protein sequences created for this study

Primer	Sequence	Notes
synRFR_del120_139_gib_REV	ATTATTCAGATTTGCCTGTTCCAGGTTGGCATCAGACAG	Used to create synRFR20.1 from synRFR24.1 by deleting one turn
synRFR_del120_139_gib_FOR	GCCAACCTGGAACAGGCAAATCTGAATAATGCGAACCTGAGC	Used to create synRFR20.1 from synRFR24.1 by deleting one turn
synRFR_ins20_restrict_REV	CCTTAAAGTTATAAATCGGCACCGTTGAGGTCCGCGCCATGCAGATTAGCACCGTCC	Used to create synRFR28.1 from synRFR24.1 by inserting one turn
synRFR_ins20_restrict_FOR	CCTTAAAGGTTTAAACAGGCTGATTTATCTGGAGCAGATTTAGGTGGCGCAAATCTGAATAATGCGAACCTGAGC	Used to create synRFR28.1 from synRFR24.1 by inserting one turn
synRFR_loop_prep_FOR	GCAATGCTGACCCGTGCG	Used to PCR linearise synRFR24.1 plasmid in preparation for gBlock loop inserts
synRFR_loop_prep_REV	CAGATTCGCATGTGACAGATTG	Used to PCR linearise synRFR24.1 plasmid in preparation for gBlock loop inserts
synRFR_mut2_FOR	TATGATGCTAGCGCCGATCTGAGCTATGC	Used to carry out D196S and R198H mutations on synRFR24.1 to create synRFR24.2
synRFR_mut2_REV	GTGCGCCCATGGAGGTCGGCATCATCCAGAC	Used to carry out D196S and R198H mutations on synRFR24.1 to create synRFR24.2
t1428_GFP_FOR	TGGGGCACCGTGGGCGCTGATCTGTCTGAT	Used to linearise the synRFR24.t1428 plasmid for sfGFP insertion to create synRFR24.t1428_GFP
t1428_GFP_REV	CGGATAGGTCTGGCCCAGCATCGCCTGGGT	Used to linearise the synRFR24.t1428 plasmid for sfGFP insertion to create synRFR24.t1428_GFP
t1428_W113A_GFP_FOR	GCTGGCACCGTGGGCGCTGATCTGTCTGAT	Used to linearise the synRFR24.t1428 plasmid for sfGFP insertion to create synRFR24.t1428_GFP_mut
sfGFP_FOR	GGCGATGCTGGGCCAGACCTATCCGGGAGGTGGAGGCTCAATGCGTAAAGGCGAAGAGCTGTTCA	Used to create sfGFP part for insertion into synRFR24.t1428 to create synRFR24.t1428_GFP and synRFR24.t1428_GFP_mut

sfGFP_REV	ACAGATCAGCGCCCACGGTGCC CCATCCACCGCCTCCAGACAGTT CATCCATACCATGCGTGATG	Used to create sfGFP part for insertion into synRFR24.t1428 to create synRFR24.t1428_GFP
sfGFP_W113A_REV	ACAGATCAGCGCCCACGGTGCC AGCTCCACCGCCTCCAGACAGTT CATCCATACCATGCGTGATG	Used to create sfGFP part for insertion into synRFR24.t1428 to create synRFR24.t1428_GFP_mut
Eurofins T7 sequencing primer	TAATACGACTCACTATAGG	Sequencing primer
Eurofins T7 terminator sequencing primer	CTAGTTATTGCTCAGCGGT	Sequencing primer

Table S4: Oligonucleotide primers used in this study

gBlock	Sequence
t754	TCACATGCGAATCTGAAAGGTGCAAATCTGGAAGAAGCCAATCTG GAAGCCGCTAATCTGCGTGGTGCGAACCTGGCGGGCGCGAATCTG AGTGGCGCTGATCTGCAAGAGGCAAATCTGACCCAGGCGCAGCTG GGCGGCTGGAGCGATAACGGCGAAACCGGCGCTGATCTGTCTGAT GCCAACCTGGAACAGGCAGATCTGGCAGGGGCTGATCTGTATGGT GCAGTTCTGGACGGTGCTAATCTGCATGGCGCAAATCTGAATAAT GCGAACCTGGATAACGCAATGCTGACCCGT
t801	TCACATGCGAATCTGCGCGGTGCAAATCTGGAAGAAGCCAATCTG GAAGCCGCTAATCTGCGTGGTGCGGATCTGATTGGCGCGAATCTG AGTGGCGCTGATCTGCAAGAGGCAAATCTGACCCAGGCGCAGCTG GGCCTGGGCGTGGAAGATGGCGGCCTGGGCGCTGATCTGTCTGAT GCCAACCTGGAACAGGCAGATCTGGCAGGGGCTAACCTGGCGGGT GCAGTTCTGGACGGTGCTAATCTGCATGGCGCAAATCTGAATAAT GCGAACCTGGATTATGCAATGCTGACCCGT
t1117	TCACATGCGAATCTGCGCGGTGCAAATCTGGAAGAAGCCAATCTG GAAGCCGCTAATCTGCGTGGTGCGGATCTGGTGGGCGCGAATCTG AGTGGCGCTGATCTGCAAGAGGCAAATCTGACCCAGGCGCAGCTG GGCGGCGTGTATCGCCTGGGCGAACCGGGCGCTGATCTGTCTGAT GCCAACCTGGAACAGGCAGATCTGGCAGGGGCTAACCTGATGGGT GCAGTTCTGGACGGTGCTAATCTGCATGGCGCAAATCTGAATAAT GCGAACCTGGATTATGCAATGCTGACCCGT
t1166	TCACATGCGAATCTGTCAGGTGCAAATCTGGAAGAAGCCAATCTG GAAGCCGCTAATCTGCGTGGTGCGGATCTGCGCGGCGCGAATCTG AGTGGCGCTGATCTGCAAGAGGCAAATCTGACCCAGGCGAAACTG GGCACCTGGAGCAGCAGCGGCCTGACCGGCGCTGATCTGTCTGAT GCCAACCTGGAACAGGCAGATCTGGCAGGGGCTGATCTGAAAGGT GCAGTTCTGGACGGTGCTAATCTGCATGGCGCAAATCTGAATAAT GCGAACCTGGATTATGCAATGCTGACCCGT
t1428	TCACATGCGAATCTGTCAGGTGCAAATCTGGAAGAAGCCAATCTG GAAGCCGCTAATCTGCGTGGTGCGAACCTGGTGGGCGCGAATCTG AGTGGCGCTGATCTGCAAGAGGCAAATCTGACCCAGGCGATGCTG GGCCAGACCTATCCGTGGGGCACCGTGGGCGCTGATCTGTCTGAT GCCAACCTGGAACAGGCAGATCTGGCAGGGGCTCAGCTGGTGGGT GCAGTTCTGGACGGTGCTAATCTGCATGGCGCAAATCTGAATAAT GCGAACCTGGATAACGCAATGCTGACCCGT
t1555	TCACATGCGAATCTGTCAGGTGCAAATCTGGAAGAAGCCAATCTG GAAGCCGCTAATCTGCGTGGTGCGGATCTGGCGGGCGCGAATCTG AGTGGCGCTGATCTGCAAGAGGCAAATCTGACCCAGGCGATGCTG GGCAAAGATGAAGATGGCGTGGTGTATGGCGCTGATCTGTCTGAT GCCAACCTGGAACAGGCAGATCTGGCAGGGGCTCAGCTGGTGGGT GCAGTTCTGGACGGTGCTAATCTGCATGGCGCAAATCTGAATAAT GCGAACCTGGATAACGCAATGCTGACCCGT
t1916	TCACATGCGAATCTGTCAGGTGCAAATCTGGAAGAAGCCAATCTG GAAGCCGCTAATCTGCGTGGTGCGCTGCTGACCGGCGCGAATCTG AGTGGCGCTGATCTGCAAGAGGCAAATCTGACCCAGGCGTGGCTG GGCCGCGATCCGCGCCTGGGCCTGAGCGGCGCTGATCTGTCTGAT GCCAACCTGGAACAGGCAGATCTGGCAGGGGCTCAGCTGAAAGGT GCAGTTCTGGACGGTGCTAATCTGCATGGCGCAAATCTGAATAAT GCGAACCTGGATAACGCAATGCTGACCCGT

t2570	TCACATGCGAATCTGAAAGGTGCAAATCTGGAAGAAGCCAATCTG GAAGCCGCTAATCTGCGTGGTGCGAACCTGGCGGGCGCGAATCTG AGTGGCGCTGATCTGCAAGAGGCAAATCTGACCCAGGCGGATCTG GGCGGCCCGCCGGATGAAGGCAAAACCGGCGCTGATCTGTCTGAT GCCAACCTGGAACAGGCAGATCTGGCAGGGGCTCAGCTGTATGGT GCAGTTCTGGACGGTGCTAATCTGCATGGCGCAAATCTGAATAAT GCGAACCTGGATTATGCAATGCTGACCCGT
t3280	TCACATGCGAATCTGAGCGGTGCAAATCTGGAAGAAGCCAATCTG GAAGCCGCTAATCTGCGTGGTGCGGATCTGCGCGGCGCGAATCTG AGTGGCGCTGATCTGCAAGAGGCAAATCTGACCCAGGCGAAACTG GGCGGCTATGATGATGAAGGCCTGGGCGGCGCTGATCTGTCTGAT GCCAACCTGGAACAGGCAGATCTGGCAGGGGCTGAACTGTTTGGT GCAGTTCTGGACGGTGCTAATCTGCATGGCGCAAATCTGAATAAT GCGAACCTGGATAAAGCAATGCTGACCCGT
t3284	TCACATGCGAATCTGGAAGGTGCAAATCTGGAAGAAGCCAATCTG GAAGCCGCTAATCTGCGTGGTGCGCGCCTGGCGGGCGCGAATCTG AGTGGCGCTGATCTGCAAGAGGCAAATCTGACCCAGGCGAACCTG GGCGGCCCGCCGGATGATGGCGATCCGGGCGCTGATCTGTCTGAT GCCAACCTGGAACAGGCAGATCTGGCAGGGGCTAACCTGGCGGGT GCAGTTCTGGACGGTGCTAATCTGCATGGCGCAAATCTGAATAAT GCGAACCTGGATAACGCAATGCTGACCCGT

Table S5: Linear DNA fragments used in this study

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1.9 Computational protein design model coordinates

PDB backbone coordinates for models of the designed loops plus surrounding residues (residues 98-127) are given below. Full coordinates are available from the authors upon request.

1.9.1 SynRFR24.t754

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ATOM   1444  N   GLN A  98       4.575 -24.236  8.271  1.00 20.00           N
ATOM   1445  CA  GLN A  98       3.419 -25.003  8.728  1.00 20.00           C
ATOM   1446  C   GLN A  98       3.074 -26.134  7.797  1.00 20.00           C
ATOM   1447  O   GLN A  98       3.175 -25.988  6.542  1.00 20.00           O
ATOM   1448  CB  GLN A  98       2.286 -24.077  8.955  1.00 20.00           C
ATOM   1461  N   GLU A  99       2.713 -27.305  8.360  1.00 20.00           N
ATOM   1462  CA  GLU A  99       2.377 -28.482  7.588  1.00 20.00           C
ATOM   1463  C   GLU A  99       3.530 -29.033  6.733  1.00 20.00           C
ATOM   1464  O   GLU A  99       3.360 -29.943  5.880  1.00 20.00           O
ATOM   1465  CB  GLU A  99       1.102 -28.211  6.751  1.00 20.00           C
ATOM   1476  N   ALA A 100       4.743 -28.544  7.004  1.00 20.00           N
ATOM   1477  CA  ALA A 100       5.858 -28.997  6.209  1.00 20.00           C
ATOM   1478  C   ALA A 100       6.285 -30.431  6.630  1.00 20.00           C
ATOM   1479  O   ALA A 100       6.178 -30.803  7.819  1.00 20.00           O
ATOM   1480  CB  ALA A 100       7.051 -27.989  6.317  1.00 20.00           C
ATOM   1486  N   ASN A 101       6.806 -31.144  5.647  1.00 20.00           N
ATOM   1487  CA  ASN A 101       7.354 -32.487  5.838  1.00 20.00           C
ATOM   1488  C   ASN A 101       8.830 -32.460  6.049  1.00 20.00           C
ATOM   1489  O   ASN A 101       9.674 -32.261  5.099  1.00 20.00           O
ATOM   1490  CB  ASN A 101       7.028 -33.403  4.673  1.00 20.00           C
ATOM   1500  N   LEU A 102       9.195 -32.574  7.331  1.00 20.00           N
ATOM   1501  CA  LEU A 102      10.587 -32.507  7.795  1.00 20.00           C
ATOM   1502  C   LEU A 102      11.037 -33.841  8.366  1.00 20.00           C
ATOM   1503  O   LEU A 102      11.942 -33.906  9.212  1.00 20.00           O
ATOM   1504  CB  LEU A 102      10.751 -31.399  8.843  1.00 20.00           C
ATOM   1519  N   THR A 103      10.460 -34.953  7.871  1.00 20.00           N
ATOM   1520  CA  THR A 103      10.778 -36.265  8.349  1.00 20.00           C
ATOM   1521  C   THR A 103      12.171 -36.555  8.006  1.00 20.00           C
ATOM   1522  O   THR A 103      12.607 -36.301  6.892  1.00 20.00           O
ATOM   1523  CB  THR A 103       9.782 -37.341  7.874  1.00 20.00           C
ATOM   1533  N   GLN A 104      12.889 -37.139  8.958  1.00 20.00           N
ATOM   1534  CA  GLN A 104      14.265 -37.415  8.805  1.00 20.00           C
ATOM   1535  C   GLN A 104      15.188 -36.282  8.383  1.00 20.00           C
ATOM   1536  O   GLN A 104      16.293 -36.518  7.890  1.00 20.00           O
ATOM   1537  CB  GLN A 104      14.397 -38.558  7.794  1.00 20.00           C
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ATOM   1551  CA  ALA A 105      15.557 -33.894  8.178  1.00  0.00           C
ATOM   1552  C   ALA A 105      16.567 -33.509  9.222  1.00  0.00           C
ATOM   1553  O   ALA A 105      16.389 -33.710 10.412  1.00  0.00           O
ATOM   1554  CB  ALA A 105      14.673 -32.637  7.779  1.00  0.00           C
ATOM   1560  N   GLN A 106      17.671 -32.978  8.754  1.00  0.00           N
ATOM   1561  CA  GLN A 106      18.706 -32.459  9.656  1.00  0.00           C
ATOM   1562  C   GLN A 106      18.542 -30.919  9.821  1.00  0.00           C
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ATOM   1564  CB  GLN A 106      20.101 -32.798  9.124  1.00  0.00           C
ATOM   1577  N   LEU A 107      18.227 -30.523 11.040  1.00  0.00           N
ATOM   1578  CA  LEU A 107      18.022 -29.150 11.401  1.00  0.00           C
ATOM   1579  C   LEU A 107      19.115 -28.616 12.346  1.00  0.00           C
ATOM   1580  O   LEU A 107      18.869 -27.838 13.285  1.00  0.00           O
ATOM   1581  CB  LEU A 107      16.644 -29.003 12.058  1.00  0.00           C
ATOM   1596  N   GLY A 108      20.350 -29.057 12.094  1.00  0.00           N
ATOM   1597  CA  GLY A 108      21.412 -28.600 12.917  1.00  0.00           C
ATOM   1598  C   GLY A 108      22.592 -29.531 12.749  1.00  0.00           C
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ATOM   1603  N   GLY A 109      23.788 -28.968 12.942  1.00  0.00           N
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ATOM   1611  CA  TRP A 110     26.958 -31.502 15.680 1.00 0.00          C
ATOM   1612  C   TRP A 110     28.262 -30.840 16.121 1.00 0.00          C
ATOM   1613  O   TRP A 110     29.167 -30.648 15.305 1.00 0.00          O
ATOM   1614  CB  TRP A 110     27.168 -33.008 15.507 1.00 0.00          C
ATOM   1634  N   SER A 111     28.371 -30.632 17.445 1.00 0.00          N
ATOM   1635  CA  SER A 111     29.466 -30.040 18.217 1.00 0.00          C
ATOM   1636  C   SER A 111     30.764 -30.849 18.179 1.00 0.00          C
ATOM   1637  O   SER A 111     31.832 -30.243 18.195 1.00 0.00          O
ATOM   1638  CB  SER A 111     29.029 -29.870 19.659 1.00 0.00          C
ATOM   1645  N   ASP A 112     30.662 -32.147 17.839 1.00 0.00          N
ATOM   1646  CA  ASP A 112     31.782 -33.067 17.657 1.00 0.00          C
ATOM   1647  C   ASP A 112     32.667 -32.647 16.478 1.00 0.00          C
ATOM   1648  O   ASP A 112     33.887 -32.781 16.551 1.00 0.00          O
ATOM   1649  CB  ASP A 112     31.270 -34.493 17.437 1.00 0.00          C
ATOM   1657  N   ASN A 113     32.053 -31.971 15.491 1.00 0.00          N
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ATOM   1660  O   ASN A 113     33.204 -29.313 13.347 1.00 0.00          O
ATOM   1661  CB  ASN A 113     31.906 -31.854 13.072 1.00 0.00          C
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ATOM   1673  C   GLY A 114     31.233 -27.023 15.086 1.00 0.00          C
ATOM   1674  O   GLY A 114     31.296 -25.802 14.941 1.00 0.00          O
ATOM   1678  N   GLU A 115     30.129 -27.721 14.802 1.00 0.00          N
ATOM   1679  CA  GLU A 115     29.008 -27.114 14.105 1.00 0.00          C
ATOM   1680  C   GLU A 115     27.882 -26.797 15.071 1.00 0.00          C
ATOM   1681  O   GLU A 115     27.799 -27.389 16.145 1.00 0.00          O
ATOM   1682  CB  GLU A 115     28.501 -28.040 12.997 1.00 0.00          C
ATOM   1693  N   THR A 116     27.090 -25.774 14.733 1.00 0.00          N
ATOM   1694  CA  THR A 116     25.962 -25.367 15.549 1.00 0.00          C
ATOM   1695  C   THR A 116     24.670 -25.851 14.906 1.00 0.00          C
ATOM   1696  O   THR A 116     24.666 -26.329 13.772 1.00 0.00          O
ATOM   1697  CB  THR A 116     25.922 -23.839 15.735 1.00 0.00          C
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ATOM   1738  C   LEU A 120     13.459 -20.616 14.743 1.00 0.00          C
ATOM   1739  O   LEU A 120     12.313 -20.877 15.035 1.00 0.00          O
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ATOM   1755  N   SER A 121     14.103 -19.543 15.122 1.00 20.00         N
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ATOM   1758  O   SER A 121     12.343 -17.612 14.211 1.00 20.00         O
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ATOM   1770  CB  ASP A 122     10.143 -15.831 15.572 1.00 20.00        C
ATOM   1778  N   ALA A 123      9.792 -19.200 14.128 1.00 20.00        N
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ATOM   1781  O   ALA A 123      7.669 -20.966 14.400 1.00 20.00        O
ATOM   1782  CB  ALA A 123     10.274 -21.069 12.451 1.00 20.00        C
ATOM   1788  N   ASN A 124      7.155 -20.670 12.214 1.00 20.00        N
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ATOM   1790  C   ASN A 124      5.967 -22.719 11.922 1.00 20.00        C
ATOM   1791  O   ASN A 124      6.162 -23.024 10.733 1.00 20.00        O
ATOM   1792  CB  ASN A 124      4.842 -20.570 11.542 1.00 20.00        C
ATOM   1802  N   LEU A 125      5.890 -23.655 12.863 1.00 20.00        N
ATOM   1803  CA  LEU A 125      5.912 -25.050 12.640 1.00 20.00        C
ATOM   1804  C   LEU A 125      4.615 -25.732 13.034 1.00 20.00        C
ATOM   1805  O   LEU A 125      4.587 -26.966 13.337 1.00 20.00        O
ATOM   1806  CB  LEU A 125      7.095 -25.661 13.401 1.00 20.00        C
ATOM   1821  N   GLU A 126      3.492 -25.026 12.879 1.00 20.00        N
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ATOM   1823  C   GLU A 126      1.906 -26.842 12.406 1.00 20.00        C
ATOM   1824  O   GLU A 126      2.015 -26.812 11.165 1.00 20.00        O
ATOM   1825  CB  GLU A 126      1.078 -24.570 13.112 1.00 20.00        C
ATOM   1836  N   GLN A 127      1.553 -27.971 13.083 1.00 20.00        N
ATOM   1837  CA  GLN A 127      1.262 -29.243 12.448 1.00 20.00        C
ATOM   1838  C   GLN A 127      2.346 -29.720 11.502 1.00 20.00        C
ATOM   1839  O   GLN A 127      2.039 -30.611 10.681 1.00 20.00        O
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1.9.2 SynRFR24.t801

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ATOM   1455  C   GLN A  98       3.084 -26.160  7.784  1.00 20.00           C
ATOM   1456  O   GLN A  98       3.187 -26.016  6.529  1.00 20.00           O
ATOM   1457  CB  GLN A  98       2.297 -24.101  8.938  1.00 20.00           C
ATOM   1470  N   GLU A  99       2.722 -27.330  8.349  1.00 20.00           N
ATOM   1471  CA  GLU A  99       2.386 -28.508  7.577  1.00 20.00           C
ATOM   1472  C   GLU A  99       3.539 -29.060  6.724  1.00 20.00           C
ATOM   1473  O   GLU A  99       3.369 -29.972  5.873  1.00 20.00           O
ATOM   1474  CB  GLU A  99       1.112 -28.237  6.738  1.00 20.00           C
ATOM   1485  N   ALA A 100       4.752 -28.572  6.996  1.00 20.00           N
ATOM   1486  CA  ALA A 100       5.868 -29.027  6.204  1.00 20.00           C
ATOM   1487  C   ALA A 100       6.293 -30.461  6.627  1.00 20.00           C
ATOM   1488  O   ALA A 100       6.185 -30.831  7.816  1.00 20.00           O
ATOM   1489  CB  ALA A 100       7.061 -28.020  6.311  1.00 20.00           C
ATOM   1495  N   ASN A 101       6.815 -31.176  5.645  1.00 20.00           N
ATOM   1496  CA  ASN A 101       7.362 -32.519  5.839  1.00 20.00           C
ATOM   1497  C   ASN A 101       8.838 -32.493  6.052  1.00 20.00           C
ATOM   1498  O   ASN A 101       9.683 -32.296  5.103  1.00 20.00           O
ATOM   1499  CB  ASN A 101       7.037 -33.436  4.675  1.00 20.00           C
ATOM   1509  N   LEU A 102       9.201 -32.605  7.334  1.00 20.00           N
ATOM   1510  CA  LEU A 102      10.592 -32.538  7.799  1.00 20.00           C
ATOM   1511  C   LEU A 102      11.041 -33.871  8.373  1.00 20.00           C
ATOM   1512  O   LEU A 102      11.945 -33.936  9.220  1.00 20.00           O
ATOM   1513  CB  LEU A 102      10.756 -31.429  8.846  1.00 20.00           C
ATOM   1528  N   THR A 103      10.464 -34.984  7.878  1.00 20.00           N
ATOM   1529  CA  THR A 103      10.780 -36.296  8.359  1.00 20.00           C
ATOM   1530  C   THR A 103      12.174 -36.587  8.018  1.00 20.00           C
ATOM   1531  O   THR A 103      12.611 -36.335  6.904  1.00 20.00           O
ATOM   1532  CB  THR A 103       9.785 -37.371  7.885  1.00 20.00           C
ATOM   1542  N   GLN A 104      12.890 -37.170  8.972  1.00 20.00           N
ATOM   1543  CA  GLN A 104      14.266 -37.448  8.820  1.00 20.00           C
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ATOM   1545  O   GLN A 104      16.296 -36.553  7.907  1.00 20.00           O
ATOM   1546  CB  GLN A 104      14.399 -38.592  7.811  1.00 20.00           C
ATOM   1559  N   ALA A 105      14.763 -35.075  8.593  1.00  0.00           N
ATOM   1560  CA  ALA A 105      15.561 -33.928  8.190  1.00  0.00           C
ATOM   1561  C   ALA A 105      16.670 -33.637  9.162  1.00  0.00           C
ATOM   1562  O   ALA A 105      16.569 -33.859 10.358  1.00  0.00           O
ATOM   1563  CB  ALA A 105      14.690 -32.624  7.945  1.00  0.00           C
ATOM   1569  N   GLN A 106      17.768 -33.164  8.622  1.00  0.00           N
ATOM   1570  CA  GLN A 106      18.917 -32.780  9.451  1.00  0.00           C
ATOM   1571  C   GLN A 106      18.871 -31.251  9.745  1.00  0.00           C
ATOM   1572  O   GLN A 106      19.393 -30.433  8.938  1.00  0.00           O
ATOM   1573  CB  GLN A 106      20.229 -33.157  8.758  1.00  0.00           C
ATOM   1586  N   LEU A 107      18.355 -30.927 10.915  1.00  0.00           N
ATOM   1587  CA  LEU A 107      18.129 -29.575 11.337  1.00  0.00           C
ATOM   1588  C   LEU A 107      19.165 -29.096 12.372  1.00  0.00           C
ATOM   1589  O   LEU A 107      18.885 -28.293 13.280  1.00  0.00           O
ATOM   1590  CB  LEU A 107      16.715 -29.459 11.919  1.00  0.00           C
ATOM   1605  N   GLY A 108      20.389 -29.613 12.233  1.00  0.00           N
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ATOM   1613  CA  LEU A 109      24.362 -30.816 14.885  1.00  0.00           C
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ATOM   1631  N   GLY A 110     24.673 -31.058 17.284 1.00 0.00          N
ATOM   1632  CA  GLY A 110     24.827 -30.688 18.687 1.00 0.00          C
ATOM   1633  C   GLY A 110     26.245 -30.628 19.294 1.00 0.00          C
ATOM   1634  O   GLY A 110     27.262 -30.613 18.590 1.00 0.00          O
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ATOM   1639  CA  VAL A 111     27.392 -30.688 21.564 1.00 0.00          C
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ATOM   1641  O   VAL A 111     29.508 -31.798 21.508 1.00 0.00          O
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ATOM   1655  CA  GLU A 112     28.359 -34.396 21.215 1.00 0.00          C
ATOM   1656  C   GLU A 112     28.777 -34.637 19.764 1.00 0.00          C
ATOM   1657  O   GLU A 112     29.652 -35.466 19.504 1.00 0.00          O
ATOM   1658  CB  GLU A 112     27.459 -35.531 21.706 1.00 0.00          C
ATOM   1669  N   ASP A 113     28.225 -33.812 18.848 1.00 0.00          N
ATOM   1670  CA  ASP A 113     28.491 -33.814 17.418 1.00 0.00          C
ATOM   1671  C   ASP A 113     29.622 -32.846 17.061 1.00 0.00          C
ATOM   1672  O   ASP A 113     30.439 -33.178 16.202 1.00 0.00          O
ATOM   1673  CB  ASP A 113     27.226 -33.444 16.641 1.00 0.00          C
ATOM   1681  N   GLY A 114     29.702 -31.709 17.793 1.00 0.00          N
ATOM   1682  CA  GLY A 114     30.680 -30.639 17.649 1.00 0.00          C
ATOM   1683  C   GLY A 114     30.369 -29.659 16.521 1.00 0.00          C
ATOM   1684  O   GLY A 114     31.272 -29.195 15.826 1.00 0.00          O
ATOM   1688  N   GLY A 115     29.068 -29.481 16.231 1.00 0.00          N
ATOM   1689  CA  GLY A 115     28.641 -28.626 15.136 1.00 0.00          C
ATOM   1690  C   GLY A 115     27.671 -27.569 15.632 1.00 0.00          C
ATOM   1691  O   GLY A 115     27.650 -27.227 16.815 1.00 0.00          O
ATOM   1695  N   LEU A 116     26.990 -26.942 14.667 1.00 0.00          N
ATOM   1696  CA  LEU A 116     26.012 -25.923 14.932 1.00 0.00          C
ATOM   1697  C   LEU A 116     24.645 -26.416 14.526 1.00 0.00          C
ATOM   1698  O   LEU A 116     24.500 -27.158 13.555 1.00 0.00          O
ATOM   1699  CB  LEU A 116     26.358 -24.635 14.175 1.00 0.00          C
ATOM   1714  N   GLY A 117     23.649 -25.967 15.291 1.00 0.00          N
ATOM   1715  CA  GLY A 117     22.277 -26.316 15.039 1.00 0.00          C
ATOM   1716  C   GLY A 117     21.617 -25.353 14.053 1.00 0.00          C
ATOM   1717  O   GLY A 117     22.153 -24.304 13.766 1.00 0.00          O
ATOM   1721  N   ALA A 118     20.449 -25.711 13.542 1.00 0.00          N
ATOM   1722  CA  ALA A 118     19.669 -24.809 12.649 1.00 0.00          C
ATOM   1723  C   ALA A 118     18.917 -23.792 13.465 1.00 0.00          C
ATOM   1724  O   ALA A 118     18.563 -24.034 14.640 1.00 0.00          O
ATOM   1725  CB  ALA A 118     18.681 -25.601 11.668 1.00 0.00          C
ATOM   1731  N   ASP A 119     18.692 -22.621 12.891 1.00 0.00          N
ATOM   1732  CA  ASP A 119     17.973 -21.514 13.539 1.00 0.00          C
ATOM   1733  C   ASP A 119     16.569 -21.466 13.089 1.00 0.00          C
ATOM   1734  O   ASP A 119     16.290 -21.130 11.923 1.00 0.00          O
ATOM   1735  CB  ASP A 119     18.634 -20.166 13.243 1.00 0.00          C
ATOM   1743  N   LEU A 120     15.675 -21.827 13.984 1.00 0.00          N
ATOM   1744  CA  LEU A 120     14.253 -21.809 13.786 1.00 0.00          C
ATOM   1745  C   LEU A 120     13.508 -20.791 14.688 1.00 0.00          C
ATOM   1746  O   LEU A 120     12.359 -21.037 14.981 1.00 0.00          O
ATOM   1747  CB  LEU A 120     13.705 -23.221 14.032 1.00 0.00          C
ATOM   1762  N   SER A 121     14.167 -19.727 15.067 1.00 20.00         N
ATOM   1763  CA  SER A 121     13.662 -18.704 15.972 1.00 20.00         C
ATOM   1764  C   SER A 121     12.442 -18.148 15.327 1.00 20.00         C
ATOM   1765  O   SER A 121     12.426 -17.773 14.170 1.00 20.00         O
ATOM   1766  CB  SER A 121     14.689 -17.619 16.234 1.00 20.00         C
ATOM   1773  N   ASP A 122     11.400 -18.057 16.141 1.00 20.00         N
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ATOM   1774  CA  ASP A 122     10.083 -17.452 15.705 1.00 20.00        C
ATOM   1775  C   ASP A 122      9.498 -18.088 14.396 1.00 20.00        C
ATOM   1776  O   ASP A 122      8.637 -17.472 13.720 1.00 20.00        O
ATOM   1777  CB  ASP A 122     10.255 -15.969 15.547 1.00 20.00        C
ATOM   1785  N   ALA A 123      9.856 -19.329 14.096 1.00 20.00        N
ATOM   1786  CA  ALA A 123      9.329 -20.065 12.942 1.00 20.00        C
ATOM   1787  C   ALA A 123      7.992 -20.689 13.224 1.00 20.00        C
ATOM   1788  O   ALA A 123      7.712 -21.070 14.375 1.00 20.00        O
ATOM   1789  CB  ALA A 123     10.306 -21.199 12.412 1.00 20.00        C
ATOM   1795  N   ASN A 124      7.191 -20.762 12.192 1.00 20.00        N
ATOM   1796  CA  ASN A 124      5.897 -21.352 12.326 1.00 20.00        C
ATOM   1797  C   ASN A 124      5.977 -22.796 11.901 1.00 20.00        C
ATOM   1798  O   ASN A 124      6.162 -23.099 10.709 1.00 20.00        O
ATOM   1799  CB  ASN A 124      4.876 -20.632 11.532 1.00 20.00        C
ATOM   1809  N   LEU A 125      5.894 -23.733 12.839 1.00 20.00        N
ATOM   1810  CA  LEU A 125      5.897 -25.127 12.612 1.00 20.00        C
ATOM   1811  C   LEU A 125      4.594 -25.796 13.011 1.00 20.00        C
ATOM   1812  O   LEU A 125      4.553 -27.029 13.311 1.00 20.00        O
ATOM   1813  CB  LEU A 125      7.077 -25.755 13.365 1.00 20.00        C
ATOM   1828  N   GLU A 126      3.479 -25.075 12.865 1.00 20.00        N
ATOM   1829  CA  GLU A 126      2.180 -25.641 13.243 1.00 20.00        C
ATOM   1830  C   GLU A 126      1.869 -26.870 12.395 1.00 20.00        C
ATOM   1831  O   GLU A 126      1.972 -26.839 11.153 1.00 20.00        O
ATOM   1832  CB  GLU A 126      1.072 -24.591 13.111 1.00 20.00        C
ATOM   1843  N   GLN A 127      1.505 -27.997 13.070 1.00 20.00        N
ATOM   1844  CA  GLN A 127      1.196 -29.264 12.433 1.00 20.00        C
ATOM   1845  C   GLN A 127      2.269 -29.752 11.480 1.00 20.00        C
ATOM   1846  O   GLN A 127      1.947 -30.636 10.658 1.00 20.00        O
ATOM   1847  CB  GLN A 127     -0.131 -29.152 11.678 1.00 20.00        C
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ATOM   1450  N   GLN A  98       4.565 -24.288  8.235  1.00 20.00           N
ATOM   1451  CA  GLN A  98       3.406 -25.050  8.690  1.00 20.00           C
ATOM   1452  C   GLN A  98       3.059 -26.181  7.759  1.00 20.00           C
ATOM   1453  O   GLN A  98       3.164 -26.037  6.504  1.00 20.00           O
ATOM   1454  CB  GLN A  98       2.276 -24.121  8.913  1.00 20.00           C
ATOM   1467  N   GLU A  99       2.693 -27.351  8.323  1.00 20.00           N
ATOM   1468  CA  GLU A  99       2.355 -28.528  7.551  1.00 20.00           C
ATOM   1469  C   GLU A  99       3.509 -29.083  6.699  1.00 20.00           C
ATOM   1470  O   GLU A  99       3.337 -29.994  5.847  1.00 20.00           O
ATOM   1471  CB  GLU A  99       1.084 -28.253  6.711  1.00 20.00           C
ATOM   1482  N   ALA A 100       4.723 -28.597  6.973  1.00 20.00           N
ATOM   1483  CA  ALA A 100       5.838 -29.055  6.181  1.00 20.00           C
ATOM   1484  C   ALA A 100       6.259 -30.490  6.605  1.00 20.00           C
ATOM   1485  O   ALA A 100       6.148 -30.861  7.794  1.00 20.00           O
ATOM   1486  CB  ALA A 100       7.034 -28.051  6.291  1.00 20.00           C
ATOM   1492  N   ASN A 101       6.780 -31.206  5.623  1.00 20.00           N
ATOM   1493  CA  ASN A 101       7.324 -32.550  5.817  1.00 20.00           C
ATOM   1494  C   ASN A 101       8.799 -32.528  6.032  1.00 20.00           C
ATOM   1495  O   ASN A 101       9.646 -32.333  5.083  1.00 20.00           O
ATOM   1496  CB  ASN A 101       6.997 -33.466  4.652  1.00 20.00           C
ATOM   1506  N   LEU A 102       9.161 -32.642  7.315  1.00 20.00           N
ATOM   1507  CA  LEU A 102      10.552 -32.578  7.781  1.00 20.00           C
ATOM   1508  C   LEU A 102      10.996 -33.913  8.355  1.00 20.00           C
ATOM   1509  O   LEU A 102      11.899 -33.980  9.203  1.00 20.00           O
ATOM   1510  CB  LEU A 102      10.717 -31.470  8.828  1.00 20.00           C
ATOM   1525  N   THR A 103      10.417 -35.024  7.859  1.00 20.00           N
ATOM   1526  CA  THR A 103      10.729 -36.336  8.340  1.00 20.00           C
ATOM   1527  C   THR A 103      12.122 -36.631  8.000  1.00 20.00           C
ATOM   1528  O   THR A 103      12.561 -36.380  6.887  1.00 20.00           O
ATOM   1529  CB  THR A 103       9.732 -37.410  7.864  1.00 20.00           C
ATOM   1539  N   GLN A 104      12.836 -37.216  8.954  1.00 20.00           N
ATOM   1540  CA  GLN A 104      14.211 -37.497  8.805  1.00 20.00           C
ATOM   1541  C   GLN A 104      15.139 -36.367  8.383  1.00 20.00           C
ATOM   1542  O   GLN A 104      16.245 -36.608  7.894  1.00 20.00           O
ATOM   1543  CB  GLN A 104      14.343 -38.642  7.795  1.00 20.00           C
ATOM   1556  N   ALA A 105      14.714 -35.126  8.579  1.00  0.00           N
ATOM   1557  CA  ALA A 105      15.516 -33.981  8.177  1.00  0.00           C
ATOM   1558  C   ALA A 105      16.629 -33.697  9.147  1.00  0.00           C
ATOM   1559  O   ALA A 105      16.544 -33.955 10.337  1.00  0.00           O
ATOM   1560  CB  ALA A 105      14.650 -32.673  7.938  1.00  0.00           C
ATOM   1566  N   GLN A 106      17.712 -33.188  8.611  1.00  0.00           N
ATOM   1567  CA  GLN A 106      18.852 -32.783  9.443  1.00  0.00           C
ATOM   1568  C   GLN A 106      18.774 -31.257  9.743  1.00  0.00           C
ATOM   1569  O   GLN A 106      19.286 -30.425  8.944  1.00  0.00           O
ATOM   1570  CB  GLN A 106      20.173 -33.129  8.750  1.00  0.00           C
ATOM   1583  N   LEU A 107      18.242 -30.948 10.911  1.00  0.00           N
ATOM   1584  CA  LEU A 107      18.063 -29.601 11.371  1.00  0.00           C
ATOM   1585  C   LEU A 107      19.130 -29.179 12.399  1.00  0.00           C
ATOM   1586  O   LEU A 107      18.902 -28.355 13.302  1.00  0.00           O
ATOM   1587  CB  LEU A 107      16.662 -29.460 11.980  1.00  0.00           C
ATOM   1602  N   GLY A 108      20.319 -29.770 12.260  1.00  0.00           N
ATOM   1603  CA  GLY A 108      21.346 -29.446 13.184  1.00  0.00           C
ATOM   1604  C   GLY A 108      22.365 -30.568 13.148  1.00  0.00           C
ATOM   1605  O   GLY A 108      22.005 -31.708 12.852  1.00  0.00           O
ATOM   1609  N   GLY A 109      23.629 -30.251 13.465  1.00  0.00           N
ATOM   1610  CA  GLY A 109      24.688 -31.239 13.504  1.00  0.00           C
ATOM   1611  C   GLY A 109      24.863 -31.819 14.904  1.00  0.00           C
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ATOM   1612  O   GLY A 109     23.891 -32.113 15.597 1.00 0.00          O
ATOM   1616  N   VAL A 110     26.125 -32.054 15.273 1.00 0.00          N
ATOM   1617  CA  VAL A 110     26.478 -32.568 16.583 1.00 0.00          C
ATOM   1618  C   VAL A 110     27.022 -31.485 17.518 1.00 0.00          C
ATOM   1619  O   VAL A 110     28.201 -31.133 17.451 1.00 0.00          O
ATOM   1620  CB  VAL A 110     27.529 -33.683 16.436 1.00 0.00          C
ATOM   1632  N   TYR A 111     26.235 -31.211 18.573 1.00 0.00          N
ATOM   1633  CA  TYR A 111     26.517 -30.277 19.669 1.00 0.00          C
ATOM   1634  C   TYR A 111     27.867 -30.517 20.367 1.00 0.00          C
ATOM   1635  O   TYR A 111     28.708 -29.618 20.412 1.00 0.00          O
ATOM   1636  CB  TYR A 111     25.388 -30.339 20.699 1.00 0.00          C
ATOM   1653  N   ARG A 112     28.121 -31.782 20.735 1.00 0.00          N
ATOM   1654  CA  ARG A 112     29.316 -32.263 21.406 1.00 0.00          C
ATOM   1655  C   ARG A 112     30.597 -32.144 20.555 1.00 0.00          C
ATOM   1656  O   ARG A 112     31.686 -32.122 21.131 1.00 0.00          O
ATOM   1657  CB  ARG A 112     29.121 -33.717 21.811 1.00 0.00          C
ATOM   1677  N   LEU A 113     30.486 -31.964 19.222 1.00 0.00          N
ATOM   1678  CA  LEU A 113     31.648 -31.734 18.361 1.00 0.00          C
ATOM   1679  C   LEU A 113     31.897 -30.297 17.873 1.00 0.00          C
ATOM   1680  O   LEU A 113     32.885 -30.054 17.179 1.00 0.00          O
ATOM   1681  CB  LEU A 113     31.524 -32.645 17.134 1.00 0.00          C
ATOM   1696  N   GLY A 114     31.090 -29.336 18.347 1.00 0.00          N
ATOM   1697  CA  GLY A 114     31.114 -27.904 18.026 1.00 0.00          C
ATOM   1698  C   GLY A 114     30.447 -27.495 16.706 1.00 0.00          C
ATOM   1699  O   GLY A 114     30.715 -26.424 16.158 1.00 0.00          O
ATOM   1703  N   GLU A 115     29.514 -28.340 16.247 1.00 0.00          N
ATOM   1704  CA  GLU A 115     28.768 -28.141 15.014 1.00 0.00          C
ATOM   1705  C   GLU A 115     27.493 -27.337 15.257 1.00 0.00          C
ATOM   1706  O   GLU A 115     26.897 -27.420 16.331 1.00 0.00          O
ATOM   1707  CB  GLU A 115     28.421 -29.491 14.382 1.00 0.00          C
ATOM   1718  N   PRO A 116     27.091 -26.549 14.256 1.00 0.00          N
ATOM   1719  CA  PRO A 116     25.911 -25.713 14.334 1.00 0.00          C
ATOM   1720  C   PRO A 116     24.594 -26.469 14.212 1.00 0.00          C
ATOM   1721  O   PRO A 116     24.528 -27.569 13.661 1.00 0.00          O
ATOM   1722  CB  PRO A 116     26.116 -24.763 13.149 1.00 0.00          C
ATOM   1732  N   GLY A 117     23.576 -25.894 14.868 1.00 0.00          N
ATOM   1733  CA  GLY A 117     22.195 -26.364 14.900 1.00 0.00          C
ATOM   1734  C   GLY A 117     21.468 -25.375 13.989 1.00 0.00          C
ATOM   1735  O   GLY A 117     21.915 -24.262 13.811 1.00 0.00          O
ATOM   1739  N   ALA A 118     20.344 -25.784 13.422 1.00 0.00          N
ATOM   1740  CA  ALA A 118     19.524 -24.886 12.561 1.00 0.00          C
ATOM   1741  C   ALA A 118     18.813 -23.863 13.405 1.00 0.00          C
ATOM   1742  O   ALA A 118     18.449 -24.123 14.574 1.00 0.00          O
ATOM   1743  CB  ALA A 118     18.489 -25.682 11.633 1.00 0.00          C
ATOM   1749  N   ASP A 119     18.634 -22.668 12.864 1.00 0.00          N
ATOM   1750  CA  ASP A 119     17.940 -21.559 13.534 1.00 0.00          C
ATOM   1751  C   ASP A 119     16.535 -21.476 13.093 1.00 0.00          C
ATOM   1752  O   ASP A 119     16.256 -21.099 11.940 1.00 0.00          O
ATOM   1753  CB  ASP A 119     18.626 -20.219 13.256 1.00 0.00          C
ATOM   1761  N   LEU A 120     15.640 -21.852 13.981 1.00 0.00          N
ATOM   1762  CA  LEU A 120     14.219 -21.835 13.781 1.00 0.00          C
ATOM   1763  C   LEU A 120     13.471 -20.816 14.679 1.00 0.00          C
ATOM   1764  O   LEU A 120     12.322 -21.063 14.970 1.00 0.00          O
ATOM   1765  CB  LEU A 120     13.671 -23.247 14.027 1.00 0.00          C
ATOM   1780  N   SER A 121     14.128 -19.751 15.058 1.00 20.00         N
ATOM   1781  CA  SER A 121     13.621 -18.728 15.961 1.00 20.00         C
ATOM   1782  C   SER A 121     12.402 -18.173 15.311 1.00 20.00         C
ATOM   1783  O   SER A 121     12.389 -17.799 14.154 1.00 20.00         O
ATOM   1784  CB  SER A 121     14.647 -17.642 16.224 1.00 20.00         C
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ATOM   1791  N   ASP A 122     11.358 -18.081 16.122 1.00 20.00        N
ATOM   1792  CA  ASP A 122     10.042 -17.477 15.682 1.00 20.00        C
ATOM   1793  C   ASP A 122      9.461 -18.115 14.372 1.00 20.00        C
ATOM   1794  O   ASP A 122      8.602 -17.501 13.693 1.00 20.00        O
ATOM   1795  CB  ASP A 122     10.214 -15.994 15.522 1.00 20.00        C
ATOM   1803  N   ALA A 123      9.820 -19.357 14.075 1.00 20.00        N
ATOM   1804  CA  ALA A 123      9.297 -20.094 12.920 1.00 20.00        C
ATOM   1805  C   ALA A 123      7.960 -20.719 13.200 1.00 20.00        C
ATOM   1806  O   ALA A 123      7.676 -21.097 14.350 1.00 20.00        O
ATOM   1807  CB  ALA A 123     10.276 -21.229 12.395 1.00 20.00        C
ATOM   1813  N   ASN A 124      7.161 -20.793 12.165 1.00 20.00        N
ATOM   1814  CA  ASN A 124      5.867 -21.383 12.296 1.00 20.00        C
ATOM   1815  C   ASN A 124      5.948 -22.827 11.873 1.00 20.00        C
ATOM   1816  O   ASN A 124      6.137 -23.132 10.683 1.00 20.00        O
ATOM   1817  CB  ASN A 124      4.848 -20.664 11.498 1.00 20.00        C
ATOM   1827  N   LEU A 125      5.863 -23.763 12.813 1.00 20.00        N
ATOM   1828  CA  LEU A 125      5.867 -25.158 12.588 1.00 20.00        C
ATOM   1829  C   LEU A 125      4.563 -25.826 12.984 1.00 20.00        C
ATOM   1830  O   LEU A 125      4.522 -27.059 13.286 1.00 20.00        O
ATOM   1831  CB  LEU A 125      7.045 -25.784 13.346 1.00 20.00        C
ATOM   1846  N   GLU A 126      3.449 -25.106 12.833 1.00 20.00        N
ATOM   1847  CA  GLU A 126      2.148 -25.671 13.209 1.00 20.00        C
ATOM   1848  C   GLU A 126      1.840 -26.902 12.361 1.00 20.00        C
ATOM   1849  O   GLU A 126      1.947 -26.873 11.120 1.00 20.00        O
ATOM   1850  CB  GLU A 126      1.040 -24.622 13.073 1.00 20.00        C
ATOM   1861  N   GLN A 127      1.475 -28.029 13.037 1.00 20.00        N
ATOM   1862  CA  GLN A 127      1.168 -29.296 12.402 1.00 20.00        C
ATOM   1863  C   GLN A 127      2.244 -29.785 11.452 1.00 20.00        C
ATOM   1864  O   GLN A 127      1.925 -30.671 10.630 1.00 20.00        O
ATOM   1865  CB  GLN A 127     -0.157 -29.185 11.642 1.00 20.00        C
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ATOM   1445  N   GLN A  98       4.602 -24.204  8.281  1.00 20.00           N
ATOM   1446  CA  GLN A  98       3.444 -24.966  8.739  1.00 20.00           C
ATOM   1447  C   GLN A  98       3.096 -26.098  7.810  1.00 20.00           C
ATOM   1448  O   GLN A  98       3.197 -25.954  6.555  1.00 20.00           O
ATOM   1449  CB  GLN A  98       2.314 -24.038  8.965  1.00 20.00           C
ATOM   1462  N   GLU A  99       2.732 -27.268  8.376  1.00 20.00           N
ATOM   1463  CA  GLU A  99       2.393 -28.445  7.605  1.00 20.00           C
ATOM   1464  C   GLU A  99       3.545 -29.000  6.751  1.00 20.00           C
ATOM   1465  O   GLU A  99       3.372 -29.911  5.899  1.00 20.00           O
ATOM   1466  CB  GLU A  99       1.119 -28.172  6.768  1.00 20.00           C
ATOM   1477  N   ALA A 100       4.759 -28.513  7.021  1.00 20.00           N
ATOM   1478  CA  ALA A 100       5.872 -28.971  6.226  1.00 20.00           C
ATOM   1479  C   ALA A 100       6.296 -30.405  6.649  1.00 20.00           C
ATOM   1480  O   ALA A 100       6.188 -30.775  7.839  1.00 20.00           O
ATOM   1481  CB  ALA A 100       7.068 -27.965  6.332  1.00 20.00           C
ATOM   1487  N   ASN A 101       6.814 -31.121  5.667  1.00 20.00           N
ATOM   1488  CA  ASN A 101       7.360 -32.465  5.860  1.00 20.00           C
ATOM   1489  C   ASN A 101       8.836 -32.441  6.071  1.00 20.00           C
ATOM   1490  O   ASN A 101       9.680 -32.246  5.120  1.00 20.00           O
ATOM   1491  CB  ASN A 101       7.031 -33.381  4.697  1.00 20.00           C
ATOM   1501  N   LEU A 102       9.201 -32.554  7.353  1.00 20.00           N
ATOM   1502  CA  LEU A 102      10.593 -32.490  7.815  1.00 20.00           C
ATOM   1503  C   LEU A 102      11.040 -33.824  8.389  1.00 20.00           C
ATOM   1504  O   LEU A 102      11.945 -33.890  9.234  1.00 20.00           O
ATOM   1505  CB  LEU A 102      10.760 -31.381  8.862  1.00 20.00           C
ATOM   1520  N   THR A 103      10.460 -34.936  7.895  1.00 20.00           N
ATOM   1521  CA  THR A 103      10.775 -36.247  8.375  1.00 20.00           C
ATOM   1522  C   THR A 103      12.167 -36.541  8.032  1.00 20.00           C
ATOM   1523  O   THR A 103      12.603 -36.290  6.918  1.00 20.00           O
ATOM   1524  CB  THR A 103       9.777 -37.322  7.903  1.00 20.00           C
ATOM   1534  N   GLN A 104      12.884 -37.125  8.985  1.00 20.00           N
ATOM   1535  CA  GLN A 104      14.259 -37.406  8.832  1.00 20.00           C
ATOM   1536  C   GLN A 104      15.185 -36.275  8.408  1.00 20.00           C
ATOM   1537  O   GLN A 104      16.289 -36.515  7.915  1.00 20.00           O
ATOM   1538  CB  GLN A 104      14.389 -38.550  7.823  1.00 20.00           C
ATOM   1551  N   ALA A 105      14.760 -35.034  8.604  1.00  0.00           N
ATOM   1552  CA  ALA A 105      15.560 -33.888  8.199  1.00  0.00           C
ATOM   1553  C   ALA A 105      16.677 -33.606  9.164  1.00  0.00           C
ATOM   1554  O   ALA A 105      16.573 -33.803 10.364  1.00  0.00           O
ATOM   1555  CB  ALA A 105      14.692 -32.580  7.966  1.00  0.00           C
ATOM   1561  N   LYS A 106      17.784 -33.169  8.614  1.00  0.00           N
ATOM   1562  CA  LYS A 106      18.942 -32.790  9.435  1.00  0.00           C
ATOM   1563  C   LYS A 106      18.870 -31.275  9.785  1.00  0.00           C
ATOM   1564  O   LYS A 106      19.423 -30.422  9.036  1.00  0.00           O
ATOM   1565  CB  LYS A 106      20.246 -33.118  8.706  1.00  0.00           C
ATOM   1583  N   LEU A 107      18.297 -30.999 10.941  1.00  0.00           N
ATOM   1584  CA  LEU A 107      18.020 -29.667 11.394  1.00  0.00           C
ATOM   1585  C   LEU A 107      19.006 -29.192 12.479  1.00  0.00           C
ATOM   1586  O   LEU A 107      18.797 -28.188 13.182  1.00  0.00           O
ATOM   1587  CB  LEU A 107      16.583 -29.604 11.928  1.00  0.00           C
ATOM   1602  N   GLY A 108      20.101 -29.944 12.619  1.00  0.00           N
ATOM   1603  CA  GLY A 108      21.081 -29.539 13.563  1.00  0.00           C
ATOM   1604  C   GLY A 108      22.241 -30.486 13.777  1.00  0.00           C
ATOM   1605  O   GLY A 108      22.231 -31.652 13.380  1.00  0.00           O
ATOM   1609  N   THR A 109      23.152 -29.948 14.586  1.00  0.00           N
ATOM   1610  CA  THR A 109      24.398 -30.539 15.012  1.00  0.00           C
ATOM   1611  C   THR A 109      24.829 -29.787 16.263  1.00  0.00           C
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ATOM   1612  O   THR A 109     24.360 -28.676 16.504 1.00 0.00          O
ATOM   1613  CB  THR A 109     25.482 -30.463 13.921 1.00 0.00          C
ATOM   1623  N   TRP A 110     25.744 -30.385 17.036 1.00 0.00          N
ATOM   1624  CA  TRP A 110     26.164 -29.839 18.313 1.00 0.00          C
ATOM   1625  C   TRP A 110     27.500 -30.401 18.782 1.00 0.00          C
ATOM   1626  O   TRP A 110     27.806 -31.582 18.606 1.00 0.00          O
ATOM   1627  CB  TRP A 110     25.097 -30.116 19.373 1.00 0.00          C
ATOM   1647  N   SER A 111     28.293 -29.496 19.361 1.00 0.00          N
ATOM   1648  CA  SER A 111     29.563 -29.757 20.025 1.00 0.00          C
ATOM   1649  C   SER A 111     29.725 -28.776 21.189 1.00 0.00          C
ATOM   1650  O   SER A 111     29.309 -27.620 21.096 1.00 0.00          O
ATOM   1651  CB  SER A 111     30.715 -29.619 19.049 1.00 0.00          C
ATOM   1658  N   SER A 112     30.370 -29.228 22.274 1.00 0.00          N
ATOM   1659  CA  SER A 112     30.604 -28.417 23.470 1.00 0.00          C
ATOM   1660  C   SER A 112     31.539 -27.227 23.199 1.00 0.00          C
ATOM   1661  O   SER A 112     31.461 -26.209 23.883 1.00 0.00          O
ATOM   1662  CB  SER A 112     31.186 -29.285 24.568 1.00 0.00          C
ATOM   1669  N   SER A 113     32.249 -27.293 22.062 1.00 0.00          N
ATOM   1670  CA  SER A 113     33.134 -26.276 21.494 1.00 0.00          C
ATOM   1671  C   SER A 113     32.528 -25.129 20.653 1.00 0.00          C
ATOM   1672  O   SER A 113     33.233 -24.558 19.814 1.00 0.00          O
ATOM   1673  CB  SER A 113     34.163 -26.992 20.641 1.00 0.00          C
ATOM   1680  N   GLY A 114     31.281 -24.729 20.957 1.00 0.00          N
ATOM   1681  CA  GLY A 114     30.502 -23.653 20.345 1.00 0.00          C
ATOM   1682  C   GLY A 114     29.791 -23.903 19.008 1.00 0.00          C
ATOM   1683  O   GLY A 114     29.592 -22.964 18.234 1.00 0.00          O
ATOM   1687  N   LEU A 115     29.302 -25.132 18.803 1.00 0.00          N
ATOM   1688  CA  LEU A 115     28.613 -25.541 17.585 1.00 0.00          C
ATOM   1689  C   LEU A 115     27.114 -25.725 17.824 1.00 0.00          C
ATOM   1690  O   LEU A 115     26.714 -26.552 18.643 1.00 0.00          O
ATOM   1691  CB  LEU A 115     29.216 -26.847 17.053 1.00 0.00          C
ATOM   1706  N   THR A 116     26.295 -24.934 17.115 1.00 0.00          N
ATOM   1707  CA  THR A 116     24.839 -25.015 17.194 1.00 0.00          C
ATOM   1708  C   THR A 116     24.243 -25.620 15.927 1.00 0.00          C
ATOM   1709  O   THR A 116     24.939 -25.782 14.922 1.00 0.00          O
ATOM   1710  CB  THR A 116     24.221 -23.627 17.442 1.00 0.00          C
ATOM   1720  N   GLY A 117     22.929 -25.909 15.979 1.00 0.00          N
ATOM   1721  CA  GLY A 117     22.179 -26.544 14.896 1.00 0.00          C
ATOM   1722  C   GLY A 117     21.484 -25.445 14.093 1.00 0.00          C
ATOM   1723  O   GLY A 117     21.939 -24.321 14.067 1.00 0.00          O
ATOM   1727  N   ALA A 118     20.377 -25.772 13.445 1.00 0.00          N
ATOM   1728  CA  ALA A 118     19.652 -24.798 12.581 1.00 0.00          C
ATOM   1729  C   ALA A 118     18.925 -23.790 13.430 1.00 0.00          C
ATOM   1730  O   ALA A 118     18.584 -24.054 14.604 1.00 0.00          O
ATOM   1731  CB  ALA A 118     18.652 -25.504 11.547 1.00 0.00          C
ATOM   1737  N   ASP A 119     18.708 -22.603 12.885 1.00 0.00          N
ATOM   1738  CA  ASP A 119     17.997 -21.508 13.560 1.00 0.00          C
ATOM   1739  C   ASP A 119     16.594 -21.437 13.111 1.00 0.00          C
ATOM   1740  O   ASP A 119     16.319 -21.074 11.952 1.00 0.00          O
ATOM   1741  CB  ASP A 119     18.669 -20.158 13.299 1.00 0.00          C
ATOM   1749  N   LEU A 120     15.696 -21.810 13.997 1.00 0.00          N
ATOM   1750  CA  LEU A 120     14.275 -21.780 13.797 1.00 0.00          C
ATOM   1751  C   LEU A 120     13.536 -20.761 14.703 1.00 0.00          C
ATOM   1752  O   LEU A 120     12.387 -21.004 15.000 1.00 0.00          O
ATOM   1753  CB  LEU A 120     13.716 -23.189 14.034 1.00 0.00          C
ATOM   1768  N   SER A 121     14.199 -19.700 15.081 1.00 20.00         N
ATOM   1769  CA  SER A 121     13.699 -18.676 15.988 1.00 20.00         C
ATOM   1770  C   SER A 121     12.481 -18.114 15.343 1.00 20.00         C
ATOM   1771  O   SER A 121     12.465 -17.738 14.187 1.00 20.00         O
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ATOM   1772  CB  SER A 121     14.731 -17.595 16.248 1.00 20.00        C
ATOM   1779  N   ASP A 122     11.440 -18.020 16.158 1.00 20.00        N
ATOM   1780  CA  ASP A 122     10.125 -17.408 15.724 1.00 20.00        C
ATOM   1781  C   ASP A 122      9.537 -18.042 14.415 1.00 20.00        C
ATOM   1782  O   ASP A 122      8.678 -17.423 13.740 1.00 20.00        O
ATOM   1783  CB  ASP A 122     10.303 -15.926 15.566 1.00 20.00        C
ATOM   1791  N   ALA A 123      9.889 -19.285 14.114 1.00 20.00        N
ATOM   1792  CA  ALA A 123      9.358 -20.018 12.960 1.00 20.00        C
ATOM   1793  C   ALA A 123      8.019 -20.637 13.244 1.00 20.00        C
ATOM   1794  O   ALA A 123      7.739 -21.017 14.394 1.00 20.00        O
ATOM   1795  CB  ALA A 123     10.330 -21.156 12.429 1.00 20.00        C
ATOM   1801  N   ASN A 124      7.217 -20.706 12.212 1.00 20.00        N
ATOM   1802  CA  ASN A 124      5.920 -21.291 12.347 1.00 20.00        C
ATOM   1803  C   ASN A 124      5.994 -22.735 11.921 1.00 20.00        C
ATOM   1804  O   ASN A 124      6.177 -23.039 10.730 1.00 20.00        O
ATOM   1805  CB  ASN A 124      4.902 -20.566 11.554 1.00 20.00        C
ATOM   1815  N   LEU A 125      5.908 -23.672 12.859 1.00 20.00        N
ATOM   1816  CA  LEU A 125      5.906 -25.066 12.632 1.00 20.00        C
ATOM   1817  C   LEU A 125      4.600 -25.729 13.032 1.00 20.00        C
ATOM   1818  O   LEU A 125      4.555 -26.963 13.331 1.00 20.00        O
ATOM   1819  CB  LEU A 125      7.083 -25.699 13.384 1.00 20.00        C
ATOM   1834  N   GLU A 126      3.488 -25.005 12.886 1.00 20.00        N
ATOM   1835  CA  GLU A 126      2.187 -25.565 13.266 1.00 20.00        C
ATOM   1836  C   GLU A 126      1.870 -26.793 12.417 1.00 20.00        C
ATOM   1837  O   GLU A 126      1.973 -26.762 11.176 1.00 20.00        O
ATOM   1838  CB  GLU A 126      1.083 -24.510 13.135 1.00 20.00        C
ATOM   1849  N   GLN A 127      1.503 -27.919 13.093 1.00 20.00        N
ATOM   1850  CA  GLN A 127      1.188 -29.184 12.456 1.00 20.00        C
ATOM   1851  C   GLN A 127      2.258 -29.676 11.502 1.00 20.00        C
ATOM   1852  O   GLN A 127      1.932 -30.559 10.680 1.00 20.00        O
ATOM   1853  CB  GLN A 127     -0.139 -29.066 11.702 1.00 20.00        C
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ATOM   1439  N   GLN A  98       4.616 -24.270  8.248  1.00 20.00           N
ATOM   1440  CA  GLN A  98       3.454 -25.026  8.704  1.00 20.00           C
ATOM   1441  C   GLN A  98       3.101 -26.156  7.774  1.00 20.00           C
ATOM   1442  O   GLN A  98       3.205 -26.013  6.519  1.00 20.00           O
ATOM   1443  CB  GLN A  98       2.328 -24.092  8.928  1.00 20.00           C
ATOM   1456  N   GLU A  99       2.730 -27.324  8.339  1.00 20.00           N
ATOM   1457  CA  GLU A  99       2.386 -28.499  7.567  1.00 20.00           C
ATOM   1458  C   GLU A  99       3.535 -29.060  6.715  1.00 20.00           C
ATOM   1459  O   GLU A  99       3.359 -29.971  5.863  1.00 20.00           O
ATOM   1460  CB  GLU A  99       1.114 -28.219  6.728  1.00 20.00           C
ATOM   1471  N   ALA A 100       4.752 -28.581  6.987  1.00 20.00           N
ATOM   1472  CA  ALA A 100       5.864 -29.044  6.195  1.00 20.00           C
ATOM   1473  C   ALA A 100       6.279 -30.481  6.618  1.00 20.00           C
ATOM   1474  O   ALA A 100       6.167 -30.850  7.807  1.00 20.00           O
ATOM   1475  CB  ALA A 100       7.065 -28.045  6.303  1.00 20.00           C
ATOM   1481  N   ASN A 101       6.795 -31.200  5.636  1.00 20.00           N
ATOM   1482  CA  ASN A 101       7.333 -32.546  5.831  1.00 20.00           C
ATOM   1483  C   ASN A 101       8.809 -32.531  6.044  1.00 20.00           C
ATOM   1484  O   ASN A 101       9.655 -32.340  5.095  1.00 20.00           O
ATOM   1485  CB  ASN A 101       7.001 -33.461  4.666  1.00 20.00           C
ATOM   1495  N   LEU A 102       9.171 -32.646  7.326  1.00 20.00           N
ATOM   1496  CA  LEU A 102      10.563 -32.589  7.791  1.00 20.00           C
ATOM   1497  C   LEU A 102      11.001 -33.926  8.366  1.00 20.00           C
ATOM   1498  O   LEU A 102      11.904 -33.997  9.213  1.00 20.00           O
ATOM   1499  CB  LEU A 102      10.734 -31.482  8.838  1.00 20.00           C
ATOM   1514  N   THR A 103      10.416 -35.034  7.871  1.00 20.00           N
ATOM   1515  CA  THR A 103      10.723 -36.348  8.351  1.00 20.00           C
ATOM   1516  C   THR A 103      12.114 -36.649  8.010  1.00 20.00           C
ATOM   1517  O   THR A 103      12.553 -36.400  6.897  1.00 20.00           O
ATOM   1518  CB  THR A 103       9.720 -37.416  7.877  1.00 20.00           C
ATOM   1528  N   GLN A 104      12.826 -37.237  8.964  1.00 20.00           N
ATOM   1529  CA  GLN A 104      14.200 -37.525  8.814  1.00 20.00           C
ATOM   1530  C   GLN A 104      15.133 -36.400  8.391  1.00 20.00           C
ATOM   1531  O   GLN A 104      16.237 -36.646  7.901  1.00 20.00           O
ATOM   1532  CB  GLN A 104      14.325 -38.670  7.804  1.00 20.00           C
ATOM   1545  N   ALA A 105      14.714 -35.157  8.587  1.00  0.00           N
ATOM   1546  CA  ALA A 105      15.521 -34.015  8.184  1.00  0.00           C
ATOM   1547  C   ALA A 105      16.682 -33.785  9.110  1.00  0.00           C
ATOM   1548  O   ALA A 105      16.628 -34.029 10.304  1.00  0.00           O
ATOM   1549  CB  ALA A 105      14.672 -32.683  8.025  1.00  0.00           C
ATOM   1555  N   MET A 106      17.771 -33.338  8.530  1.00  0.00           N
ATOM   1556  CA  MET A 106      18.964 -32.997  9.315  1.00  0.00           C
ATOM   1557  C   MET A 106      18.904 -31.503  9.748  1.00  0.00           C
ATOM   1558  O   MET A 106      19.419 -30.609  9.020  1.00  0.00           O
ATOM   1559  CB  MET A 106      20.228 -33.285  8.507  1.00  0.00           C
ATOM   1572  N   LEU A 107      18.386 -31.292 10.943  1.00  0.00           N
ATOM   1573  CA  LEU A 107      18.236 -29.991 11.526  1.00  0.00           C
ATOM   1574  C   LEU A 107      19.293 -29.700 12.608  1.00  0.00           C
ATOM   1575  O   LEU A 107      19.191 -28.755 13.410  1.00  0.00           O
ATOM   1576  CB  LEU A 107      16.828 -29.865 12.122  1.00  0.00           C
ATOM   1591  N   GLY A 108      20.328 -30.544 12.633  1.00  0.00           N
ATOM   1592  CA  GLY A 108      21.368 -30.310 13.569  1.00  0.00           C
ATOM   1593  C   GLY A 108      22.230 -31.579 13.712  1.00  0.00           C
ATOM   1594  O   GLY A 108      21.711 -32.689 13.563  1.00  0.00           O
ATOM   1598  N   GLN A 109      23.543 -31.390 13.971  1.00  0.00           N
ATOM   1599  CA  GLN A 109      24.574 -32.432 14.032  1.00  0.00           C
ATOM   1600  C   GLN A 109      25.767 -32.026 14.906  1.00  0.00           C
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ATOM   1601  O   GLN A 109     26.377 -30.976 14.712 1.00 0.00          O
ATOM   1602  CB  GLN A 109     25.062 -32.773 12.622 1.00 0.00          C
ATOM   1615  N   THR A 110     26.253 -32.910 15.765 1.00 0.00          N
ATOM   1616  CA  THR A 110     27.468 -32.549 16.477 1.00 0.00          C
ATOM   1617  C   THR A 110     28.673 -32.923 15.647 1.00 0.00          C
ATOM   1618  O   THR A 110     28.667 -33.998 15.057 1.00 0.00          O
ATOM   1619  CB  THR A 110     27.546 -33.236 17.853 1.00 0.00          C
ATOM   1629  N   TYR A 111     29.625 -31.989 15.494 1.00 0.00          N
ATOM   1630  CA  TYR A 111     30.842 -32.215 14.735 1.00 0.00          C
ATOM   1631  C   TYR A 111     32.039 -32.222 15.693 1.00 0.00          C
ATOM   1632  O   TYR A 111     31.957 -31.681 16.795 1.00 0.00          O
ATOM   1633  CB  TYR A 111     31.014 -31.149 13.650 1.00 0.00          C
ATOM   1650  N   PRO A 112     33.170 -32.781 15.239 1.00 0.00          N
ATOM   1651  CA  PRO A 112     34.457 -32.824 15.929 1.00 0.00          C
ATOM   1652  C   PRO A 112     34.955 -31.484 16.474 1.00 0.00          C
ATOM   1653  O   PRO A 112     35.646 -31.452 17.490 1.00 0.00          O
ATOM   1654  CB  PRO A 112     35.386 -33.344 14.827 1.00 0.00          C
ATOM   1664  N   TRP A 113     34.543 -30.377 15.838 1.00 0.00          N
ATOM   1665  CA  TRP A 113     34.914 -29.035 16.240 1.00 0.00          C
ATOM   1666  C   TRP A 113     33.842 -28.235 16.992 1.00 0.00          C
ATOM   1667  O   TRP A 113     34.091 -27.057 17.215 1.00 0.00          O
ATOM   1668  CB  TRP A 113     35.330 -28.249 14.996 1.00 0.00          C
ATOM   1688  N   GLY A 114     32.702 -28.848 17.385 1.00 0.00          N
ATOM   1689  CA  GLY A 114     31.531 -28.329 18.117 1.00 0.00          C
ATOM   1690  C   GLY A 114     30.206 -28.736 17.438 1.00 0.00          C
ATOM   1691  O   GLY A 114     30.177 -29.114 16.265 1.00 0.00          O
ATOM   1695  N   THR A 115     29.092 -28.497 18.151 1.00 0.00          N
ATOM   1696  CA  THR A 115     27.750 -28.787 17.688 1.00 0.00          C
ATOM   1697  C   THR A 115     27.164 -27.623 16.873 1.00 0.00          C
ATOM   1698  O   THR A 115     27.218 -26.475 17.283 1.00 0.00          O
ATOM   1699  CB  THR A 115     26.826 -29.112 18.876 1.00 0.00          C
ATOM   1709  N   VAL A 116     26.624 -27.976 15.689 1.00 0.00          N
ATOM   1710  CA  VAL A 116     26.017 -27.067 14.732 1.00 0.00          C
ATOM   1711  C   VAL A 116     24.522 -27.375 14.612 1.00 0.00          C
ATOM   1712  O   VAL A 116     24.077 -28.492 14.351 1.00 0.00          O
ATOM   1713  CB  VAL A 116     26.693 -27.200 13.355 1.00 0.00          C
ATOM   1725  N   GLY A 117     23.673 -26.349 14.665 1.00 0.00          N
ATOM   1726  CA  GLY A 117     22.265 -26.776 14.558 1.00 0.00          C
ATOM   1727  C   GLY A 117     21.483 -25.737 13.756 1.00 0.00          C
ATOM   1728  O   GLY A 117     21.931 -24.621 13.593 1.00 0.00          O
ATOM   1732  N   ALA A 118     20.310 -26.104 13.262 1.00 0.00          N
ATOM   1733  CA  ALA A 118     19.467 -25.176 12.459 1.00 0.00          C
ATOM   1734  C   ALA A 118     18.854 -24.128 13.349 1.00 0.00          C
ATOM   1735  O   ALA A 118     18.546 -24.382 14.535 1.00 0.00          O
ATOM   1736  CB  ALA A 118     18.341 -25.933 11.606 1.00 0.00          C
ATOM   1742  N   ASP A 119     18.702 -22.922 12.827 1.00 0.00          N
ATOM   1743  CA  ASP A 119     18.053 -21.802 13.523 1.00 0.00          C
ATOM   1744  C   ASP A 119     16.650 -21.657 13.093 1.00 0.00          C
ATOM   1745  O   ASP A 119     16.378 -21.221 11.959 1.00 0.00          O
ATOM   1746  CB  ASP A 119     18.787 -20.483 13.269 1.00 0.00          C
ATOM   1754  N   LEU A 120     15.747 -22.047 13.967 1.00 0.00          N
ATOM   1755  CA  LEU A 120     14.326 -21.994 13.767 1.00 0.00          C
ATOM   1756  C   LEU A 120     13.602 -20.977 14.688 1.00 0.00          C
ATOM   1757  O   LEU A 120     12.454 -21.214 14.992 1.00 0.00          O
ATOM   1758  CB  LEU A 120     13.746 -23.397 13.984 1.00 0.00          C
ATOM   1773  N   SER A 121     14.276 -19.923 15.068 1.00 20.00         N
ATOM   1774  CA  SER A 121     13.784 -18.894 15.973 1.00 20.00         C
ATOM   1775  C   SER A 121     12.574 -18.318 15.325 1.00 20.00         C
ATOM   1776  O   SER A 121     12.567 -17.942 14.168 1.00 20.00         O
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ATOM   1777  CB  SER A 121     14.827 -17.824 16.238 1.00 20.00        C
ATOM   1784  N   ASP A 122     11.532 -18.212 16.136 1.00 20.00        N
ATOM   1785  CA  ASP A 122     10.226 -17.586 15.697 1.00 20.00        C
ATOM   1786  C   ASP A 122      9.635 -18.213 14.386 1.00 20.00        C
ATOM   1787  O   ASP A 122      8.785 -17.584 13.708 1.00 20.00        O
ATOM   1788  CB  ASP A 122     10.420 -16.106 15.540 1.00 20.00        C
ATOM   1796  N   ALA A 123      9.974 -19.459 14.087 1.00 20.00        N
ATOM   1797  CA  ALA A 123      9.439 -20.186 12.931 1.00 20.00        C
ATOM   1798  C   ALA A 123      8.092 -20.790 13.209 1.00 20.00        C
ATOM   1799  O   ALA A 123      7.804 -21.167 14.358 1.00 20.00        O
ATOM   1800  CB  ALA A 123     10.400 -21.335 12.402 1.00 20.00        C
ATOM   1806  N   ASN A 124      7.293 -20.850 12.174 1.00 20.00        N
ATOM   1807  CA  ASN A 124      5.989 -21.421 12.305 1.00 20.00        C
ATOM   1808  C   ASN A 124      6.048 -22.865 11.879 1.00 20.00        C
ATOM   1809  O   ASN A 124      6.232 -23.171 10.688 1.00 20.00        O
ATOM   1810  CB  ASN A 124      4.982 -20.684 11.508 1.00 20.00        C
ATOM   1820  N   LEU A 125      5.948 -23.801 12.816 1.00 20.00        N
ATOM   1821  CA  LEU A 125      5.931 -25.196 12.589 1.00 20.00        C
ATOM   1822  C   LEU A 125      4.617 -25.844 12.984 1.00 20.00        C
ATOM   1823  O   LEU A 125      4.557 -27.077 13.283 1.00 20.00        O
ATOM   1824  CB  LEU A 125      7.099 -25.842 13.345 1.00 20.00        C
ATOM   1839  N   GLU A 126      3.514 -25.107 12.835 1.00 20.00        N
ATOM   1840  CA  GLU A 126      2.205 -25.652 13.209 1.00 20.00        C
ATOM   1841  C   GLU A 126      1.877 -26.876 12.360 1.00 20.00        C
ATOM   1842  O   GLU A 126      1.984 -26.846 11.118 1.00 20.00        O
ATOM   1843  CB  GLU A 126      1.113 -24.585 13.076 1.00 20.00        C
ATOM   1854  N   GLN A 127      1.495 -27.998 13.034 1.00 20.00        N
ATOM   1855  CA  GLN A 127      1.168 -29.259 12.396 1.00 20.00        C
ATOM   1856  C   GLN A 127      2.236 -29.763 11.445 1.00 20.00        C
ATOM   1857  O   GLN A 127      1.903 -30.642 10.622 1.00 20.00        O
ATOM   1858  CB  GLN A 127     -0.155 -29.127 11.637 1.00 20.00        C
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ATOM   1431  N   GLN A  98       4.626 -24.219  8.289  1.00 20.00           N
ATOM   1432  CA  GLN A  98       3.470 -24.983  8.748  1.00 20.00           C
ATOM   1433  C   GLN A  98       3.123 -26.116  7.819  1.00 20.00           C
ATOM   1434  O   GLN A  98       3.223 -25.971  6.563  1.00 20.00           O
ATOM   1435  CB  GLN A  98       2.339 -24.057  8.975  1.00 20.00           C
ATOM   1448  N   GLU A  99       2.761 -27.286  8.384  1.00 20.00           N
ATOM   1449  CA  GLU A  99       2.423 -28.463  7.613  1.00 20.00           C
ATOM   1450  C   GLU A  99       3.574 -29.016  6.757  1.00 20.00           C
ATOM   1451  O   GLU A  99       3.402 -29.927  5.906  1.00 20.00           O
ATOM   1452  CB  GLU A  99       1.148 -28.191  6.777  1.00 20.00           C
ATOM   1463  N   ALA A 100       4.788 -28.528  7.026  1.00 20.00           N
ATOM   1464  CA  ALA A 100       5.901 -28.984  6.231  1.00 20.00           C
ATOM   1465  C   ALA A 100       6.327 -30.418  6.653  1.00 20.00           C
ATOM   1466  O   ALA A 100       6.221 -30.789  7.842  1.00 20.00           O
ATOM   1467  CB  ALA A 100       7.096 -27.977  6.336  1.00 20.00           C
ATOM   1473  N   ASN A 101       6.846 -31.133  5.669  1.00 20.00           N
ATOM   1474  CA  ASN A 101       7.393 -32.476  5.862  1.00 20.00           C
ATOM   1475  C   ASN A 101       8.869 -32.451  6.071  1.00 20.00           C
ATOM   1476  O   ASN A 101       9.712 -32.254  5.119  1.00 20.00           O
ATOM   1477  CB  ASN A 101       7.064 -33.393  4.698  1.00 20.00           C
ATOM   1487  N   LEU A 102       9.235 -32.564  7.352  1.00 20.00           N
ATOM   1488  CA  LEU A 102      10.628 -32.498  7.814  1.00 20.00           C
ATOM   1489  C   LEU A 102      11.077 -33.831  8.387  1.00 20.00           C
ATOM   1490  O   LEU A 102      11.983 -33.896  9.231  1.00 20.00           O
ATOM   1491  CB  LEU A 102      10.795 -31.389  8.860  1.00 20.00           C
ATOM   1506  N   THR A 103      10.498 -34.944  7.893  1.00 20.00           N
ATOM   1507  CA  THR A 103      10.815 -36.255  8.372  1.00 20.00           C
ATOM   1508  C   THR A 103      12.208 -36.547  8.027  1.00 20.00           C
ATOM   1509  O   THR A 103      12.642 -36.295  6.913  1.00 20.00           O
ATOM   1510  CB  THR A 103       9.818 -37.331  7.900  1.00 20.00           C
ATOM   1520  N   GLN A 104      12.926 -37.131  8.979  1.00 20.00           N
ATOM   1521  CA  GLN A 104      14.301 -37.409  8.825  1.00 20.00           C
ATOM   1522  C   GLN A 104      15.225 -36.277  8.400  1.00 20.00           C
ATOM   1523  O   GLN A 104      16.330 -36.516  7.906  1.00 20.00           O
ATOM   1524  CB  GLN A 104      14.431 -38.553  7.815  1.00 20.00           C
ATOM   1537  N   ALA A 105      14.799 -35.037  8.597  1.00  0.00           N
ATOM   1538  CA  ALA A 105      15.597 -33.890  8.192  1.00  0.00           C
ATOM   1539  C   ALA A 105      16.678 -33.570  9.187  1.00  0.00           C
ATOM   1540  O   ALA A 105      16.591 -33.866 10.367  1.00  0.00           O
ATOM   1541  CB  ALA A 105      14.720 -32.600  7.899  1.00  0.00           C
ATOM   1547  N   MET A 106      17.736 -32.983  8.682  1.00  0.00           N
ATOM   1548  CA  MET A 106      18.847 -32.551  9.540  1.00  0.00           C
ATOM   1549  C   MET A 106      18.698 -31.038  9.877  1.00  0.00           C
ATOM   1550  O   MET A 106      19.045 -30.163  9.037  1.00  0.00           O
ATOM   1551  CB  MET A 106      20.183 -32.834  8.857  1.00  0.00           C
ATOM   1564  N   LEU A 107      18.298 -30.781 11.108  1.00  0.00           N
ATOM   1565  CA  LEU A 107      18.117 -29.456 11.624  1.00  0.00           C
ATOM   1566  C   LEU A 107      19.108 -29.119 12.755  1.00  0.00           C
ATOM   1567  O   LEU A 107      18.989 -28.111 13.474  1.00  0.00           O
ATOM   1568  CB  LEU A 107      16.676 -29.303 12.128  1.00  0.00           C
ATOM   1583  N   GLY A 108      20.104 -29.994 12.917  1.00  0.00           N
ATOM   1584  CA  GLY A 108      21.034 -29.772 13.965  1.00  0.00           C
ATOM   1585  C   GLY A 108      21.987 -30.959 13.794  1.00  0.00           C
ATOM   1586  O   GLY A 108      21.634 -32.072 14.182  1.00  0.00           O
ATOM   1590  N   LYS A 109      23.151 -30.753 13.159  1.00  0.00           N
ATOM   1591  CA  LYS A 109      24.103 -31.814 12.882  1.00  0.00           C
ATOM   1592  C   LYS A 109      25.230 -31.883 13.903  1.00  0.00           C
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ATOM   1593  O   LYS A 109     25.799 -30.853 14.273 1.00 0.00          O
ATOM   1594  CB  LYS A 109     24.687 -31.637 11.479 1.00 0.00          C
ATOM   1612  N   ASP A 110     25.585 -33.127 14.253 1.00 0.00          N
ATOM   1613  CA  ASP A 110     26.682 -33.461 15.150 1.00 0.00          C
ATOM   1614  C   ASP A 110     27.597 -34.556 14.576 1.00 0.00          C
ATOM   1615  O   ASP A 110     28.510 -34.996 15.277 1.00 0.00          O
ATOM   1616  CB  ASP A 110     26.129 -33.910 16.505 1.00 0.00          C
ATOM   1624  N   GLU A 111     27.460 -34.858 13.268 1.00 0.00          N
ATOM   1625  CA  GLU A 111     28.188 -35.863 12.484 1.00 0.00          C
ATOM   1626  C   GLU A 111     29.706 -35.945 12.708 1.00 0.00          C
ATOM   1627  O   GLU A 111     30.226 -37.032 12.958 1.00 0.00          O
ATOM   1628  CB  GLU A 111     27.929 -35.609 10.997 1.00 0.00          C
ATOM   1639  N   ASP A 112     30.388 -34.789 12.712 1.00 0.00          N
ATOM   1640  CA  ASP A 112     31.832 -34.704 12.847 1.00 0.00          C
ATOM   1641  C   ASP A 112     32.251 -34.269 14.261 1.00 0.00          C
ATOM   1642  O   ASP A 112     33.433 -34.003 14.492 1.00 0.00          O
ATOM   1643  CB  ASP A 112     32.399 -33.726 11.815 1.00 0.00          C
ATOM   1651  N   GLY A 113     31.284 -34.244 15.203 1.00 0.00          N
ATOM   1652  CA  GLY A 113     31.380 -33.821 16.604 1.00 0.00          C
ATOM   1653  C   GLY A 113     31.128 -32.336 16.889 1.00 0.00          C
ATOM   1654  O   GLY A 113     31.051 -31.940 18.051 1.00 0.00          O
ATOM   1658  N   VAL A 114     30.945 -31.535 15.831 1.00 0.00          N
ATOM   1659  CA  VAL A 114     30.685 -30.111 15.907 1.00 0.00          C
ATOM   1660  C   VAL A 114     29.223 -29.850 15.567 1.00 0.00          C
ATOM   1661  O   VAL A 114     28.695 -30.368 14.584 1.00 0.00          O
ATOM   1662  CB  VAL A 114     31.597 -29.338 14.936 1.00 0.00          C
ATOM   1674  N   VAL A 115     28.572 -29.085 16.448 1.00 0.00          N
ATOM   1675  CA  VAL A 115     27.184 -28.721 16.312 1.00 0.00          C
ATOM   1676  C   VAL A 115     26.950 -27.635 15.271 1.00 0.00          C
ATOM   1677  O   VAL A 115     27.576 -26.574 15.294 1.00 0.00          O
ATOM   1678  CB  VAL A 115     26.643 -28.240 17.672 1.00 0.00          C
ATOM   1690  N   TYR A 116     26.084 -27.982 14.312 1.00 0.00          N
ATOM   1691  CA  TYR A 116     25.684 -27.122 13.224 1.00 0.00          C
ATOM   1692  C   TYR A 116     24.186 -27.042 13.432 1.00 0.00          C
ATOM   1693  O   TYR A 116     23.468 -27.854 12.863 1.00 0.00          O
ATOM   1694  CB  TYR A 116     26.061 -27.679 11.850 1.00 0.00          C
ATOM   1711  N   GLY A 117     23.796 -26.402 14.540 1.00 0.00          N
ATOM   1712  CA  GLY A 117     22.416 -26.220 14.934 1.00 0.00          C
ATOM   1713  C   GLY A 117     21.701 -25.244 14.001 1.00 0.00          C
ATOM   1714  O   GLY A 117     22.178 -24.153 13.770 1.00 0.00          O
ATOM   1718  N   ALA A 118     20.553 -25.638 13.472 1.00 0.00          N
ATOM   1719  CA  ALA A 118     19.741 -24.747 12.597 1.00 0.00          C
ATOM   1720  C   ALA A 118     18.988 -23.745 13.431 1.00 0.00          C
ATOM   1721  O   ALA A 118     18.631 -24.010 14.600 1.00 0.00          O
ATOM   1722  CB  ALA A 118     18.747 -25.553 11.633 1.00 0.00          C
ATOM   1728  N   ASP A 119     18.767 -22.563 12.880 1.00 0.00          N
ATOM   1729  CA  ASP A 119     18.053 -21.466 13.550 1.00 0.00          C
ATOM   1730  C   ASP A 119     16.646 -21.411 13.115 1.00 0.00          C
ATOM   1731  O   ASP A 119     16.355 -21.058 11.957 1.00 0.00          O
ATOM   1732  CB  ASP A 119     18.712 -20.113 13.267 1.00 0.00          C
ATOM   1740  N   LEU A 120     15.760 -21.786 14.012 1.00 0.00          N
ATOM   1741  CA  LEU A 120     14.337 -21.774 13.826 1.00 0.00          C
ATOM   1742  C   LEU A 120     13.594 -20.762 14.736 1.00 0.00          C
ATOM   1743  O   LEU A 120     12.448 -21.012 15.035 1.00 0.00          O
ATOM   1744  CB  LEU A 120     13.797 -23.189 14.071 1.00 0.00          C
ATOM   1759  N   SER A 121     14.252 -19.698 15.116 1.00 20.00         N
ATOM   1760  CA  SER A 121     13.745 -18.674 16.018 1.00 20.00         C
ATOM   1761  C   SER A 121     12.528 -18.117 15.367 1.00 20.00         C
ATOM   1762  O   SER A 121     12.516 -17.744 14.210 1.00 20.00         O
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ATOM   1763  CB  SER A 121     14.772 -17.589 16.282 1.00 20.00        C
ATOM   1770  N   ASP A 122     11.482 -18.025 16.177 1.00 20.00        N
ATOM   1771  CA  ASP A 122     10.168 -17.419 15.736 1.00 20.00        C
ATOM   1772  C   ASP A 122      9.588 -18.057 14.425 1.00 20.00        C
ATOM   1773  O   ASP A 122      8.730 -17.441 13.745 1.00 20.00        O
ATOM   1774  CB  ASP A 122     10.341 -15.936 15.576 1.00 20.00        C
ATOM   1782  N   ALA A 123      9.945 -19.298 14.128 1.00 20.00        N
ATOM   1783  CA  ALA A 123      9.423 -20.035 12.973 1.00 20.00        C
ATOM   1784  C   ALA A 123      8.084 -20.658 13.250 1.00 20.00        C
ATOM   1785  O   ALA A 123      7.800 -21.037 14.400 1.00 20.00        O
ATOM   1786  CB  ALA A 123     10.401 -21.171 12.448 1.00 20.00        C
ATOM   1792  N   ASN A 124      7.287 -20.731 12.215 1.00 20.00        N
ATOM   1793  CA  ASN A 124      5.992 -21.320 12.345 1.00 20.00        C
ATOM   1794  C   ASN A 124      6.072 -22.764 11.922 1.00 20.00        C
ATOM   1795  O   ASN A 124      6.262 -23.070 10.732 1.00 20.00        O
ATOM   1796  CB  ASN A 124      4.975 -20.600 11.546 1.00 20.00        C
ATOM   1806  N   LEU A 125      5.985 -23.701 12.861 1.00 20.00        N
ATOM   1807  CA  LEU A 125      5.988 -25.095 12.636 1.00 20.00        C
ATOM   1808  C   LEU A 125      4.683 -25.762 13.031 1.00 20.00        C
ATOM   1809  O   LEU A 125      4.640 -26.995 13.332 1.00 20.00        O
ATOM   1810  CB  LEU A 125      7.164 -25.723 13.395 1.00 20.00        C
ATOM   1825  N   GLU A 126      3.569 -25.041 12.879 1.00 20.00        N
ATOM   1826  CA  GLU A 126      2.268 -25.605 13.253 1.00 20.00        C
ATOM   1827  C   GLU A 126      1.959 -26.835 12.405 1.00 20.00        C
ATOM   1828  O   GLU A 126      2.067 -26.805 11.164 1.00 20.00        O
ATOM   1829  CB  GLU A 126      1.161 -24.554 13.116 1.00 20.00        C
ATOM   1840  N   GLN A 127      1.592 -27.961 13.080 1.00 20.00        N
ATOM   1841  CA  GLN A 127      1.285 -29.228 12.444 1.00 20.00        C
ATOM   1842  C   GLN A 127      2.361 -29.718 11.495 1.00 20.00        C
ATOM   1843  O   GLN A 127      2.042 -30.603 10.673 1.00 20.00        O
ATOM   1844  CB  GLN A 127     -0.039 -29.116 11.684 1.00 20.00        C
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ATOM   1442  N   GLN A  98       4.557 -24.256  8.257  1.00 20.00           N
ATOM   1443  CA  GLN A  98       3.397 -25.015  8.715  1.00 20.00           C
ATOM   1444  C   GLN A  98       3.043 -26.144  7.784  1.00 20.00           C
ATOM   1445  O   GLN A  98       3.144 -25.997  6.529  1.00 20.00           O
ATOM   1446  CB  GLN A  98       2.271 -24.083  8.944  1.00 20.00           C
ATOM   1459  N   GLU A  99       2.675 -27.313  8.347  1.00 20.00           N
ATOM   1460  CA  GLU A  99       2.331 -28.487  7.574  1.00 20.00           C
ATOM   1461  C   GLU A  99       3.479 -29.044  6.717  1.00 20.00           C
ATOM   1462  O   GLU A  99       3.301 -29.954  5.864  1.00 20.00           O
ATOM   1463  CB  GLU A  99       1.057 -28.207  6.739  1.00 20.00           C
ATOM   1474  N   ALA A 100       4.695 -28.564  6.987  1.00 20.00           N
ATOM   1475  CA  ALA A 100       5.806 -29.024  6.190  1.00 20.00           C
ATOM   1476  C   ALA A 100       6.224 -30.461  6.609  1.00 20.00           C
ATOM   1477  O   ALA A 100       6.116 -30.833  7.798  1.00 20.00           O
ATOM   1478  CB  ALA A 100       7.006 -28.024  6.297  1.00 20.00           C
ATOM   1484  N   ASN A 101       6.739 -31.177  5.625  1.00 20.00           N
ATOM   1485  CA  ASN A 101       7.279 -32.523  5.815  1.00 20.00           C
ATOM   1486  C   ASN A 101       8.755 -32.506  6.024  1.00 20.00           C
ATOM   1487  O   ASN A 101       9.599 -32.312  5.073  1.00 20.00           O
ATOM   1488  CB  ASN A 101       6.945 -33.436  4.649  1.00 20.00           C
ATOM   1498  N   LEU A 102       9.121 -32.623  7.305  1.00 20.00           N
ATOM   1499  CA  LEU A 102      10.514 -32.566  7.766  1.00 20.00           C
ATOM   1500  C   LEU A 102      10.956 -33.903  8.337  1.00 20.00           C
ATOM   1501  O   LEU A 102      11.862 -33.974  9.181  1.00 20.00           O
ATOM   1502  CB  LEU A 102      10.687 -31.460  8.815  1.00 20.00           C
ATOM   1517  N   THR A 103      10.371 -35.011  7.841  1.00 20.00           N
ATOM   1518  CA  THR A 103      10.681 -36.325  8.318  1.00 20.00           C
ATOM   1519  C   THR A 103      12.072 -36.624  7.972  1.00 20.00           C
ATOM   1520  O   THR A 103      12.508 -36.372  6.858  1.00 20.00           O
ATOM   1521  CB  THR A 103       9.678 -37.394  7.844  1.00 20.00           C
ATOM   1531  N   GLN A 104      12.788 -37.213  8.923  1.00 20.00           N
ATOM   1532  CA  GLN A 104      14.161 -37.499  8.768  1.00 20.00           C
ATOM   1533  C   GLN A 104      15.091 -36.371  8.345  1.00 20.00           C
ATOM   1534  O   GLN A 104      16.194 -36.614  7.851  1.00 20.00           O
ATOM   1535  CB  GLN A 104      14.285 -38.641  7.756  1.00 20.00           C
ATOM   1548  N   ALA A 105      14.671 -35.129  8.545  1.00  0.00           N
ATOM   1549  CA  ALA A 105      15.476 -33.985  8.142  1.00  0.00           C
ATOM   1550  C   ALA A 105      16.568 -33.682  9.129  1.00  0.00           C
ATOM   1551  O   ALA A 105      16.481 -33.969 10.311  1.00  0.00           O
ATOM   1552  CB  ALA A 105      14.608 -32.685  7.867  1.00  0.00           C
ATOM   1558  N   TRP A 106      17.637 -33.122  8.615  1.00  0.00           N
ATOM   1559  CA  TRP A 106      18.744 -32.674  9.469  1.00  0.00           C
ATOM   1560  C   TRP A 106      18.574 -31.164  9.809  1.00  0.00           C
ATOM   1561  O   TRP A 106      19.082 -30.283  9.062  1.00  0.00           O
ATOM   1562  CB  TRP A 106      20.085 -32.913  8.773  1.00  0.00           C
ATOM   1582  N   LEU A 107      17.970 -30.919 10.956  1.00  0.00           N
ATOM   1583  CA  LEU A 107      17.740 -29.599 11.467  1.00  0.00           C
ATOM   1584  C   LEU A 107      18.706 -29.228 12.609  1.00  0.00           C
ATOM   1585  O   LEU A 107      18.575 -28.196 13.290  1.00  0.00           O
ATOM   1586  CB  LEU A 107      16.289 -29.492 11.952  1.00  0.00           C
ATOM   1601  N   GLY A 108      19.692 -30.103 12.826  1.00  0.00           N
ATOM   1602  CA  GLY A 108      20.639 -29.813 13.842  1.00  0.00           C
ATOM   1603  C   GLY A 108      21.986 -30.299 13.322  1.00  0.00           C
ATOM   1604  O   GLY A 108      22.091 -30.573 12.128  1.00  0.00           O
ATOM   1608  N   ARG A 109      22.931 -30.707 14.183  1.00  0.00           N
ATOM   1609  CA  ARG A 109      24.204 -31.202 13.704  1.00  0.00           C
ATOM   1610  C   ARG A 109      24.235 -32.565 13.045  1.00  0.00           C
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ATOM   1611  O   ARG A 109     23.501 -33.464 13.445 1.00 0.00          O
ATOM   1612  CB  ARG A 109     25.183 -31.230 14.868 1.00 0.00          C
ATOM   1632  N   ASP A 110     24.863 -32.587 11.858 1.00 0.00          N
ATOM   1633  CA  ASP A 110     25.052 -33.800 11.094 1.00 0.00          C
ATOM   1634  C   ASP A 110     26.471 -34.059 11.603 1.00 0.00          C
ATOM   1635  O   ASP A 110     27.339 -33.200 11.387 1.00 0.00          O
ATOM   1636  CB  ASP A 110     24.960 -33.621  9.577 1.00 0.00          C
ATOM   1644  N   PRO A 111     26.664 -35.169 12.341 1.00 0.00          N
ATOM   1645  CA  PRO A 111     27.953 -35.591 12.868 1.00 0.00          C
ATOM   1646  C   PRO A 111     29.154 -35.575 11.903 1.00 0.00          C
ATOM   1647  O   PRO A 111     30.251 -35.186 12.313 1.00 0.00          O
ATOM   1648  CB  PRO A 111     27.633 -37.022 13.311 1.00 0.00          C
ATOM   1658  N   ARG A 112     28.854 -35.764 10.607 1.00 0.00          N
ATOM   1659  CA  ARG A 112     29.780 -35.720  9.499 1.00 0.00          C
ATOM   1660  C   ARG A 112     30.273 -34.311  9.121 1.00 0.00          C
ATOM   1661  O   ARG A 112     31.326 -34.208  8.494 1.00 0.00          O
ATOM   1662  CB  ARG A 112     29.127 -36.357  8.281 1.00 0.00          C
ATOM   1682  N   LEU A 113     29.576 -33.252  9.580 1.00 0.00          N
ATOM   1683  CA  LEU A 113     29.962 -31.859  9.376 1.00 0.00          C
ATOM   1684  C   LEU A 113     30.608 -31.129 10.566 1.00 0.00          C
ATOM   1685  O   LEU A 113     31.501 -30.313 10.335 1.00 0.00          O
ATOM   1686  CB  LEU A 113     28.719 -31.073  8.941 1.00 0.00          C
ATOM   1701  N   GLY A 114     30.109 -31.359 11.802 1.00 0.00          N
ATOM   1702  CA  GLY A 114     30.543 -30.718 13.047 1.00 0.00          C
ATOM   1703  C   GLY A 114     30.082 -29.265 13.278 1.00 0.00          C
ATOM   1704  O   GLY A 114     30.708 -28.523 14.035 1.00 0.00          O
ATOM   1708  N   LEU A 115     28.948 -28.880 12.668 1.00 0.00          N
ATOM   1709  CA  LEU A 115     28.471 -27.505 12.681 1.00 0.00          C
ATOM   1710  C   LEU A 115     27.328 -27.325 13.685 1.00 0.00          C
ATOM   1711  O   LEU A 115     26.824 -28.303 14.240 1.00 0.00          O
ATOM   1712  CB  LEU A 115     28.003 -27.098 11.278 1.00 0.00          C
ATOM   1727  N   SER A 116     26.928 -26.064 13.905 1.00 0.00          N
ATOM   1728  CA  SER A 116     25.815 -25.724 14.769 1.00 0.00          C
ATOM   1729  C   SER A 116     24.499 -26.154 14.126 1.00 0.00          C
ATOM   1730  O   SER A 116     24.432 -26.402 12.920 1.00 0.00          O
ATOM   1731  CB  SER A 116     25.801 -24.233 15.045 1.00 0.00          C
ATOM   1738  N   GLY A 117     23.439 -26.183 14.939 1.00 0.00          N
ATOM   1739  CA  GLY A 117     22.130 -26.599 14.480 1.00 0.00          C
ATOM   1740  C   GLY A 117     21.376 -25.531 13.688 1.00 0.00          C
ATOM   1741  O   GLY A 117     21.844 -24.420 13.554 1.00 0.00          O
ATOM   1745  N   ALA A 118     20.206 -25.871 13.170 1.00 0.00          N
ATOM   1746  CA  ALA A 118     19.391 -24.915 12.368 1.00 0.00          C
ATOM   1747  C   ALA A 118     18.739 -23.902 13.270 1.00 0.00          C
ATOM   1748  O   ALA A 118     18.404 -24.193 14.440 1.00 0.00          O
ATOM   1749  CB  ALA A 118     18.304 -25.643 11.443 1.00 0.00          C
ATOM   1755  N   ASP A 119     18.582 -22.684 12.777 1.00 0.00          N
ATOM   1756  CA  ASP A 119     17.909 -21.590 13.492 1.00 0.00          C
ATOM   1757  C   ASP A 119     16.499 -21.480 13.078 1.00 0.00          C
ATOM   1758  O   ASP A 119     16.203 -21.037 11.953 1.00 0.00          O
ATOM   1759  CB  ASP A 119     18.603 -20.248 13.245 1.00 0.00          C
ATOM   1767  N   LEU A 120     15.616 -21.907 13.956 1.00 0.00          N
ATOM   1768  CA  LEU A 120     14.192 -21.883 13.775 1.00 0.00          C
ATOM   1769  C   LEU A 120     13.461 -20.873 14.697 1.00 0.00          C
ATOM   1770  O   LEU A 120     12.315 -21.119 15.002 1.00 0.00          O
ATOM   1771  CB  LEU A 120     13.643 -23.295 14.011 1.00 0.00          C
ATOM   1786  N   SER A 121     14.127 -19.814 15.079 1.00 20.00         N
ATOM   1787  CA  SER A 121     13.628 -18.790 15.986 1.00 20.00         C
ATOM   1788  C   SER A 121     12.413 -18.223 15.340 1.00 20.00         C
ATOM   1789  O   SER A 121     12.402 -17.845 14.184 1.00 20.00         O
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ATOM   1790  CB  SER A 121     14.663 -17.713 16.251 1.00 20.00        C
ATOM   1797  N   ASP A 122     11.370 -18.127 16.153 1.00 20.00        N
ATOM   1798  CA  ASP A 122     10.059 -17.510 15.716 1.00 20.00        C
ATOM   1799  C   ASP A 122      9.471 -18.139 14.405 1.00 20.00        C
ATOM   1800  O   ASP A 122      8.616 -17.516 13.729 1.00 20.00        O
ATOM   1801  CB  ASP A 122     10.242 -16.028 15.562 1.00 20.00        C
ATOM   1809  N   ALA A 123      9.820 -19.382 14.103 1.00 20.00        N
ATOM   1810  CA  ALA A 123      9.290 -20.112 12.946 1.00 20.00        C
ATOM   1811  C   ALA A 123      7.948 -20.727 13.225 1.00 20.00        C
ATOM   1812  O   ALA A 123      7.664 -21.108 14.374 1.00 20.00        O
ATOM   1813  CB  ALA A 123     10.259 -21.252 12.415 1.00 20.00        C
ATOM   1819  N   ASN A 124      7.148 -20.791 12.191 1.00 20.00        N
ATOM   1820  CA  ASN A 124      5.849 -21.372 12.322 1.00 20.00        C
ATOM   1821  C   ASN A 124      5.919 -22.815 11.894 1.00 20.00        C
ATOM   1822  O   ASN A 124      6.103 -23.117 10.702 1.00 20.00        O
ATOM   1823  CB  ASN A 124      4.835 -20.642 11.528 1.00 20.00        C
ATOM   1833  N   LEU A 125      5.827 -23.754 12.830 1.00 20.00        N
ATOM   1834  CA  LEU A 125      5.821 -25.148 12.600 1.00 20.00        C
ATOM   1835  C   LEU A 125      4.512 -25.807 12.995 1.00 20.00        C
ATOM   1836  O   LEU A 125      4.462 -27.041 13.292 1.00 20.00        O
ATOM   1837  CB  LEU A 125      6.994 -25.786 13.353 1.00 20.00        C
ATOM   1852  N   GLU A 126      3.403 -25.078 12.849 1.00 20.00        N
ATOM   1853  CA  GLU A 126      2.099 -25.634 13.224 1.00 20.00        C
ATOM   1854  C   GLU A 126      1.780 -26.860 12.372 1.00 20.00        C
ATOM   1855  O   GLU A 126      1.885 -26.826 11.131 1.00 20.00        O
ATOM   1856  CB  GLU A 126      0.999 -24.576 13.093 1.00 20.00        C
ATOM   1867  N   GLN A 127      1.407 -27.986 13.044 1.00 20.00        N
ATOM   1868  CA  GLN A 127      1.090 -29.248 12.405 1.00 20.00        C
ATOM   1869  C   GLN A 127      2.160 -29.742 11.452 1.00 20.00        C
ATOM   1870  O   GLN A 127      1.833 -30.622 10.627 1.00 20.00        O
ATOM   1871  CB  GLN A 127     -0.235 -29.125 11.648 1.00 20.00        C
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ATOM   1444  N   GLN A  98       4.557 -24.253  8.265  1.00 20.00           N
ATOM   1445  CA  GLN A  98       3.400 -25.015  8.722  1.00 20.00           C
ATOM   1446  C   GLN A  98       3.049 -26.145  7.792  1.00 20.00           C
ATOM   1447  O   GLN A  98       3.150 -25.999  6.537  1.00 20.00           O
ATOM   1448  CB  GLN A  98       2.271 -24.086  8.951  1.00 20.00           C
ATOM   1461  N   GLU A  99       2.685 -27.316  8.355  1.00 20.00           N
ATOM   1462  CA  GLU A  99       2.344 -28.491  7.583  1.00 20.00           C
ATOM   1463  C   GLU A  99       3.494 -29.045  6.726  1.00 20.00           C
ATOM   1464  O   GLU A  99       3.319 -29.955  5.873  1.00 20.00           O
ATOM   1465  CB  GLU A  99       1.069 -28.215  6.747  1.00 20.00           C
ATOM   1476  N   ALA A 100       4.709 -28.561  6.996  1.00 20.00           N
ATOM   1477  CA  ALA A 100       5.821 -29.018  6.199  1.00 20.00           C
ATOM   1478  C   ALA A 100       6.243 -30.454  6.619  1.00 20.00           C
ATOM   1479  O   ALA A 100       6.137 -30.826  7.808  1.00 20.00           O
ATOM   1480  CB  ALA A 100       7.018 -28.014  6.306  1.00 20.00           C
ATOM   1486  N   ASN A 101       6.760 -31.168  5.635  1.00 20.00           N
ATOM   1487  CA  ASN A 101       7.304 -32.513  5.825  1.00 20.00           C
ATOM   1488  C   ASN A 101       8.781 -32.491  6.034  1.00 20.00           C
ATOM   1489  O   ASN A 101       9.624 -32.295  5.083  1.00 20.00           O
ATOM   1490  CB  ASN A 101       6.973 -33.427  4.660  1.00 20.00           C
ATOM   1500  N   LEU A 102       9.147 -32.607  7.315  1.00 20.00           N
ATOM   1501  CA  LEU A 102      10.539 -32.545  7.777  1.00 20.00           C
ATOM   1502  C   LEU A 102      10.985 -33.880  8.348  1.00 20.00           C
ATOM   1503  O   LEU A 102      11.891 -33.949  9.192  1.00 20.00           O
ATOM   1504  CB  LEU A 102      10.709 -31.438  8.825  1.00 20.00           C
ATOM   1519  N   THR A 103      10.404 -34.991  7.852  1.00 20.00           N
ATOM   1520  CA  THR A 103      10.718 -36.304  8.330  1.00 20.00           C
ATOM   1521  C   THR A 103      12.110 -36.598  7.984  1.00 20.00           C
ATOM   1522  O   THR A 103      12.544 -36.346  6.870  1.00 20.00           O
ATOM   1523  CB  THR A 103       9.718 -37.376  7.856  1.00 20.00           C
ATOM   1533  N   GLN A 104      12.827 -37.185  8.935  1.00 20.00           N
ATOM   1534  CA  GLN A 104      14.201 -37.467  8.780  1.00 20.00           C
ATOM   1535  C   GLN A 104      15.128 -36.336  8.357  1.00 20.00           C
ATOM   1536  O   GLN A 104      16.231 -36.577  7.863  1.00 20.00           O
ATOM   1537  CB  GLN A 104      14.329 -38.609  7.769  1.00 20.00           C
ATOM   1550  N   ALA A 105      14.704 -35.095  8.556  1.00  0.00           N
ATOM   1551  CA  ALA A 105      15.505 -33.950  8.153  1.00  0.00           C
ATOM   1552  C   ALA A 105      16.587 -33.634  9.147  1.00  0.00           C
ATOM   1553  O   ALA A 105      16.465 -33.853 10.341  1.00  0.00           O
ATOM   1554  CB  ALA A 105      14.632 -32.657  7.863  1.00  0.00           C
ATOM   1560  N   ASP A 106      17.687 -33.142  8.629  1.00  0.00           N
ATOM   1561  CA  ASP A 106      18.799 -32.706  9.482  1.00  0.00           C
ATOM   1562  C   ASP A 106      18.669 -31.185  9.787  1.00  0.00           C
ATOM   1563  O   ASP A 106      19.185 -30.334  9.011  1.00  0.00           O
ATOM   1564  CB  ASP A 106      20.141 -33.001  8.808  1.00  0.00           C
ATOM   1572  N   LEU A 107      18.089 -30.898 10.938  1.00  0.00           N
ATOM   1573  CA  LEU A 107      17.889 -29.560 11.416  1.00  0.00           C
ATOM   1574  C   LEU A 107      18.915 -29.155 12.491  1.00  0.00           C
ATOM   1575  O   LEU A 107      18.699 -28.251 13.317  1.00  0.00           O
ATOM   1576  CB  LEU A 107      16.466 -29.432 11.973  1.00  0.00           C
ATOM   1591  N   GLY A 108      20.054 -29.853 12.482  1.00  0.00           N
ATOM   1592  CA  GLY A 108      21.031 -29.564 13.469  1.00  0.00           C
ATOM   1593  C   GLY A 108      21.768 -30.848 13.797  1.00  0.00           C
ATOM   1594  O   GLY A 108      21.151 -31.882 14.054  1.00  0.00           O
ATOM   1598  N   GLY A 109      23.097 -30.766 13.736  1.00  0.00           N
ATOM   1599  CA  GLY A 109      23.968 -31.886 14.007  1.00  0.00           C
ATOM   1600  C   GLY A 109      25.101 -31.444 14.909  1.00  0.00           C
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ATOM   1601  O   GLY A 109     25.251 -30.252 15.182 1.00 0.00          O
ATOM   1605  N   PRO A 110     25.921 -32.420 15.326 1.00 0.00          N
ATOM   1606  CA  PRO A 110     27.034 -32.207 16.242 1.00 0.00          C
ATOM   1607  C   PRO A 110     28.275 -31.684 15.517 1.00 0.00          C
ATOM   1608  O   PRO A 110     28.493 -31.965 14.337 1.00 0.00          O
ATOM   1609  CB  PRO A 110     27.267 -33.605 16.822 1.00 0.00          C
ATOM   1619  N   PRO A 111     29.110 -30.941 16.257 1.00 0.00          N
ATOM   1620  CA  PRO A 111     30.420 -30.455 15.822 1.00 0.00          C
ATOM   1621  C   PRO A 111     31.336 -31.502 15.178 1.00 0.00          C
ATOM   1622  O   PRO A 111     31.861 -31.234 14.098 1.00 0.00          O
ATOM   1623  CB  PRO A 111     31.016 -29.947 17.139 1.00 0.00          C
ATOM   1633  N   ASP A 112     31.264 -32.751 15.667 1.00 0.00          N
ATOM   1634  CA  ASP A 112     31.948 -33.955 15.181 1.00 0.00          C
ATOM   1635  C   ASP A 112     31.633 -34.448 13.758 1.00 0.00          C
ATOM   1636  O   ASP A 112     32.466 -35.135 13.166 1.00 0.00          O
ATOM   1637  CB  ASP A 112     31.658 -35.100 16.154 1.00 0.00          C
ATOM   1645  N   GLU A 113     30.498 -34.026 13.175 1.00 0.00          N
ATOM   1646  CA  GLU A 113     30.155 -34.298 11.781 1.00 0.00          C
ATOM   1647  C   GLU A 113     30.378 -33.109 10.839 1.00 0.00          C
ATOM   1648  O   GLU A 113     30.243 -33.273  9.629 1.00  0.00          O
ATOM   1649  CB  GLU A 113     28.693 -34.743 11.693 1.00 0.00          C
ATOM   1660  N   GLY A 114     30.906 -31.998 11.378 1.00 0.00          N
ATOM   1661  CA  GLY A 114     31.138 -30.695 10.736 1.00 0.00          C
ATOM   1662  C   GLY A 114     29.857 -29.873 10.617 1.00 0.00          C
ATOM   1663  O   GLY A 114     29.662 -29.087  9.686 1.00  0.00          O
ATOM   1667  N   LYS A 115     29.000 -30.087 11.622 1.00 0.00          N
ATOM   1668  CA  LYS A 115     27.653 -29.558 11.692 1.00 0.00          C
ATOM   1669  C   LYS A 115     27.458 -28.702 12.937 1.00 0.00          C
ATOM   1670  O   LYS A 115     28.299 -28.670 13.839 1.00 0.00          O
ATOM   1671  CB  LYS A 115     26.633 -30.698 11.667 1.00 0.00          C
ATOM   1689  N   THR A 116     26.310 -28.019 12.955 1.00 0.00          N
ATOM   1690  CA  THR A 116     25.810 -27.232 14.066 1.00 0.00          C
ATOM   1691  C   THR A 116     24.288 -27.206 13.992 1.00 0.00          C
ATOM   1692  O   THR A 116     23.699 -27.868 13.136 1.00 0.00          O
ATOM   1693  CB  THR A 116     26.375 -25.800 14.049 1.00 0.00          C
ATOM   1703  N   GLY A 117     23.658 -26.388 14.848 1.00 0.00          N
ATOM   1704  CA  GLY A 117     22.213 -26.289 14.951 1.00 0.00          C
ATOM   1705  C   GLY A 117     21.532 -25.317 13.987 1.00 0.00          C
ATOM   1706  O   GLY A 117     22.030 -24.238 13.749 1.00 0.00          O
ATOM   1710  N   ALA A 118     20.389 -25.702 13.442 1.00 0.00          N
ATOM   1711  CA  ALA A 118     19.589 -24.799 12.567 1.00 0.00          C
ATOM   1712  C   ALA A 118     18.854 -23.784 13.400 1.00 0.00          C
ATOM   1713  O   ALA A 118     18.494 -24.041 14.570 1.00 0.00          O
ATOM   1714  CB  ALA A 118     18.580 -25.591 11.606 1.00 0.00          C
ATOM   1720  N   ASP A 119     18.651 -22.599 12.847 1.00 0.00          N
ATOM   1721  CA  ASP A 119     17.948 -21.493 13.512 1.00 0.00          C
ATOM   1722  C   ASP A 119     16.542 -21.425 13.074 1.00 0.00          C
ATOM   1723  O   ASP A 119     16.257 -21.062 11.917 1.00 0.00          O
ATOM   1724  CB  ASP A 119     18.621 -20.148 13.227 1.00 0.00          C
ATOM   1732  N   LEU A 120     15.651 -21.799 13.967 1.00 0.00          N
ATOM   1733  CA  LEU A 120     14.229 -21.781 13.774 1.00 0.00          C
ATOM   1734  C   LEU A 120     13.486 -20.771 14.686 1.00 0.00          C
ATOM   1735  O   LEU A 120     12.341 -21.024 14.989 1.00 0.00          O
ATOM   1736  CB  LEU A 120     13.683 -23.195 14.011 1.00 0.00          C
ATOM   1751  N   SER A 121     14.142 -19.704 15.064 1.00 20.00          N
ATOM   1752  CA  SER A 121     13.636 -18.683 15.969 1.00 20.00          C
ATOM   1753  C   SER A 121     12.413 -18.130 15.325 1.00 20.00          C
ATOM   1754  O   SER A 121     12.394 -17.756 14.168 1.00 20.00          O
ATOM   1755  CB  SER A 121     14.660 -17.595 16.229 1.00 20.00          C
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ATOM   1762  N   ASP A 122     11.371 -18.043 16.141 1.00 20.00        N
ATOM   1763  CA  ASP A 122     10.052 -17.441 15.706 1.00 20.00        C
ATOM   1764  C   ASP A 122      9.468 -18.080 14.398 1.00 20.00        C
ATOM   1765  O   ASP A 122      8.604 -17.467 13.723 1.00 20.00        O
ATOM   1766  CB  ASP A 122     10.220 -15.957 15.547 1.00 20.00        C
ATOM   1774  N   ALA A 123      9.828 -19.320 14.099 1.00 20.00        N
ATOM   1775  CA  ALA A 123      9.302 -20.058 12.945 1.00 20.00        C
ATOM   1776  C   ALA A 123      7.968 -20.686 13.230 1.00 20.00        C
ATOM   1777  O   ALA A 123      7.691 -21.067 14.381 1.00 20.00        O
ATOM   1778  CB  ALA A 123     10.282 -21.190 12.415 1.00 20.00        C
ATOM   1784  N   ASN A 124      7.166 -20.762 12.199 1.00 20.00        N
ATOM   1785  CA  ASN A 124      5.873 -21.356 12.335 1.00 20.00        C
ATOM   1786  C   ASN A 124      5.957 -22.799 11.910 1.00 20.00        C
ATOM   1787  O   ASN A 124      6.141 -23.103 10.719 1.00 20.00        O
ATOM   1788  CB  ASN A 124      4.849 -20.639 11.542 1.00 20.00        C
ATOM   1798  N   LEU A 125      5.878 -23.736 12.849 1.00 20.00        N
ATOM   1799  CA  LEU A 125      5.885 -25.131 12.623 1.00 20.00        C
ATOM   1800  C   LEU A 125      4.584 -25.802 13.024 1.00 20.00        C
ATOM   1801  O   LEU A 125      4.548 -27.036 13.325 1.00 20.00        O
ATOM   1802  CB  LEU A 125      7.067 -25.755 13.375 1.00 20.00        C
ATOM   1817  N   GLU A 126      3.467 -25.086 12.879 1.00 20.00        N
ATOM   1818  CA  GLU A 126      2.170 -25.654 13.259 1.00 20.00        C
ATOM   1819  C   GLU A 126      1.861 -26.885 12.412 1.00 20.00        C
ATOM   1820  O   GLU A 126      1.963 -26.854 11.170 1.00 20.00        O
ATOM   1821  CB  GLU A 126      1.059 -24.608 13.128 1.00 20.00        C
ATOM   1832  N   GLN A 127      1.502 -28.013 13.088 1.00 20.00        N
ATOM   1833  CA  GLN A 127      1.196 -29.281 12.453 1.00 20.00        C
ATOM   1834  C   GLN A 127      2.269 -29.766 11.498 1.00 20.00        C
ATOM   1835  O   GLN A 127      1.949 -30.652 10.677 1.00 20.00        O
ATOM   1836  CB  GLN A 127     -0.132 -29.173 11.699 1.00 20.00        C
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ATOM   1445  N   GLN A  98       4.608 -24.197  8.281  1.00 20.00           N
ATOM   1446  CA  GLN A  98       3.450 -24.959  8.738  1.00 20.00           C
ATOM   1447  C   GLN A  98       3.101 -26.090  7.809  1.00 20.00           C
ATOM   1448  O   GLN A  98       3.203 -25.946  6.554  1.00 20.00           O
ATOM   1449  CB  GLN A  98       2.320 -24.030  8.965  1.00 20.00           C
ATOM   1462  N   GLU A  99       2.736 -27.260  8.374  1.00 20.00           N
ATOM   1463  CA  GLU A  99       2.397 -28.437  7.603  1.00 20.00           C
ATOM   1464  C   GLU A  99       3.548 -28.992  6.749  1.00 20.00           C
ATOM   1465  O   GLU A  99       3.374 -29.903  5.897  1.00 20.00           O
ATOM   1466  CB  GLU A  99       1.123 -28.162  6.766  1.00 20.00           C
ATOM   1477  N   ALA A 100       4.762 -28.506  7.019  1.00 20.00           N
ATOM   1478  CA  ALA A 100       5.876 -28.964  6.225  1.00 20.00           C
ATOM   1479  C   ALA A 100       6.298 -30.399  6.648  1.00 20.00           C
ATOM   1480  O   ALA A 100       6.190 -30.769  7.837  1.00 20.00           O
ATOM   1481  CB  ALA A 100       7.072 -27.960  6.331  1.00 20.00           C
ATOM   1487  N   ASN A 101       6.816 -31.116  5.665  1.00 20.00           N
ATOM   1488  CA  ASN A 101       7.361 -32.460  5.859  1.00 20.00           C
ATOM   1489  C   ASN A 101       8.837 -32.437  6.069  1.00 20.00           C
ATOM   1490  O   ASN A 101       9.681 -32.242  5.119  1.00 20.00           O
ATOM   1491  CB  ASN A 101       7.031 -33.376  4.695  1.00 20.00           C
ATOM   1501  N   LEU A 102       9.201 -32.551  7.351  1.00 20.00           N
ATOM   1502  CA  LEU A 102      10.593 -32.487  7.814  1.00 20.00           C
ATOM   1503  C   LEU A 102      11.039 -33.821  8.388  1.00 20.00           C
ATOM   1504  O   LEU A 102      11.944 -33.888  9.233  1.00 20.00           O
ATOM   1505  CB  LEU A 102      10.761 -31.379  8.860  1.00 20.00           C
ATOM   1520  N   THR A 103      10.459 -34.933  7.893  1.00 20.00           N
ATOM   1521  CA  THR A 103      10.773 -36.245  8.373  1.00 20.00           C
ATOM   1522  C   THR A 103      12.165 -36.539  8.030  1.00 20.00           C
ATOM   1523  O   THR A 103      12.601 -36.289  6.916  1.00 20.00           O
ATOM   1524  CB  THR A 103       9.774 -37.318  7.900  1.00 20.00           C
ATOM   1534  N   GLN A 104      12.881 -37.124  8.983  1.00 20.00           N
ATOM   1535  CA  GLN A 104      14.256 -37.406  8.830  1.00 20.00           C
ATOM   1536  C   GLN A 104      15.183 -36.276  8.406  1.00 20.00           C
ATOM   1537  O   GLN A 104      16.287 -36.516  7.914  1.00 20.00           O
ATOM   1538  CB  GLN A 104      14.385 -38.550  7.821  1.00 20.00           C
ATOM   1551  N   ALA A 105      14.758 -35.034  8.603  1.00  0.00           N
ATOM   1552  CA  ALA A 105      15.559 -33.889  8.198  1.00  0.00           C
ATOM   1553  C   ALA A 105      16.651 -33.582  9.185  1.00  0.00           C
ATOM   1554  O   ALA A 105      16.527 -33.780 10.382  1.00  0.00           O
ATOM   1555  CB  ALA A 105      14.687 -32.592  7.922  1.00  0.00           C
ATOM   1561  N   LYS A 106      17.760 -33.122  8.657  1.00  0.00           N
ATOM   1562  CA  LYS A 106      18.898 -32.733  9.499  1.00  0.00           C
ATOM   1563  C   LYS A 106      18.829 -31.209  9.811  1.00  0.00           C
ATOM   1564  O   LYS A 106      19.327 -30.372  9.009  1.00  0.00           O
ATOM   1565  CB  LYS A 106      20.218 -33.087  8.813  1.00  0.00           C
ATOM   1583  N   LEU A 107      18.321 -30.908 10.992  1.00  0.00           N
ATOM   1584  CA  LEU A 107      18.115 -29.564 11.449  1.00  0.00           C
ATOM   1585  C   LEU A 107      19.161 -29.125 12.492  1.00  0.00           C
ATOM   1586  O   LEU A 107      18.926 -28.261 13.354  1.00  0.00           O
ATOM   1587  CB  LEU A 107      16.704 -29.443 12.038  1.00  0.00           C
ATOM   1602  N   GLY A 108      20.340 -29.748 12.412  1.00  0.00           N
ATOM   1603  CA  GLY A 108      21.373 -29.354 13.300  1.00  0.00           C
ATOM   1604  C   GLY A 108      22.426 -30.448 13.309  1.00  0.00           C
ATOM   1605  O   GLY A 108      22.105 -31.625 13.140  1.00  0.00           O
ATOM   1609  N   GLY A 109      23.688 -30.039 13.462  1.00  0.00           N
ATOM   1610  CA  GLY A 109      24.830 -30.933 13.408  1.00  0.00           C
ATOM   1611  C   GLY A 109      25.169 -31.427 14.807  1.00  0.00           C
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ATOM   1612  O   GLY A 109     24.504 -31.055 15.772 1.00 0.00          O
ATOM   1616  N   TYR A 110     26.199 -32.276 14.902 1.00 0.00          N
ATOM   1617  CA  TYR A 110     26.599 -32.889 16.154 1.00 0.00          C
ATOM   1618  C   TYR A 110     27.981 -32.395 16.607 1.00 0.00          C
ATOM   1619  O   TYR A 110     28.755 -31.841 15.817 1.00 0.00          O
ATOM   1620  CB  TYR A 110     26.593 -34.414 16.017 1.00 0.00          C
ATOM   1637  N   ASP A 111     28.265 -32.608 17.903 1.00 0.00          N
ATOM   1638  CA  ASP A 111     29.520 -32.290 18.574 1.00 0.00          C
ATOM   1639  C   ASP A 111     30.723 -33.008 17.949 1.00 0.00          C
ATOM   1640  O   ASP A 111     31.734 -32.361 17.681 1.00 0.00          O
ATOM   1641  CB  ASP A 111     29.425 -32.650 20.059 1.00 0.00          C
ATOM   1649  N   ASP A 112     30.529 -34.285 17.571 1.00 0.00          N
ATOM   1650  CA  ASP A 112     31.490 -35.125 16.866 1.00 0.00          C
ATOM   1651  C   ASP A 112     31.786 -34.611 15.445 1.00 0.00          C
ATOM   1652  O   ASP A 112     32.916 -34.758 14.975 1.00 0.00          O
ATOM   1653  CB  ASP A 112     30.972 -36.564 16.796 1.00 0.00          C
ATOM   1661  N   GLU A 113     30.783 -33.979 14.800 1.00 0.00          N
ATOM   1662  CA  GLU A 113     30.888 -33.310 13.505 1.00 0.00          C
ATOM   1663  C   GLU A 113     31.545 -31.926 13.599 1.00 0.00          C
ATOM   1664  O   GLU A 113     32.201 -31.510 12.644 1.00 0.00          O
ATOM   1665  CB  GLU A 113     29.499 -33.176 12.876 1.00 0.00          C
ATOM   1676  N   GLY A 114     31.363 -31.245 14.751 1.00 0.00          N
ATOM   1677  CA  GLY A 114     31.832 -29.898 15.079 1.00 0.00          C
ATOM   1678  C   GLY A 114     30.934 -28.749 14.624 1.00 0.00          C
ATOM   1679  O   GLY A 114     31.363 -27.602 14.479 1.00 0.00          O
ATOM   1683  N   LEU A 115     29.654 -29.079 14.467 1.00 0.00          N
ATOM   1684  CA  LEU A 115     28.663 -28.172 13.933 1.00 0.00          C
ATOM   1685  C   LEU A 115     27.587 -27.856 14.969 1.00 0.00          C
ATOM   1686  O   LEU A 115     27.305 -28.653 15.870 1.00 0.00          O
ATOM   1687  CB  LEU A 115     28.020 -28.777 12.679 1.00 0.00          C
ATOM   1702  N   GLY A 116     27.035 -26.645 14.836 1.00 0.00          N
ATOM   1703  CA  GLY A 116     25.958 -26.122 15.660 1.00 0.00          C
ATOM   1704  C   GLY A 116     24.625 -26.547 15.043 1.00 0.00          C
ATOM   1705  O   GLY A 116     24.603 -27.231 14.017 1.00 0.00          O
ATOM   1709  N   GLY A 117     23.517 -26.058 15.602 1.00 0.00          N
ATOM   1710  CA  GLY A 117     22.216 -26.374 15.065 1.00 0.00          C
ATOM   1711  C   GLY A 117     21.582 -25.389 14.083 1.00 0.00          C
ATOM   1712  O   GLY A 117     22.138 -24.345 13.814 1.00 0.00          O
ATOM   1716  N   ALA A 118     20.414 -25.722 13.556 1.00 0.00          N
ATOM   1717  CA  ALA A 118     19.660 -24.798 12.663 1.00 0.00          C
ATOM   1718  C   ALA A 118     18.921 -23.772 13.479 1.00 0.00          C
ATOM   1719  O   ALA A 118     18.554 -24.015 14.650 1.00 0.00          O
ATOM   1720  CB  ALA A 118     18.665 -25.564 11.667 1.00 0.00          C
ATOM   1726  N   ASP A 119     18.721 -22.594 12.911 1.00 0.00          N
ATOM   1727  CA  ASP A 119     18.015 -21.479 13.558 1.00 0.00          C
ATOM   1728  C   ASP A 119     16.611 -21.417 13.112 1.00 0.00          C
ATOM   1729  O   ASP A 119     16.332 -21.082 11.946 1.00 0.00          O
ATOM   1730  CB  ASP A 119     18.689 -20.138 13.258 1.00 0.00          C
ATOM   1738  N   LEU A 120     15.716 -21.767 14.011 1.00 0.00          N
ATOM   1739  CA  LEU A 120     14.294 -21.747 13.812 1.00 0.00          C
ATOM   1740  C   LEU A 120     13.549 -20.730 14.716 1.00 0.00          C
ATOM   1741  O   LEU A 120     12.401 -20.977 15.010 1.00 0.00          O
ATOM   1742  CB  LEU A 120     13.745 -23.159 14.055 1.00 0.00          C
ATOM   1757  N   SER A 121     14.207 -19.666 15.094 1.00 20.00         N
ATOM   1758  CA  SER A 121     13.701 -18.642 15.997 1.00 20.00         C
ATOM   1759  C   SER A 121     12.482 -18.086 15.349 1.00 20.00         C
ATOM   1760  O   SER A 121     12.468 -17.712 14.192 1.00 20.00         O
ATOM   1761  CB  SER A 121     14.728 -17.557 16.259 1.00 20.00         C
ATOM   1768  N   ASP A 122     11.438 -17.994 16.161 1.00 20.00         N
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ATOM   1769  CA  ASP A 122     10.123 -17.389 15.722 1.00 20.00        C
ATOM   1770  C   ASP A 122      9.541 -18.027 14.412 1.00 20.00        C
ATOM   1771  O   ASP A 122      8.681 -17.412 13.734 1.00 20.00        O
ATOM   1772  CB  ASP A 122     10.295 -15.906 15.562 1.00 20.00        C
ATOM   1780  N   ALA A 123      9.898 -19.268 14.114 1.00 20.00        N
ATOM   1781  CA  ALA A 123      9.374 -20.005 12.960 1.00 20.00        C
ATOM   1782  C   ALA A 123      8.036 -20.629 13.241 1.00 20.00        C
ATOM   1783  O   ALA A 123      7.754 -21.008 14.391 1.00 20.00        O
ATOM   1784  CB  ALA A 123     10.351 -21.141 12.433 1.00 20.00        C
ATOM   1790  N   ASN A 124      7.237 -20.703 12.207 1.00 20.00        N
ATOM   1791  CA  ASN A 124      5.942 -21.293 12.339 1.00 20.00        C
ATOM   1792  C   ASN A 124      6.023 -22.736 11.916 1.00 20.00        C
ATOM   1793  O   ASN A 124      6.210 -23.042 10.725 1.00 20.00        O
ATOM   1794  CB  ASN A 124      4.923 -20.573 11.542 1.00 20.00        C
ATOM   1804  N   LEU A 125      5.937 -23.673 12.855 1.00 20.00        N
ATOM   1805  CA  LEU A 125      5.941 -25.067 12.630 1.00 20.00        C
ATOM   1806  C   LEU A 125      4.637 -25.735 13.027 1.00 20.00        C
ATOM   1807  O   LEU A 125      4.595 -26.968 13.329 1.00 20.00        O
ATOM   1808  CB  LEU A 125      7.119 -25.694 13.387 1.00 20.00        C
ATOM   1823  N   GLU A 126      3.522 -25.014 12.878 1.00 20.00        N
ATOM   1824  CA  GLU A 126      2.222 -25.579 13.254 1.00 20.00        C
ATOM   1825  C   GLU A 126      1.912 -26.809 12.407 1.00 20.00        C
ATOM   1826  O   GLU A 126      2.018 -26.779 11.165 1.00 20.00        O
ATOM   1827  CB  GLU A 126      1.115 -24.528 13.119 1.00 20.00        C
ATOM   1838  N   GLN A 127      1.547 -27.935 13.083 1.00 20.00        N
ATOM   1839  CA  GLN A 127      1.239 -29.202 12.447 1.00 20.00        C
ATOM   1840  C   GLN A 127      2.314 -29.692 11.497 1.00 20.00        C
ATOM   1841  O   GLN A 127      1.993 -30.577 10.675 1.00 20.00        O
ATOM   1842  CB  GLN A 127     -0.086 -29.091 11.689 1.00 20.00        C
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ATOM   1447  N   GLN A  98       4.545 -24.272  8.213  1.00 20.00           N
ATOM   1448  CA  GLN A  98       3.384 -25.033  8.664  1.00 20.00           C
ATOM   1449  C   GLN A  98       3.041 -26.165  7.734  1.00 20.00           C
ATOM   1450  O   GLN A  98       3.151 -26.023  6.479  1.00 20.00           O
ATOM   1451  CB  GLN A  98       2.253 -24.103  8.881  1.00 20.00           C
ATOM   1464  N   GLU A  99       2.672 -27.334  8.298  1.00 20.00           N
ATOM   1465  CA  GLU A  99       2.337 -28.512  7.526  1.00 20.00           C
ATOM   1466  C   GLU A  99       3.494 -29.068  6.680  1.00 20.00           C
ATOM   1467  O   GLU A  99       3.326 -29.980  5.828  1.00 20.00           O
ATOM   1468  CB  GLU A  99       1.069 -28.238  6.679  1.00 20.00           C
ATOM   1479  N   ALA A 100       4.707 -28.583  6.958  1.00 20.00           N
ATOM   1480  CA  ALA A 100       5.825 -29.042  6.172  1.00 20.00           C
ATOM   1481  C   ALA A 100       6.244 -30.477  6.599  1.00 20.00           C
ATOM   1482  O   ALA A 100       6.128 -30.845  7.788  1.00 20.00           O
ATOM   1483  CB  ALA A 100       7.021 -28.038  6.285  1.00 20.00           C
ATOM   1489  N   ASN A 101       6.769 -31.194  5.621  1.00 20.00           N
ATOM   1490  CA  ASN A 101       7.312 -32.539  5.819  1.00 20.00           C
ATOM   1491  C   ASN A 101       8.786 -32.516  6.040  1.00 20.00           C
ATOM   1492  O   ASN A 101       9.637 -32.323  5.095  1.00 20.00           O
ATOM   1493  CB  ASN A 101       6.990 -33.456  4.654  1.00 20.00           C
ATOM   1503  N   LEU A 102       9.142 -32.628  7.324  1.00 20.00           N
ATOM   1504  CA  LEU A 102      10.531 -32.565  7.797  1.00 20.00           C
ATOM   1505  C   LEU A 102      10.972 -33.899  8.375  1.00 20.00           C
ATOM   1506  O   LEU A 102      11.871 -33.965  9.226  1.00 20.00           O
ATOM   1507  CB  LEU A 102      10.692 -31.455  8.843  1.00 20.00           C
ATOM   1522  N   THR A 103      10.395 -35.011  7.878  1.00 20.00           N
ATOM   1523  CA  THR A 103      10.705 -36.322  8.362  1.00 20.00           C
ATOM   1524  C   THR A 103      12.099 -36.618  8.028  1.00 20.00           C
ATOM   1525  O   THR A 103      12.543 -36.368  6.917  1.00 20.00           O
ATOM   1526  CB  THR A 103       9.709 -37.396  7.883  1.00 20.00           C
ATOM   1536  N   GLN A 104      12.809 -37.202  8.987  1.00 20.00           N
ATOM   1537  CA  GLN A 104      14.185 -37.484  8.843  1.00 20.00           C
ATOM   1538  C   GLN A 104      15.115 -36.354  8.425  1.00 20.00           C
ATOM   1539  O   GLN A 104      16.222 -36.596  7.940  1.00 20.00           O
ATOM   1540  CB  GLN A 104      14.320 -38.629  7.836  1.00 20.00           C
ATOM   1553  N   ALA A 105      14.689 -35.113  8.616  1.00  0.00           N
ATOM   1554  CA  ALA A 105      15.493 -33.968  8.216  1.00  0.00           C
ATOM   1555  C   ALA A 105      16.632 -33.714  9.164  1.00  0.00           C
ATOM   1556  O   ALA A 105      16.575 -33.997 10.349  1.00  0.00           O
ATOM   1557  CB  ALA A 105      14.635 -32.648  8.023  1.00  0.00           C
ATOM   1563  N   ASN A 106      17.706 -33.203  8.612  1.00  0.00           N
ATOM   1564  CA  ASN A 106      18.881 -32.851  9.419  1.00  0.00           C
ATOM   1565  C   ASN A 106      18.819 -31.347  9.816  1.00  0.00           C
ATOM   1566  O   ASN A 106      19.247 -30.462  9.024  1.00  0.00           O
ATOM   1567  CB  ASN A 106      20.161 -33.171  8.669  1.00  0.00           C
ATOM   1577  N   LEU A 107      18.399 -31.115 11.046  1.00  0.00           N
ATOM   1578  CA  LEU A 107      18.310 -29.804 11.621  1.00  0.00           C
ATOM   1579  C   LEU A 107      19.353 -29.571 12.731  1.00  0.00           C
ATOM   1580  O   LEU A 107      19.136 -28.839 13.712  1.00  0.00           O
ATOM   1581  CB  LEU A 107      16.897 -29.593 12.178  1.00  0.00           C
ATOM   1596  N   GLY A 108      20.509 -30.221 12.570  1.00  0.00           N
ATOM   1597  CA  GLY A 108      21.483 -30.129 13.597  1.00  0.00           C
ATOM   1598  C   GLY A 108      21.859 -31.509 14.117  1.00  0.00           C
ATOM   1599  O   GLY A 108      20.981 -32.312 14.450  1.00  0.00           O
ATOM   1603  N   GLY A 109      23.166 -31.786 14.177  1.00  0.00           N
ATOM   1604  CA  GLY A 109      23.693 -33.045 14.635  1.00  0.00           C
ATOM   1605  C   GLY A 109      24.414 -32.872 15.959  1.00  0.00           C
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ATOM   1606  O   GLY A 109     24.770 -31.798 16.425 1.00 0.00          O
ATOM   1610  N   PRO A 110     24.681 -33.976 16.653 1.00 0.00          N
ATOM   1611  CA  PRO A 110     25.402 -33.873 17.898 1.00 0.00          C
ATOM   1612  C   PRO A 110     26.879 -33.556 17.592 1.00 0.00          C
ATOM   1613  O   PRO A 110     27.357 -33.680 16.454 1.00 0.00          O
ATOM   1614  CB  PRO A 110     25.218 -35.260 18.524 1.00 0.00          C
ATOM   1624  N   PRO A 111     27.612 -33.093 18.608 1.00 0.00          N
ATOM   1625  CA  PRO A 111     29.021 -32.746 18.500 1.00 0.00          C
ATOM   1626  C   PRO A 111     29.866 -33.852 17.849 1.00 0.00          C
ATOM   1627  O   PRO A 111     30.740 -33.543 17.042 1.00 0.00          O
ATOM   1628  CB  PRO A 111     29.416 -32.527 19.963 1.00 0.00          C
ATOM   1638  N   ASP A 112     29.459 -35.121 18.062 1.00 0.00          N
ATOM   1639  CA  ASP A 112     30.015 -36.344 17.523 1.00 0.00          C
ATOM   1640  C   ASP A 112     30.016 -36.361 15.992 1.00 0.00          C
ATOM   1641  O   ASP A 112     30.979 -36.857 15.404 1.00 0.00          O
ATOM   1642  CB  ASP A 112     29.232 -37.549 18.051 1.00 0.00          C
ATOM   1650  N   ASP A 113     29.007 -35.745 15.348 1.00 0.00          N
ATOM   1651  CA  ASP A 113     28.899 -35.642 13.901 1.00 0.00          C
ATOM   1652  C   ASP A 113     29.388 -34.283 13.412 1.00 0.00          C
ATOM   1653  O   ASP A 113     29.937 -34.202 12.309 1.00 0.00          O
ATOM   1654  CB  ASP A 113     27.452 -35.865 13.455 1.00 0.00          C
ATOM   1662  N   GLY A 114     29.156 -33.229 14.227 1.00 0.00          N
ATOM   1663  CA  GLY A 114     29.537 -31.830 14.031 1.00 0.00          C
ATOM   1664  C   GLY A 114     28.667 -31.018 13.076 1.00 0.00          C
ATOM   1665  O   GLY A 114     29.116 -29.988 12.573 1.00 0.00          O
ATOM   1669  N   ASP A 115     27.401 -31.401 12.870 1.00 0.00          N
ATOM   1670  CA  ASP A 115     26.533 -30.672 11.964 1.00 0.00          C
ATOM   1671  C   ASP A 115     25.930 -29.507 12.773 1.00 0.00          C
ATOM   1672  O   ASP A 115     25.301 -29.767 13.726 1.00 0.00          O
ATOM   1673  CB  ASP A 115     25.437 -31.573 11.391 1.00 0.00          C
ATOM   1681  N   PRO A 116     26.165 -28.232 12.446 1.00 0.00          N
ATOM   1682  CA  PRO A 116     25.610 -27.138 13.257 1.00 0.00          C
ATOM   1683  C   PRO A 116     24.094 -27.148 13.416 1.00 0.00          C
ATOM   1684  O   PRO A 116     23.372 -27.552 12.482 1.00 0.00          O
ATOM   1685  CB  PRO A 116     26.064 -25.899 12.478 1.00 0.00          C
ATOM   1695  N   GLY A 117     23.607 -26.771 14.591 1.00 0.00          N
ATOM   1696  CA  GLY A 117     22.187 -26.708 14.863 1.00 0.00          C
ATOM   1697  C   GLY A 117     21.456 -25.706 13.972 1.00 0.00          C
ATOM   1698  O   GLY A 117     21.933 -24.611 13.757 1.00 0.00          O
ATOM   1702  N   ALA A 118     20.294 -26.081 13.460 1.00 0.00          N
ATOM   1703  CA  ALA A 118     19.478 -25.173 12.606 1.00 0.00          C
ATOM   1704  C   ALA A 118     18.806 -24.126 13.453 1.00 0.00          C
ATOM   1705  O   ALA A 118     18.453 -24.370 14.629 1.00 0.00          O
ATOM   1706  CB  ALA A 118     18.409 -25.955 11.704 1.00 0.00          C
ATOM   1712  N   ASP A 119     18.649 -22.932 12.906 1.00 0.00          N
ATOM   1713  CA  ASP A 119     17.985 -21.803 13.575 1.00 0.00          C
ATOM   1714  C   ASP A 119     16.585 -21.678 13.130 1.00 0.00          C
ATOM   1715  O   ASP A 119     16.320 -21.284 11.979 1.00 0.00          O
ATOM   1716  CB  ASP A 119     18.711 -20.484 13.301 1.00 0.00          C
ATOM   1724  N   LEU A 120     15.676 -22.039 14.010 1.00 0.00          N
ATOM   1725  CA  LEU A 120     14.257 -21.992 13.800 1.00 0.00          C
ATOM   1726  C   LEU A 120     13.524 -20.966 14.704 1.00 0.00          C
ATOM   1727  O   LEU A 120     12.371 -21.196 14.993 1.00 0.00          O
ATOM   1728  CB  LEU A 120     13.680 -23.394 14.030 1.00 0.00          C
ATOM   1743  N   SER A 121     14.197 -19.913 15.088 1.00 20.00         N
ATOM   1744  CA  SER A 121     13.701 -18.882 15.989 1.00 20.00         C
ATOM   1745  C   SER A 121     12.496 -18.305 15.332 1.00 20.00         C
ATOM   1746  O   SER A 121     12.498 -17.930 14.175 1.00 20.00         O
ATOM   1747  CB  SER A 121     14.744 -17.814 16.260 1.00 20.00         C
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ATOM   1754  N   ASP A 122     11.448 -18.197 16.136 1.00 20.00        N
ATOM   1755  CA  ASP A 122     10.146 -17.569 15.688 1.00 20.00        C
ATOM   1756  C   ASP A 122      9.563 -18.196 14.373 1.00 20.00        C
ATOM   1757  O   ASP A 122      8.719 -17.566 13.689 1.00 20.00        O
ATOM   1758  CB  ASP A 122     10.345 -16.089 15.531 1.00 20.00        C
ATOM   1766  N   ALA A 123      9.903 -19.443 14.077 1.00 20.00        N
ATOM   1767  CA  ALA A 123      9.374 -20.170 12.918 1.00 20.00        C
ATOM   1768  C   ALA A 123      8.025 -20.772 13.188 1.00 20.00        C
ATOM   1769  O   ALA A 123      7.728 -21.147 14.335 1.00 20.00        O
ATOM   1770  CB  ALA A 123     10.337 -21.321 12.397 1.00 20.00        C
ATOM   1776  N   ASN A 124      7.232 -20.831 12.148 1.00 20.00        N
ATOM   1777  CA  ASN A 124      5.927 -21.400 12.270 1.00 20.00        C
ATOM   1778  C   ASN A 124      5.987 -22.844 11.845 1.00 20.00        C
ATOM   1779  O   ASN A 124      6.178 -23.151 10.656 1.00 20.00        O
ATOM   1780  CB  ASN A 124      4.926 -20.662 11.466 1.00 20.00        C
ATOM   1790  N   LEU A 125      5.879 -23.780 12.783 1.00 20.00        N
ATOM   1791  CA  LEU A 125      5.861 -25.174 12.556 1.00 20.00        C
ATOM   1792  C   LEU A 125      4.543 -25.820 12.943 1.00 20.00        C
ATOM   1793  O   LEU A 125      4.478 -27.053 13.243 1.00 20.00        O
ATOM   1794  CB  LEU A 125      7.022 -25.821 13.321 1.00 20.00        C
ATOM   1809  N   GLU A 126      3.442 -25.081 12.786 1.00 20.00        N
ATOM   1810  CA  GLU A 126      2.129 -25.624 13.152 1.00 20.00        C
ATOM   1811  C   GLU A 126      1.806 -26.848 12.301 1.00 20.00        C
ATOM   1812  O   GLU A 126      1.921 -26.819 11.060 1.00 20.00        O
ATOM   1813  CB  GLU A 126      1.041 -24.555 13.010 1.00 20.00        C
ATOM   1824  N   GLN A 127      1.417 -27.969 12.973 1.00 20.00        N
ATOM   1825  CA  GLN A 127      1.093 -29.230 12.334 1.00 20.00        C
ATOM   1826  C   GLN A 127      2.166 -29.737 11.391 1.00 20.00        C
ATOM   1827  O   GLN A 127      1.837 -30.616 10.566 1.00 20.00        O
ATOM   1828  CB  GLN A 127     -0.225 -29.096 11.566 1.00 20.00        C
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