

Supporting Information

Aminoquinoline–rhodium(II) conjugates as Src-family SH3 ligands

Samuel C. Martin, Zachary T. Ball

Department of Chemistry, Rice University, Houston, Texas

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General methods

Synthesis procedures: Large scale reactions were performed in oven-dried round-bottom flasks. Small scale reactions were performed in 4-mL vials or scintillation vials. Air- or moisture-sensitive reactions were performed in vials sealed with septum caps. Insensitive reactions used bulk solvent without further purification, while air- or moisture-sensitive ones used solvent stored under argon or nitrogen. Reaction vessels were stirred magnetically; flasks were heated in an oil bath and vials in an aluminum heating block. Flash chromatography was performed with 40-63 μM particle size silica gel (Silicycle).

Chemicals: Chemical reagents were purchased and used without further purification. All solvents used were ACS reagent grade. Solvents used under inert atmosphere were bought and maintained in inert packaging or purified and degassed by a solvent dispensing system (Pure Process Technology).

NMR spectroscopy: NMR data was acquired with Bruker Avance 400 MHz, Bruker Avance 500 MHz, or Bruker Avance III 600 MHz instrument. ^1H and ^{13}C NMR spectra were referenced relative to residual solvent or TMS.

Mass spectroscopy: Compatible samples were analyzed using an Agilent 6890 gas chromatograph. All other samples were analyzed by electrospray ionization (ESI-MS) by direct injection into a Bruker Daltonics microTOF instrument.

Synthesis of known compounds: N-Boc-piperazine,¹ *tert*-butyl 4-bromobutanoate,² methyl 6-bromohexanoate,³ and $\text{Rh}_2(\text{OAc})_3(\text{tfa})^4$ were prepared according to previously reported protocols.

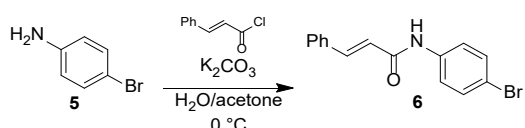
HPLC: HPLC analyses were performed on reverse phase columns using a Shimadzu CBM-20A instrument monitoring at 254 and 350 nm. Mobile phase consisted of acetonitrile/water mixtures with 0.1% trifluoroacetic acid in both constituents. Analytical and preparative separations employed a Phenomenex Jupiter 4 μ Proteo 90A (250 \times 4.6 mm) column at 1 mL/min and a Phenomenex Jupiter 4 μ Proteo 90A (250 \times 15 mm) at 8 mL/min, respectively.

ITC analysis: ITC experiments were performed using a MicroCal ITC200 instrument at 25 $^\circ\text{C}$. Solutions of 275 μM ligand were titrated into 18-20 μM solutions of SH3 domain. Heats of dilution were measured independently for each experiment by titrating the ligand solution into buffer (20 mM phosphate buffer, pH 7.0, 150 mM NaCl, 1 mM EDTA). The linear regression for the heat of dilution and the observed baseline were subtracted from the raw data. The experimental data were fit in Origin (MicroCal) using a one set of sites binding model minimizing the residual sum of squared deviations.

Computational docking and model building: Docking was performed using the GOLD program (v. 5.7.2, CSD-Discovery suite). Docking was conducted assuming protonation at both basic nitrogens of the ligand **4.2**, and the GOLD program found 10 low-energy docked structures. A promising candidate was used as a starting point to build a two-point binding model: the ligand was locked in place except for the 3-carbon alkyl linker. Manual manipulation of the linker torsional angles (Swiss PDB Viewer) was then used to build a reasonable binding model based on the docked structure.

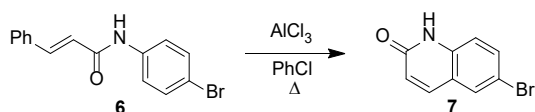
Chemical synthesis

N-(4-bromophenyl)cinnamamide (**6**)



The procedure was adapted from the literature.⁵ A 500-mL round-bottom flask was charged with 4-bromoaniline, **5**, (5.3 g, 31 mmol), water (70 mL), and potassium carbonate (60.0 g, 434 mmol). The mixture was gently heated to dissolve the solid then held at $0\text{ }^\circ\text{C}$. With stirring, a solution of cinnamoyl chloride in acetone (7.1 g, 43 mmol in 25 mL) was added dropwise by addition funnel over 30 min. The flask was placed in the freezer for 30 min to precipitate the product. The mixture was filtered on a glass frit, washed with cold water (20 mL) and cold diethyl ether (15 mL), and dried under vacuum to afford the product as a white powder (9.2 g, 99%). Spectral data was consistent with that previously reported.⁶ ^1H NMR (500 MHz, DMSO-d_6) δ 10.37 (s, 1H), 7.70–7.66 (m, 2H), 7.65–7.63 (m, 2H), 7.61 (d, 1H, $J = 15.7$ Hz), 7.48–7.40 (m, 3H), 6.81 (d, 1H, $J = 15.7$ Hz). ^{13}C NMR (125 MHz, DMSO-d_6) δ 163.7, 140.6, 138.6, 134.6, 131.6, 129.9, 129.1, 127.8, 121.9, 121.1, 115.0. GC–MS, m/z : calculated for $\text{C}_{15}\text{H}_{12}\text{BrNO}^+$ [M^+]⁺ 303.0, found 302.9.

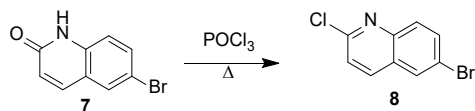
6-bromoquinolin-2(1H)-one (**7**)



The procedure was adapted from the literature.⁵ A 500-mL round-bottom flask was charged with amide **6** (9.2 g, 30 mmol), chlorobenzene (150 mL), and aluminum chloride (24.3 g, 182 mmol). The flask was fitted with a reflux condenser, and the solution was heated at reflux, quickly turning yellow to black. After 2 h, the mixture was concentrated by rotary evaporation to ~ 65 mL, then poured onto ice (900 mL). The reaction flask was rinsed with water, and the resulting aqueous suspension was filtered on a glass frit. The solid was

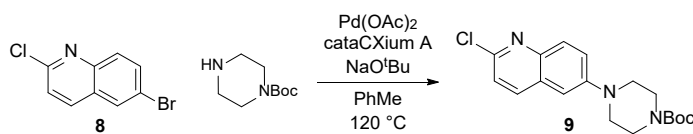
dried under vacuum to afford the product as a light orange solid (3.75 g, 55%). Spectral data were consistent with that previously reported.⁷ ¹H NMR (400 MHz, DMSO-*d*₆) δ 11.87 (br s, 1H), 7.91 (d, 1H, *J* = 2.3 Hz), 7.87 (d, 1H, *J* = 9.6 Hz), 7.63 (dd, 1H, *J* = 8.7, 2.3 Hz), 7.24 (d, 1H, *J* = 8.8 Hz), 6.55 (d, 1H, *J* = 9.6 Hz). ¹³C NMR (125 MHz, DMSO-*d*₆) δ 161.7, 139.2, 138.0, 132.9, 129.9, 123.2, 120.9, 117.3, 113.4, 39.5. GC–MS, *m/z*: calculated for C₉H₆BrNO⁺ [*M*]⁺ 223.0, found 222.9.

6-bromo-2-chloroquinoline (8)



The procedure was adapted from the literature.⁵ To a 500-mL round-bottom flask charged with phosphoryl chloride (20.5 g), lactam **7** (1.50 g, 6.69 mmol) was slowly added. The mixture was refluxed for 75 min, then cooled to rt and quenched by slowly pouring the solution onto ice. The flask was rinsed with cold water, and the precipitate was collected on a glass frit and washed with cold water. The solid was dried under vacuum to afford the product as an orange solid (1.62 g, 100%). Spectral data were consistent with that previously reported.⁸ ¹H NMR (500 MHz, CDCl₃) δ 8.02 (ddd, 1H, *J* = 8.6, 0.7, 0.4 Hz), 7.98 (d, 1H, *J* = 2.2 Hz), 7.89 (dt, 1H, *J* = 9, 0.6 Hz), 7.80 (dd, 1H, *J* = 9, 2.2 Hz), 7.41 (d, 1H, *J* = 8.6 Hz). ¹³C NMR (125 MHz, CDCl₃) δ 151.1, 146.4, 137.7, 134.0, 130.3, 129.63, 127.9, 123.3, 120.9. GC–MS, *m/z*: calculated for C₉H₅BrClN⁺ [*M*]⁺ 242.9, found 243.0.

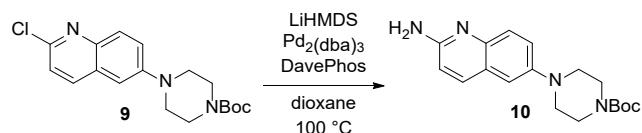
tert-butyl 4-(2-chloroquinolin-6-yl)piperazine-1-carboxylate (9)



The procedure was adapted from the literature.⁵ To a 4-mL vial, charged with bromide **8** (200 mg, 825 μmol), *N*-Boc-piperazine (154 mg, 825 μmol), Pd(OAc)₂ (3.6 mg, 16 μmol), and cataCXium[®] A (11.8 mg, 33 μmol) and equipped with a magnetic stir bar under nitrogen, was added sodium *tert*-butoxide (95 mg, 990 μmol) and toluene (1 mL). The vial was sealed and stirred at 120 °C in an aluminum heating block for 24 h. Upon cooling, the mixture was extracted with ethyl acetate, the combined organic phases were washed with brine, dried over sodium sulfate, filtered, and concentrated by rotary evaporation. Purification on silica gel column (Et₂O/hexanes, 20→50% v/v) afforded the product as a yellow-orange solid (126 mg, 44% yield). Spectral data were consistent with that previously reported.⁵ ¹H NMR (500 MHz, CDCl₃) δ 7.93 (d, 1H, *J* = 8.6 Hz), 7.89 (d, 1H, *J* = 9.3 Hz), 7.48 (dd, 1H, *J* = 9.3, 2.7 Hz), 7.29 (d, 1H, *J* = 8.6 Hz), 7.01 (d, 1H, *J* = 2.7 Hz), 3.66–3.61 (m, 4H), 3.28–3.24 (m, 4H), 1.50 (s, 9H). ¹³C NMR (125 MHz, CDCl₃) δ 154.6,

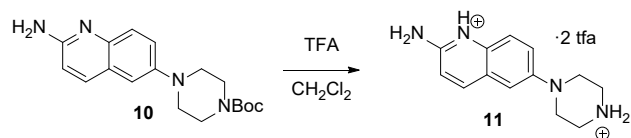
149.5, 147.8, 143.3, 137.5, 129.3, 127.9, 123.4, 122.5, 109.4, 80.1, 49.1, 28.4. GC–MS, m/z: calculated for $C_{18}H_{22}ClN_3O_2$ $[M]^+$ 347.1, found 347.2.

tert-butyl 4-(2-aminoquinolin-6-yl)piperazine-1-carboxylate (10)



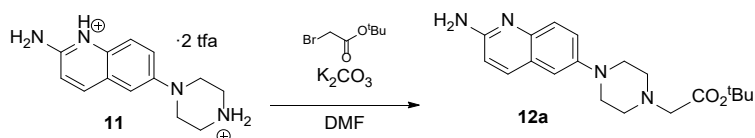
The procedure was adapted from the literature.⁵ To a 4-mL vial, charged with chloride **9** (45 mg, 129 μ mol), Pd₂(dba)₃ (1.8 mg, 1.9 μ mol), and DavePhos (1.5 mg, 3.9 μ mol) and equipped with a magnetic stir bar under nitrogen, was added anhydrous dioxane (1.5 mL). The vial was sealed, and lithium bis(trimethylsilyl)amide (1.0 M in tetrahydrofuran, 170 μ L) was added via syringe. The vial was stirred at 100 °C in an aluminum heating block for 20 h. Upon cooling, the mixture was quenched with 5 drops of 2.0 M hydrochloric acid, stirred for 10 minutes, then adjusted to pH 12 with 1.0 M potassium hydroxide. The mixture was then extracted with methylene chloride, washed with brine, dried over sodium sulfate, filtered, and concentrated by rotary evaporation. Purification on silica gel column (methanol/methylene chloride/triethylamine, 5:94:1 \rightarrow 15:84:1 v/v) afforded the product as a yellow-orange solid (32 mg, 73% yield). Spectral data were consistent with that previously reported.⁵ ¹H NMR (500 MHz, CDCl₃) δ 7.79 (d, 1H, J = 8.7 Hz), 7.60 (d, 1H, J = 9.1 Hz), 7.35 (dd, 1H, J = 9.2, 2.8 Hz), 6.98 (d, 1H, J = 2.7 Hz), 6.70 (d, 1H, J = 8.8 Hz), 4.78 (br s, 2H), 3.65–3.60 (m, 4H), 3.18–3.13 (m, 4H), 1.49 (s, 9H). GC–MS, m/z: calculated for $C_{18}H_{24}N_4O_2$ $[M]^+$ 328.2, found 328.2.

6-(piperazin-1-yl)quinolin-2-amine (11)



A scintillation vial was charged with Boc-amine **10** (260 mg, 792 μ mol), trifluoroacetic acid (4.0 mL), and methylene chloride (4.0 mL) and equipped with a magnetic stir bar. After 4 h, starting material was consumed, and the mixture was concentrated by rotary evaporation, resuspended in toluene, and concentrated once more to obtain the pure bis(trifluoroacetate) salt as a dark yellow solid (350 mg, 97%). ¹H NMR (500 MHz, CD₃OD) δ 8.26 (d, 1H, J = 9.4 Hz), 7.62–7.61 (m, 2H), 7.39 (t, 1H, J = 1.3 Hz), 7.03 (d, 1H, J = 9.4 Hz), 3.53–3.50 (m, 4H), 3.44–3.41 (m, 4H). ¹³C NMR (150 MHz, CD₃OD) δ 149.3, 144.5, 132.1, 125.6, 123.7, 119.3, 114.7, 114.4, 47.7, 44.7. GC–MS, m/z: calculated for $C_{13}H_{16}N_4$ $[M]^+$ 228.1, found 228.1.

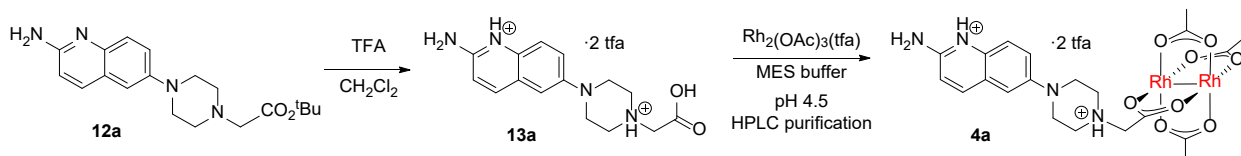
tert-butyl 2-(4-(2-aminoquinolin-6-yl)piperazin-1-yl)acetate (**12a**)



To a 4-mL vial was added the bis-TFA salt **11** (105 mg, 230 μmol), *tert*-butyl bromoacetate (37 μL , 253 μmol), potassium carbonate (163 mg, 1.15 mmol), and dry *N,N*-dimethylformamide (1.0 mL). The vial was equipped with a magnetic stir bar and stirred at 40 °C for 16 h. The mixture was extracted with ethyl acetate, dried over sodium sulfate, filtered, and concentrated by rotary evaporation. Purification on silica gel column (ethyl acetate/hexanes/triethylamine, 80:19:1 \rightarrow 99:0:1 v/v) afforded the product as a light orange solid (71 mg, 90% yield). ^1H NMR (600 MHz, CD_3OD) δ 7.83 (d, 1H, $J = 8.9$ Hz), 7.45 (d, 1H, $J = 9.2$ Hz), 7.36 (dd, 1H, $J = 9.2, 2.7$ Hz), 7.07 (d, 1H, $J = 2.6$ Hz), 6.77 (d, 1H, $J = 8.9$ Hz), 3.25–3.22 (m, 4H), 3.20 (s, 2H), 2.78–2.76 (m, 4H), 1.49 (s, 9H). ^{13}C NMR (150 MHz, CD_3OD) δ 171.0, 158.3, 148.0, 143.5, 138.8, 126.2, 125.1, 124.0, 113.6, 112.8, 82.5, 60.7, 54.0, 50.9, 28.4. GC–MS, m/z : calculated for $\text{C}_{19}\text{H}_{26}\text{N}_4\text{O}_2^+$ $[\text{M}]^+$ 342.2, found 342.2.

dirhodium ligation of 2-(4-(2-aminoquinolin-6-yl)piperazin-1-yl)acetic acid (**4a**)

Two steps:



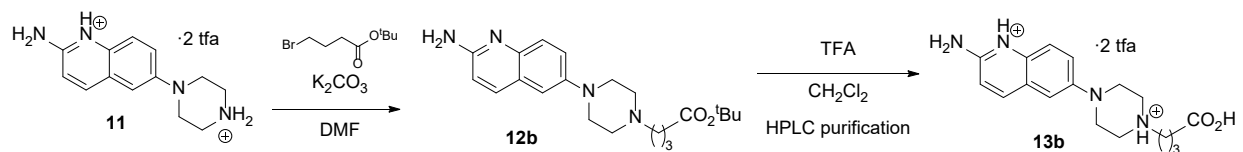
A 4-mL vial was charged with ester **12a** (8 mg, 23 μmol), trifluoroacetic acid (1 mL), and dry methylene chloride (1 mL) and equipped with a magnetic stir bar. After 3 h stirring at rt, the starting material was consumed, and the mixture was concentrated by rotary evaporation, resuspended in toluene, and concentrated once more to obtain the bis(trifluoroacetate) intermediate **13a** as a yellow solid (12 mg, 99% yield). ^1H NMR (400 MHz, CD_3OD) δ 8.25 (d, 1H, $J = 9.4$ Hz), 7.62 (s, 1H), 7.61 (s, 1H), 7.39 (s, 1H), 7.03 (d, 1H, $J = 9.3$ Hz), 4.17 (s, 2H), 3.61 (br s, 8H). ESI–MS, m/z : calculated for $\text{C}_{15}\text{H}_{19}\text{N}_4\text{O}_2$ $[\text{M}+\text{H}]^+$ 287.2, found 287.0.

A 4-mL vial was charged with acid **13a** as the bis(trifluoroacetate) salt (2.0 mg, 3.9 μmol), $\text{Rh}_2(\text{OAc})_3(\text{tfa})$ (4.2 mg, 8.7 μmol), and MES buffer (1.4 mL, 25 mg/mL, pH = 4.5) and equipped with a magnetic stir bar. The vial was stirred at rt, and the reaction was monitored by analytical HPLC. After 24 h, the mixture was purified by preparative HPLC. Fractions were combined, concentrated by rotary evaporation, and dried by

lyophilization to afford the product as the bis(trifluoroacetate) salt as a light green solid (3.0 mg, 86%). ESI-MS, m/z : calculated for $C_{21}H_{27}N_4O_8Rh_2$ $[M+H]^+$ 669.0, found 668.8.

4-(4-(2-aminoquinolin-6-yl)piperazin-1-yl)butanoic acid (**13b**)

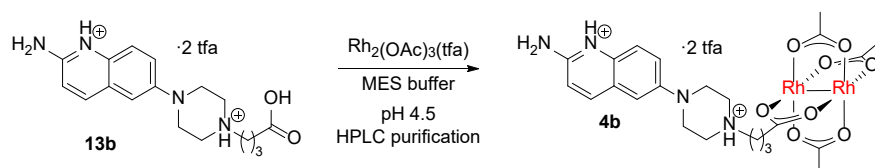
Two steps:



To a 4-mL vial was added the bis-TFA salt **11** (81 mg, 178 μ mol), *tert*-butyl 4-bromobutyrate (50 mg, 213 μ mol), potassium carbonate (120 mg, 888 mmol), and dry *N,N*-dimethylformamide (1.0 mL) and equipped with a magnetic stir bar. The vial was stirred at 40 °C for 16 h. The mixture was extracted with ethyl acetate, dried over sodium sulfate, filtered, and concentrated by rotary evaporation. Purification on silica gel column (methanol/methylene chloride/triethylamine, 0:99:1 \rightarrow 10:89:1 v/v) afforded the ester intermediate **12b** as a light orange solid (52 mg, 78%). 1H NMR (500 MHz, CD_3OD) δ 7.85 (d, 1H, J = 8.9 Hz), 7.45 (d, 1H, J = 9.2 Hz), 7.37 (dd, 1H, J = 9.2, 2.7 Hz), 7.08 (d, 1H, J = 2.7 Hz), 6.77 (d, 1H, J = 8.9 Hz), 3.24–3.21 (m, 4H), 2.70–2.66 (m, 4H), 2.47–2.42 (m, 2H), 2.30 (t, 2H, J = 7.3 Hz), 1.86–1.79 (m, 2H), 1.46 (s, 9H). ^{13}C NMR (125 MHz, CD_3OD) δ 174.5, 158.3, 148.0, 143.3, 138.9, 126.1, 125.1, 123.9, 113.6, 112.8, 81.5, 58.8, 54.3, 51.0, 34.2, 28.4, 23.0.

A 4-mL vial was charged with ester **12b** (24 mg, 60 μ mol), trifluoroacetic acid (0.5 mL), and dry methylene chloride (0.5 mL) and equipped with a magnetic stir bar. After stirring at rt for 4.5 h, the starting material was consumed, and the mixture was concentrated by rotary evaporation. Purification was performed by preparative HPLC. Fractions were combined, concentrated by rotary evaporation, and dried by lyophilization to obtain the pure bis(trifluoroacetate) salt as a yellow solid (12 mg, 38%). 1H NMR (600 MHz, CD_3OD) δ 8.25 (d, 1H, J = 9.4 Hz), 7.63–7.61 (m, 2H), 7.38 (d, 1H, J = 2.0 Hz), 7.03 (d, 1H, J = 9.4 Hz), 3.53 (br s, 1H), 3.30–3.27 (m, 2H), 2.50 (t, 2H, J = 6.9 Hz), 2.11–2.05 (m, 2H). ^{13}C NMR (150 MHz, CD_3OD) δ 175.8, 155.2, 148.8, 144.5, 132.1, 125.5, 123.7, 119.4, 114.8, 114.4, 57.4, 53.0, 47.9, 31.4, 20.4. ESI-MS, m/z : calculated for $C_{17}H_{23}N_4O_2$ $[M+H]^+$ 315.2, found 315.1.

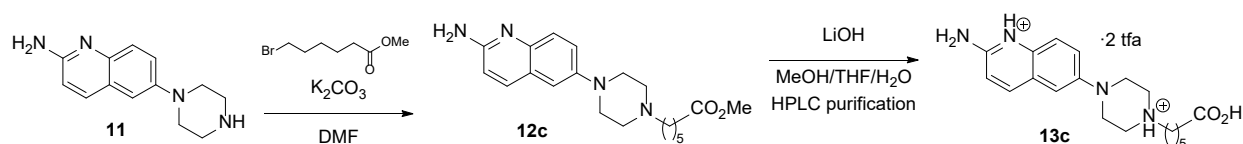
dirhodium ligation of 4-(4-(2-aminoquinolin-6-yl)piperazin-1-yl)butanoic acid (**4b**)



A 4-mL vial was charged with acid **13b** as the bis(trifluoroacetate) salt (3.3 mg, 6.1 μmol), $\text{Rh}_2(\text{OAc})_3(\text{tfa})$ (6.3 mg, 9.1 μmol), and MES buffer (1.2 mL, 25 mg/mL, pH = 4.5) and equipped with a magnetic stir bar. The vial was stirred at 40 °C and monitored by analytical HPLC. After 24 h, the mixture was purified by preparative HPLC. Fractions were combined, concentrated by rotary evaporation, and dried by lyophilization to afford the product as the bis(trifluoroacetate) salt as a light green solid (5.5 mg, 98%). ESI-MS, m/z : calculated for $\text{C}_{23}\text{H}_{31}\text{N}_4\text{O}_8\text{Rh}_2$ $[\text{M}+\text{H}]^+$ 697.0, found 696.8; calculated for $[\text{M}+2\text{H}]^{2+}$ 349.0, found 348.9; calculated for $[\text{M}+2\text{H}+\text{MeOH}]^{2+}$ 365.0, found 364.9.

6-(4-(2-aminoquinolin-6-yl)piperazin-1-yl)hexanoic acid (**13c**)

Two steps:

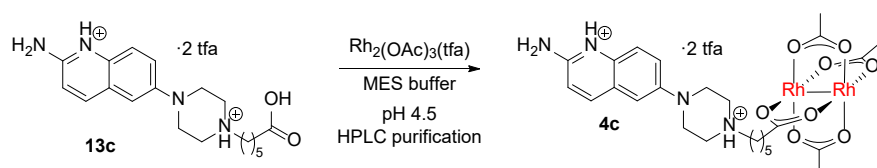


A 4-mL vial was charged with **11** as the free amine (55 mg, 240 μmol), methyl 6-bromohexanoate (64 mg, 290 μmol), potassium carbonate (167 mg, 1.21 mmol), and dry *N,N*-dimethylformamide (1.0 mL) and equipped with a magnetic stir bar. After 25 h stirring at rt, *N,N*-diisopropylethylamine (42 μL , 240 μmol) was added to speed the reaction. After an additional 19 h, 6-bromohexanoate (30 mg, 140 μmol) was added. After 3 h, the mixture was extracted with ethyl acetate, dried over sodium sulfate, filtered, and concentrated by rotary evaporation. Purification on silica gel column (methanol/ethyl acetate/hexanes/triethylamine, 0:80:19:1→0:99:0:1→2:97:0:1 v/v) afforded the ester intermediate **12c** as a light orange solid (42 mg, 30%). ^1H NMR (600 MHz, CD_3OD) δ 7.85 (d, 1H, $J = 8.9$ Hz), 7.46 (d, 1H, $J = 9.2$ Hz), 7.38 (dd, 1H, $J = 9.2, 2.7$ Hz), 7.08 (d, 1H, $J = 2.7$ Hz), 6.78 (d, 1H, $J = 8.9$ Hz), 3.66 (s, 3H), 3.25–3.22 (m, 4H), 2.71–2.67 (m, 4H), 2.47–2.43 (m, 2H), 2.36 (t, 2H, $J = 7.4$ Hz), 1.70–1.63 (m, 2H), 1.63–1.56 (m, 2H), 1.41–1.35 (m, 2H). ^{13}C NMR (150 MHz, CD_3OD) δ 175.9, 158.3, 148.0, 143.3, 138.9, 126.1, 125.1, 123.9, 113.6, 112.8, 59.5, 54.3, 52.0, 50.9, 34.7, 28.1, 27.2, 25.9.

A 4-mL vial was charged with ester **12c** (20 mg, 56 μmol), lithium hydroxide (5.2 mg, 224 μmol), methanol (1.7 mL), water (0.5 mL), and tetrahydrofuran (0.2 mL) and equipped with a magnetic stir bar. After stirring

at 40 °C for 20 h, the starting material was consumed, and the mixture was dried under a gentle stream of nitrogen, resuspended in methanol, and filtered. Purification was performed by preparative HPLC. Fractions were combined, concentrated by rotary evaporation, and dried by lyophilization to obtain the pure bis(trifluoroacetate) salt as a yellow solid (9.0 mg, 28%). ¹H NMR (600 MHz, CD₃OD) δ 8.26 (d, 1H, *J* = 9.4 Hz), 7.62 (d, 2H, *J* = 1.3 Hz), 7.39 (s, 1H), 7.04 (d, 1H, *J* = 9.4 Hz), 3.51 (br s, 8H), 3.26–3.21 (m, 2H), 2.36 (t, 2H, *J* = 7.3 Hz), 1.86–1.79 (m, 2H), 1.73–1.67 (m, 2H), 1.51–1.44 (m, 2H). ¹³C NMR (150 MHz, CD₃OD) δ 177.2, 155.1, 148.8, 144.5, 132.1, 125.5, 123.7, 119.4, 114.8, 114.4, 57.8, 52.9, 47.8, 34.4, 27.0, 25.3, 24.8. ESI–MS, *m/z*: calculated for C₁₉H₂₇N₄O₂ [M+H]⁺ 343.2, found 343.1.

dirhodium ligation of 6-(4-(2-aminoquinolin-6-yl)piperazin-1-yl)hexanoic acid (**4c**)



A 4-mL vial was charged with acid **13c** as the bis(trifluoroacetate) salt (3.2 mg, 5.6 μmol), Rh₂(OAc)₃(tfa) (4.2 mg, 8.4 μmol), and MES buffer (1.2 mL, 25 mg/mL, pH = 4.5) and equipped with a magnetic stir bar. The vial was stirred at 40 °C, and the reaction was monitored by analytical HPLC. After 36 h, the mixture was purified by preparative HPLC. Fractions were combined, concentrated by rotary evaporation, and dried by lyophilization, to afford the product as the bis(trifluoroacetate) salt as a light green solid (5.1 mg, 95%). ESI–MS, *m/z*: calculated for C₂₅H₃₅N₄O₈Rh₂ [M+H]⁺ 725.1, found 724.9; calculated for [M+2H]²⁺ 363.0, found 362.9; calculated for [M+2H+MeOH]²⁺ 379.0, found 378.9.

Compound characterization

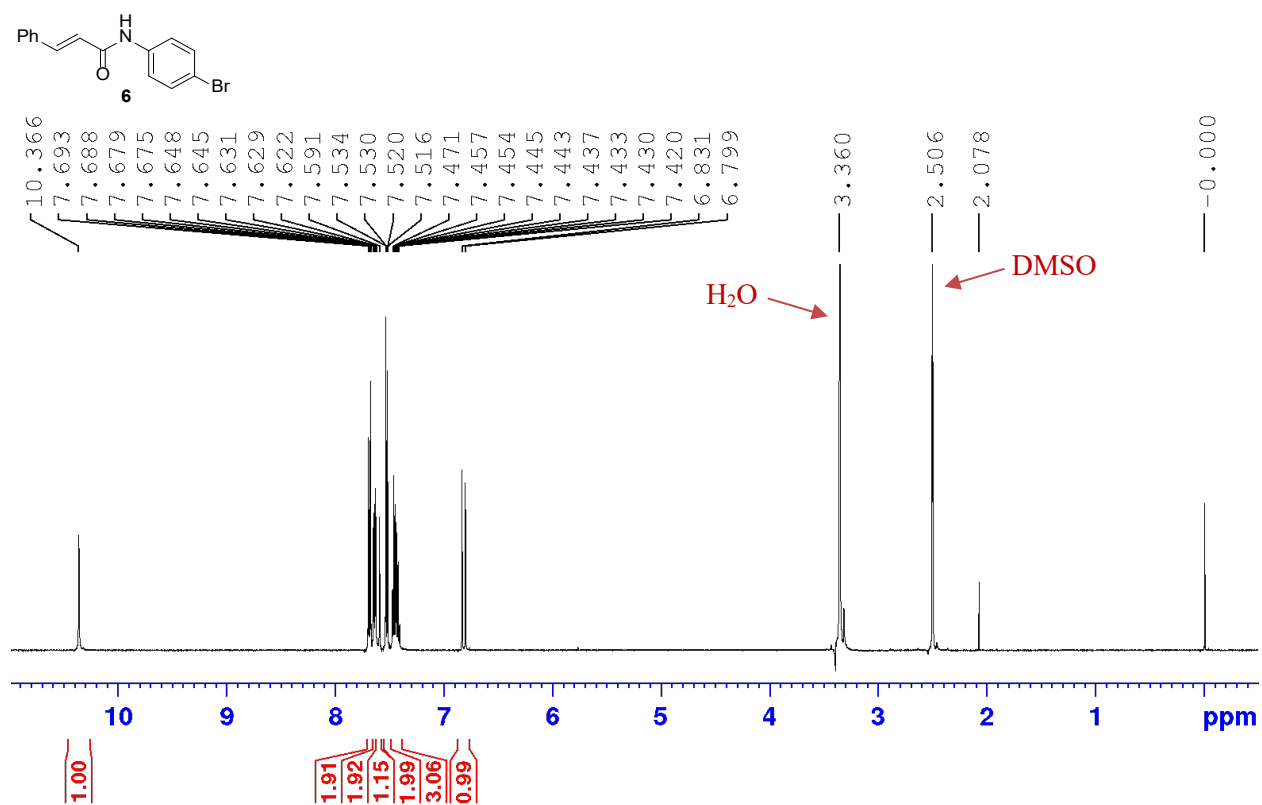


Figure 1. ¹H NMR spectrum of compound 6 in DMSO-d₆.

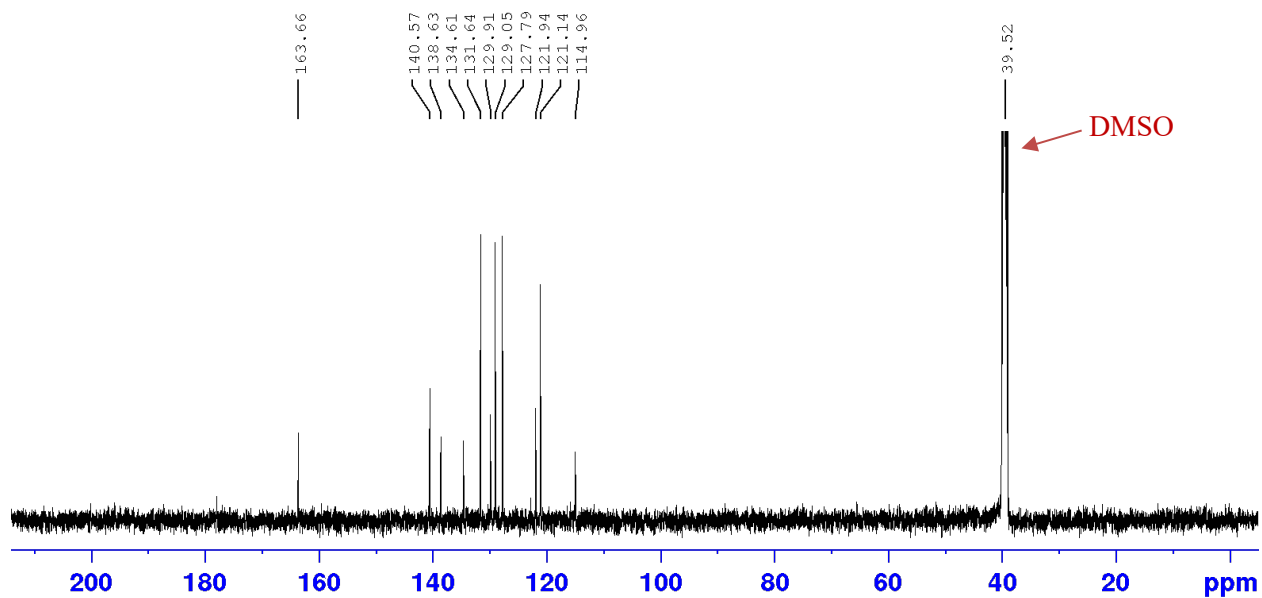


Figure 2. ¹³C NMR spectrum of compound 6 in DMSO-d₆.

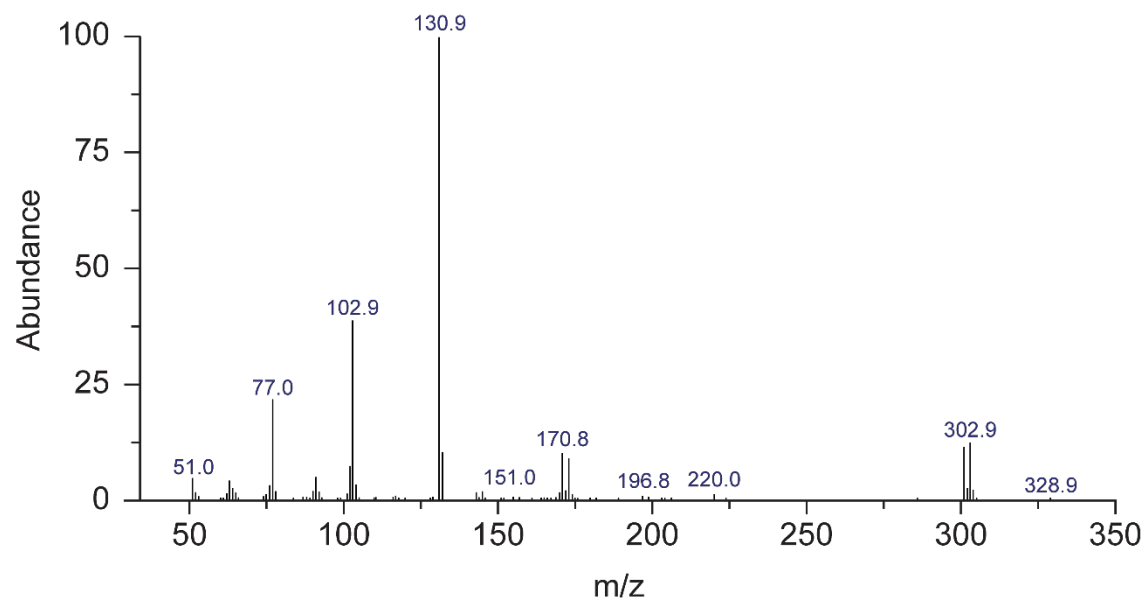


Figure 3. GC-MS spectrum of compound 6.

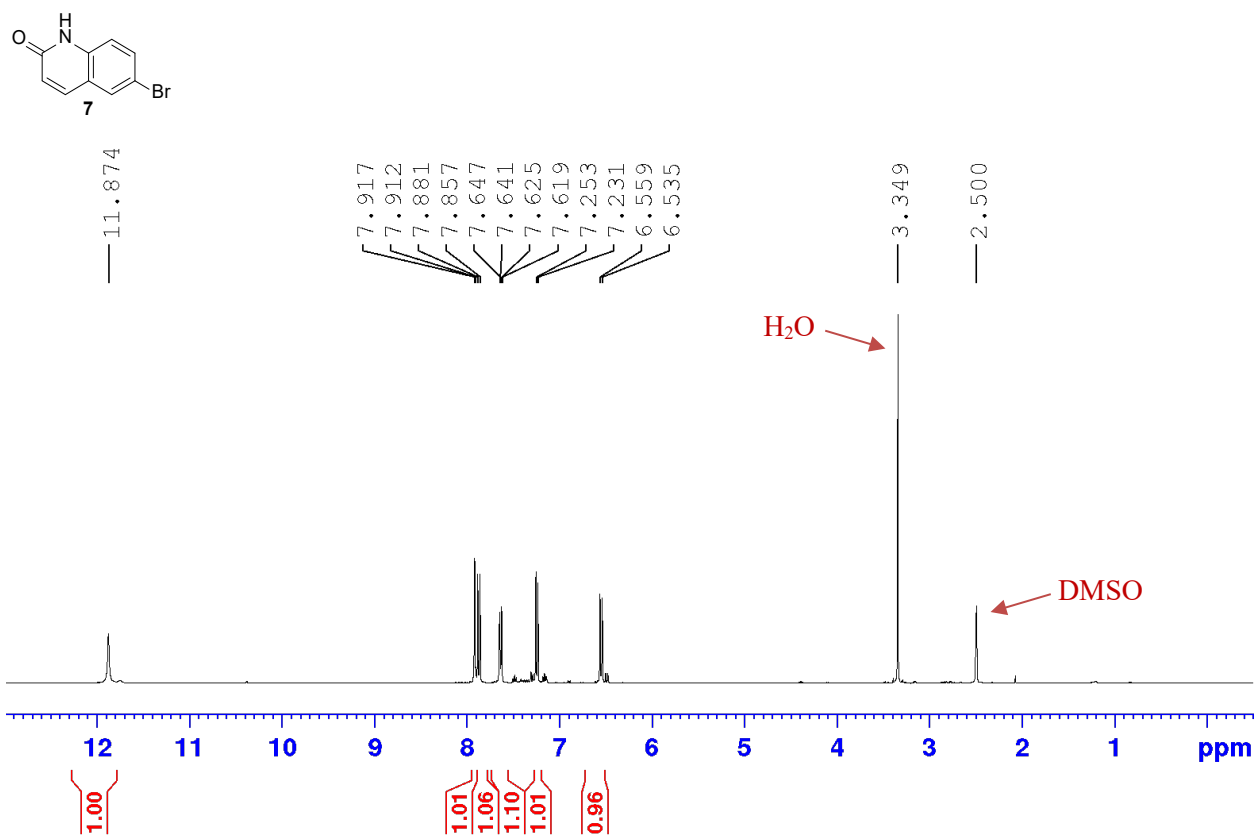


Figure 4. ¹H NMR spectrum of compound 7 in DMSO-d₆.

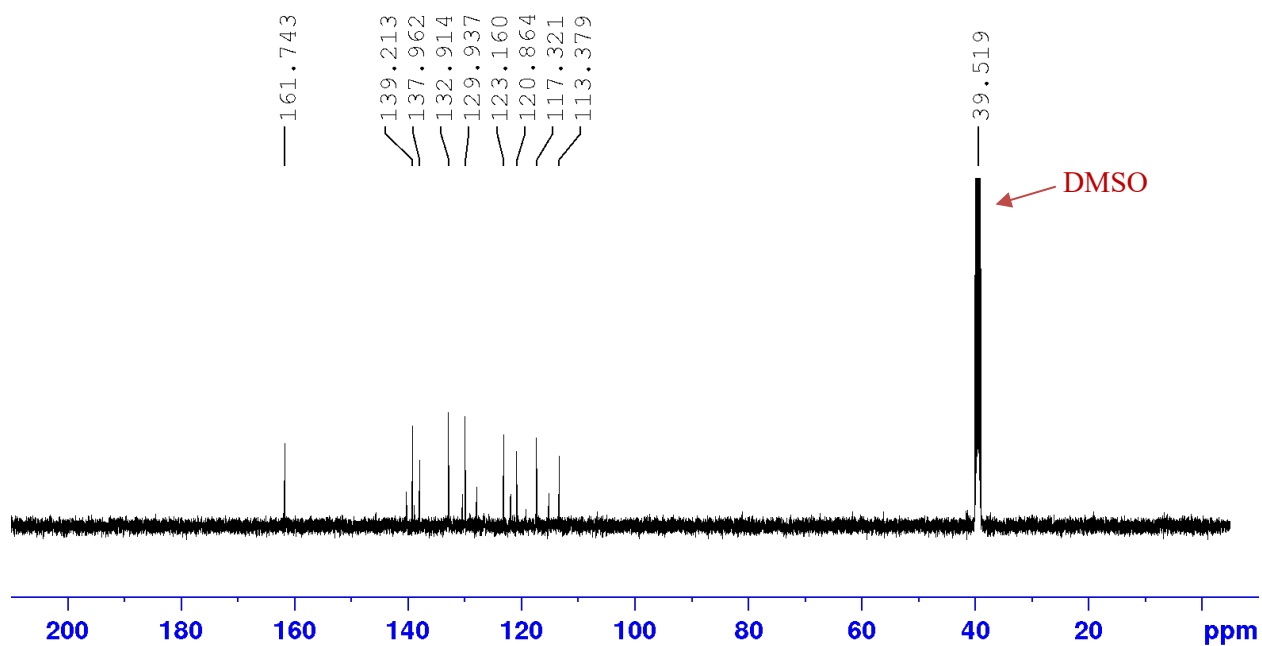


Figure 5. ¹³C NMR spectrum of compound 7 in DMSO-d₆.

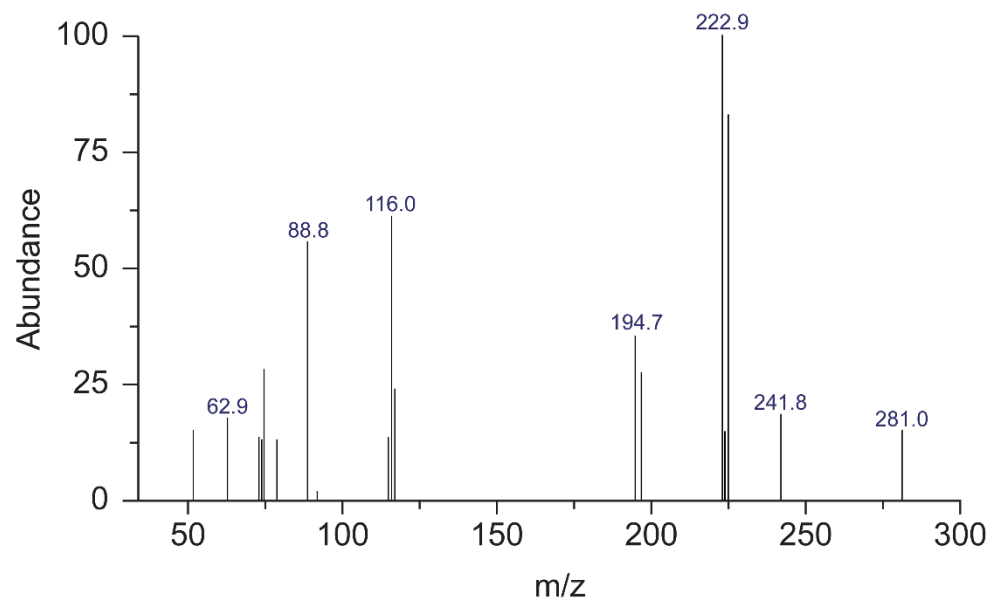


Figure 6. GC-MS spectrum of compound 7.

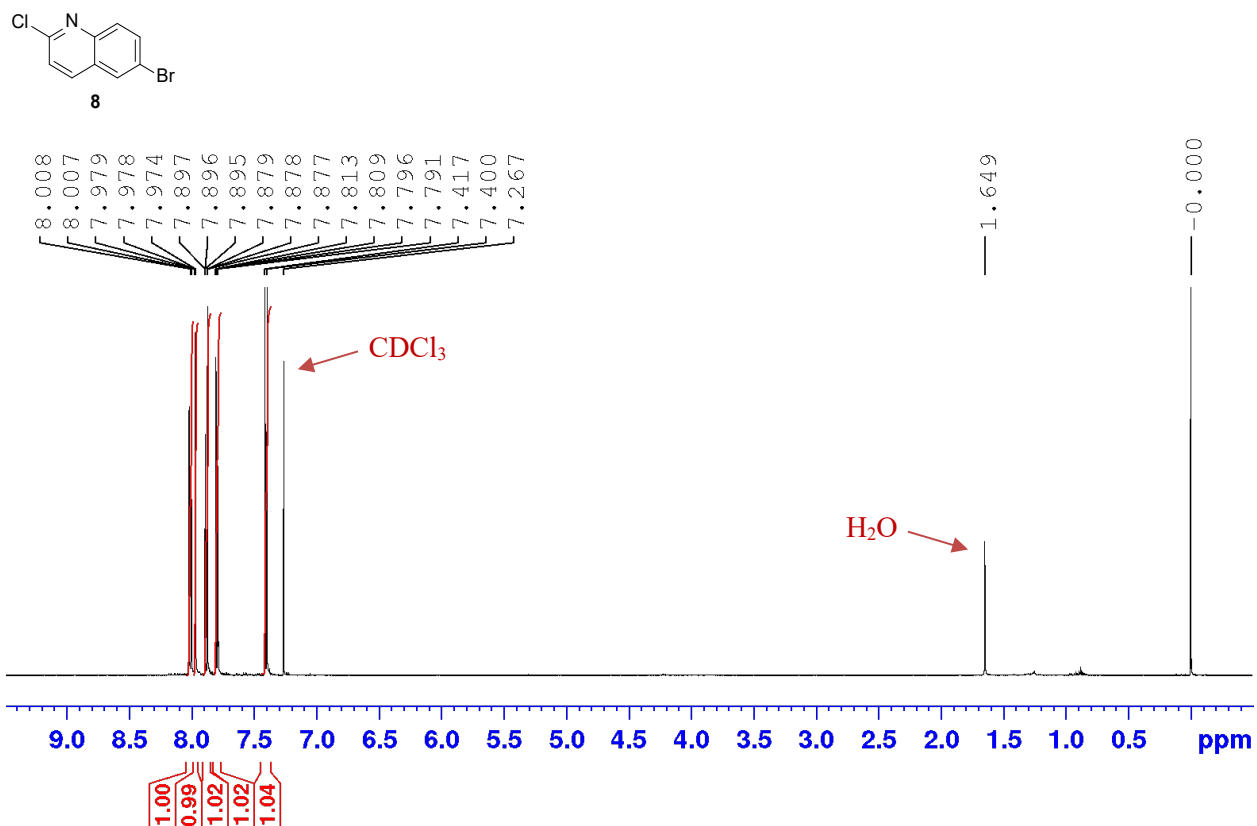


Figure 7. ¹H NMR spectrum of compound **8** in CDCl₃.

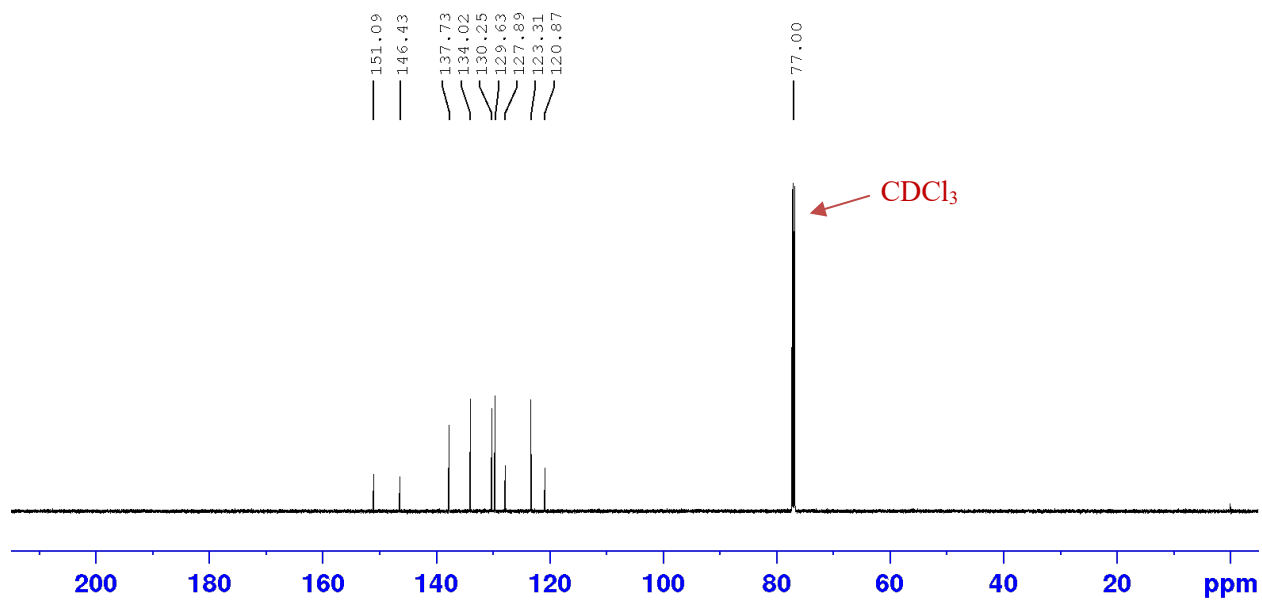


Figure 8. ¹³C NMR spectrum of compound **8** in CDCl₃.

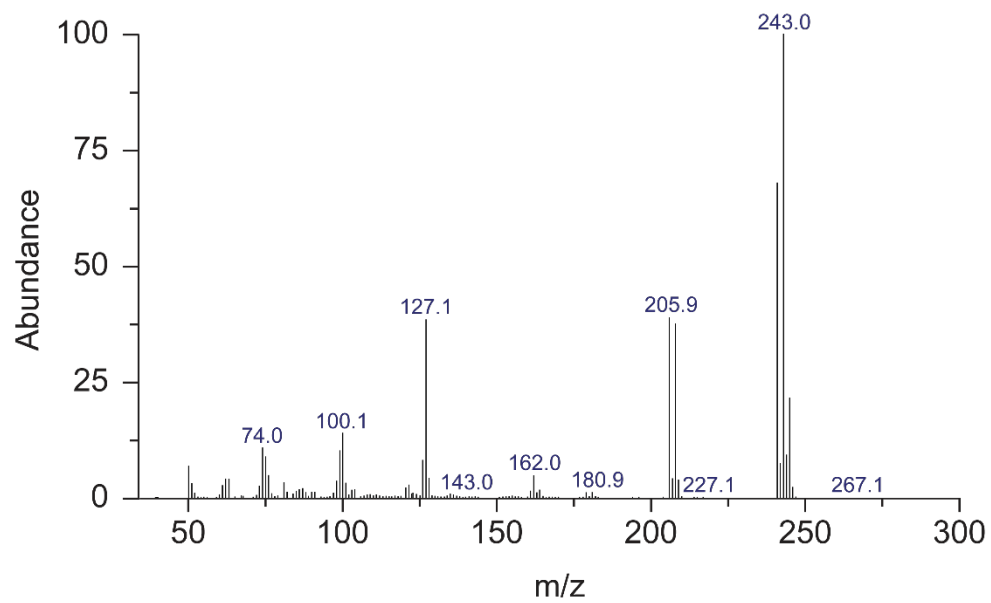


Figure 9. GC-MS spectrum of compound **8**.

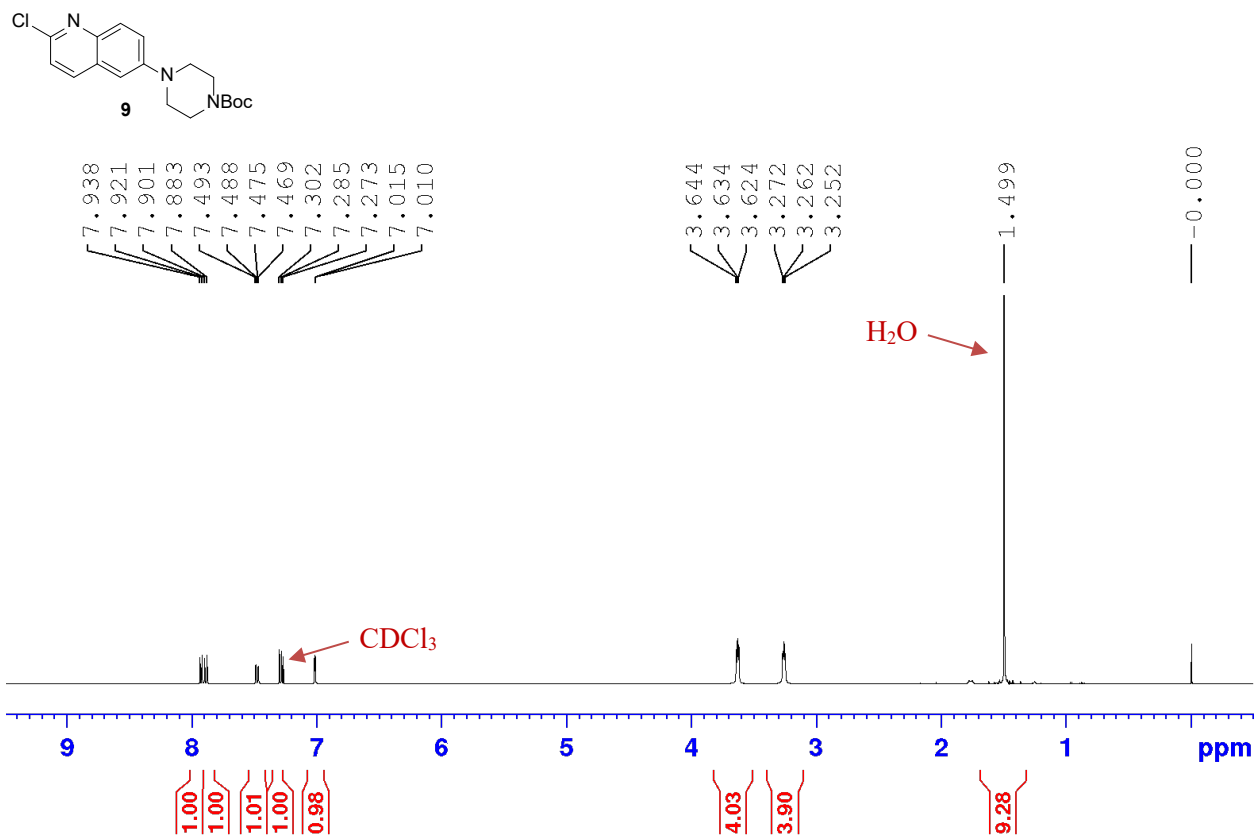


Figure 10. ¹H NMR spectrum of compound **9** in CDCl₃.

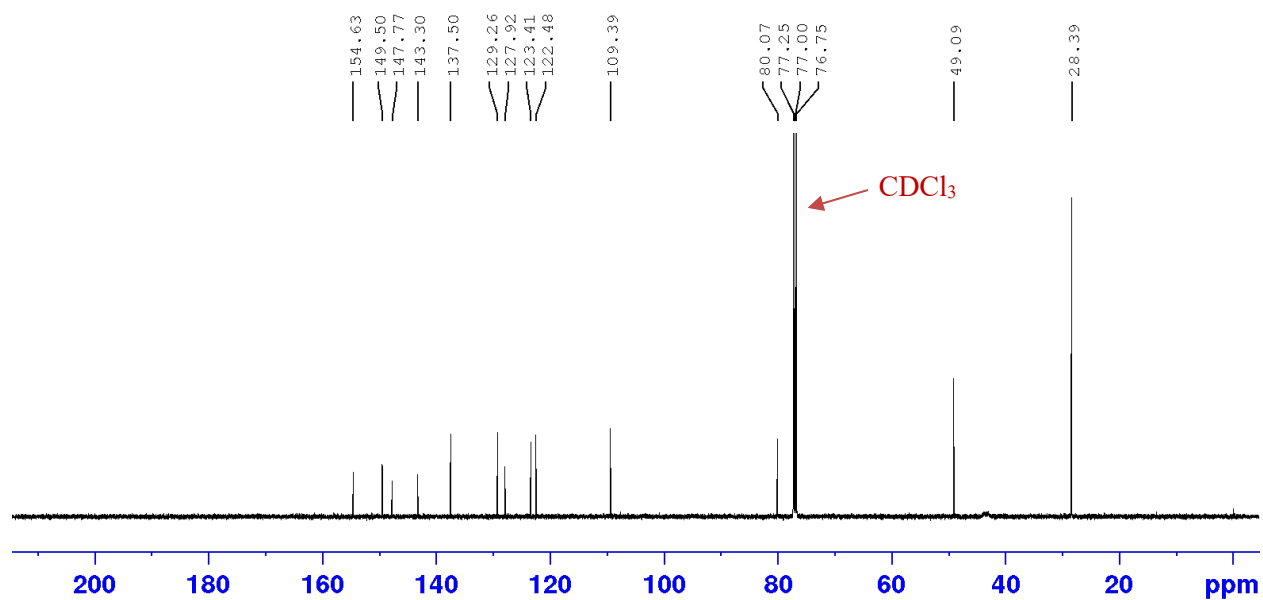


Figure 11. ¹³C NMR spectrum of compound **9** in CDCl₃.

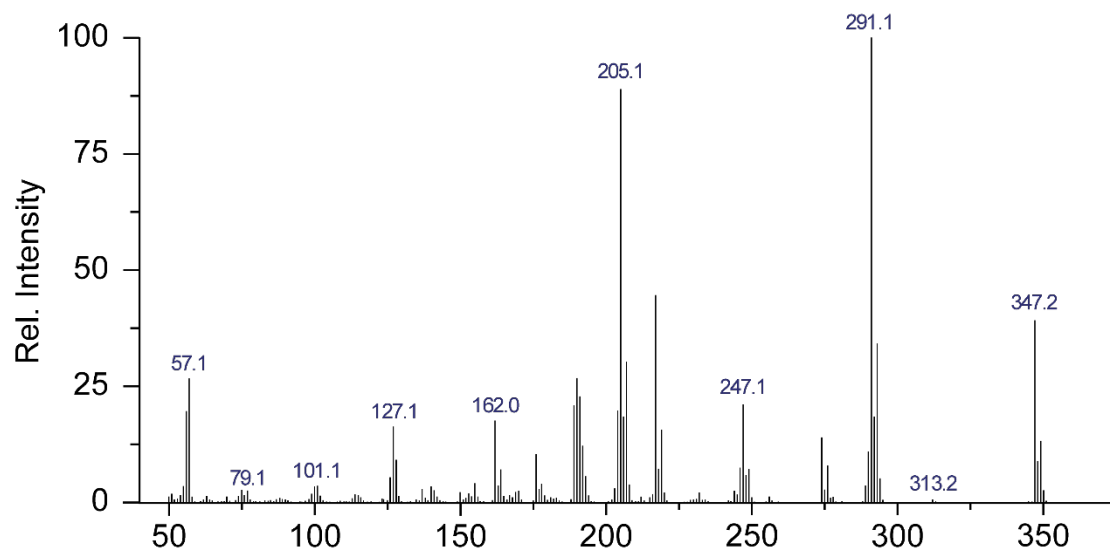


Figure 12. GC-MS spectrum of compound 9.

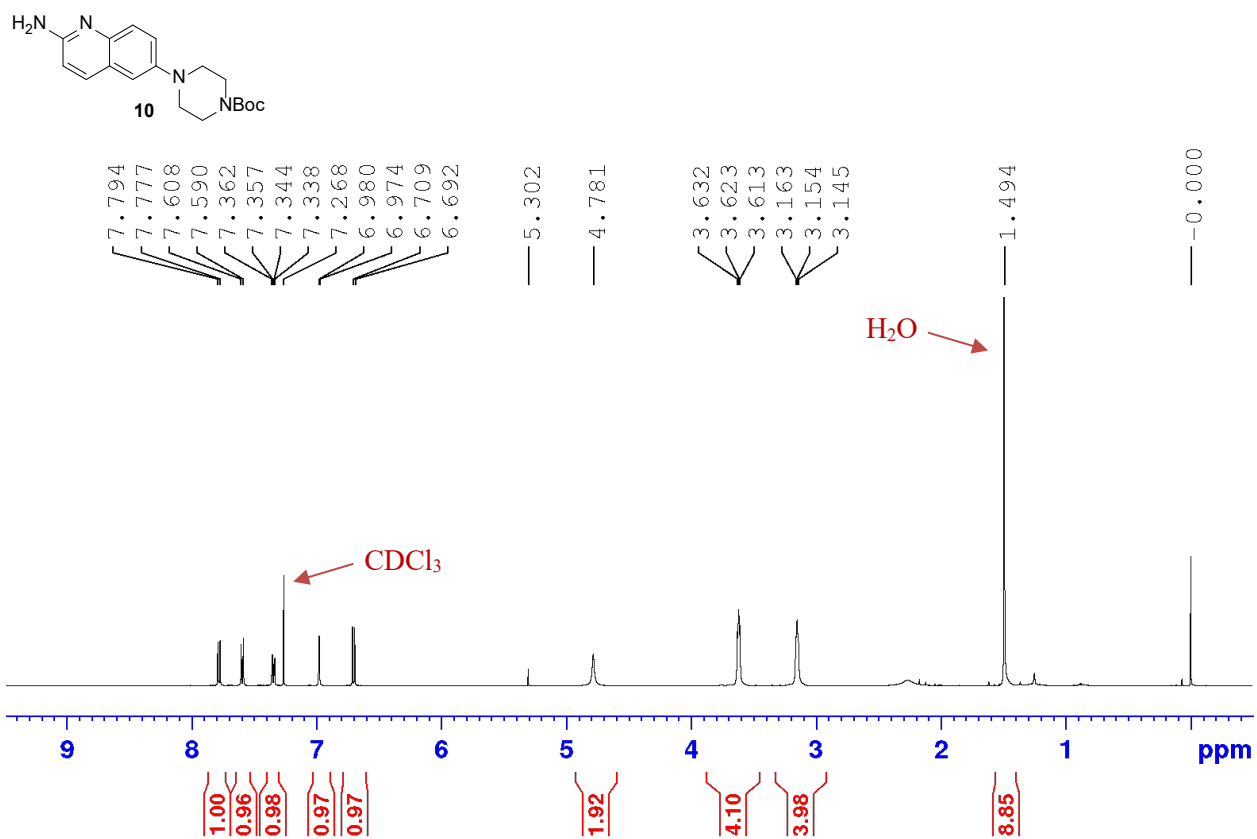


Figure 13. ¹H NMR spectrum of compound **10** in CDCl₃.

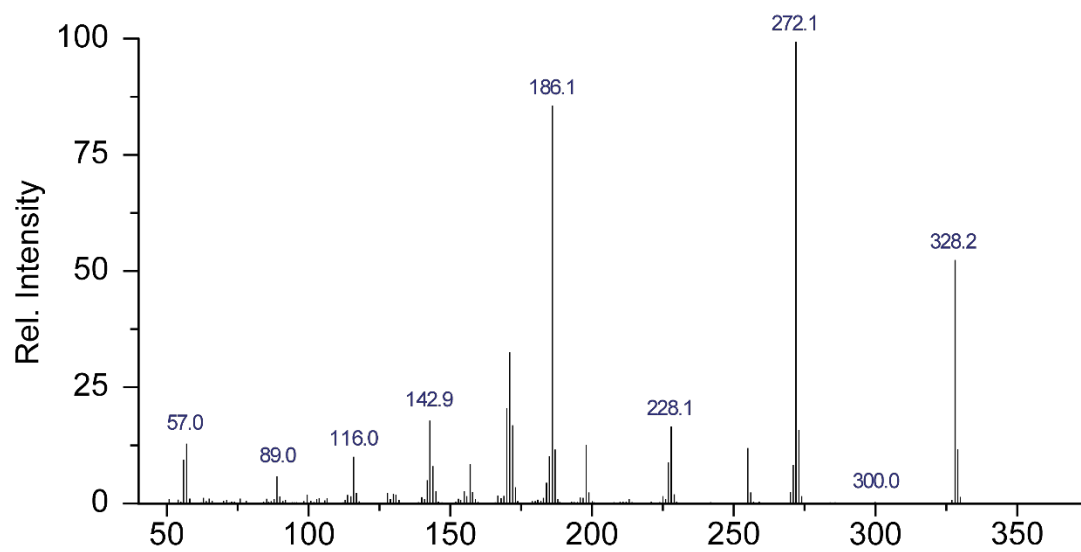


Figure 14. GC-MS spectrum of compound **10**.

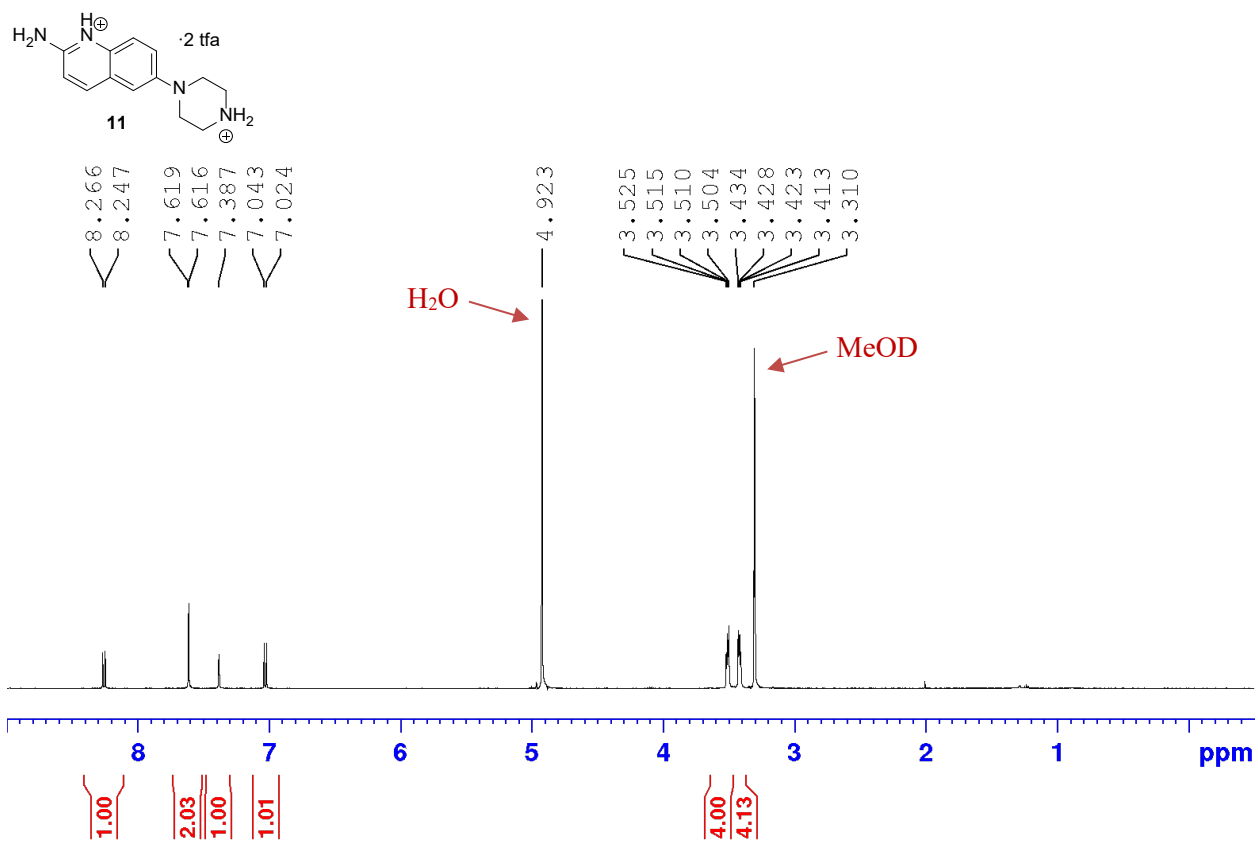


Figure 15. ¹H NMR spectrum of compound **11** in CD₃OD.

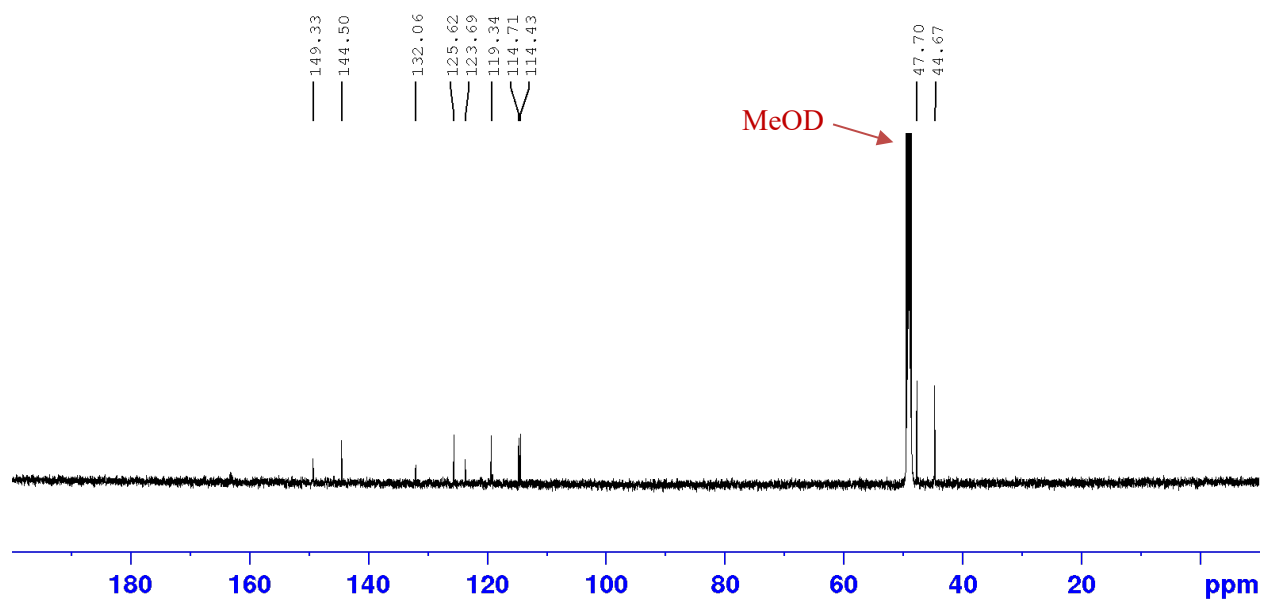


Figure 16. ¹³C NMR spectrum of compound **11** in CD₃OD.

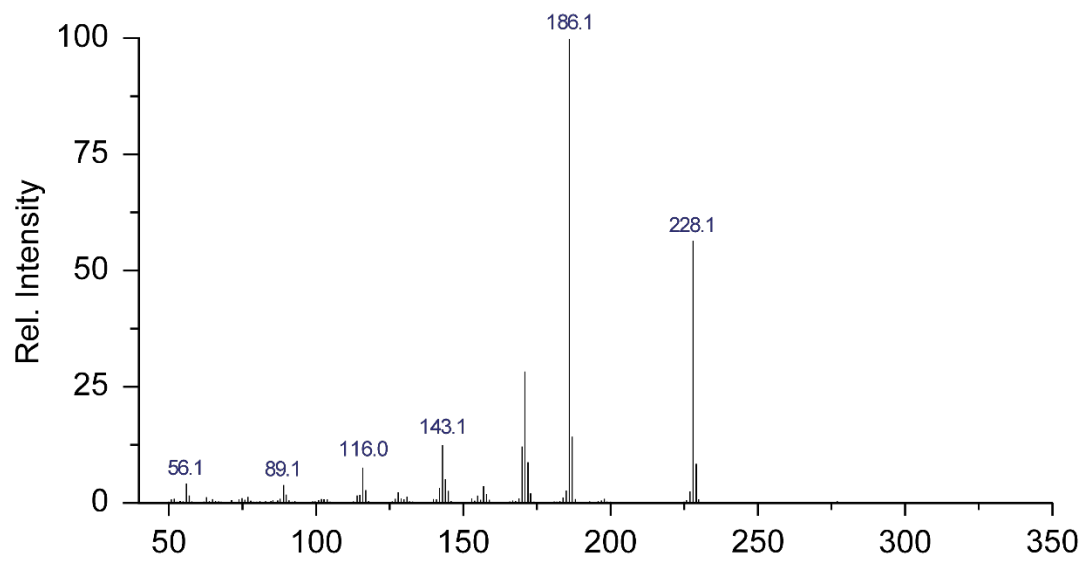


Figure 17. GC-MS spectrum of compound **11**.

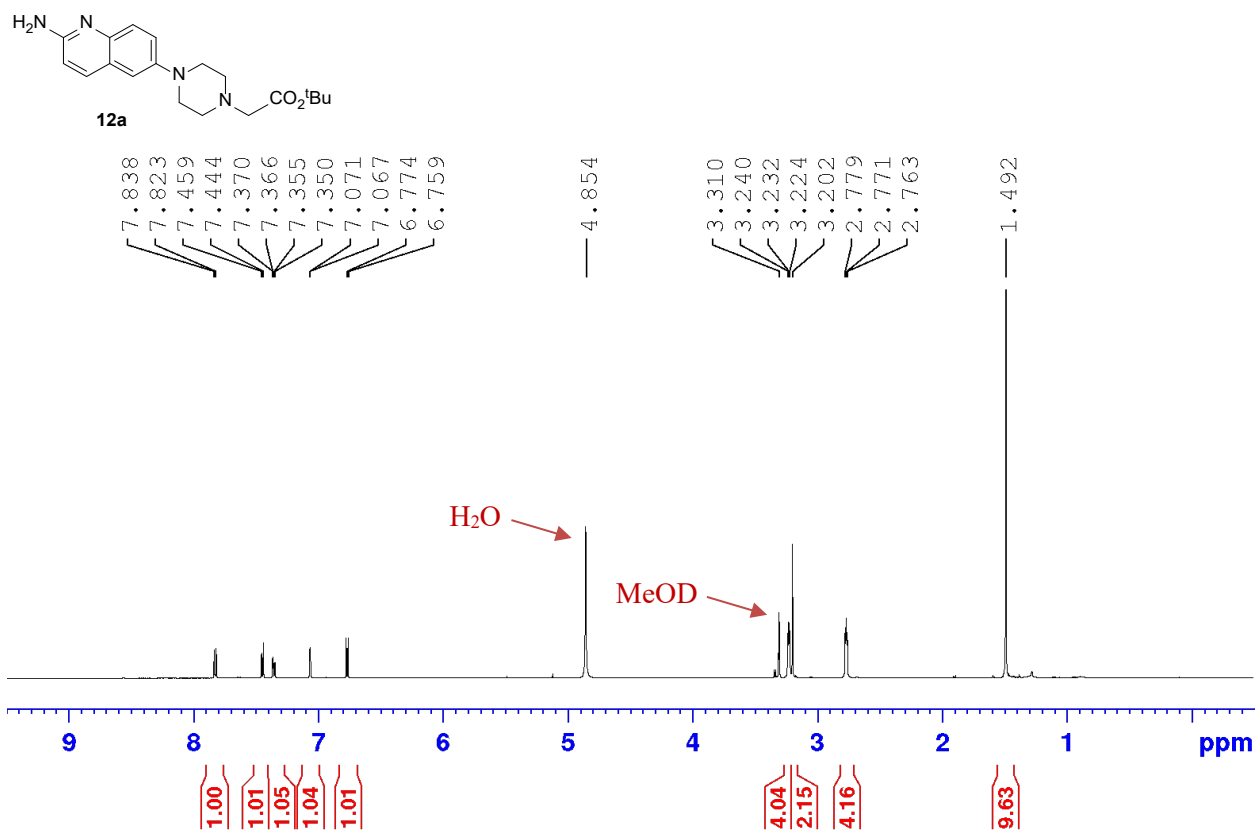


Figure 18. ^1H NMR spectrum of compound **12a** in CD_3OD .

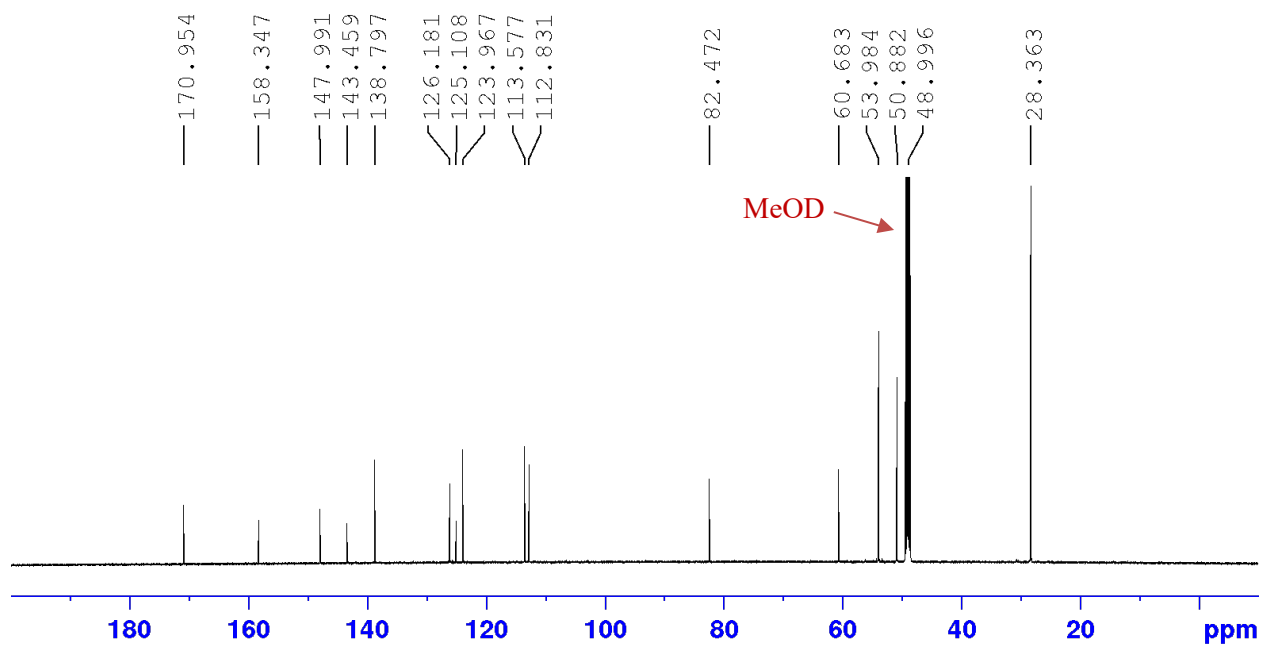


Figure 19. ^{13}C NMR spectrum of compound **12a** in CD_3OD .

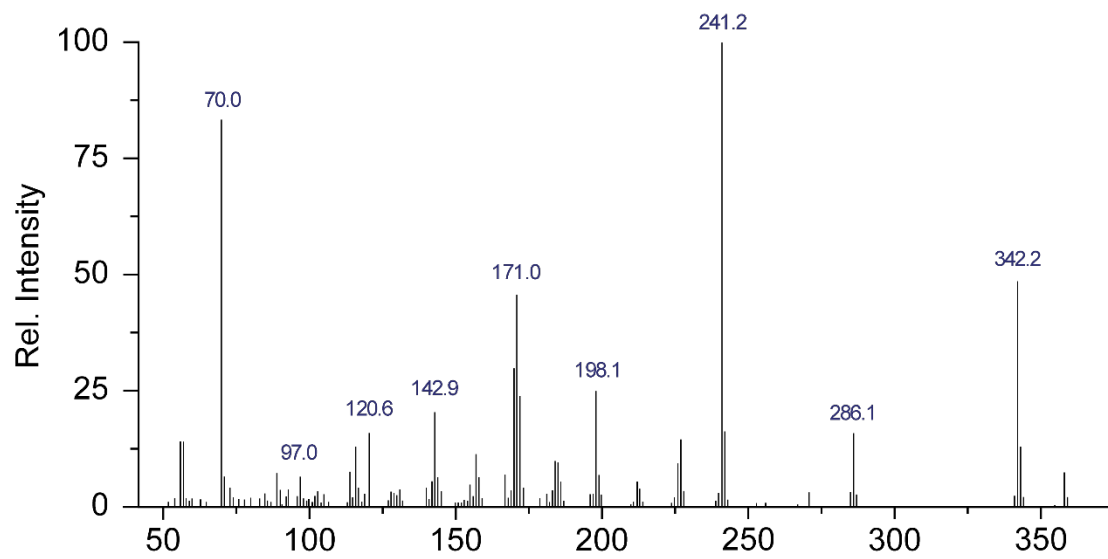


Figure 20. GC-MS spectrum of compound **12a**.

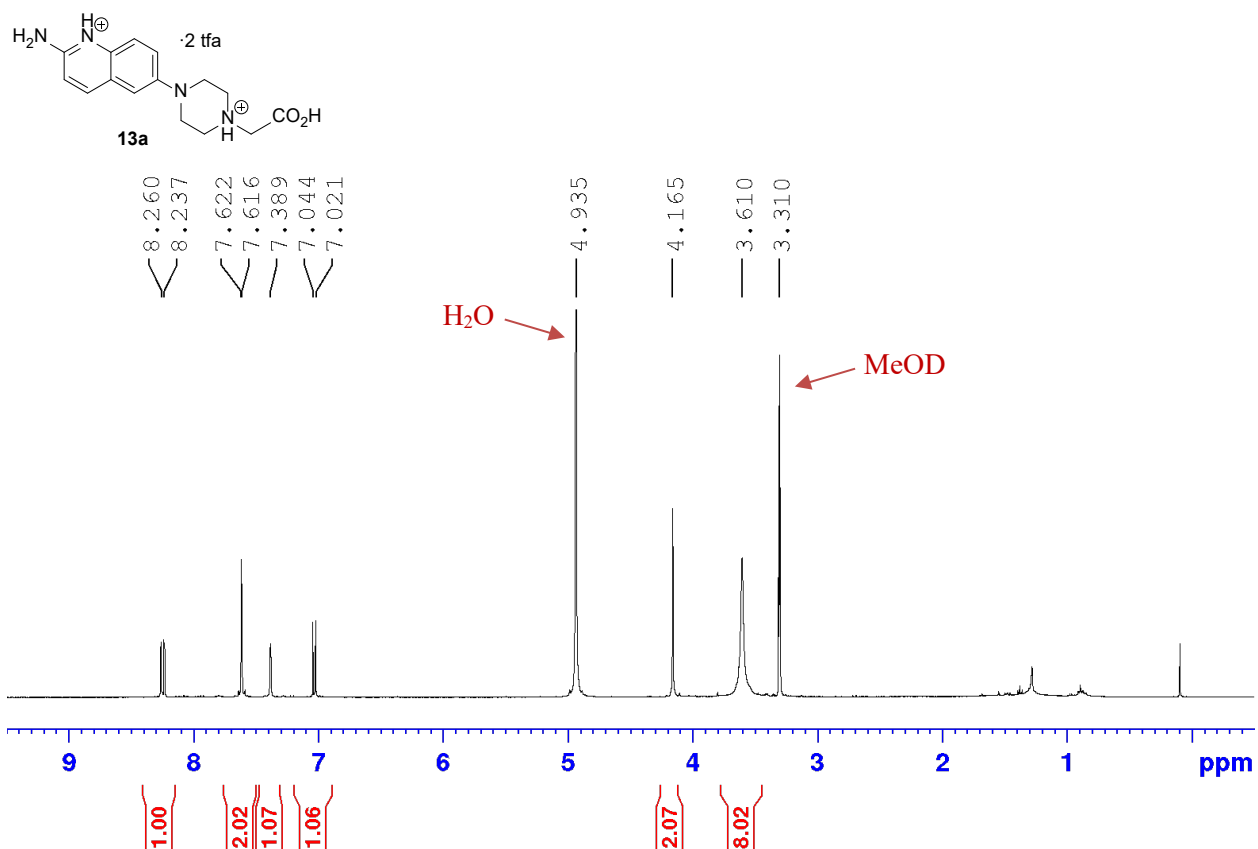


Figure 21. ^1H NMR spectrum of compound **13a** in CD_3OD .

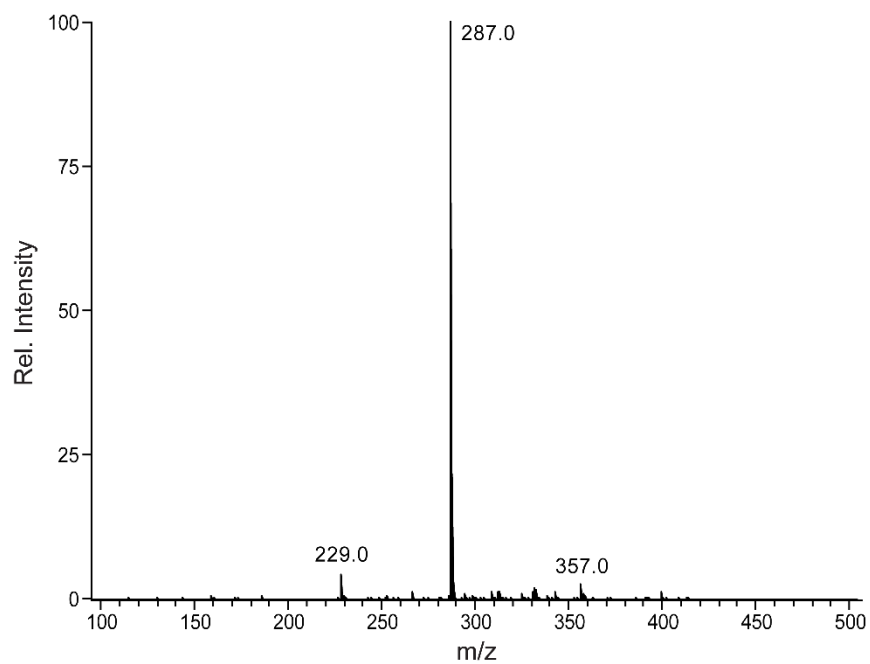


Figure 22. ESI-MS spectrum of compound **13a**.

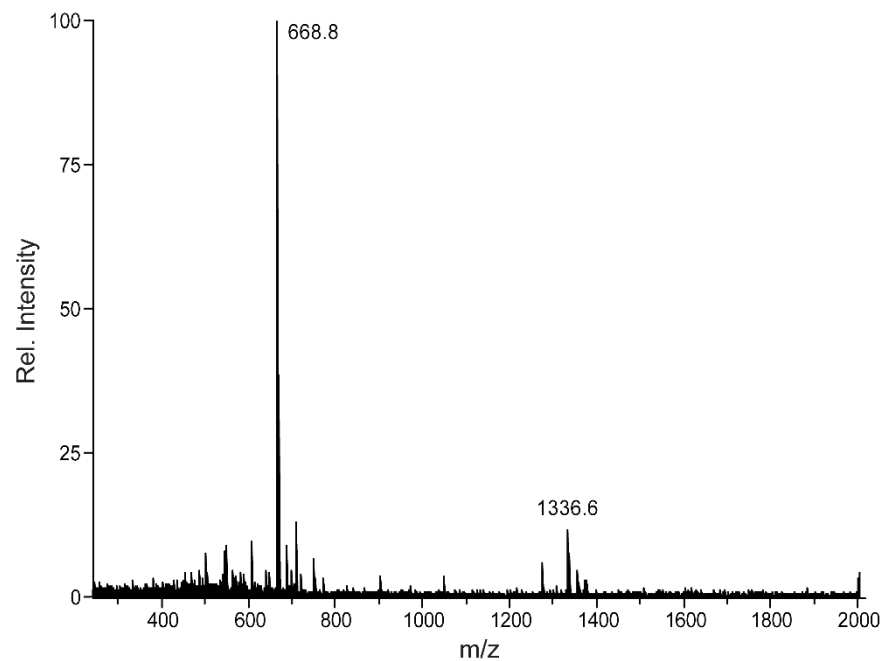
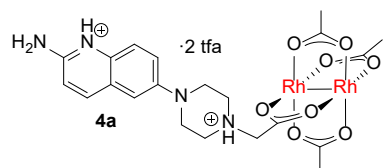


Figure 23. ESI-MS spectrum of compound 4a.

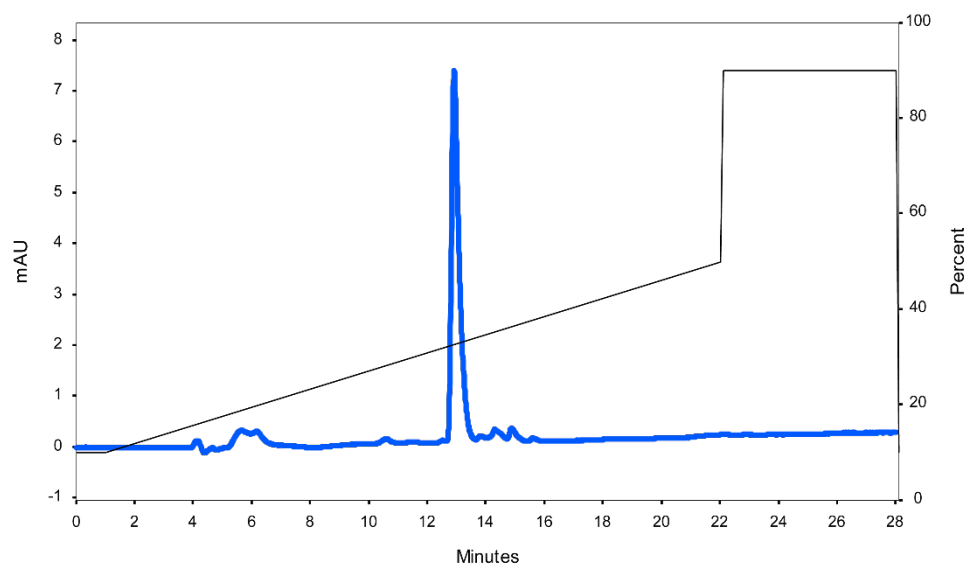


Figure 24. HPLC chromatogram of compound 4a.

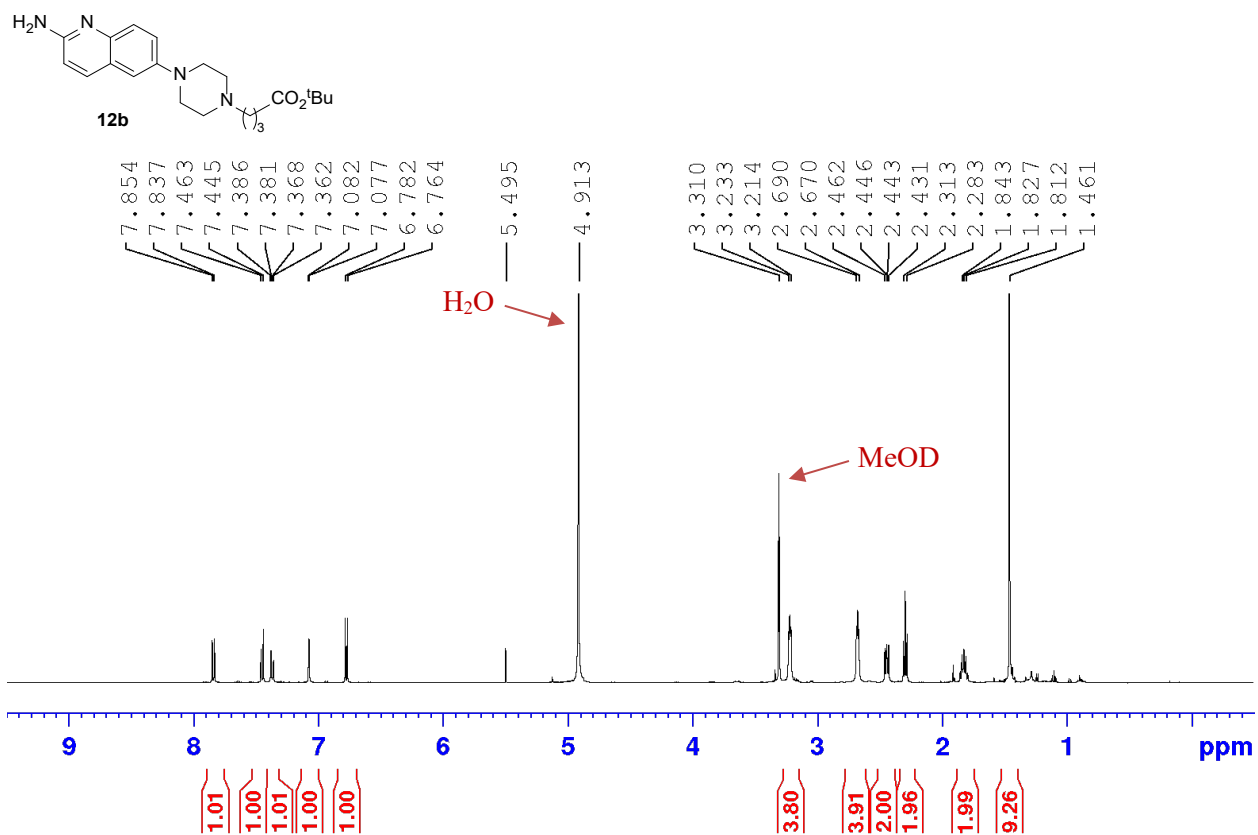


Figure 25. ¹H NMR spectrum of compound **12b** in CD₃OD.

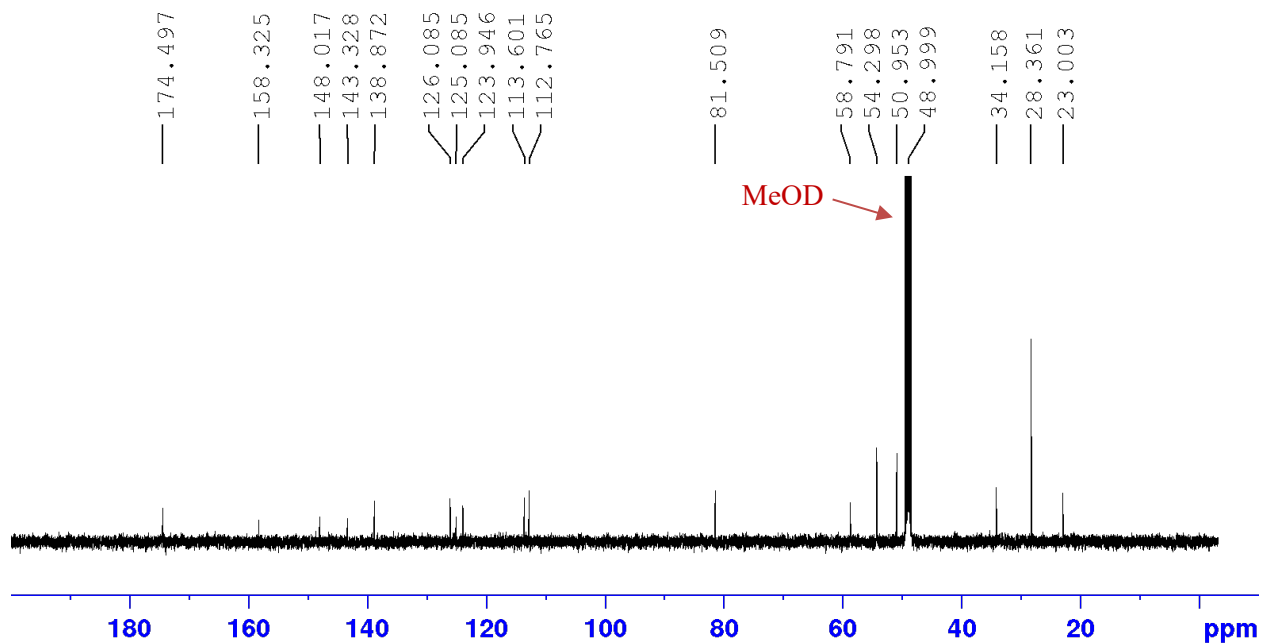


Figure 26. ¹³C NMR spectrum of compound **12b** in CD₃OD.

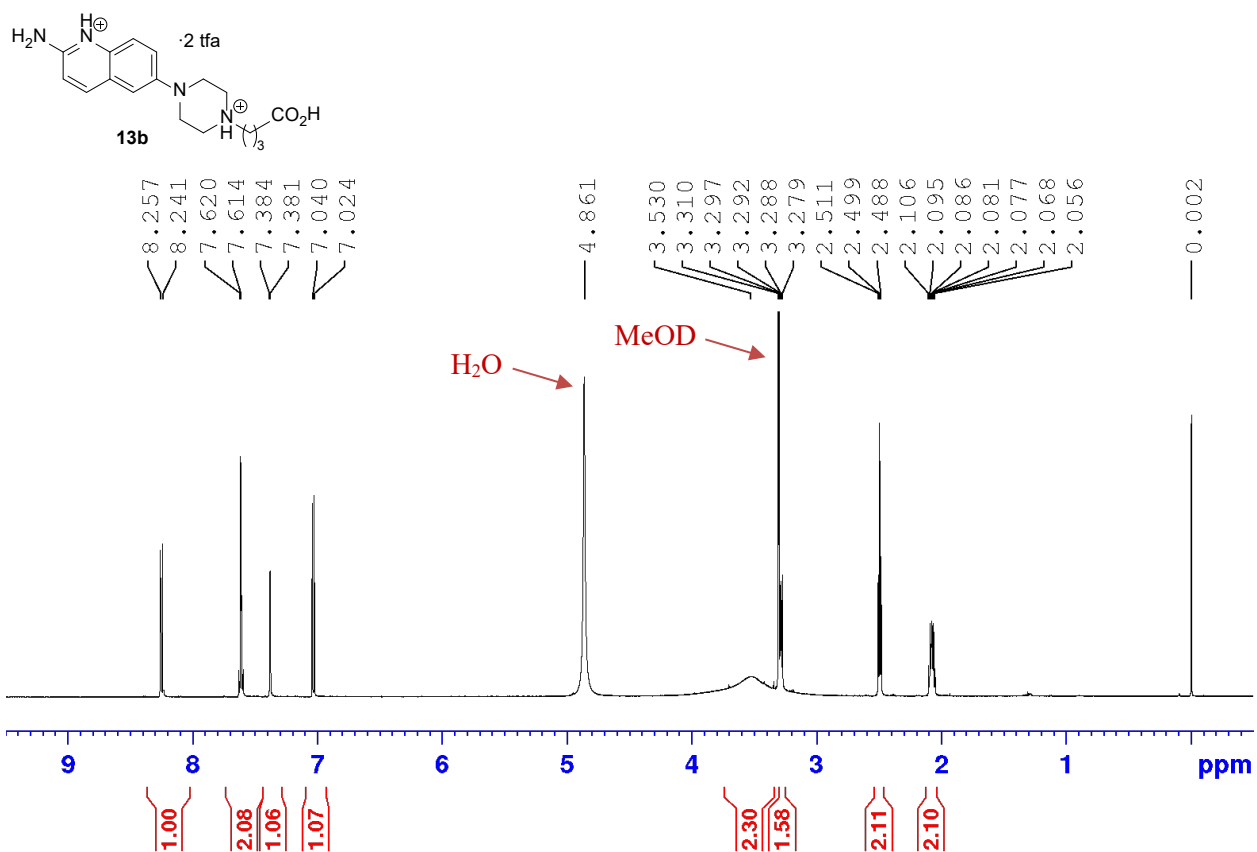


Figure 27. ¹H NMR spectrum of compound **13b** in CD₃OD.

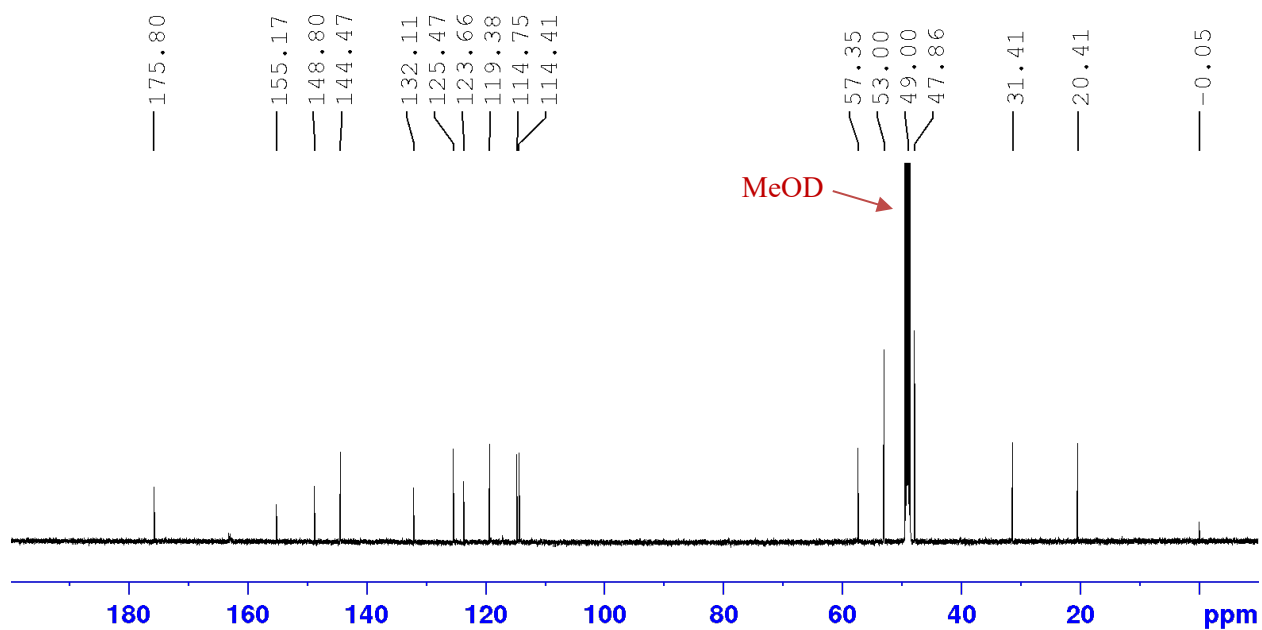


Figure 28. ¹³C NMR spectrum of compound **13b** in CD₃OD.

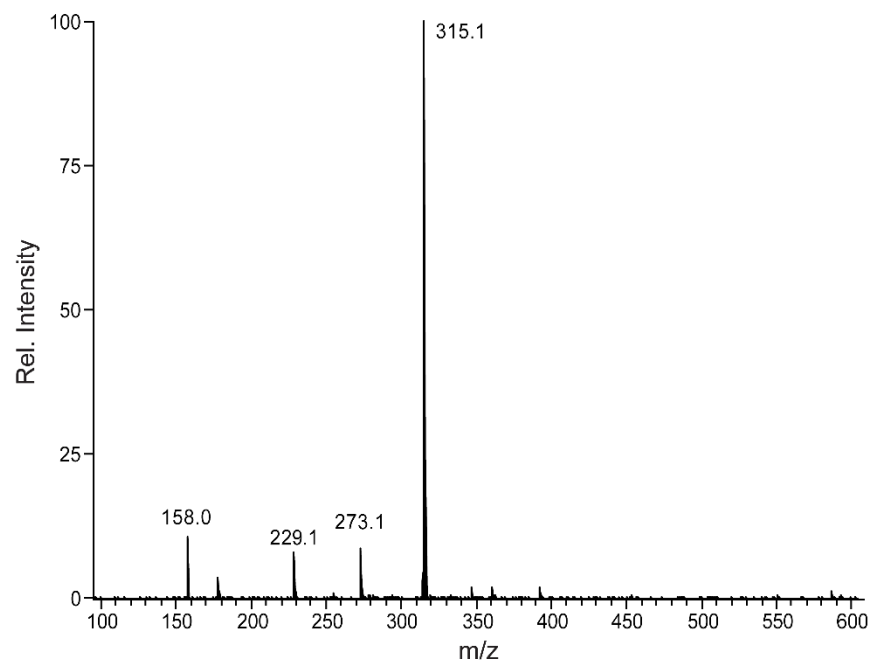


Figure 29.ESI-MS spectrum of compound **13b**.

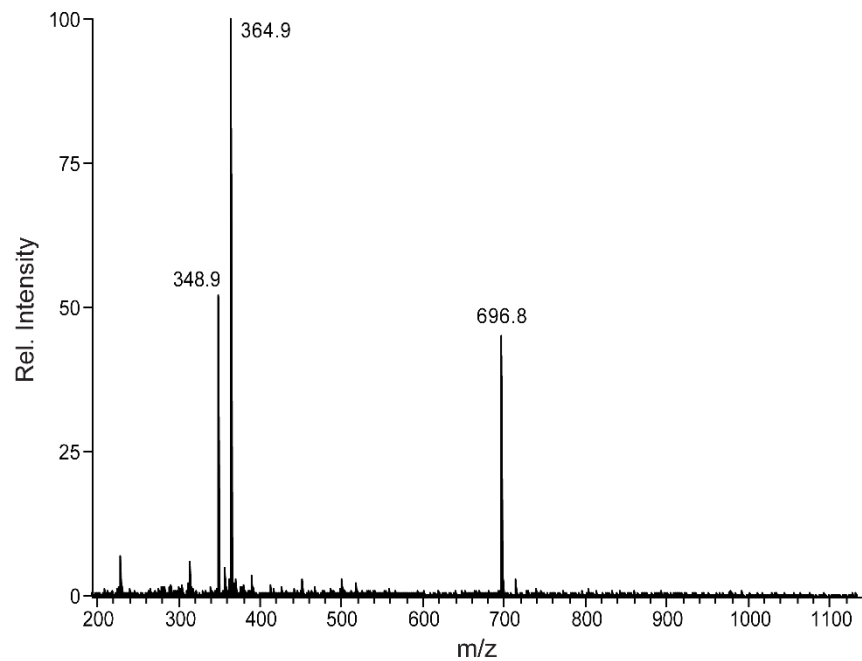
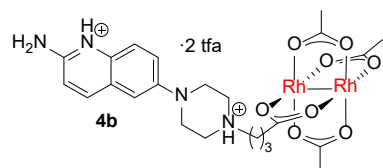


Figure 30. ESI-MS spectrum of compound **4b**.

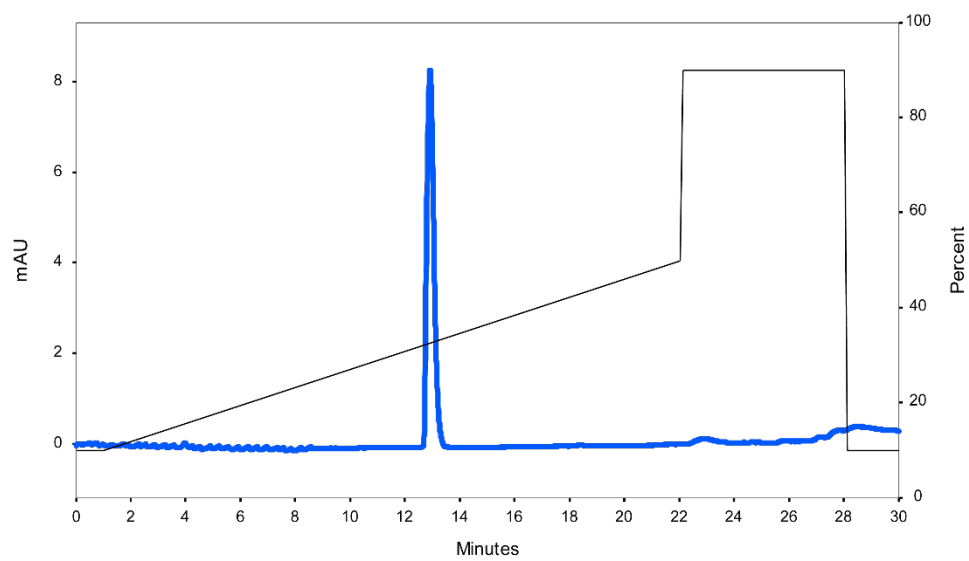


Figure 31. HPLC chromatogram of compound **4b**.

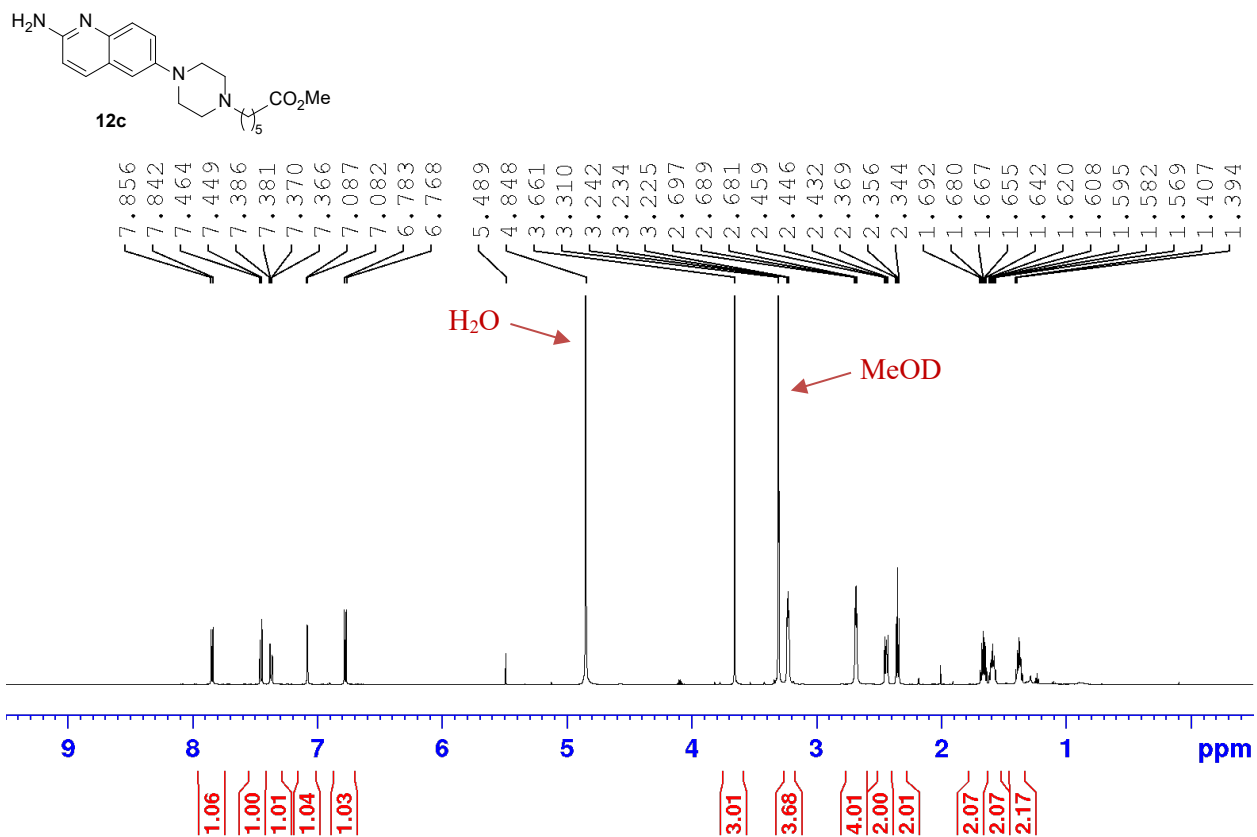


Figure 32. ¹H NMR spectrum of compound **12c** in CD₃OD.

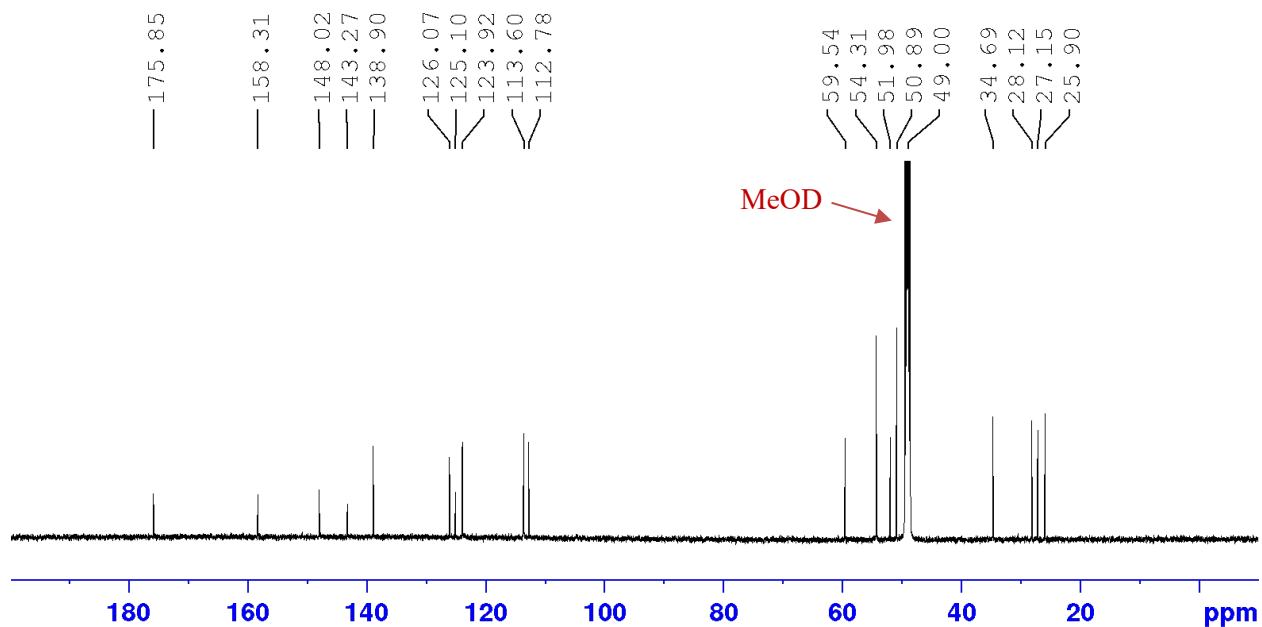


Figure 33. ¹³C NMR spectrum of compound **12c** in CD₃OD.

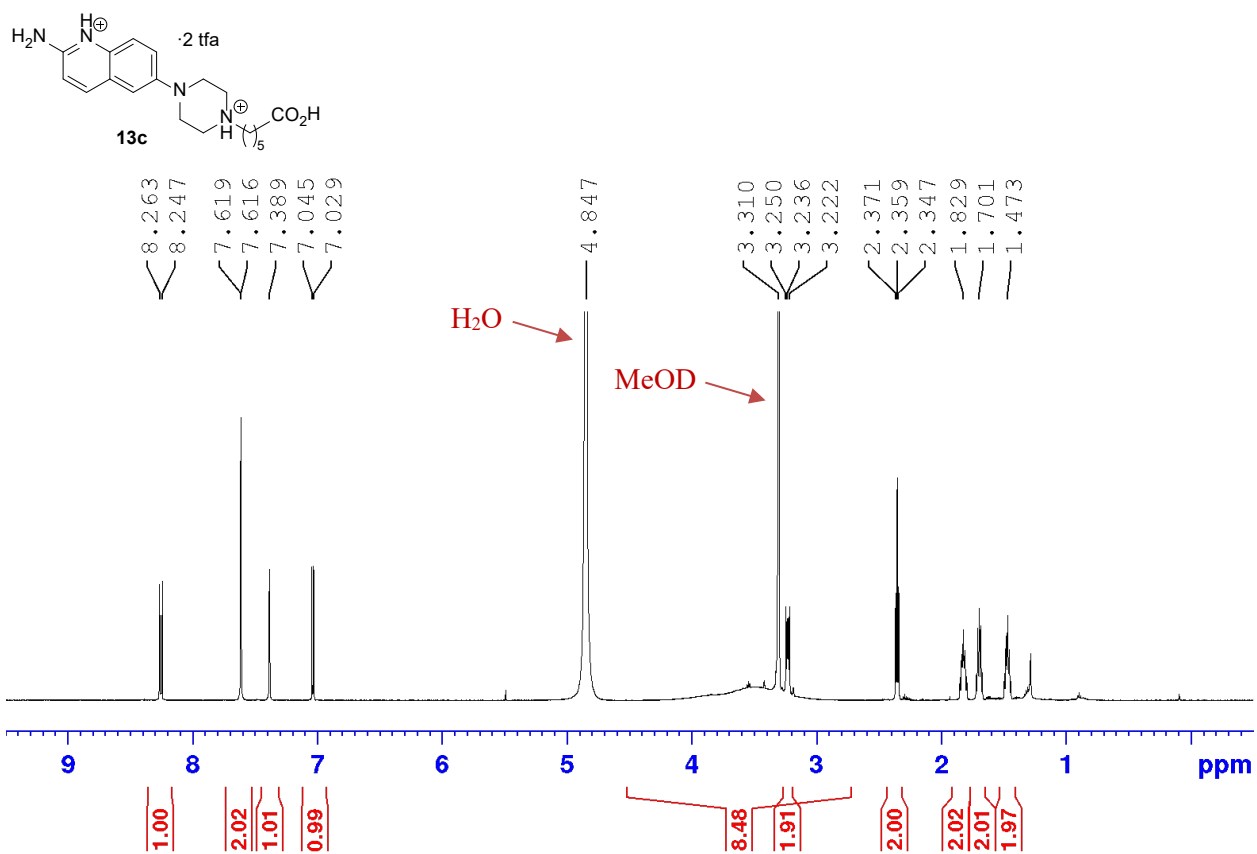


Figure 34. ¹H NMR spectrum of compound **13c** in CD₃OD.

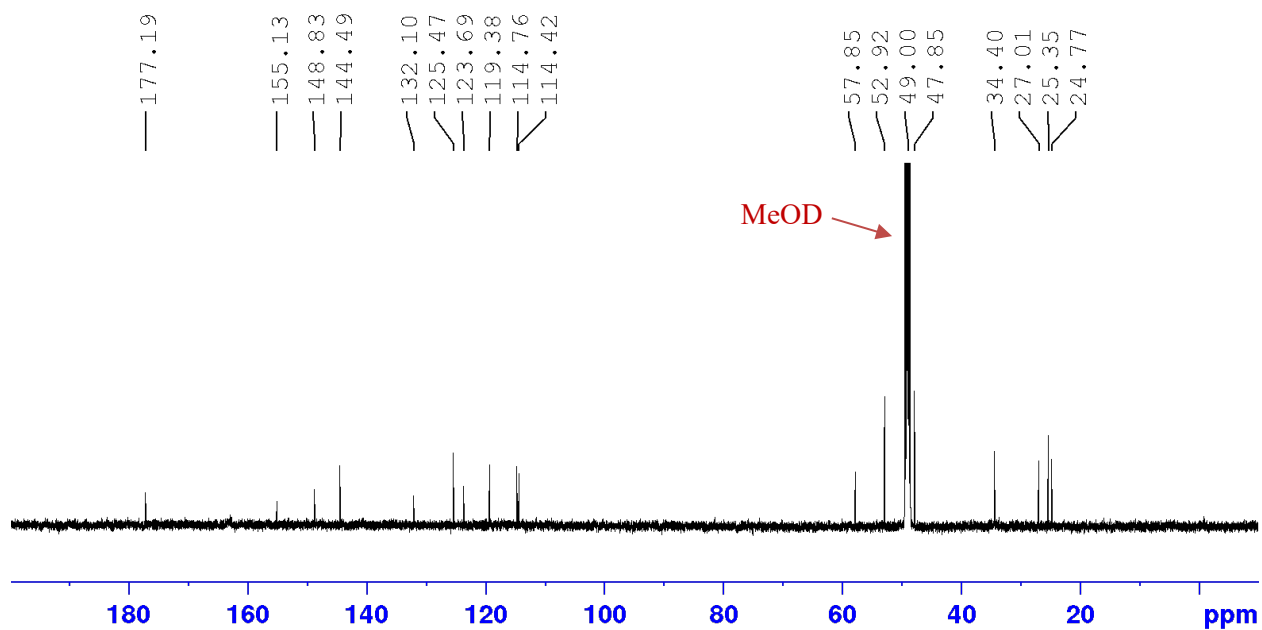


Figure 35. ¹³C NMR spectrum of compound **13c** in CD₃OD.

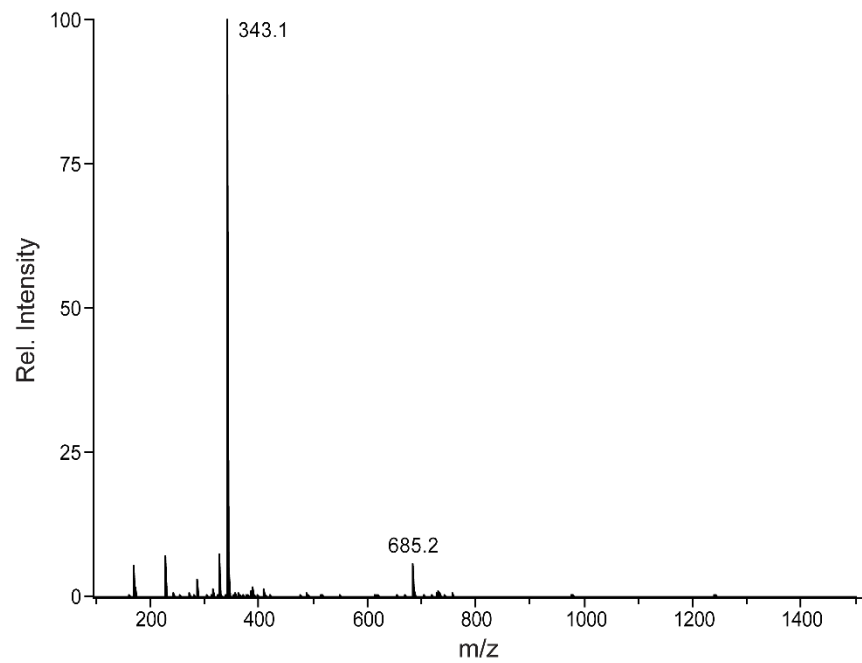


Figure 36. ESI-MS spectrum of compound **13c**.

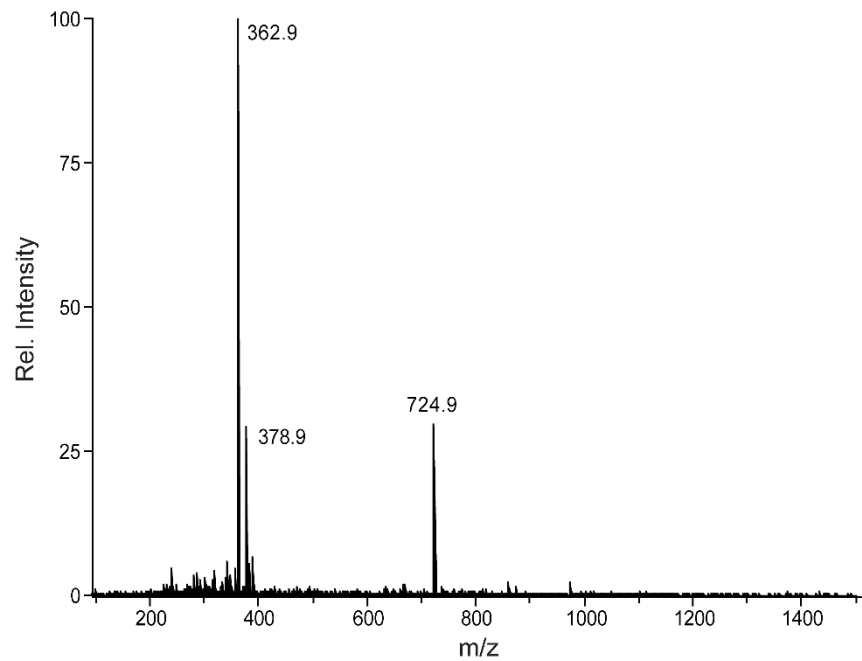
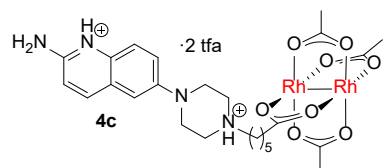


Figure 37. ESI-MS spectrum of compound **4c**.

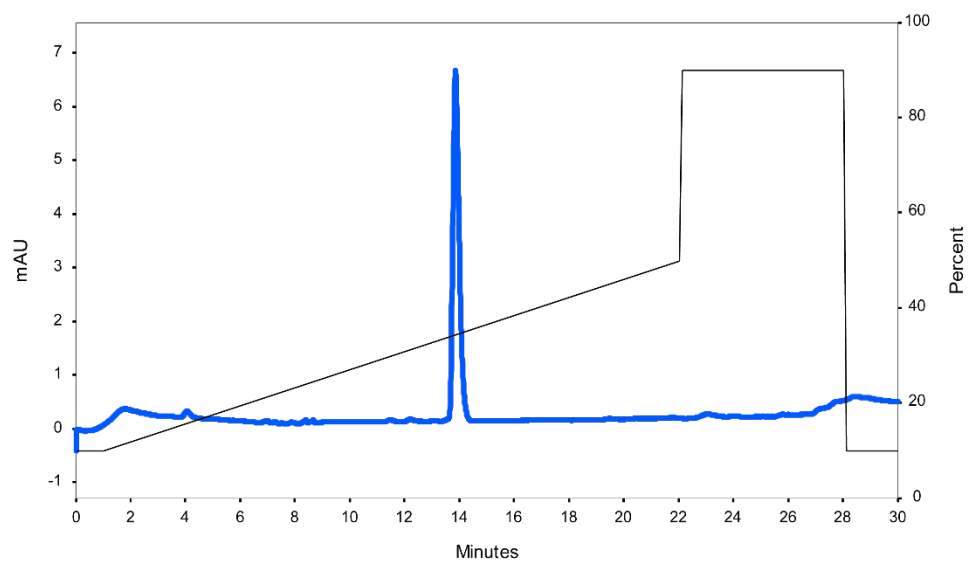
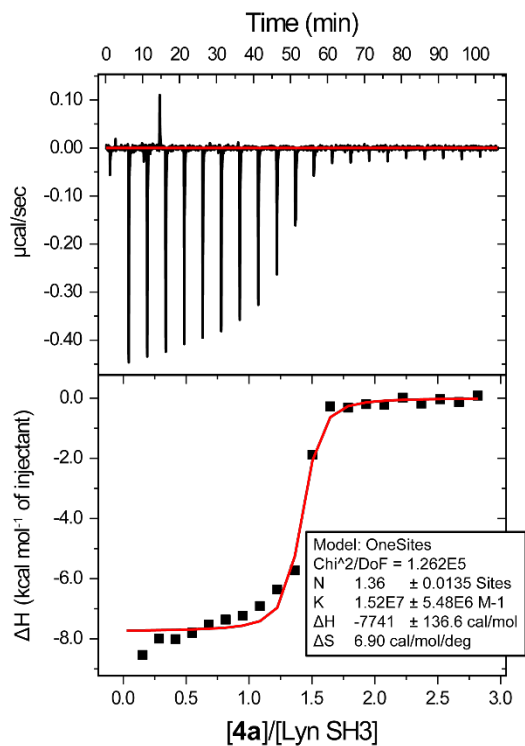
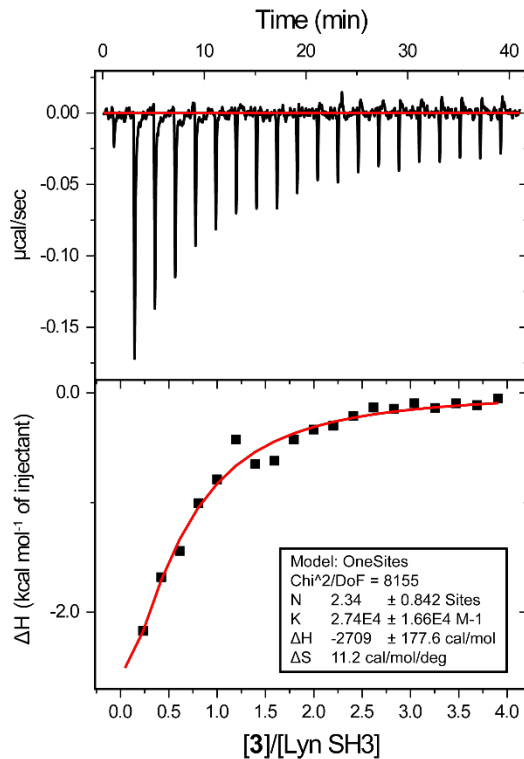
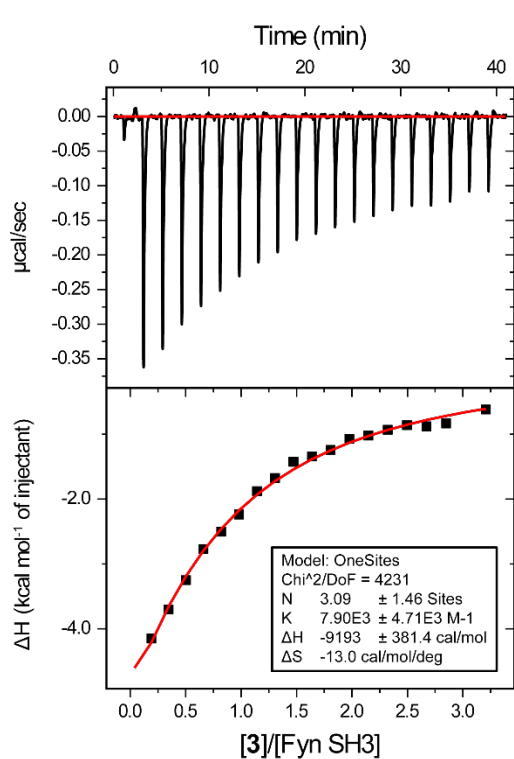
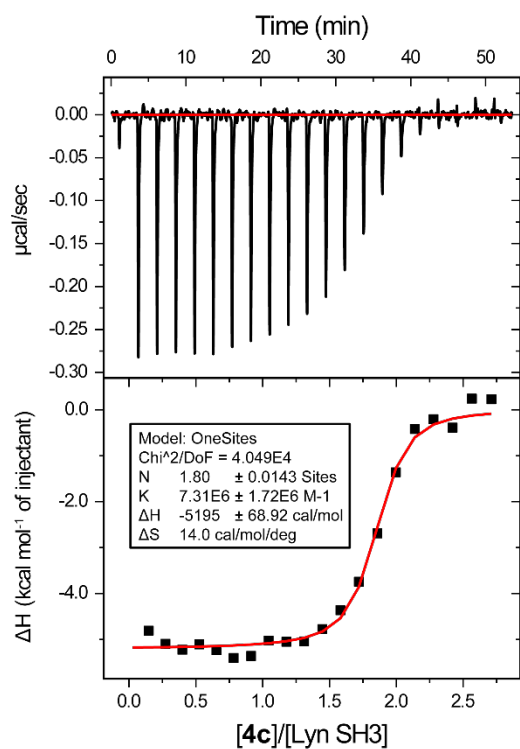
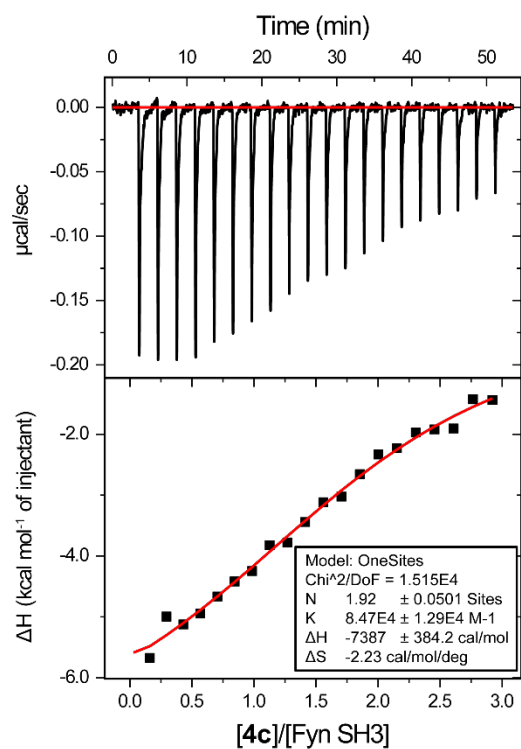
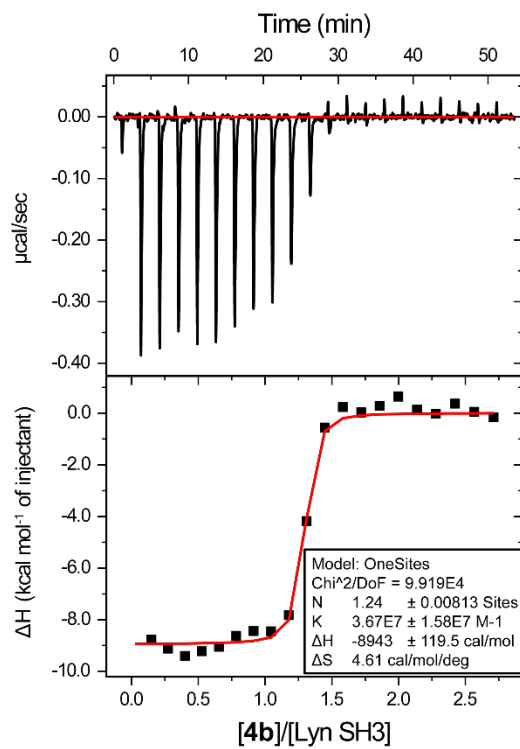
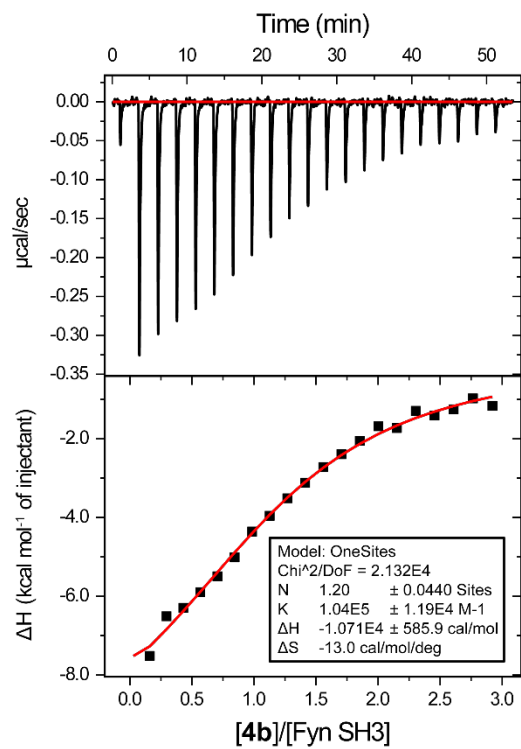
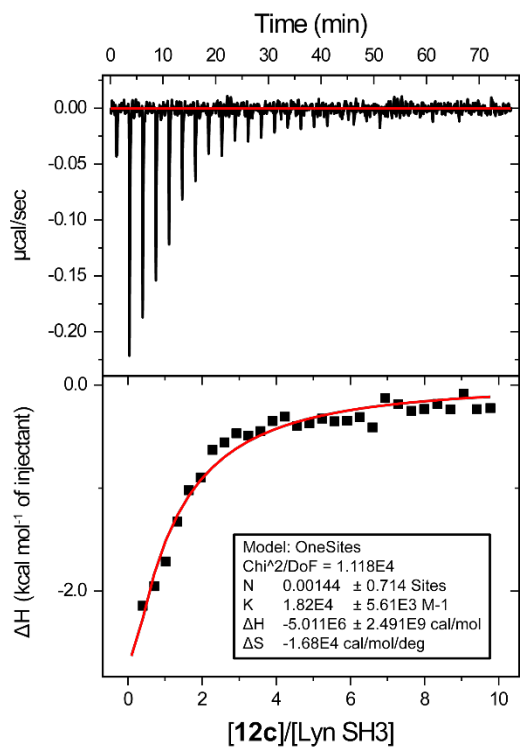
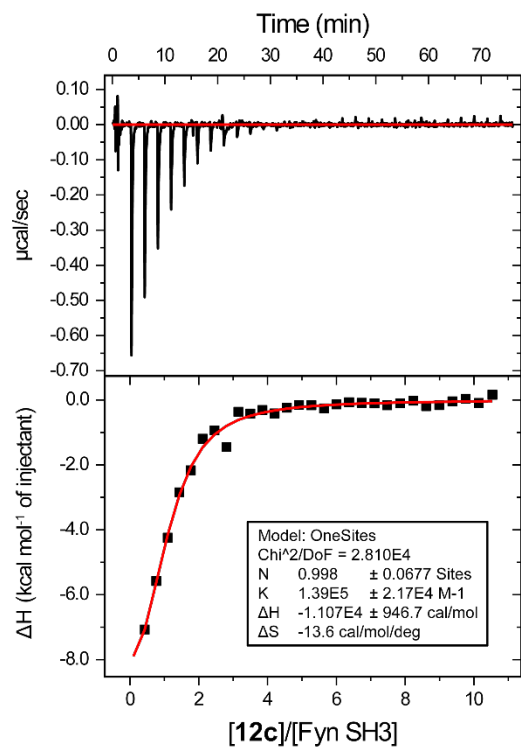


Figure 38. HPLC chromatogram of compound **4c**.

ITC binding data

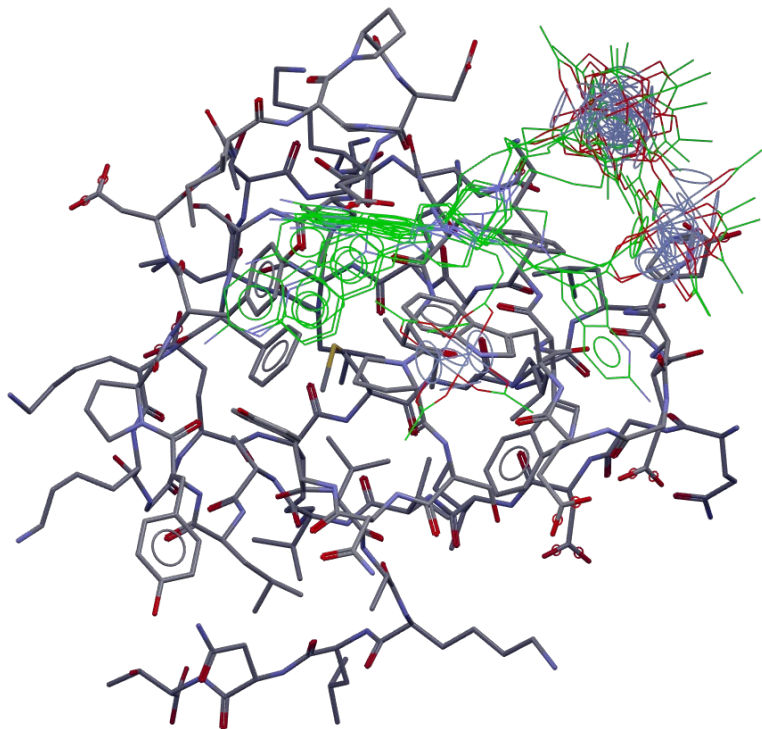




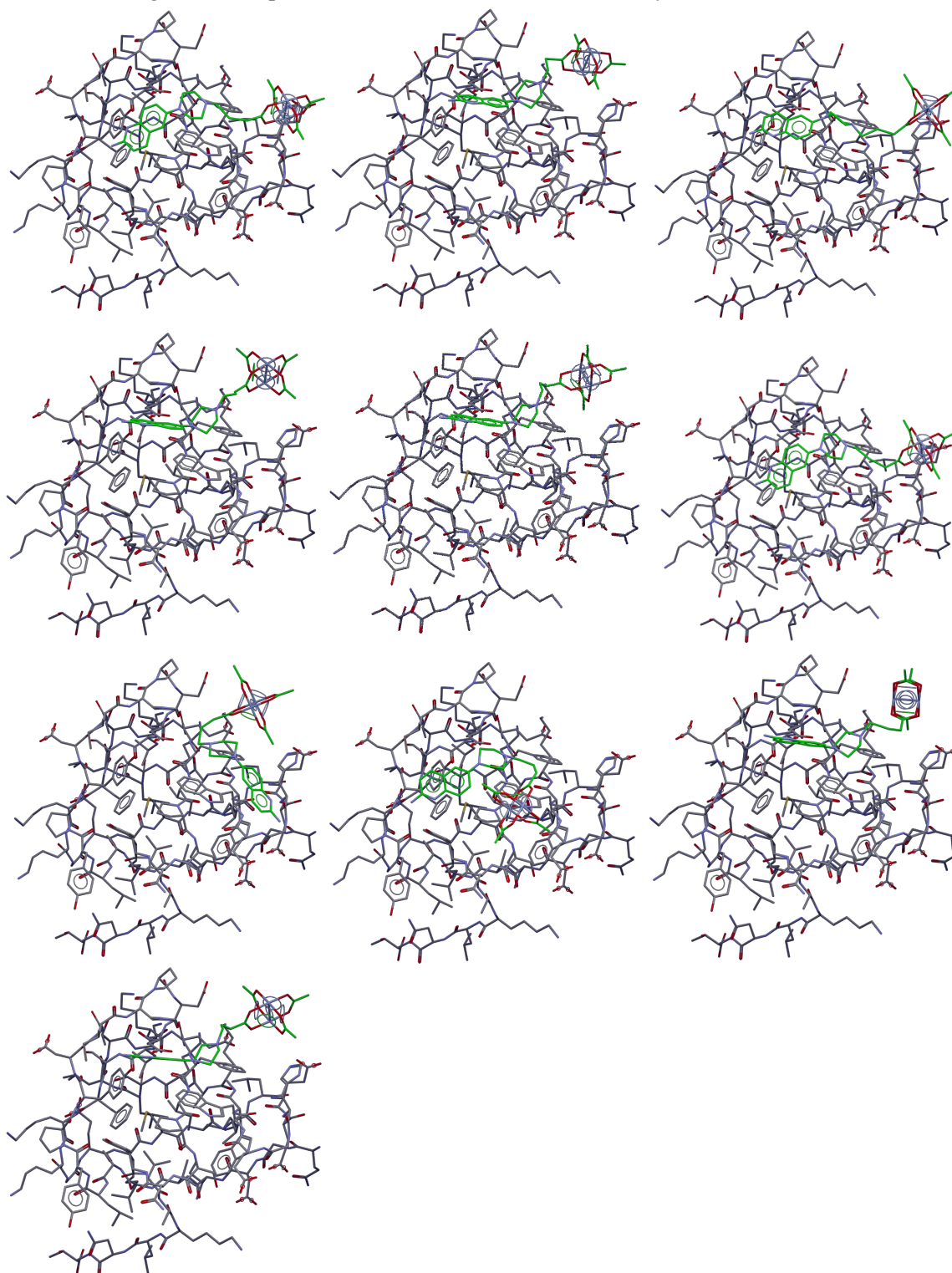


Computational docking

Overlay of the top 10 docked conformations identified by GOLD:



Individual images of the top 10 docked conformations identified by Gold:



Coordinates of final binding model:

HETATM	1	N	d	1	10.619	-4.445	-30.483	1.00	99.99	N
HETATM	2	N	d	1	11.993	-2.499	-31.882	1.00	99.99	N
HETATM	3	N	d	1	19.244	-1.024	-32.077	1.00	99.99	N
HETATM	4	N	d	1	17.194	-1.268	-31.204	1.00	99.99	N
HETATM	5	C	d	1	4.279	-5.456	-28.891	1.00	99.99	C
HETATM	6	C	d	1	3.825	-4.061	-29.134	1.00	99.99	C
HETATM	7	C	d	1	7.123	-7.792	-29.808	1.00	99.99	C
HETATM	8	C	d	1	8.348	-7.770	-30.659	1.00	99.99	C
HETATM	9	C	d	1	5.714	-10.394	-27.737	1.00	99.99	C
HETATM	10	C	d	1	2.871	-8.058	-26.820	1.00	99.99	C
HETATM	11	C	d	1	6.169	-11.789	-27.495	1.00	99.99	C
HETATM	12	C	d	1	1.646	-8.080	-25.969	1.00	99.99	C
HETATM	13	C	d	1	10.874	-1.988	-31.048	1.00	99.99	C
HETATM	14	C	d	1	10.755	-3.031	-29.928	1.00	99.99	C
HETATM	15	C	d	1	11.503	-4.792	-31.681	1.00	99.99	C
HETATM	16	C	d	1	11.556	-3.651	-32.708	1.00	99.99	C
HETATM	17	C	d	1	15.922	-1.535	-31.384	1.00	99.99	C
HETATM	18	C	d	1	15.044	-1.496	-30.366	1.00	99.99	C
HETATM	19	C	d	1	13.745	-1.790	-30.541	1.00	99.99	C
HETATM	20	C	d	1	13.222	-2.155	-31.732	1.00	99.99	C
HETATM	21	C	d	1	14.124	-2.159	-32.741	1.00	99.99	C

HETATM	22	C	d	1	15.430	-1.856	-32.593	1.00	99.99	C
HETATM	23	C	d	1	16.275	-1.880	-33.641	1.00	99.99	C
HETATM	24	C	d	1	17.570	-1.591	-33.457	1.00	99.99	C
HETATM	25	C	d	1	18.011	-1.290	-32.224	1.00	99.99	C
HETATM	26	C	d	1	10.755	-5.558	-29.462	1.00	99.99	C
HETATM	27	C	d	1	9.962	-7.065	-30.233	1.00	99.99	C
HETATM	28	O	d	1	3.846	-6.388	-29.627	1.00	99.99	O
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HETATM	31	O	d	1	2.763	-8.402	-28.029	1.00	99.99	O
HETATM	32	O	d	1	5.084	-5.658	-27.933	1.00	99.99	O
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HETATM	35	O	d	1	3.962	-7.692	-26.293	1.00	99.99	O
HETATM	36	Cr	d	1	4.361	-8.311	-29.231	1.00	99.99	Cr
HETATM	37	Cr	d	1	5.633	-7.539	-27.398	1.00	99.99	Cr
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HETATM	39	H	d	1	3.325	-3.981	-29.754	1.00	99.99	H
HETATM	40	H	d	1	4.552	-3.434	-29.263	1.00	99.99	H
HETATM	41	H	d	1	8.054	-7.814	-31.741	1.00	99.99	H
HETATM	42	H	d	1	8.428	-8.734	-31.226	1.00	99.99	H
HETATM	43	H	d	1	6.449	-12.146	-28.267	1.00	99.99	H

HETATM	44	H	d	1	6.669	-11.869	-26.876	1.00	99.99	H
HETATM	45	H	d	1	5.442	-12.416	-27.365	1.00	99.99	H
HETATM	46	H	d	1	1.631	-7.359	-25.444	1.00	99.99	H
HETATM	47	H	d	1	0.921	-8.238	-26.422	1.00	99.99	H
HETATM	48	H	d	1	1.817	-8.648	-25.379	1.00	99.99	H
HETATM	49	H	d	1	10.987	-0.951	-30.672	1.00	99.99	H
HETATM	50	H	d	1	9.927	-1.952	-31.636	1.00	99.99	H
HETATM	51	H	d	1	9.870	-2.795	-29.292	1.00	99.99	H
HETATM	52	H	d	1	11.685	-2.920	-29.330	1.00	99.99	H
HETATM	53	H	d	1	9.636	-4.501	-30.845	1.00	99.99	H
HETATM	54	H	d	1	11.102	-5.710	-32.172	1.00	99.99	H
HETATM	55	H	d	1	12.545	-4.998	-31.341	1.00	99.99	H
HETATM	56	H	d	1	12.182	-3.890	-33.590	1.00	99.99	H
HETATM	57	H	d	1	10.542	-3.472	-33.136	1.00	99.99	H
HETATM	58	H	d	1	19.906	-1.036	-32.893	1.00	99.99	H
HETATM	59	H	d	1	19.621	-0.791	-31.124	1.00	99.99	H
HETATM	60	H	d	1	15.395	-1.237	-29.353	1.00	99.99	H
HETATM	61	H	d	1	13.141	-1.752	-29.621	1.00	99.99	H
HETATM	62	H	d	1	13.826	-2.437	-33.762	1.00	99.99	H
HETATM	63	H	d	1	15.926	-2.128	-34.657	1.00	99.99	H
HETATM	64	H	d	1	18.256	-1.600	-34.322	1.00	99.99	H
HETATM	65	H	d	1	17.554	-1.033	-30.269	1.00	99.99	H

HETATM	66	H	d	1	10.136	-5.364	-28.552	1.00	99.99	H	
HETATM	67	H	d	1	11.741	-5.936	-29.093	1.00	99.99	H	
HETATM	68	H	d	1	10.632	-7.406	-31.056	1.00	99.99	H	
HETATM	69	H	d	1	10.184	-7.788	-29.402	1.00	99.99	H	
ATOM	70	N	GLN	A	1	10.473	-14.506	-14.094	1.00	0.00	N
ATOM	71	CA	GLN	A	1	11.422	-14.806	-12.985	1.00	0.00	C
ATOM	72	C	GLN	A	1	12.711	-14.008	-13.187	1.00	0.00	C
ATOM	73	O	GLN	A	1	13.327	-13.554	-12.243	1.00	0.00	O
ATOM	74	CB	GLN	A	1	11.745	-16.301	-12.981	1.00	0.00	C
ATOM	75	CG	GLN	A	1	11.817	-16.803	-11.537	1.00	0.00	C
ATOM	76	CD	GLN	A	1	13.260	-17.185	-11.202	1.00	0.00	C
ATOM	77	NE2	GLN	A	1	13.490	-18.051	-10.254	1.00	0.00	N
ATOM	78	OE1	GLN	A	1	14.188	-16.689	-11.810	1.00	0.00	O
ATOM	79	H	GLN	A	1	10.139	-13.593	-14.219	1.00	99.99	H
ATOM	80	HA	GLN	A	1	10.974	-14.531	-12.043	1.00	99.99	H
ATOM	81	HB2	GLN	A	1	10.973	-16.838	-13.511	1.00	99.99	H
ATOM	82	HB3	GLN	A	1	12.696	-16.465	-13.466	1.00	99.99	H
ATOM	83	HG2	GLN	A	1	11.486	-16.023	-10.868	1.00	99.99	H
ATOM	84	HG3	GLN	A	1	11.180	-17.668	-11.425	1.00	99.99	H
ATOM	85	HE21	GLN	A	1	12.742	-18.451	-9.764	1.00	99.99	H
ATOM	86	HE22	GLN	A	1	14.411	-18.302	-10.033	1.00	99.99	H
ATOM	87	N	GLY	A	2	13.122	-13.835	-14.412	1.00	0.00	N

ATOM	88	CA	GLY	A	2	14.370	-13.068	-14.678	1.00	0.00	C
ATOM	89	C	GLY	A	2	15.465	-14.025	-15.155	1.00	0.00	C
ATOM	90	O	GLY	A	2	15.910	-14.887	-14.424	1.00	0.00	O
ATOM	91	H	GLY	A	2	12.608	-14.211	-15.156	1.00	99.99	H
ATOM	92	HA2	GLY	A	2	14.692	-12.577	-13.772	1.00	99.99	H
ATOM	93	HA3	GLY	A	2	14.182	-12.327	-15.441	1.00	99.99	H
ATOM	94	N	ASP	A	3	15.902	-13.880	-16.376	1.00	0.00	N
ATOM	95	CA	ASP	A	3	16.968	-14.781	-16.897	1.00	0.00	C
ATOM	96	C	ASP	A	3	18.304	-14.037	-16.900	1.00	0.00	C
ATOM	97	O	ASP	A	3	18.353	-12.831	-17.034	1.00	0.00	O
ATOM	98	CB	ASP	A	3	16.619	-15.209	-18.324	1.00	0.00	C
ATOM	99	CG	ASP	A	3	17.202	-16.597	-18.597	1.00	0.00	C
ATOM	100	OD1	ASP	A	3	16.785	-17.534	-17.936	1.00	0.00	O
ATOM	101	OD2	ASP	A	3	18.056	-16.699	-19.463	1.00	0.00	O1-
ATOM	102	H	ASP	A	3	15.531	-13.177	-16.950	1.00	99.99	H
ATOM	103	HA	ASP	A	3	17.042	-15.654	-16.267	1.00	99.99	H
ATOM	104	HB2	ASP	A	3	15.546	-15.241	-18.439	1.00	99.99	H
ATOM	105	HB3	ASP	A	3	17.035	-14.500	-19.025	1.00	99.99	H
ATOM	106	N	ILE	A	4	19.391	-14.745	-16.755	1.00	0.00	N
ATOM	107	CA	ILE	A	4	20.720	-14.071	-16.753	1.00	0.00	C
ATOM	108	C	ILE	A	4	21.432	-14.350	-18.079	1.00	0.00	C
ATOM	109	O	ILE	A	4	21.537	-15.480	-18.514	1.00	0.00	O

ATOM	110	CB	ILE	A	4	21.564	-14.595	-15.586	1.00	0.00	C
ATOM	111	CG1	ILE	A	4	22.523	-13.498	-15.119	1.00	0.00	C
ATOM	112	CG2	ILE	A	4	22.372	-15.816	-16.035	1.00	0.00	C
ATOM	113	CD1	ILE	A	4	21.952	-12.816	-13.874	1.00	0.00	C
ATOM	114	H	ILE	A	4	19.333	-15.718	-16.651	1.00	99.99	H
ATOM	115	HA	ILE	A	4	20.578	-13.006	-16.643	1.00	99.99	H
ATOM	116	HB	ILE	A	4	20.915	-14.875	-14.770	1.00	99.99	H
ATOM	117	HG12	ILE	A	4	23.482	-13.935	-14.882	1.00	99.99	H
ATOM	118	HG13	ILE	A	4	22.644	-12.768	-15.905	1.00	99.99	H
ATOM	119	HG21	ILE	A	4	21.725	-16.502	-16.561	1.00	99.99	H
ATOM	120	HG22	ILE	A	4	23.169	-15.497	-16.692	1.00	99.99	H
ATOM	121	HG23	ILE	A	4	22.793	-16.307	-15.171	1.00	99.99	H
ATOM	122	HD11	ILE	A	4	21.819	-13.549	-13.091	1.00	99.99	H
ATOM	123	HD12	ILE	A	4	22.635	-12.050	-13.538	1.00	99.99	H
ATOM	124	HD13	ILE	A	4	20.999	-12.368	-14.114	1.00	99.99	H
ATOM	125	N	VAL	A	5	21.919	-13.328	-18.723	1.00	0.00	N
ATOM	126	CA	VAL	A	5	22.622	-13.524	-20.019	1.00	0.00	C
ATOM	127	C	VAL	A	5	23.968	-12.808	-19.964	1.00	0.00	C
ATOM	128	O	VAL	A	5	24.138	-11.854	-19.231	1.00	0.00	O
ATOM	129	CB	VAL	A	5	21.779	-12.925	-21.148	1.00	0.00	C
ATOM	130	CG1	VAL	A	5	20.763	-13.961	-21.631	1.00	0.00	C
ATOM	131	CG2	VAL	A	5	21.041	-11.688	-20.632	1.00	0.00	C

ATOM	132	H	VAL A	5	21.822	-12.424	-18.355	1.00	99.99	H
ATOM	133	HA	VAL A	5	22.771	-14.577	-20.205	1.00	99.99	H
ATOM	134	HB	VAL A	5	22.424	-12.643	-21.967	1.00	99.99	H
ATOM	135	HG11	VAL A	5	20.498	-14.614	-20.813	1.00	99.99	H
ATOM	136	HG12	VAL A	5	19.878	-13.457	-21.991	1.00	99.99	H
ATOM	137	HG13	VAL A	5	21.196	-14.544	-22.431	1.00	99.99	H
ATOM	138	HG21	VAL A	5	21.638	-11.202	-19.875	1.00	99.99	H
ATOM	139	HG22	VAL A	5	20.870	-11.003	-21.450	1.00	99.99	H
ATOM	140	HG23	VAL A	5	20.093	-11.985	-20.208	1.00	99.99	H
ATOM	141	N	VAL A	6	24.924	-13.240	-20.733	1.00	0.00	N
ATOM	142	CA	VAL A	6	26.239	-12.550	-20.706	1.00	0.00	C
ATOM	143	C	VAL A	6	26.468	-11.873	-22.055	1.00	0.00	C
ATOM	144	O	VAL A	6	26.242	-12.452	-23.100	1.00	0.00	O
ATOM	145	CB	VAL A	6	27.358	-13.555	-20.421	1.00	0.00	C
ATOM	146	CG1	VAL A	6	27.233	-14.743	-21.376	1.00	0.00	C
ATOM	147	CG2	VAL A	6	28.715	-12.879	-20.623	1.00	0.00	C
ATOM	148	H	VAL A	6	24.775	-14.003	-21.330	1.00	99.99	H
ATOM	149	HA	VAL A	6	26.212	-11.797	-19.934	1.00	99.99	H
ATOM	150	HB	VAL A	6	27.277	-13.903	-19.402	1.00	99.99	H
ATOM	151	HG11	VAL A	6	26.778	-14.417	-22.299	1.00	99.99	H
ATOM	152	HG12	VAL A	6	28.214	-15.146	-21.580	1.00	99.99	H
ATOM	153	HG13	VAL A	6	26.618	-15.507	-20.922	1.00	99.99	H

ATOM	154	HG21	VAL	A	6	28.724	-11.929	-20.110	1.00	99.99	H
ATOM	155	HG22	VAL	A	6	29.495	-13.511	-20.223	1.00	99.99	H
ATOM	156	HG23	VAL	A	6	28.885	-12.721	-21.678	1.00	99.99	H
ATOM	157	N	ALA	A	7	26.899	-10.644	-22.037	1.00	0.00	N
ATOM	158	CA	ALA	A	7	27.129	-9.916	-23.312	1.00	0.00	C
ATOM	159	C	ALA	A	7	28.104	-10.701	-24.187	1.00	0.00	C
ATOM	160	O	ALA	A	7	29.260	-10.871	-23.852	1.00	0.00	O
ATOM	161	CB	ALA	A	7	27.714	-8.535	-23.012	1.00	0.00	C
ATOM	162	H	ALA	A	7	27.065	-10.195	-21.182	1.00	99.99	H
ATOM	163	HA	ALA	A	7	26.191	-9.802	-23.834	1.00	99.99	H
ATOM	164	HB1	ALA	A	7	28.484	-8.625	-22.260	1.00	99.99	H
ATOM	165	HB2	ALA	A	7	26.932	-7.883	-22.651	1.00	99.99	H
ATOM	166	HB3	ALA	A	7	28.139	-8.120	-23.915	1.00	99.99	H
ATOM	167	N	LEU	A	8	27.652	-11.159	-25.319	1.00	0.00	N
ATOM	168	CA	LEU	A	8	28.558	-11.906	-26.231	1.00	0.00	C
ATOM	169	C	LEU	A	8	29.243	-10.891	-27.141	1.00	0.00	C
ATOM	170	O	LEU	A	8	30.346	-11.093	-27.608	1.00	0.00	O
ATOM	171	CB	LEU	A	8	27.748	-12.896	-27.071	1.00	0.00	C
ATOM	172	CG	LEU	A	8	27.162	-13.977	-26.160	1.00	0.00	C
ATOM	173	CD1	LEU	A	8	26.037	-14.708	-26.895	1.00	0.00	C
ATOM	174	CD2	LEU	A	8	28.258	-14.975	-25.783	1.00	0.00	C
ATOM	175	H	LEU	A	8	26.723	-10.986	-25.578	1.00	99.99	H

ATOM	176	HA	LEU	A	8	29.303	-12.434	-25.653	1.00	99.99	H
ATOM	177	HB2	LEU	A	8	26.947	-12.373	-27.571	1.00	99.99	H
ATOM	178	HB3	LEU	A	8	28.392	-13.355	-27.807	1.00	99.99	H
ATOM	179	HG	LEU	A	8	26.769	-13.518	-25.265	1.00	99.99	H
ATOM	180	HD11	LEU	A	8	26.177	-14.606	-27.961	1.00	99.99	H
ATOM	181	HD12	LEU	A	8	26.054	-15.755	-26.628	1.00	99.99	H
ATOM	182	HD13	LEU	A	8	25.086	-14.281	-26.614	1.00	99.99	H
ATOM	183	HD21	LEU	A	8	29.125	-14.810	-26.405	1.00	99.99	H
ATOM	184	HD22	LEU	A	8	28.528	-14.838	-24.746	1.00	99.99	H
ATOM	185	HD23	LEU	A	8	27.895	-15.981	-25.930	1.00	99.99	H
ATOM	186	N	TYR	A	9	28.587	-9.790	-27.380	1.00	0.00	N
ATOM	187	CA	TYR	A	9	29.173	-8.732	-28.243	1.00	0.00	C
ATOM	188	C	TYR	A	9	28.919	-7.370	-27.592	1.00	0.00	C
ATOM	189	O	TYR	A	9	27.859	-7.122	-27.054	1.00	0.00	O
ATOM	190	CB	TYR	A	9	28.504	-8.769	-29.619	1.00	0.00	C
ATOM	191	CG	TYR	A	9	29.024	-9.952	-30.400	1.00	0.00	C
ATOM	192	CD1	TYR	A	9	28.485	-11.226	-30.184	1.00	0.00	C
ATOM	193	CD2	TYR	A	9	30.045	-9.774	-31.341	1.00	0.00	C
ATOM	194	CE1	TYR	A	9	28.967	-12.322	-30.908	1.00	0.00	C
ATOM	195	CE2	TYR	A	9	30.528	-10.871	-32.065	1.00	0.00	C
ATOM	196	CZ	TYR	A	9	29.989	-12.145	-31.849	1.00	0.00	C
ATOM	197	OH	TYR	A	9	30.464	-13.225	-32.563	1.00	0.00	O

ATOM	198	H	TYR	A	9	27.701	-9.656	-26.984	1.00	99.99	H
ATOM	199	HA	TYR	A	9	30.234	-8.897	-28.353	1.00	99.99	H
ATOM	200	HB2	TYR	A	9	27.434	-8.861	-29.497	1.00	99.99	H
ATOM	201	HB3	TYR	A	9	28.728	-7.858	-30.153	1.00	99.99	H
ATOM	202	HD1	TYR	A	9	27.697	-11.362	-29.458	1.00	99.99	H
ATOM	203	HD2	TYR	A	9	30.461	-8.792	-31.508	1.00	99.99	H
ATOM	204	HE1	TYR	A	9	28.551	-13.305	-30.741	1.00	99.99	H
ATOM	205	HE2	TYR	A	9	31.315	-10.734	-32.791	1.00	99.99	H
ATOM	206	HH	TYR	A	9	30.630	-12.936	-33.463	1.00	99.99	H
ATOM	207	N	PRO	A	10	29.908	-6.470	-27.649	1.00	0.00	N
ATOM	208	CA	PRO	A	10	29.792	-5.123	-27.072	1.00	0.00	C
ATOM	209	C	PRO	A	10	28.658	-4.321	-27.718	1.00	0.00	C
ATOM	210	O	PRO	A	10	28.421	-4.402	-28.907	1.00	0.00	O
ATOM	211	CB	PRO	A	10	31.154	-4.491	-27.383	1.00	0.00	C
ATOM	212	CG	PRO	A	10	31.651	-5.268	-28.554	1.00	0.00	C
ATOM	213	CD	PRO	A	10	31.216	-6.678	-28.284	1.00	0.00	C
ATOM	214	HA	PRO	A	10	29.653	-5.150	-26.004	1.00	99.99	H
ATOM	215	HB2	PRO	A	10	31.025	-3.446	-27.621	1.00	99.99	H
ATOM	216	HB3	PRO	A	10	31.807	-4.593	-26.529	1.00	99.99	H
ATOM	217	HG2	PRO	A	10	31.204	-4.892	-29.463	1.00	99.99	H
ATOM	218	HG3	PRO	A	10	32.727	-5.198	-28.613	1.00	99.99	H
ATOM	219	HD2	PRO	A	10	31.131	-7.241	-29.198	1.00	99.99	H

ATOM	220	HD3	PRO	A	10	31.909	-7.170	-27.617	1.00	99.99	H
ATOM	221	N	TYR	A	11	27.948	-3.555	-26.934	1.00	0.00	N
ATOM	222	CA	TYR	A	11	26.818	-2.753	-27.482	1.00	0.00	C
ATOM	223	C	TYR	A	11	26.905	-1.321	-26.955	1.00	0.00	C
ATOM	224	O	TYR	A	11	26.929	-1.094	-25.761	1.00	0.00	O
ATOM	225	CB	TYR	A	11	25.497	-3.373	-27.023	1.00	0.00	C
ATOM	226	CG	TYR	A	11	24.350	-2.774	-27.806	1.00	0.00	C
ATOM	227	CD1	TYR	A	11	23.752	-1.581	-27.377	1.00	0.00	C
ATOM	228	CD2	TYR	A	11	23.881	-3.416	-28.958	1.00	0.00	C
ATOM	229	CE1	TYR	A	11	22.686	-1.031	-28.101	1.00	0.00	C
ATOM	230	CE2	TYR	A	11	22.815	-2.866	-29.682	1.00	0.00	C
ATOM	231	CZ	TYR	A	11	22.218	-1.674	-29.254	1.00	0.00	C
ATOM	232	OH	TYR	A	11	21.169	-1.133	-29.967	1.00	0.00	O
ATOM	233	H	TYR	A	11	28.156	-3.512	-25.977	1.00	99.99	H
ATOM	234	HA	TYR	A	11	26.855	-2.755	-28.562	1.00	99.99	H
ATOM	235	HB2	TYR	A	11	25.526	-4.440	-27.189	1.00	99.99	H
ATOM	236	HB3	TYR	A	11	25.354	-3.178	-25.971	1.00	99.99	H
ATOM	237	HD1	TYR	A	11	24.112	-1.085	-26.489	1.00	99.99	H
ATOM	238	HD2	TYR	A	11	24.341	-4.335	-29.290	1.00	99.99	H
ATOM	239	HE1	TYR	A	11	22.225	-0.112	-27.770	1.00	99.99	H
ATOM	240	HE2	TYR	A	11	22.454	-3.362	-30.570	1.00	99.99	H
ATOM	241	HH	TYR	A	11	21.012	-1.691	-30.733	1.00	99.99	H

ATOM	242	N	ASP	A	12	26.943	-0.350	-27.823	1.00	0.00	N
ATOM	243	CA	ASP	A	12	27.017	1.058	-27.345	1.00	0.00	C
ATOM	244	C	ASP	A	12	25.633	1.695	-27.461	1.00	0.00	C
ATOM	245	O	ASP	A	12	25.130	1.914	-28.544	1.00	0.00	O
ATOM	246	CB	ASP	A	12	28.026	1.842	-28.187	1.00	0.00	C
ATOM	247	CG	ASP	A	12	28.959	2.627	-27.264	1.00	0.00	C
ATOM	248	OD1	ASP	A	12	28.466	3.474	-26.537	1.00	0.00	O
ATOM	249	OD2	ASP	A	12	30.151	2.368	-27.299	1.00	0.00	O1-
ATOM	250	H	ASP	A	12	26.916	-0.545	-28.783	1.00	99.99	H
ATOM	251	HA	ASP	A	12	27.321	1.060	-26.309	1.00	99.99	H
ATOM	252	HB2	ASP	A	12	28.605	1.156	-28.786	1.00	99.99	H
ATOM	253	HB3	ASP	A	12	27.498	2.528	-28.833	1.00	99.99	H
ATOM	254	N	GLY	A	13	25.014	1.976	-26.343	1.00	0.00	N
ATOM	255	CA	GLY	A	13	23.652	2.587	-26.351	1.00	0.00	C
ATOM	256	C	GLY	A	13	23.439	3.419	-27.618	1.00	0.00	C
ATOM	257	O	GLY	A	13	23.705	4.604	-27.647	1.00	0.00	O
ATOM	258	H	GLY	A	13	25.447	1.774	-25.488	1.00	99.99	H
ATOM	259	HA2	GLY	A	13	23.543	3.224	-25.485	1.00	99.99	H
ATOM	260	HA3	GLY	A	13	22.910	1.803	-26.311	1.00	99.99	H
ATOM	261	N	ILE	A	14	22.944	2.809	-28.661	1.00	0.00	N
ATOM	262	CA	ILE	A	14	22.696	3.567	-29.917	1.00	0.00	C
ATOM	263	C	ILE	A	14	21.239	4.028	-29.925	1.00	0.00	C

ATOM	264	O	ILE A 14	20.843	4.877	-30.700	1.00	0.00	O
ATOM	265	CB	ILE A 14	22.957	2.664	-31.125	1.00	0.00	C
ATOM	266	CG1	ILE A 14	24.458	2.400	-31.250	1.00	0.00	C
ATOM	267	CG2	ILE A 14	22.453	3.353	-32.394	1.00	0.00	C
ATOM	268	CD1	ILE A 14	24.718	0.893	-31.182	1.00	0.00	C
ATOM	269	H	ILE A 14	22.725	1.855	-28.612	1.00	99.99	H
ATOM	270	HA	ILE A 14	23.351	4.426	-29.955	1.00	99.99	H
ATOM	271	HB	ILE A 14	22.436	1.728	-30.992	1.00	99.99	H
ATOM	272	HG12	ILE A 14	24.814	2.784	-32.195	1.00	99.99	H
ATOM	273	HG13	ILE A 14	24.979	2.891	-30.442	1.00	99.99	H
ATOM	274	HG21	ILE A 14	22.961	4.298	-32.517	1.00	99.99	H
ATOM	275	HG22	ILE A 14	22.652	2.723	-33.249	1.00	99.99	H
ATOM	276	HG23	ILE A 14	21.390	3.524	-32.313	1.00	99.99	H
ATOM	277	HD11	ILE A 14	23.966	0.426	-30.563	1.00	99.99	H
ATOM	278	HD12	ILE A 14	24.676	0.476	-32.177	1.00	99.99	H
ATOM	279	HD13	ILE A 14	25.695	0.715	-30.758	1.00	99.99	H
ATOM	280	N	HIS A 15	20.441	3.471	-29.055	1.00	0.00	N
ATOM	281	CA	HIS A 15	19.008	3.864	-28.984	1.00	0.00	C
ATOM	282	C	HIS A 15	18.751	4.563	-27.649	1.00	0.00	C
ATOM	283	O	HIS A 15	19.622	4.646	-26.806	1.00	0.00	O
ATOM	284	CB	HIS A 15	18.133	2.613	-29.080	1.00	0.00	C
ATOM	285	CG	HIS A 15	17.330	2.660	-30.351	1.00	0.00	C

ATOM	286	CD2	HIS	A	15	17.638	3.096	-31.616	1.00	0.00	C
ATOM	287	ND1	HIS	A	15	16.018	2.216	-30.413	1.00	0.00	N
ATOM	288	CE1	HIS	A	15	15.590	2.393	-31.676	1.00	0.00	C
ATOM	289	NE2	HIS	A	15	16.538	2.927	-32.451	1.00	0.00	N
ATOM	290	H	HIS	A	15	20.791	2.794	-28.439	1.00	99.99	H
ATOM	291	HA	HIS	A	15	18.771	4.533	-29.798	1.00	99.99	H
ATOM	292	HB2	HIS	A	15	18.760	1.734	-29.084	1.00	99.99	H
ATOM	293	HB3	HIS	A	15	17.464	2.575	-28.233	1.00	99.99	H
ATOM	294	HD1	HIS	A	15	15.498	1.841	-29.672	1.00	99.99	H
ATOM	295	HD2	HIS	A	15	18.590	3.508	-31.917	1.00	99.99	H
ATOM	296	HE1	HIS	A	15	14.599	2.136	-32.022	1.00	99.99	H
ATOM	297	N	PRO	A	16	17.530	5.077	-27.455	1.00	0.00	N
ATOM	298	CA	PRO	A	16	17.155	5.773	-26.220	1.00	0.00	C
ATOM	299	C	PRO	A	16	17.009	4.809	-25.038	1.00	0.00	C
ATOM	300	O	PRO	A	16	17.300	5.150	-23.909	1.00	0.00	O
ATOM	301	CB	PRO	A	16	15.801	6.395	-26.556	1.00	0.00	C
ATOM	302	CG	PRO	A	16	15.246	5.532	-27.640	1.00	0.00	C
ATOM	303	CD	PRO	A	16	16.422	5.022	-28.425	1.00	0.00	C
ATOM	304	HA	PRO	A	16	17.849	6.553	-25.964	1.00	99.99	H
ATOM	305	HB2	PRO	A	16	15.170	6.386	-25.679	1.00	99.99	H
ATOM	306	HB3	PRO	A	16	15.942	7.412	-26.890	1.00	99.99	H
ATOM	307	HG2	PRO	A	16	14.693	4.712	-27.205	1.00	99.99	H

ATOM	308	HG3 PRO A 16	14.592	6.117	-28.270	1.00	99.99	H
ATOM	309	HD2 PRO A 16	16.242	4.012	-28.763	1.00	99.99	H
ATOM	310	HD3 PRO A 16	16.612	5.658	-29.277	1.00	99.99	H
ATOM	311	N ASP A 17	16.548	3.615	-25.284	1.00	0.00	N
ATOM	312	CA ASP A 17	16.369	2.641	-24.168	1.00	0.00	C
ATOM	313	C ASP A 17	17.362	1.481	-24.301	1.00	0.00	C
ATOM	314	O ASP A 17	17.509	0.678	-23.401	1.00	0.00	O
ATOM	315	CB ASP A 17	14.944	2.086	-24.211	1.00	0.00	C
ATOM	316	CG ASP A 17	13.968	3.212	-24.558	1.00	0.00	C
ATOM	317	OD1 ASP A 17	13.595	3.944	-23.656	1.00	0.00	O
ATOM	318	OD2 ASP A 17	13.610	3.322	-25.719	1.00	0.00	O1-
ATOM	319	H ASP A 17	16.303	3.362	-26.198	1.00	99.99	H
ATOM	320	HA ASP A 17	16.523	3.143	-23.224	1.00	99.99	H
ATOM	321	HB2 ASP A 17	14.882	1.312	-24.962	1.00	99.99	H
ATOM	322	HB3 ASP A 17	14.689	1.673	-23.246	1.00	99.99	H
ATOM	323	N ASP A 18	18.038	1.374	-25.412	1.00	0.00	N
ATOM	324	CA ASP A 18	19.003	0.252	-25.584	1.00	0.00	C
ATOM	325	C ASP A 18	20.086	0.332	-24.507	1.00	0.00	C
ATOM	326	O ASP A 18	20.857	1.271	-24.465	1.00	0.00	O
ATOM	327	CB ASP A 18	19.658	0.351	-26.962	1.00	0.00	C
ATOM	328	CG ASP A 18	18.764	-0.330	-28.001	1.00	0.00	C
ATOM	329	OD1 ASP A 18	17.722	-0.835	-27.616	1.00	0.00	O

ATOM	330	OD2	ASP	A	18	19.135	-0.334	-29.163	1.00	0.00	O1-
ATOM	331	H	ASP	A	18	17.906	2.022	-26.135	1.00	99.99	H
ATOM	332	HA	ASP	A	18	18.473	-0.686	-25.509	1.00	99.99	H
ATOM	333	HB2	ASP	A	18	19.790	1.390	-27.225	1.00	99.99	H
ATOM	334	HB3	ASP	A	18	20.621	-0.140	-26.938	1.00	99.99	H
ATOM	335	N	LEU	A	19	20.168	-0.642	-23.642	1.00	0.00	N
ATOM	336	CA	LEU	A	19	21.219	-0.607	-22.588	1.00	0.00	C
ATOM	337	C	LEU	A	19	22.548	-1.041	-23.214	1.00	0.00	C
ATOM	338	O	LEU	A	19	22.610	-1.999	-23.959	1.00	0.00	O
ATOM	339	CB	LEU	A	19	20.815	-1.552	-21.445	1.00	0.00	C
ATOM	340	CG	LEU	A	19	22.044	-1.998	-20.646	1.00	0.00	C
ATOM	341	CD1	LEU	A	19	22.792	-3.090	-21.415	1.00	0.00	C
ATOM	342	CD2	LEU	A	19	22.969	-0.803	-20.411	1.00	0.00	C
ATOM	343	H	LEU	A	19	19.553	-1.404	-23.684	1.00	99.99	H
ATOM	344	HA	LEU	A	19	21.313	0.400	-22.209	1.00	99.99	H
ATOM	345	HB2	LEU	A	19	20.138	-1.034	-20.785	1.00	99.99	H
ATOM	346	HB3	LEU	A	19	20.318	-2.420	-21.854	1.00	99.99	H
ATOM	347	HG	LEU	A	19	21.724	-2.392	-19.693	1.00	99.99	H
ATOM	348	HD11	LEU	A	19	22.126	-3.545	-22.134	1.00	99.99	H
ATOM	349	HD12	LEU	A	19	23.634	-2.656	-21.930	1.00	99.99	H
ATOM	350	HD13	LEU	A	19	23.142	-3.842	-20.723	1.00	99.99	H
ATOM	351	HD21	LEU	A	19	22.504	0.094	-20.790	1.00	99.99	H

ATOM	352	HD22	LEU	A	19	23.153	-0.695	-19.353	1.00	99.99	H
ATOM	353	HD23	LEU	A	19	23.904	-0.966	-20.921	1.00	99.99	H
ATOM	354	N	SER	A	20	23.609	-0.336	-22.930	1.00	0.00	N
ATOM	355	CA	SER	A	20	24.930	-0.695	-23.521	1.00	0.00	C
ATOM	356	C	SER	A	20	25.600	-1.797	-22.697	1.00	0.00	C
ATOM	357	O	SER	A	20	25.625	-1.755	-21.484	1.00	0.00	O
ATOM	358	CB	SER	A	20	25.830	0.542	-23.525	1.00	0.00	C
ATOM	359	OG	SER	A	20	26.616	0.560	-22.342	1.00	0.00	O
ATOM	360	H	SER	A	20	23.540	0.438	-22.333	1.00	99.99	H
ATOM	361	HA	SER	A	20	24.797	-1.036	-24.536	1.00	99.99	H
ATOM	362	HB2	SER	A	20	26.478	0.513	-24.388	1.00	99.99	H
ATOM	363	HB3	SER	A	20	25.219	1.432	-23.564	1.00	99.99	H
ATOM	364	HG	SER	A	20	27.513	0.312	-22.579	1.00	99.99	H
ATOM	365	N	PHE	A	21	26.168	-2.771	-23.353	1.00	0.00	N
ATOM	366	CA	PHE	A	21	26.862	-3.861	-22.615	1.00	0.00	C
ATOM	367	C	PHE	A	21	28.151	-4.213	-23.357	1.00	0.00	C
ATOM	368	O	PHE	A	21	28.227	-4.109	-24.565	1.00	0.00	O
ATOM	369	CB	PHE	A	21	25.960	-5.097	-22.513	1.00	0.00	C
ATOM	370	CG	PHE	A	21	25.277	-5.367	-23.834	1.00	0.00	C
ATOM	371	CD1	PHE	A	21	24.029	-4.794	-24.108	1.00	0.00	C
ATOM	372	CD2	PHE	A	21	25.883	-6.207	-24.775	1.00	0.00	C
ATOM	373	CE1	PHE	A	21	23.389	-5.058	-25.325	1.00	0.00	C

ATOM	374	CE2	PHE	A	21	25.242	-6.474	-25.991	1.00	0.00	C
ATOM	375	CZ	PHE	A	21	23.995	-5.899	-26.267	1.00	0.00	C
ATOM	376	H	PHE	A	21	26.158	-2.772	-24.333	1.00	99.99	H
ATOM	377	HA	PHE	A	21	27.104	-3.516	-21.619	1.00	99.99	H
ATOM	378	HB2	PHE	A	21	26.558	-5.953	-22.240	1.00	99.99	H
ATOM	379	HB3	PHE	A	21	25.211	-4.928	-21.753	1.00	99.99	H
ATOM	380	HD1	PHE	A	21	23.562	-4.145	-23.382	1.00	99.99	H
ATOM	381	HD2	PHE	A	21	26.846	-6.649	-24.564	1.00	99.99	H
ATOM	382	HE1	PHE	A	21	22.428	-4.615	-25.537	1.00	99.99	H
ATOM	383	HE2	PHE	A	21	25.710	-7.122	-26.717	1.00	99.99	H
ATOM	384	HZ	PHE	A	21	23.499	-6.107	-27.204	1.00	99.99	H
ATOM	385	N	LYS	A	22	29.170	-4.616	-22.651	1.00	0.00	N
ATOM	386	CA	LYS	A	22	30.450	-4.956	-23.331	1.00	0.00	C
ATOM	387	C	LYS	A	22	30.659	-6.467	-23.297	1.00	0.00	C
ATOM	388	O	LYS	A	22	30.390	-7.112	-22.304	1.00	0.00	O
ATOM	389	CB	LYS	A	22	31.606	-4.271	-22.600	1.00	0.00	C
ATOM	390	CG	LYS	A	22	32.827	-4.210	-23.520	1.00	0.00	C
ATOM	391	CD	LYS	A	22	34.063	-4.696	-22.760	1.00	0.00	C
ATOM	392	CE	LYS	A	22	35.059	-5.312	-23.745	1.00	0.00	C
ATOM	393	NZ	LYS	A	22	35.333	-4.345	-24.846	1.00	0.00	N1+
ATOM	394	H	LYS	A	22	29.096	-4.691	-21.674	1.00	99.99	H
ATOM	395	HA	LYS	A	22	30.423	-4.613	-24.354	1.00	99.99	H

ATOM	396	HB2	LYS	A	22	31.314	-3.270	-22.322	1.00	99.99	H
ATOM	397	HB3	LYS	A	22	31.854	-4.833	-21.711	1.00	99.99	H
ATOM	398	HG2	LYS	A	22	32.662	-4.842	-24.380	1.00	99.99	H
ATOM	399	HG3	LYS	A	22	32.982	-3.192	-23.845	1.00	99.99	H
ATOM	400	HD2	LYS	A	22	34.527	-3.861	-22.255	1.00	99.99	H
ATOM	401	HD3	LYS	A	22	33.770	-5.438	-22.033	1.00	99.99	H
ATOM	402	HE2	LYS	A	22	35.980	-5.542	-23.230	1.00	99.99	H
ATOM	403	HE3	LYS	A	22	34.641	-6.218	-24.159	1.00	99.99	H
ATOM	404	HZ1	LYS	A	22	34.896	-3.429	-24.619	1.00	99.99	H
ATOM	405	HZ2	LYS	A	22	36.359	-4.220	-24.951	1.00	99.99	H
ATOM	406	HZ3	LYS	A	22	34.934	-4.710	-25.735	1.00	99.99	H
ATOM	407	N	LYS	A	23	31.147	-7.041	-24.365	1.00	0.00	N
ATOM	408	CA	LYS	A	23	31.377	-8.511	-24.359	1.00	0.00	C
ATOM	409	C	LYS	A	23	31.988	-8.897	-23.013	1.00	0.00	C
ATOM	410	O	LYS	A	23	32.648	-8.104	-22.371	1.00	0.00	O
ATOM	411	CB	LYS	A	23	32.332	-8.903	-25.485	1.00	0.00	C
ATOM	412	CG	LYS	A	23	33.545	-7.971	-25.473	1.00	0.00	C
ATOM	413	CD	LYS	A	23	34.333	-8.142	-26.773	1.00	0.00	C
ATOM	414	CE	LYS	A	23	35.209	-9.394	-26.678	1.00	0.00	C
ATOM	415	NZ	LYS	A	23	35.966	-9.568	-27.949	1.00	0.00	N1+
ATOM	416	H	LYS	A	23	31.368	-6.509	-25.157	1.00	99.99	H
ATOM	417	HA	LYS	A	23	30.438	-9.031	-24.477	1.00	99.99	H

ATOM	418	HB2	LYS	A	23	32.657	-9.923	-25.334	1.00	99.99	H
ATOM	419	HB3	LYS	A	23	31.823	-8.823	-26.434	1.00	99.99	H
ATOM	420	HG2	LYS	A	23	33.211	-6.947	-25.387	1.00	99.99	H
ATOM	421	HG3	LYS	A	23	34.178	-8.215	-24.633	1.00	99.99	H
ATOM	422	HD2	LYS	A	23	33.646	-8.246	-27.600	1.00	99.99	H
ATOM	423	HD3	LYS	A	23	34.959	-7.277	-26.932	1.00	99.99	H
ATOM	424	HE2	LYS	A	23	35.902	-9.286	-25.857	1.00	99.99	H
ATOM	425	HE3	LYS	A	23	34.583	-10.258	-26.510	1.00	99.99	H
ATOM	426	HZ1	LYS	A	23	36.297	-8.642	-28.286	1.00	99.99	H
ATOM	427	HZ2	LYS	A	23	36.784	-10.190	-27.783	1.00	99.99	H
ATOM	428	HZ3	LYS	A	23	35.346	-9.994	-28.667	1.00	99.99	H
ATOM	429	N	GLY	A	24	31.765	-10.102	-22.572	1.00	0.00	N
ATOM	430	CA	GLY	A	24	32.325	-10.528	-21.258	1.00	0.00	C
ATOM	431	C	GLY	A	24	31.463	-9.962	-20.119	1.00	0.00	C
ATOM	432	O	GLY	A	24	31.540	-10.410	-18.992	1.00	0.00	O
ATOM	433	H	GLY	A	24	31.229	-10.727	-23.103	1.00	99.99	H
ATOM	434	HA2	GLY	A	24	33.335	-10.158	-21.161	1.00	99.99	H
ATOM	435	HA3	GLY	A	24	32.330	-11.606	-21.202	1.00	99.99	H
ATOM	436	N	GLU	A	25	30.644	-8.982	-20.402	1.00	0.00	N
ATOM	437	CA	GLU	A	25	29.783	-8.391	-19.334	1.00	0.00	C
ATOM	438	C	GLU	A	25	28.529	-9.250	-19.146	1.00	0.00	C
ATOM	439	O	GLU	A	25	28.074	-9.916	-20.054	1.00	0.00	O

ATOM	440	CB	GLU	A	25	29.378	-6.969	-19.726	1.00	0.00	C
ATOM	441	CG	GLU	A	25	29.128	-6.143	-18.463	1.00	0.00	C
ATOM	442	CD	GLU	A	25	29.999	-4.885	-18.495	1.00	0.00	C
ATOM	443	OE1	GLU	A	25	31.202	-5.025	-18.637	1.00	0.00	O
ATOM	444	OE2	GLU	A	25	29.447	-3.803	-18.379	1.00	0.00	O1-
ATOM	445	H	GLU	A	25	30.595	-8.632	-21.314	1.00	99.99	H
ATOM	446	HA	GLU	A	25	30.321	-8.370	-18.401	1.00	99.99	H
ATOM	447	HB2	GLU	A	25	30.171	-6.515	-20.302	1.00	99.99	H
ATOM	448	HB3	GLU	A	25	28.476	-7.002	-20.319	1.00	99.99	H
ATOM	449	HG2	GLU	A	25	28.087	-5.859	-18.418	1.00	99.99	H
ATOM	450	HG3	GLU	A	25	29.379	-6.732	-17.592	1.00	99.99	H
ATOM	451	N	LYS	A	26	27.975	-9.243	-17.961	1.00	0.00	N
ATOM	452	CA	LYS	A	26	26.756	-10.060	-17.690	1.00	0.00	C
ATOM	453	C	LYS	A	26	25.528	-9.153	-17.605	1.00	0.00	C
ATOM	454	O	LYS	A	26	25.598	-8.028	-17.152	1.00	0.00	O
ATOM	455	CB	LYS	A	26	26.930	-10.803	-16.364	1.00	0.00	C
ATOM	456	CG	LYS	A	26	27.319	-12.257	-16.640	1.00	0.00	C
ATOM	457	CD	LYS	A	26	28.365	-12.708	-15.618	1.00	0.00	C
ATOM	458	CE	LYS	A	26	27.671	-13.059	-14.300	1.00	0.00	C
ATOM	459	NZ	LYS	A	26	28.662	-13.659	-13.362	1.00	0.00	N1+
ATOM	460	H	LYS	A	26	28.367	-8.701	-17.244	1.00	99.99	H
ATOM	461	HA	LYS	A	26	26.614	-10.777	-18.485	1.00	99.99	H

ATOM	462	HB2	LYS	A	26	27.707	-10.327	-15.784	1.00	99.99	H
ATOM	463	HB3	LYS	A	26	26.002	-10.777	-15.812	1.00	99.99	H
ATOM	464	HG2	LYS	A	26	26.444	-12.885	-16.561	1.00	99.99	H
ATOM	465	HG3	LYS	A	26	27.731	-12.337	-17.635	1.00	99.99	H
ATOM	466	HD2	LYS	A	26	28.885	-13.576	-15.994	1.00	99.99	H
ATOM	467	HD3	LYS	A	26	29.072	-11.909	-15.450	1.00	99.99	H
ATOM	468	HE2	LYS	A	26	27.256	-12.164	-13.861	1.00	99.99	H
ATOM	469	HE3	LYS	A	26	26.878	-13.768	-14.488	1.00	99.99	H
ATOM	470	HZ1	LYS	A	26	29.250	-14.348	-13.873	1.00	99.99	H
ATOM	471	HZ2	LYS	A	26	29.267	-12.909	-12.970	1.00	99.99	H
ATOM	472	HZ3	LYS	A	26	28.161	-14.137	-12.586	1.00	99.99	H
ATOM	473	N	MET	A	27	24.403	-9.642	-18.045	1.00	0.00	N
ATOM	474	CA	MET	A	27	23.154	-8.833	-18.009	1.00	0.00	C
ATOM	475	C	MET	A	27	21.985	-9.705	-17.559	1.00	0.00	C
ATOM	476	O	MET	A	27	21.980	-10.907	-17.735	1.00	0.00	O
ATOM	477	CB	MET	A	27	22.843	-8.306	-19.407	1.00	0.00	C
ATOM	478	CG	MET	A	27	23.342	-6.864	-19.535	1.00	0.00	C
ATOM	479	SD	MET	A	27	23.192	-6.322	-21.257	1.00	0.00	S
ATOM	480	CE	MET	A	27	23.963	-7.769	-22.025	1.00	0.00	C
ATOM	481	H	MET	A	27	24.376	-10.551	-18.411	1.00	99.99	H
ATOM	482	HA	MET	A	27	23.244	-7.993	-17.334	1.00	99.99	H
ATOM	483	HB2	MET	A	27	23.330	-8.926	-20.144	1.00	99.99	H

ATOM	484	HB3	MET	A	27	21.774	-8.329	-19.561	1.00	99.99	H
ATOM	485	HG2	MET	A	27	22.746	-6.221	-18.904	1.00	99.99	H
ATOM	486	HG3	MET	A	27	24.375	-6.809	-19.228	1.00	99.99	H
ATOM	487	HE1	MET	A	27	24.617	-8.250	-21.311	1.00	99.99	H
ATOM	488	HE2	MET	A	27	23.199	-8.464	-22.335	1.00	99.99	H
ATOM	489	HE3	MET	A	27	24.533	-7.455	-22.890	1.00	99.99	H
ATOM	490	N	LYS	A	28	20.988	-9.093	-16.990	1.00	0.00	N
ATOM	491	CA	LYS	A	28	19.795	-9.855	-16.530	1.00	0.00	C
ATOM	492	C	LYS	A	28	18.565	-9.288	-17.236	1.00	0.00	C
ATOM	493	O	LYS	A	28	18.416	-8.091	-17.359	1.00	0.00	O
ATOM	494	CB	LYS	A	28	19.636	-9.699	-15.016	1.00	0.00	C
ATOM	495	CG	LYS	A	28	18.406	-10.481	-14.549	1.00	0.00	C
ATOM	496	CD	LYS	A	28	17.833	-9.827	-13.290	1.00	0.00	C
ATOM	497	CE	LYS	A	28	17.750	-10.864	-12.169	1.00	0.00	C
ATOM	498	NZ	LYS	A	28	19.071	-10.966	-11.488	1.00	0.00	N1+
ATOM	499	H	LYS	A	28	21.024	-8.121	-16.871	1.00	99.99	H
ATOM	500	HA	LYS	A	28	19.910	-10.899	-16.781	1.00	99.99	H
ATOM	501	HB2	LYS	A	28	20.516	-10.083	-14.521	1.00	99.99	H
ATOM	502	HB3	LYS	A	28	19.513	-8.654	-14.772	1.00	99.99	H
ATOM	503	HG2	LYS	A	28	17.660	-10.476	-15.329	1.00	99.99	H
ATOM	504	HG3	LYS	A	28	18.690	-11.499	-14.328	1.00	99.99	H
ATOM	505	HD2	LYS	A	28	18.475	-9.014	-12.982	1.00	99.99	H

ATOM	506	HD3	LYS	A	28	16.845	-9.445	-13.501	1.00	99.99	H
ATOM	507	HE2	LYS	A	28	16.999	-10.563	-11.455	1.00	99.99	H
ATOM	508	HE3	LYS	A	28	17.485	-11.825	-12.587	1.00	99.99	H
ATOM	509	HZ1	LYS	A	28	19.547	-10.041	-11.516	1.00	99.99	H
ATOM	510	HZ2	LYS	A	28	18.931	-11.255	-10.499	1.00	99.99	H
ATOM	511	HZ3	LYS	A	28	19.659	-11.674	-11.973	1.00	99.99	H
ATOM	512	N	VAL	A	29	17.690	-10.128	-17.714	1.00	0.00	N
ATOM	513	CA	VAL	A	29	16.489	-9.604	-18.424	1.00	0.00	C
ATOM	514	C	VAL	A	29	15.292	-9.566	-17.473	1.00	0.00	C
ATOM	515	O	VAL	A	29	14.874	-10.575	-16.940	1.00	0.00	O
ATOM	516	CB	VAL	A	29	16.168	-10.500	-19.619	1.00	0.00	C
ATOM	517	CG1	VAL	A	29	15.467	-9.675	-20.696	1.00	0.00	C
ATOM	518	CG2	VAL	A	29	17.465	-11.083	-20.183	1.00	0.00	C
ATOM	519	H	VAL	A	29	17.826	-11.092	-17.615	1.00	99.99	H
ATOM	520	HA	VAL	A	29	16.705	-8.603	-18.764	1.00	99.99	H
ATOM	521	HB	VAL	A	29	15.520	-11.303	-19.302	1.00	99.99	H
ATOM	522	HG11	VAL	A	29	14.755	-9.008	-20.234	1.00	99.99	H
ATOM	523	HG12	VAL	A	29	16.200	-9.098	-21.240	1.00	99.99	H
ATOM	524	HG13	VAL	A	29	14.952	-10.337	-21.376	1.00	99.99	H
ATOM	525	HG21	VAL	A	29	18.257	-10.356	-20.091	1.00	99.99	H
ATOM	526	HG22	VAL	A	29	17.728	-11.974	-19.632	1.00	99.99	H
ATOM	527	HG23	VAL	A	29	17.325	-11.333	-21.225	1.00	99.99	H

ATOM	528	N	LEU	A	30	14.741	-8.404	-17.256	1.00	0.00	N
ATOM	529	CA	LEU	A	30	13.574	-8.289	-16.339	1.00	0.00	C
ATOM	530	C	LEU	A	30	12.277	-8.555	-17.109	1.00	0.00	C
ATOM	531	O	LEU	A	30	11.250	-8.836	-16.525	1.00	0.00	O
ATOM	532	CB	LEU	A	30	13.530	-6.879	-15.745	1.00	0.00	C
ATOM	533	CG	LEU	A	30	14.815	-6.612	-14.958	1.00	0.00	C
ATOM	534	CD1	LEU	A	30	15.142	-7.825	-14.084	1.00	0.00	C
ATOM	535	CD2	LEU	A	30	15.968	-6.360	-15.932	1.00	0.00	C
ATOM	536	H	LEU	A	30	15.101	-7.604	-17.693	1.00	99.99	H
ATOM	537	HA	LEU	A	30	13.672	-9.010	-15.542	1.00	99.99	H
ATOM	538	HB2	LEU	A	30	13.440	-6.156	-16.542	1.00	99.99	H
ATOM	539	HB3	LEU	A	30	12.680	-6.794	-15.085	1.00	99.99	H
ATOM	540	HG	LEU	A	30	14.679	-5.744	-14.330	1.00	99.99	H
ATOM	541	HD11	LEU	A	30	14.224	-8.273	-13.732	1.00	99.99	H
ATOM	542	HD12	LEU	A	30	15.696	-8.548	-14.664	1.00	99.99	H
ATOM	543	HD13	LEU	A	30	15.736	-7.510	-13.239	1.00	99.99	H
ATOM	544	HD21	LEU	A	30	15.577	-5.966	-16.858	1.00	99.99	H
ATOM	545	HD22	LEU	A	30	16.656	-5.649	-15.500	1.00	99.99	H
ATOM	546	HD23	LEU	A	30	16.485	-7.289	-16.126	1.00	99.99	H
ATOM	547	N	GLU	A	31	12.307	-8.470	-18.413	1.00	0.00	N
ATOM	548	CA	GLU	A	31	11.063	-8.719	-19.194	1.00	0.00	C
ATOM	549	C	GLU	A	31	11.423	-9.193	-20.602	1.00	0.00	C

ATOM	550	O	GLU A 31	12.357	-8.711	-21.211	1.00	0.00	O
ATOM	551	CB	GLU A 31	10.250	-7.427	-19.282	1.00	0.00	C
ATOM	552	CG	GLU A 31	8.757	-7.763	-19.280	1.00	0.00	C
ATOM	553	CD	GLU A 31	7.953	-6.521	-19.668	1.00	0.00	C
ATOM	554	OE1	GLU A 31	8.555	-5.577	-20.154	1.00	0.00	O
ATOM	555	OE2	GLU A 31	6.749	-6.534	-19.473	1.00	0.00	O1-
ATOM	556	H	GLU A 31	13.141	-8.240	-18.877	1.00	99.99	H
ATOM	557	HA	GLU A 31	10.476	-9.479	-18.699	1.00	99.99	H
ATOM	558	HB2	GLU A 31	10.479	-6.799	-18.434	1.00	99.99	H
ATOM	559	HB3	GLU A 31	10.500	-6.905	-20.194	1.00	99.99	H
ATOM	560	HG2	GLU A 31	8.566	-8.553	-19.992	1.00	99.99	H
ATOM	561	HG3	GLU A 31	8.463	-8.088	-18.293	1.00	99.99	H
ATOM	562	N	GLU A 32	10.682	-10.129	-21.126	1.00	0.00	N
ATOM	563	CA	GLU A 32	10.972	-10.631	-22.497	1.00	0.00	C
ATOM	564	C	GLU A 32	9.883	-10.141	-23.451	1.00	0.00	C
ATOM	565	O	GLU A 32	8.707	-10.196	-23.148	1.00	0.00	O
ATOM	566	CB	GLU A 32	10.996	-12.161	-22.489	1.00	0.00	C
ATOM	567	CG	GLU A 32	11.111	-12.679	-23.924	1.00	0.00	C
ATOM	568	CD	GLU A 32	12.017	-13.912	-23.950	1.00	0.00	C
ATOM	569	OE1	GLU A 32	11.803	-14.798	-23.140	1.00	0.00	O
ATOM	570	OE2	GLU A 32	12.911	-13.948	-24.780	1.00	0.00	O1-
ATOM	571	H	GLU A 32	9.929	-10.500	-20.620	1.00	99.99	H

ATOM	572	HA	GLU	A	32	11.932	-10.256	-22.824	1.00	99.99	H
ATOM	573	HB2	GLU	A	32	11.844	-12.505	-21.914	1.00	99.99	H
ATOM	574	HB3	GLU	A	32	10.085	-12.533	-22.044	1.00	99.99	H
ATOM	575	HG2	GLU	A	32	10.130	-12.946	-24.290	1.00	99.99	H
ATOM	576	HG3	GLU	A	32	11.533	-11.909	-24.552	1.00	99.99	H
ATOM	577	N	HIS	A	33	10.262	-9.661	-24.602	1.00	0.00	N
ATOM	578	CA	HIS	A	33	9.253	-9.167	-25.576	1.00	0.00	C
ATOM	579	C	HIS	A	33	9.381	-9.958	-26.878	1.00	0.00	C
ATOM	580	O	HIS	A	33	9.184	-9.410	-27.960	1.00	0.00	O
ATOM	581	CB	HIS	A	33	9.507	-7.686	-25.855	1.00	99.99	C
ATOM	582	CG	HIS	A	33	8.519	-6.853	-25.087	1.00	99.99	C
ATOM	583	CD2	HIS	A	33	8.673	-5.990	-24.029	1.00	99.99	C
ATOM	584	ND1	HIS	A	33	7.165	-6.849	-25.383	1.00	99.99	N
ATOM	585	CE1	HIS	A	33	6.563	-6.009	-24.521	1.00	99.99	C
ATOM	586	NE2	HIS	A	33	7.437	-5.458	-23.674	1.00	99.99	N
ATOM	587	N	GLY	A	34	9.703	-11.219	-26.786	1.00	0.00	N
ATOM	588	CA	GLY	A	34	9.847	-12.042	-28.018	1.00	0.00	C
ATOM	589	C	GLY	A	34	11.318	-12.069	-28.441	1.00	0.00	C
ATOM	590	O	GLY	A	34	12.149	-12.674	-27.794	1.00	0.00	O
ATOM	591	H	GLY	A	34	9.851	-11.624	-25.906	1.00	99.99	H
ATOM	592	HA2	GLY	A	34	9.252	-11.613	-28.810	1.00	99.99	H
ATOM	593	HA3	GLY	A	34	9.511	-13.049	-27.820	1.00	99.99	H

ATOM	594	N	GLU	A	35	11.644	-11.423	-29.527	1.00	0.00	N
ATOM	595	CA	GLU	A	35	13.060	-11.417	-29.994	1.00	0.00	C
ATOM	596	C	GLU	A	35	13.833	-10.295	-29.296	1.00	0.00	C
ATOM	597	O	GLU	A	35	15.035	-10.183	-29.433	1.00	0.00	O
ATOM	598	CB	GLU	A	35	13.095	-11.193	-31.507	1.00	0.00	C
ATOM	599	CG	GLU	A	35	14.164	-12.092	-32.130	1.00	0.00	C
ATOM	600	CD	GLU	A	35	13.537	-13.429	-32.529	1.00	0.00	C
ATOM	601	OE1	GLU	A	35	12.357	-13.439	-32.837	1.00	0.00	O
ATOM	602	OE2	GLU	A	35	14.248	-14.420	-32.520	1.00	0.00	O1-
ATOM	603	H	GLU	A	35	10.957	-10.946	-30.037	1.00	99.99	H
ATOM	604	HA	GLU	A	35	13.518	-12.367	-29.762	1.00	99.99	H
ATOM	605	HB2	GLU	A	35	12.131	-11.434	-31.929	1.00	99.99	H
ATOM	606	HB3	GLU	A	35	13.330	-10.159	-31.712	1.00	99.99	H
ATOM	607	HG2	GLU	A	35	14.573	-11.610	-33.007	1.00	99.99	H
ATOM	608	HG3	GLU	A	35	14.953	-12.264	-31.413	1.00	99.99	H
ATOM	609	N	TRP	A	36	13.159	-9.460	-28.553	1.00	0.00	N
ATOM	610	CA	TRP	A	36	13.871	-8.349	-27.859	1.00	0.00	C
ATOM	611	C	TRP	A	36	13.477	-8.325	-26.380	1.00	0.00	C
ATOM	612	O	TRP	A	36	12.337	-8.550	-26.028	1.00	0.00	O
ATOM	613	CB	TRP	A	36	13.489	-7.017	-28.507	1.00	0.00	C
ATOM	614	CG	TRP	A	36	14.308	-6.809	-29.740	1.00	0.00	C
ATOM	615	CD1	TRP	A	36	14.096	-7.423	-30.927	1.00	0.00	C

ATOM	616	CD2	TRP	A	36	15.461	-5.938	-29.931	1.00	0.00	C
ATOM	617	CE2	TRP	A	36	15.909	-6.070	-31.266	1.00	0.00	C
ATOM	618	CE3	TRP	A	36	16.154	-5.056	-29.082	1.00	0.00	C
ATOM	619	NE1	TRP	A	36	15.046	-6.986	-31.833	1.00	0.00	N
ATOM	620	CZ2	TRP	A	36	17.006	-5.352	-31.743	1.00	0.00	C
ATOM	621	CZ3	TRP	A	36	17.259	-4.332	-29.560	1.00	0.00	C
ATOM	622	CH2	TRP	A	36	17.684	-4.479	-30.887	1.00	0.00	C
ATOM	623	H	TRP	A	36	12.190	-9.561	-28.455	1.00	99.99	H
ATOM	624	HA	TRP	A	36	14.937	-8.499	-27.947	1.00	99.99	H
ATOM	625	HB2	TRP	A	36	12.441	-7.031	-28.769	1.00	99.99	H
ATOM	626	HB3	TRP	A	36	13.675	-6.212	-27.812	1.00	99.99	H
ATOM	627	HD1	TRP	A	36	13.313	-8.139	-31.133	1.00	99.99	H
ATOM	628	HE1	TRP	A	36	15.114	-7.278	-32.766	1.00	99.99	H
ATOM	629	HE3	TRP	A	36	15.835	-4.935	-28.058	1.00	99.99	H
ATOM	630	HZ2	TRP	A	36	17.330	-5.469	-32.767	1.00	99.99	H
ATOM	631	HZ3	TRP	A	36	17.784	-3.657	-28.900	1.00	99.99	H
ATOM	632	HH2	TRP	A	36	18.534	-3.920	-31.248	1.00	99.99	H
ATOM	633	N	TRP	A	37	14.411	-8.041	-25.512	1.00	0.00	N
ATOM	634	CA	TRP	A	37	14.083	-7.992	-24.058	1.00	0.00	C
ATOM	635	C	TRP	A	37	14.816	-6.819	-23.407	1.00	0.00	C
ATOM	636	O	TRP	A	37	15.715	-6.238	-23.981	1.00	0.00	O
ATOM	637	CB	TRP	A	37	14.527	-9.284	-23.368	1.00	0.00	C

ATOM	638	CG	TRP	A	37	14.637	-10.400	-24.355	1.00	0.00	C
ATOM	639	CD1	TRP	A	37	13.646	-10.828	-25.169	1.00	0.00	C
ATOM	640	CD2	TRP	A	37	15.789	-11.247	-24.630	1.00	0.00	C
ATOM	641	CE2	TRP	A	37	15.434	-12.180	-25.631	1.00	0.00	C
ATOM	642	CE3	TRP	A	37	17.096	-11.294	-24.112	1.00	0.00	C
ATOM	643	NE1	TRP	A	37	14.117	-11.885	-25.928	1.00	0.00	N
ATOM	644	CZ2	TRP	A	37	16.343	-13.127	-26.101	1.00	0.00	C
ATOM	645	CZ3	TRP	A	37	18.014	-12.245	-24.583	1.00	0.00	C
ATOM	646	CH2	TRP	A	37	17.638	-13.161	-25.575	1.00	0.00	C
ATOM	647	H	TRP	A	37	15.321	-7.854	-25.822	1.00	99.99	H
ATOM	648	HA	TRP	A	37	13.015	-7.873	-23.940	1.00	99.99	H
ATOM	649	HB2	TRP	A	37	15.489	-9.124	-22.907	1.00	99.99	H
ATOM	650	HB3	TRP	A	37	13.806	-9.548	-22.609	1.00	99.99	H
ATOM	651	HD1	TRP	A	37	12.650	-10.413	-25.220	1.00	99.99	H
ATOM	652	HE1	TRP	A	37	13.598	-12.376	-26.597	1.00	99.99	H
ATOM	653	HE3	TRP	A	37	17.395	-10.593	-23.347	1.00	99.99	H
ATOM	654	HZ2	TRP	A	37	16.046	-13.831	-26.864	1.00	99.99	H
ATOM	655	HZ3	TRP	A	37	19.015	-12.272	-24.178	1.00	99.99	H
ATOM	656	HH2	TRP	A	37	18.350	-13.889	-25.934	1.00	99.99	H
ATOM	657	N	LYS	A	38	14.453	-6.483	-22.202	1.00	0.00	N
ATOM	658	CA	LYS	A	38	15.141	-5.367	-21.498	1.00	0.00	C
ATOM	659	C	LYS	A	38	15.956	-5.953	-20.346	1.00	0.00	C

ATOM	660	O	LYS A 38	15.425	-6.578	-19.450	1.00	0.00	O
ATOM	661	CB	LYS A 38	14.105	-4.382	-20.959	1.00	0.00	C
ATOM	662	CG	LYS A 38	14.701	-2.974	-20.932	1.00	0.00	C
ATOM	663	CD	LYS A 38	13.656	-1.989	-20.403	1.00	0.00	C
ATOM	664	CE	LYS A 38	13.993	-0.579	-20.892	1.00	0.00	C
ATOM	665	NZ	LYS A 38	13.465	-0.392	-22.272	1.00	0.00	N1+
ATOM	666	H	LYS A 38	13.735	-6.977	-21.752	1.00	99.99	H
ATOM	667	HA	LYS A 38	15.804	-4.860	-22.184	1.00	99.99	H
ATOM	668	HB2	LYS A 38	13.238	-4.393	-21.601	1.00	99.99	H
ATOM	669	HB3	LYS A 38	13.820	-4.671	-19.959	1.00	99.99	H
ATOM	670	HG2	LYS A 38	15.567	-2.962	-20.286	1.00	99.99	H
ATOM	671	HG3	LYS A 38	14.992	-2.687	-21.931	1.00	99.99	H
ATOM	672	HD2	LYS A 38	12.679	-2.272	-20.765	1.00	99.99	H
ATOM	673	HD3	LYS A 38	13.659	-2.006	-19.323	1.00	99.99	H
ATOM	674	HE2	LYS A 38	13.542	0.148	-20.232	1.00	99.99	H
ATOM	675	HE3	LYS A 38	15.065	-0.445	-20.895	1.00	99.99	H
ATOM	676	HZ1	LYS A 38	12.956	-1.249	-22.568	1.00	99.99	H
ATOM	677	HZ2	LYS A 38	12.815	0.420	-22.288	1.00	99.99	H
ATOM	678	HZ3	LYS A 38	14.254	-0.218	-22.926	1.00	99.99	H
ATOM	679	N	ALA A 39	17.246	-5.773	-20.373	1.00	0.00	N
ATOM	680	CA	ALA A 39	18.099	-6.338	-19.291	1.00	0.00	C
ATOM	681	C	ALA A 39	18.766	-5.216	-18.495	1.00	0.00	C

ATOM	682	O	ALA A 39	18.484	-4.050	-18.680	1.00	0.00	O
ATOM	683	CB	ALA A 39	19.177	-7.231	-19.909	1.00	0.00	C
ATOM	684	H	ALA A 39	17.652	-5.275	-21.114	1.00	99.99	H
ATOM	685	HA	ALA A 39	17.495	-6.930	-18.620	1.00	99.99	H
ATOM	686	HB1	ALA A 39	19.061	-7.244	-20.983	1.00	99.99	H
ATOM	687	HB2	ALA A 39	19.075	-8.236	-19.524	1.00	99.99	H
ATOM	688	HB3	ALA A 39	20.153	-6.845	-19.656	1.00	99.99	H
ATOM	689	N	LYS A 40	19.656	-5.572	-17.608	1.00	0.00	N
ATOM	690	CA	LYS A 40	20.357	-4.545	-16.787	1.00	0.00	C
ATOM	691	C	LYS A 40	21.824	-4.950	-16.625	1.00	0.00	C
ATOM	692	O	LYS A 40	22.156	-6.120	-16.637	1.00	0.00	O
ATOM	693	CB	LYS A 40	19.696	-4.453	-15.411	1.00	0.00	C
ATOM	694	CG	LYS A 40	20.052	-3.114	-14.761	1.00	0.00	C
ATOM	695	CD	LYS A 40	19.836	-3.208	-13.249	1.00	0.00	C
ATOM	696	CE	LYS A 40	18.521	-2.518	-12.879	1.00	0.00	C
ATOM	697	NZ	LYS A 40	18.679	-1.816	-11.574	1.00	0.00	N1+
ATOM	698	H	LYS A 40	19.867	-6.521	-17.486	1.00	99.99	H
ATOM	699	HA	LYS A 40	20.298	-3.588	-17.283	1.00	99.99	H
ATOM	700	HB2	LYS A 40	18.624	-4.525	-15.521	1.00	99.99	H
ATOM	701	HB3	LYS A 40	20.049	-5.261	-14.787	1.00	99.99	H
ATOM	702	HG2	LYS A 40	21.087	-2.880	-14.963	1.00	99.99	H
ATOM	703	HG3	LYS A 40	19.421	-2.338	-15.168	1.00	99.99	H

ATOM	704	HD2	LYS	A	40	19.793	-4.246	-12.955	1.00	99.99	H
ATOM	705	HD3	LYS	A	40	20.654	-2.722	-12.738	1.00	99.99	H
ATOM	706	HE2	LYS	A	40	18.262	-1.802	-13.644	1.00	99.99	H
ATOM	707	HE3	LYS	A	40	17.738	-3.257	-12.797	1.00	99.99	H
ATOM	708	HZ1	LYS	A	40	19.479	-1.154	-11.630	1.00	99.99	H
ATOM	709	HZ2	LYS	A	40	17.810	-1.288	-11.356	1.00	99.99	H
ATOM	710	HZ3	LYS	A	40	18.859	-2.515	-10.824	1.00	99.99	H
ATOM	711	N	SER	A	41	22.708	-3.999	-16.489	1.00	0.00	N
ATOM	712	CA	SER	A	41	24.150	-4.348	-16.344	1.00	0.00	C
ATOM	713	C	SER	A	41	24.499	-4.506	-14.863	1.00	0.00	C
ATOM	714	O	SER	A	41	24.257	-3.623	-14.065	1.00	0.00	O
ATOM	715	CB	SER	A	41	25.007	-3.236	-16.953	1.00	0.00	C
ATOM	716	OG	SER	A	41	26.324	-3.312	-16.427	1.00	0.00	O
ATOM	717	H	SER	A	41	22.427	-3.060	-16.495	1.00	99.99	H
ATOM	718	HA	SER	A	41	24.336	-5.273	-16.871	1.00	99.99	H
ATOM	719	HB2	SER	A	41	25.040	-3.353	-18.026	1.00	99.99	H
ATOM	720	HB3	SER	A	41	24.577	-2.276	-16.708	1.00	99.99	H
ATOM	721	HG	SER	A	41	26.888	-3.705	-17.097	1.00	99.99	H
ATOM	722	N	LEU	A	42	25.063	-5.619	-14.486	1.00	0.00	N
ATOM	723	CA	LEU	A	42	25.418	-5.816	-13.052	1.00	0.00	C
ATOM	724	C	LEU	A	42	26.568	-4.876	-12.680	1.00	0.00	C
ATOM	725	O	LEU	A	42	26.888	-4.697	-11.522	1.00	0.00	O

ATOM	726	CB	LEU	A	42	25.847	-7.266	-12.824	1.00	0.00	C
ATOM	727	CG	LEU	A	42	25.071	-7.847	-11.641	1.00	0.00	C
ATOM	728	CD1	LEU	A	42	23.725	-8.387	-12.129	1.00	0.00	C
ATOM	729	CD2	LEU	A	42	25.878	-8.982	-11.009	1.00	0.00	C
ATOM	730	H	LEU	A	42	25.247	-6.323	-15.142	1.00	99.99	H
ATOM	731	HA	LEU	A	42	24.555	-5.595	-12.442	1.00	99.99	H
ATOM	732	HB2	LEU	A	42	25.640	-7.847	-13.711	1.00	99.99	H
ATOM	733	HB3	LEU	A	42	26.906	-7.299	-12.612	1.00	99.99	H
ATOM	734	HG	LEU	A	42	24.903	-7.073	-10.906	1.00	99.99	H
ATOM	735	HD11	LEU	A	42	23.885	-9.044	-12.971	1.00	99.99	H
ATOM	736	HD12	LEU	A	42	23.247	-8.936	-11.331	1.00	99.99	H
ATOM	737	HD13	LEU	A	42	23.094	-7.564	-12.429	1.00	99.99	H
ATOM	738	HD21	LEU	A	42	26.844	-9.047	-11.488	1.00	99.99	H
ATOM	739	HD22	LEU	A	42	26.011	-8.786	-9.955	1.00	99.99	H
ATOM	740	HD23	LEU	A	42	25.350	-9.915	-11.138	1.00	99.99	H
ATOM	741	N	LEU	A	43	27.194	-4.276	-13.657	1.00	0.00	N
ATOM	742	CA	LEU	A	43	28.325	-3.350	-13.367	1.00	0.00	C
ATOM	743	C	LEU	A	43	27.780	-1.966	-13.013	1.00	0.00	C
ATOM	744	O	LEU	A	43	28.075	-1.418	-11.970	1.00	0.00	O
ATOM	745	CB	LEU	A	43	29.223	-3.242	-14.602	1.00	0.00	C
ATOM	746	CG	LEU	A	43	30.233	-2.111	-14.401	1.00	0.00	C
ATOM	747	CD1	LEU	A	43	31.199	-2.484	-13.275	1.00	0.00	C

ATOM	748	CD2	LEU	A	43	31.020	-1.894	-15.696	1.00	0.00	C
ATOM	749	H	LEU	A	43	26.920	-4.437	-14.584	1.00	99.99	H
ATOM	750	HA	LEU	A	43	28.900	-3.728	-12.539	1.00	99.99	H
ATOM	751	HB2	LEU	A	43	29.749	-4.174	-14.747	1.00	99.99	H
ATOM	752	HB3	LEU	A	43	28.616	-3.032	-15.470	1.00	99.99	H
ATOM	753	HG	LEU	A	43	29.710	-1.202	-14.141	1.00	99.99	H
ATOM	754	HD11	LEU	A	43	31.665	-3.432	-13.499	1.00	99.99	H
ATOM	755	HD12	LEU	A	43	31.959	-1.722	-13.185	1.00	99.99	H
ATOM	756	HD13	LEU	A	43	30.655	-2.560	-12.345	1.00	99.99	H
ATOM	757	HD21	LEU	A	43	31.037	-2.811	-16.265	1.00	99.99	H
ATOM	758	HD22	LEU	A	43	30.546	-1.117	-16.279	1.00	99.99	H
ATOM	759	HD23	LEU	A	43	32.031	-1.599	-15.457	1.00	99.99	H
ATOM	760	N	THR	A	44	26.985	-1.400	-13.874	1.00	0.00	N
ATOM	761	CA	THR	A	44	26.415	-0.052	-13.592	1.00	0.00	C
ATOM	762	C	THR	A	44	24.922	-0.188	-13.291	1.00	0.00	C
ATOM	763	O	THR	A	44	24.211	0.790	-13.167	1.00	0.00	O
ATOM	764	CB	THR	A	44	26.614	0.855	-14.809	1.00	0.00	C
ATOM	765	CG2	THR	A	44	26.316	0.069	-16.086	1.00	0.00	C
ATOM	766	OG1	THR	A	44	25.734	1.967	-14.717	1.00	0.00	O
ATOM	767	H	THR	A	44	26.759	-1.863	-14.705	1.00	99.99	H
ATOM	768	HA	THR	A	44	26.910	0.379	-12.734	1.00	99.99	H
ATOM	769	HB	THR	A	44	27.634	1.204	-14.835	1.00	99.99	H

ATOM	770	HG1	THR	A	44	25.536	2.262	-15.609	1.00	99.99	H
ATOM	771	HG21	THR	A	44	25.655	-0.754	-15.857	1.00	99.99	H
ATOM	772	HG22	THR	A	44	25.845	0.720	-16.808	1.00	99.99	H
ATOM	773	HG23	THR	A	44	27.239	-0.314	-16.496	1.00	99.99	H
ATOM	774	N	LYS	A	45	24.443	-1.394	-13.166	1.00	0.00	N
ATOM	775	CA	LYS	A	45	22.999	-1.602	-12.865	1.00	0.00	C
ATOM	776	C	LYS	A	45	22.142	-0.803	-13.845	1.00	0.00	C
ATOM	777	O	LYS	A	45	21.014	-0.457	-13.555	1.00	0.00	O
ATOM	778	CB	LYS	A	45	22.707	-1.136	-11.438	1.00	0.00	C
ATOM	779	CG	LYS	A	45	23.846	-1.575	-10.516	1.00	0.00	C
ATOM	780	CD	LYS	A	45	23.317	-1.733	-9.089	1.00	0.00	C
ATOM	781	CE	LYS	A	45	23.350	-0.378	-8.380	1.00	0.00	C
ATOM	782	NZ	LYS	A	45	23.000	-0.560	-6.943	1.00	0.00	N1+
ATOM	783	H	LYS	A	45	25.033	-2.170	-13.265	1.00	99.99	H
ATOM	784	HA	LYS	A	45	22.769	-2.654	-12.952	1.00	99.99	H
ATOM	785	HB2	LYS	A	45	22.624	-0.060	-11.419	1.00	99.99	H
ATOM	786	HB3	LYS	A	45	21.780	-1.575	-11.099	1.00	99.99	H
ATOM	787	HG2	LYS	A	45	24.243	-2.520	-10.859	1.00	99.99	H
ATOM	788	HG3	LYS	A	45	24.628	-0.830	-10.529	1.00	99.99	H
ATOM	789	HD2	LYS	A	45	22.300	-2.098	-9.121	1.00	99.99	H
ATOM	790	HD3	LYS	A	45	23.935	-2.436	-8.551	1.00	99.99	H
ATOM	791	HE2	LYS	A	45	24.341	0.045	-8.458	1.00	99.99	H

ATOM	792	HE3	LYS	A	45	22.637	0.289	-8.843	1.00	99.99	H
ATOM	793	HZ1	LYS	A	45	23.527	-1.369	-6.558	1.00	99.99	H
ATOM	794	HZ2	LYS	A	45	23.249	0.301	-6.414	1.00	99.99	H
ATOM	795	HZ3	LYS	A	45	21.980	-0.740	-6.855	1.00	99.99	H
ATOM	796	N	LYS	A	46	22.656	-0.518	-15.008	1.00	0.00	N
ATOM	797	CA	LYS	A	46	21.851	0.244	-16.000	1.00	0.00	C
ATOM	798	C	LYS	A	46	20.925	-0.732	-16.720	1.00	0.00	C
ATOM	799	O	LYS	A	46	21.281	-1.867	-16.963	1.00	0.00	O
ATOM	800	CB	LYS	A	46	22.781	0.915	-17.013	1.00	0.00	C
ATOM	801	CG	LYS	A	46	22.330	2.359	-17.238	1.00	0.00	C
ATOM	802	CD	LYS	A	46	23.360	3.087	-18.104	1.00	0.00	C
ATOM	803	CE	LYS	A	46	22.786	4.430	-18.559	1.00	0.00	C
ATOM	804	NZ	LYS	A	46	21.566	4.195	-19.382	1.00	0.00	N1+
ATOM	805	H	LYS	A	46	23.561	-0.817	-15.235	1.00	99.99	H
ATOM	806	HA	LYS	A	46	21.264	0.994	-15.491	1.00	99.99	H
ATOM	807	HB2	LYS	A	46	23.792	0.909	-16.633	1.00	99.99	H
ATOM	808	HB3	LYS	A	46	22.744	0.376	-17.947	1.00	99.99	H
ATOM	809	HG2	LYS	A	46	21.373	2.363	-17.739	1.00	99.99	H
ATOM	810	HG3	LYS	A	46	22.241	2.862	-16.287	1.00	99.99	H
ATOM	811	HD2	LYS	A	46	24.259	3.255	-17.529	1.00	99.99	H
ATOM	812	HD3	LYS	A	46	23.594	2.484	-18.969	1.00	99.99	H
ATOM	813	HE2	LYS	A	46	22.528	5.022	-17.693	1.00	99.99	H

ATOM	814	HE3	LYS	A	46	23.523	4.956	-19.148	1.00	99.99	H
ATOM	815	HZ1	LYS	A	46	21.541	3.202	-19.689	1.00	99.99	H
ATOM	816	HZ2	LYS	A	46	20.720	4.405	-18.814	1.00	99.99	H
ATOM	817	HZ3	LYS	A	46	21.587	4.814	-20.217	1.00	99.99	H
ATOM	818	N	GLU	A	47	19.740	-0.312	-17.063	1.00	0.00	N
ATOM	819	CA	GLU	A	47	18.807	-1.237	-17.762	1.00	0.00	C
ATOM	820	C	GLU	A	47	18.426	-0.646	-19.120	1.00	0.00	C
ATOM	821	O	GLU	A	47	18.312	0.554	-19.277	1.00	0.00	O
ATOM	822	CB	GLU	A	47	17.549	-1.433	-16.913	1.00	0.00	C
ATOM	823	CG	GLU	A	47	16.752	-2.626	-17.445	1.00	0.00	C
ATOM	824	CD	GLU	A	47	15.313	-2.546	-16.933	1.00	0.00	C
ATOM	825	OE1	GLU	A	47	15.120	-2.033	-15.844	1.00	0.00	O
ATOM	826	OE2	GLU	A	47	14.428	-3.000	-17.640	1.00	0.00	O1-
ATOM	827	H	GLU	A	47	19.464	0.607	-16.864	1.00	99.99	H
ATOM	828	HA	GLU	A	47	19.296	-2.188	-17.912	1.00	99.99	H
ATOM	829	HB2	GLU	A	47	17.832	-1.618	-15.888	1.00	99.99	H
ATOM	830	HB3	GLU	A	47	16.939	-0.543	-16.963	1.00	99.99	H
ATOM	831	HG2	GLU	A	47	16.752	-2.606	-18.525	1.00	99.99	H
ATOM	832	HG3	GLU	A	47	17.206	-3.544	-17.102	1.00	99.99	H
ATOM	833	N	GLY	A	48	18.234	-1.480	-20.104	1.00	0.00	N
ATOM	834	CA	GLY	A	48	17.869	-0.967	-21.453	1.00	0.00	C
ATOM	835	C	GLY	A	48	17.339	-2.116	-22.306	1.00	0.00	C

ATOM	836	O	GLY A 48	17.051	-3.189	-21.815	1.00	0.00	O
ATOM	837	H	GLY A 48	18.336	-2.444	-19.956	1.00	99.99	H
ATOM	838	HA2	GLY A 48	18.742	-0.542	-21.925	1.00	99.99	H
ATOM	839	HA3	GLY A 48	17.106	-0.209	-21.359	1.00	99.99	H
ATOM	840	N	PHE A 49	17.213	-1.901	-23.583	1.00	0.00	N
ATOM	841	CA	PHE A 49	16.704	-2.983	-24.468	1.00	0.00	C
ATOM	842	C	PHE A 49	17.884	-3.707	-25.118	1.00	0.00	C
ATOM	843	O	PHE A 49	18.813	-3.095	-25.606	1.00	0.00	O
ATOM	844	CB	PHE A 49	15.804	-2.384	-25.551	1.00	0.00	C
ATOM	845	CG	PHE A 49	14.526	-3.185	-25.647	1.00	0.00	C
ATOM	846	CD1	PHE A 49	13.904	-3.653	-24.483	1.00	0.00	C
ATOM	847	CD2	PHE A 49	13.964	-3.458	-26.899	1.00	0.00	C
ATOM	848	CE1	PHE A 49	12.719	-4.394	-24.573	1.00	0.00	C
ATOM	849	CE2	PHE A 49	12.780	-4.199	-26.989	1.00	0.00	C
ATOM	850	CZ	PHE A 49	12.157	-4.667	-25.826	1.00	0.00	C
ATOM	851	H	PHE A 49	17.461	-1.028	-23.955	1.00	99.99	H
ATOM	852	HA	PHE A 49	16.141	-3.688	-23.874	1.00	99.99	H
ATOM	853	HB2	PHE A 49	15.569	-1.361	-25.298	1.00	99.99	H
ATOM	854	HB3	PHE A 49	16.317	-2.411	-26.501	1.00	99.99	H
ATOM	855	HD1	PHE A 49	14.337	-3.443	-23.517	1.00	99.99	H
ATOM	856	HD2	PHE A 49	14.445	-3.097	-27.797	1.00	99.99	H
ATOM	857	HE1	PHE A 49	12.239	-4.755	-23.675	1.00	99.99	H

ATOM	858	HE2	PHE	A	49	12.347	-4.410	-27.955	1.00	99.99	H
ATOM	859	HZ	PHE	A	49	11.244	-5.239	-25.895	1.00	99.99	H
ATOM	860	N	ILE	A	50	17.850	-5.010	-25.123	1.00	0.00	N
ATOM	861	CA	ILE	A	50	18.965	-5.789	-25.737	1.00	0.00	C
ATOM	862	C	ILE	A	50	18.393	-6.762	-26.769	1.00	0.00	C
ATOM	863	O	ILE	A	50	17.336	-7.328	-26.573	1.00	0.00	O
ATOM	864	CB	ILE	A	50	19.689	-6.580	-24.645	1.00	0.00	C
ATOM	865	CG1	ILE	A	50	18.686	-7.474	-23.911	1.00	0.00	C
ATOM	866	CG2	ILE	A	50	20.330	-5.609	-23.652	1.00	0.00	C
ATOM	867	CD1	ILE	A	50	19.421	-8.664	-23.292	1.00	0.00	C
ATOM	868	H	ILE	A	50	17.085	-5.479	-24.722	1.00	99.99	H
ATOM	869	HA	ILE	A	50	19.663	-5.116	-26.213	1.00	99.99	H
ATOM	870	HB	ILE	A	50	20.456	-7.194	-25.094	1.00	99.99	H
ATOM	871	HG12	ILE	A	50	18.201	-6.906	-23.132	1.00	99.99	H
ATOM	872	HG13	ILE	A	50	17.945	-7.833	-24.610	1.00	99.99	H
ATOM	873	HG21	ILE	A	50	19.960	-4.611	-23.835	1.00	99.99	H
ATOM	874	HG22	ILE	A	50	20.078	-5.906	-22.644	1.00	99.99	H
ATOM	875	HG23	ILE	A	50	21.403	-5.624	-23.774	1.00	99.99	H
ATOM	876	HD11	ILE	A	50	20.443	-8.386	-23.081	1.00	99.99	H
ATOM	877	HD12	ILE	A	50	18.930	-8.954	-22.375	1.00	99.99	H
ATOM	878	HD13	ILE	A	50	19.410	-9.494	-23.984	1.00	99.99	H
ATOM	879	N	PRO	A	51	19.102	-6.963	-27.892	1.00	0.00	N

ATOM	880	CA	PRO A	51	18.644	-7.874	-28.942	1.00	0.00	C
ATOM	881	C	PRO A	51	18.858	-9.333	-28.528	1.00	0.00	C
ATOM	882	O	PRO A	51	19.677	-9.622	-27.678	1.00	0.00	O
ATOM	883	CB	PRO A	51	19.532	-7.526	-30.133	1.00	0.00	C
ATOM	884	CG	PRO A	51	20.775	-6.951	-29.534	1.00	0.00	C
ATOM	885	CD	PRO A	51	20.387	-6.324	-28.220	1.00	0.00	C
ATOM	886	HA	PRO A	51	17.613	-7.686	-29.193	1.00	99.99	H
ATOM	887	HB2	PRO A	51	19.742	-8.420	-30.701	1.00	99.99	H
ATOM	888	HB3	PRO A	51	19.027	-6.808	-30.763	1.00	99.99	H
ATOM	889	HG2	PRO A	51	21.497	-7.738	-29.380	1.00	99.99	H
ATOM	890	HG3	PRO A	51	21.187	-6.209	-30.201	1.00	99.99	H
ATOM	891	HD2	PRO A	51	21.134	-6.534	-27.468	1.00	99.99	H
ATOM	892	HD3	PRO A	51	20.280	-5.255	-28.330	1.00	99.99	H
ATOM	893	N	SER A	52	18.138	-10.259	-29.098	1.00	0.00	N
ATOM	894	CA	SER A	52	18.331	-11.678	-28.693	1.00	0.00	C
ATOM	895	C	SER A	52	19.410	-12.333	-29.560	1.00	0.00	C
ATOM	896	O	SER A	52	19.394	-13.528	-29.782	1.00	0.00	O
ATOM	897	CB	SER A	52	17.016	-12.436	-28.845	1.00	0.00	C
ATOM	898	OG	SER A	52	17.204	-13.790	-28.462	1.00	0.00	O
ATOM	899	H	SER A	52	17.469	-10.026	-29.775	1.00	99.99	H
ATOM	900	HA	SER A	52	18.654	-11.699	-27.664	1.00	99.99	H
ATOM	901	HB2	SER A	52	16.266	-11.980	-28.217	1.00	99.99	H

ATOM	902	HB3	SER	A	52	16.694	-12.395	-29.875	1.00	99.99	H
ATOM	903	HG	SER	A	52	17.924	-13.822	-27.828	1.00	99.99	H
ATOM	904	N	ASN	A	53	20.353	-11.571	-30.042	1.00	0.00	N
ATOM	905	CA	ASN	A	53	21.430	-12.171	-30.880	1.00	0.00	C
ATOM	906	C	ASN	A	53	22.785	-11.582	-30.477	1.00	0.00	C
ATOM	907	O	ASN	A	53	23.812	-11.939	-31.020	1.00	0.00	O
ATOM	908	CB	ASN	A	53	21.162	-11.879	-32.355	1.00	0.00	C
ATOM	909	CG	ASN	A	53	21.944	-12.867	-33.222	1.00	0.00	C
ATOM	910	ND2	ASN	A	53	21.306	-13.829	-33.832	1.00	0.00	N
ATOM	911	OD1	ASN	A	53	23.148	-12.764	-33.346	1.00	0.00	O
ATOM	912	H	ASN	A	53	20.355	-10.610	-29.850	1.00	99.99	H
ATOM	913	HA	ASN	A	53	21.452	-13.238	-30.713	1.00	99.99	H
ATOM	914	HB2	ASN	A	53	20.106	-11.979	-32.556	1.00	99.99	H
ATOM	915	HB3	ASN	A	53	21.478	-10.871	-32.580	1.00	99.99	H
ATOM	916	HD21	ASN	A	53	20.334	-13.912	-33.731	1.00	99.99	H
ATOM	917	HD22	ASN	A	53	21.797	-14.467	-34.389	1.00	99.99	H
ATOM	918	N	TYR	A	54	22.800	-10.691	-29.524	1.00	0.00	N
ATOM	919	CA	TYR	A	54	24.092	-10.092	-29.084	1.00	0.00	C
ATOM	920	C	TYR	A	54	24.475	-10.667	-27.717	1.00	0.00	C
ATOM	921	O	TYR	A	54	25.634	-10.718	-27.356	1.00	0.00	O
ATOM	922	CB	TYR	A	54	23.945	-8.574	-28.975	1.00	0.00	C
ATOM	923	CG	TYR	A	54	24.064	-7.955	-30.347	1.00	0.00	C

ATOM	924	CD1	TYR	A	54	23.154	-8.302	-31.353	1.00	0.00	C
ATOM	925	CD2	TYR	A	54	25.085	-7.035	-30.614	1.00	0.00	C
ATOM	926	CE1	TYR	A	54	23.265	-7.728	-32.626	1.00	0.00	C
ATOM	927	CE2	TYR	A	54	25.196	-6.461	-31.887	1.00	0.00	C
ATOM	928	CZ	TYR	A	54	24.286	-6.808	-32.893	1.00	0.00	C
ATOM	929	OH	TYR	A	54	24.395	-6.243	-34.147	1.00	0.00	O
ATOM	930	H	TYR	A	54	21.964	-10.421	-29.094	1.00	99.99	H
ATOM	931	HA	TYR	A	54	24.863	-10.330	-29.803	1.00	99.99	H
ATOM	932	HB2	TYR	A	54	22.980	-8.335	-28.554	1.00	99.99	H
ATOM	933	HB3	TYR	A	54	24.722	-8.182	-28.335	1.00	99.99	H
ATOM	934	HD1	TYR	A	54	22.367	-9.012	-31.148	1.00	99.99	H
ATOM	935	HD2	TYR	A	54	25.787	-6.767	-29.838	1.00	99.99	H
ATOM	936	HE1	TYR	A	54	22.563	-7.996	-33.402	1.00	99.99	H
ATOM	937	HE2	TYR	A	54	25.984	-5.752	-32.092	1.00	99.99	H
ATOM	938	HH	TYR	A	54	25.078	-5.569	-34.110	1.00	99.99	H
ATOM	939	N	VAL	A	55	23.507	-11.101	-26.955	1.00	0.00	N
ATOM	940	CA	VAL	A	55	23.809	-11.676	-25.612	1.00	0.00	C
ATOM	941	C	VAL	A	55	23.239	-13.092	-25.523	1.00	0.00	C
ATOM	942	O	VAL	A	55	22.415	-13.491	-26.322	1.00	0.00	O
ATOM	943	CB	VAL	A	55	23.167	-10.806	-24.530	1.00	0.00	C
ATOM	944	CG1	VAL	A	55	23.657	-9.365	-24.676	1.00	0.00	C
ATOM	945	CG2	VAL	A	55	21.644	-10.847	-24.681	1.00	0.00	C

ATOM	946	H	VAL A 55	22.580	-11.052	-27.269	1.00	99.99	H
ATOM	947	HA	VAL A 55	24.879	-11.706	-25.464	1.00	99.99	H
ATOM	948	HB	VAL A 55	23.442	-11.183	-23.556	1.00	99.99	H
ATOM	949	HG11	VAL A 55	24.065	-9.222	-25.666	1.00	99.99	H
ATOM	950	HG12	VAL A 55	22.831	-8.687	-24.525	1.00	99.99	H
ATOM	951	HG13	VAL A 55	24.423	-9.170	-23.939	1.00	99.99	H
ATOM	952	HG21	VAL A 55	21.349	-11.788	-25.123	1.00	99.99	H
ATOM	953	HG22	VAL A 55	21.183	-10.747	-23.710	1.00	99.99	H
ATOM	954	HG23	VAL A 55	21.323	-10.035	-25.317	1.00	99.99	H
ATOM	955	N	ALA A 56	23.663	-13.857	-24.552	1.00	0.00	N
ATOM	956	CA	ALA A 56	23.132	-15.243	-24.416	1.00	0.00	C
ATOM	957	C	ALA A 56	23.382	-15.755	-22.998	1.00	0.00	C
ATOM	958	O	ALA A 56	23.691	-15.000	-22.097	1.00	0.00	O
ATOM	959	CB	ALA A 56	23.824	-16.162	-25.424	1.00	0.00	C
ATOM	960	H	ALA A 56	24.326	-13.517	-23.912	1.00	99.99	H
ATOM	961	HA	ALA A 56	22.070	-15.237	-24.601	1.00	99.99	H
ATOM	962	HB1	ALA A 56	23.706	-15.759	-26.419	1.00	99.99	H
ATOM	963	HB2	ALA A 56	23.379	-17.146	-25.380	1.00	99.99	H
ATOM	964	HB3	ALA A 56	24.875	-16.231	-25.187	1.00	99.99	H
ATOM	965	N	LYS A 57	23.246	-17.034	-22.795	1.00	0.00	N
ATOM	966	CA	LYS A 57	23.469	-17.605	-21.436	1.00	0.00	C
ATOM	967	C	LYS A 57	24.940	-17.993	-21.277	1.00	0.00	C

ATOM	968	O	LYS A 57	25.504	-18.681	-22.104	1.00	0.00	O
ATOM	969	CB	LYS A 57	22.593	-18.847	-21.254	1.00	0.00	C
ATOM	970	CG	LYS A 57	21.128	-18.478	-21.493	1.00	0.00	C
ATOM	971	CD	LYS A 57	20.272	-19.747	-21.465	1.00	0.00	C
ATOM	972	CE	LYS A 57	18.861	-19.421	-21.959	1.00	0.00	C
ATOM	973	NZ	LYS A 57	18.225	-20.657	-22.494	1.00	0.00	N1+
ATOM	974	H	LYS A 57	22.997	-17.621	-23.539	1.00	99.99	H
ATOM	975	HA	LYS A 57	23.209	-16.869	-20.689	1.00	99.99	H
ATOM	976	HB2	LYS A 57	22.893	-19.606	-21.962	1.00	99.99	H
ATOM	977	HB3	LYS A 57	22.710	-19.226	-20.250	1.00	99.99	H
ATOM	978	HG2	LYS A 57	20.796	-17.803	-20.718	1.00	99.99	H
ATOM	979	HG3	LYS A 57	21.029	-17.998	-22.455	1.00	99.99	H
ATOM	980	HD2	LYS A 57	20.715	-20.494	-22.107	1.00	99.99	H
ATOM	981	HD3	LYS A 57	20.221	-20.125	-20.455	1.00	99.99	H
ATOM	982	HE2	LYS A 57	18.272	-19.039	-21.139	1.00	99.99	H
ATOM	983	HE3	LYS A 57	18.916	-18.677	-22.740	1.00	99.99	H
ATOM	984	HZ1	LYS A 57	18.849	-21.087	-23.207	1.00	99.99	H
ATOM	985	HZ2	LYS A 57	18.068	-21.331	-21.718	1.00	99.99	H
ATOM	986	HZ3	LYS A 57	17.313	-20.417	-22.931	1.00	99.99	H
ATOM	987	N	LEU A 58	25.565	-17.560	-20.216	1.00	0.00	N
ATOM	988	CA	LEU A 58	26.999	-17.904	-20.001	1.00	0.00	C
ATOM	989	C	LEU A 58	27.775	-17.700	-21.303	1.00	0.00	C

ATOM	990	O	LEU A 58	27.259	-17.172	-22.268	1.00	0.00	O
ATOM	991	CB	LEU A 58	27.111	-19.366	-19.562	1.00	0.00	C
ATOM	992	CG	LEU A 58	28.079	-19.471	-18.382	1.00	0.00	C
ATOM	993	CD1	LEU A 58	27.478	-18.764	-17.165	1.00	0.00	C
ATOM	994	CD2	LEU A 58	28.319	-20.944	-18.048	1.00	0.00	C
ATOM	995	H	LEU A 58	25.091	-17.008	-19.560	1.00	99.99	H
ATOM	996	HA	LEU A 58	27.410	-17.266	-19.233	1.00	99.99	H
ATOM	997	HB2	LEU A 58	26.138	-19.728	-19.264	1.00	99.99	H
ATOM	998	HB3	LEU A 58	27.480	-19.961	-20.385	1.00	99.99	H
ATOM	999	HG	LEU A 58	29.017	-19.003	-18.643	1.00	99.99	H
ATOM	1000	HD11	LEU A 58	26.401	-18.816	-17.215	1.00	99.99	H
ATOM	1001	HD12	LEU A 58	27.821	-19.247	-16.263	1.00	99.99	H
ATOM	1002	HD13	LEU A 58	27.789	-17.729	-17.160	1.00	99.99	H
ATOM	1003	HD21	LEU A 58	27.617	-21.556	-18.594	1.00	99.99	H
ATOM	1004	HD22	LEU A 58	29.327	-21.217	-18.325	1.00	99.99	H
ATOM	1005	HD23	LEU A 58	28.183	-21.099	-16.988	1.00	99.99	H
ATOM	1006	N	ASN A 59	29.013	-18.112	-21.337	1.00	0.00	N
ATOM	1007	CA	ASN A 59	29.822	-17.940	-22.577	1.00	0.00	C
ATOM	1008	C	ASN A 59	31.276	-18.320	-22.294	1.00	0.00	C
ATOM	1009	O	ASN A 59	31.682	-19.450	-22.482	1.00	0.00	O
ATOM	1010	CB	ASN A 59	29.757	-16.480	-23.031	1.00	0.00	C
ATOM	1011	CG	ASN A 59	30.750	-16.256	-24.173	1.00	0.00	C

ATOM	1012	ND2	ASN	A	59	30.866	-15.066	-24.697	1.00	0.00	N
ATOM	1013	OD1	ASN	A	59	31.428	-17.173	-24.593	1.00	0.00	O
ATOM	1014	H	ASN	A	59	29.411	-18.534	-20.548	1.00	99.99	H
ATOM	1015	HA	ASN	A	59	29.429	-18.576	-23.355	1.00	99.99	H
ATOM	1016	HB2	ASN	A	59	28.758	-16.254	-23.374	1.00	99.99	H
ATOM	1017	HB3	ASN	A	59	30.008	-15.834	-22.203	1.00	99.99	H
ATOM	1018	HD21	ASN	A	59	30.319	-14.327	-24.358	1.00	99.99	H
ATOM	1019	HD22	ASN	A	59	31.499	-14.913	-25.428	1.00	99.99	H
ATOM	1020	N	THR	A	60	32.065	-17.383	-21.844	1.00	0.00	N
ATOM	1021	CA	THR	A	60	33.493	-17.688	-21.550	1.00	0.00	C
ATOM	1022	C	THR	A	60	33.654	-17.988	-20.058	1.00	0.00	C
ATOM	1023	O	THR	A	60	33.181	-17.196	-19.260	1.00	0.00	O
ATOM	1024	CB	THR	A	60	34.358	-16.482	-21.924	1.00	0.00	C
ATOM	1025	CG2	THR	A	60	35.798	-16.722	-21.469	1.00	0.00	C
ATOM	1026	OG1	THR	A	60	34.327	-16.299	-23.332	1.00	0.00	O
ATOM	1027	OXT	THR	A	60	34.247	-19.006	-19.739	1.00	0.00	O1-
ATOM	1028	H	THR	A	60	31.717	-16.479	-21.701	1.00	99.99	H
ATOM	1029	HA	THR	A	60	33.804	-18.547	-22.126	1.00	99.99	H
ATOM	1030	HB	THR	A	60	33.975	-15.598	-21.437	1.00	99.99	H
ATOM	1031	HG1	THR	A	60	34.830	-17.010	-23.735	1.00	99.99	H
ATOM	1032	HG21	THR	A	60	35.844	-17.626	-20.879	1.00	99.99	H
ATOM	1033	HG22	THR	A	60	36.436	-16.826	-22.335	1.00	99.99	H

ATOM 1034 HG22 THR A 60 36.436 -16.826 -22.335 1.00 99.99 H

CONNECT 1 15 26 53 14

CONNECT 2 20 13 16

CONNECT 3 25 58 59

CONNECT 4 65 17 25

CONNECT 5 6 28 32

CONNECT 6 5 38 39 40

CONNECT 7 8 30 33

CONNECT 8 7 27 41 42

CONNECT 9 11 34 29

CONNECT 10 12 35 31

CONNECT 11 9 43 44 45

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CONNECT 13 2 14 49 50

CONNECT 14 13 1 51 52

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CONNECT 16 15 2 56 57

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CONNECT 65 4

CONNECT 66 26

CONNECT 67 26

CONNECT 68 27

CONNECT 69 27

END

Data for computed docked structures:

Name: *****

Creating user name zbl

Creation time: Thu Jun 13 10:31:08 2019

File generated by GOLD software.

#

@<TRIPOS>MOLECULE

*****|pRh-6|mol2|1|dock1

85 91 1

SMALL

USER_CHARGES

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24 H	9.7119	-3.7864	-21.2665	H	1 <1>	0.0000
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26 H	10.1735	-3.0060	-20.2285	H	1 <1>	0.0000
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29 H	11.4305	2.4308	-20.6146	H	1 <1>	0.0000
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46 N	17.2208 -1.0572 -31.2344 N.p13	1 <1>	0.0000
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66 H	8.3372	-1.5075	-30.0998 H	1 <1>	0.0000
67 H	9.8196	-1.0203	-29.2284 H	1 <1>	0.0000
68 H	7.9160	-3.5430	-28.5867 H	1 <1>	0.0000
69 H	9.6504	-3.7619	-28.4202 H	1 <1>	0.0000
70 ****	8.6120	0.7004	-24.2032 LP	1 <1>	0.0000
71 ****	7.6473	1.9549	-24.9073 LP	1 <1>	0.0000
72 ****	8.9786	-0.7164	-22.7437 LP	1 <1>	0.0000
73 ****	8.3727	-1.7958	-21.5322 LP	1 <1>	0.0000
74 ****	8.5239	-0.6960	-24.1993 LP	1 <1>	0.0000
75 ****	7.3469	-1.7322	-24.9348 LP	1 <1>	0.0000
76 ****	9.0325	0.6535	-22.7946 LP	1 <1>	0.0000
77 ****	8.6431	1.8426	-21.5970 LP	1 <1>	0.0000
78 ****	10.7605	0.4594	-24.8958 LP	1 <1>	0.0000
79 ****	11.3665	1.5389	-26.1073 LP	1 <1>	0.0000
80 ****	10.7067	-0.9105	-24.8449 LP	1 <1>	0.0000
81 ****	11.0961	-2.0996	-26.0425 LP	1 <1>	0.0000
82 ****	11.1272	-0.9574	-23.4363 LP	1 <1>	0.0000
83 ****	12.0919	-2.2118	-22.7322 LP	1 <1>	0.0000
84 ****	11.2153	0.4390	-23.4402 LP	1 <1>	0.0000
85 ****	12.3922	1.4753	-22.7047 LP	1 <1>	0.0000

@<TRIPOS>BOND

1 1 11 ar

2 1 12 ar

3 1 13 ar

4 1 14 ar

5 1 15 1

6 2 3 1

7 2 11 ar

8 2 16 ar

9 3 6 1

10 3 7 1

11 3 8 1

12 4 5 1

13 4 13 ar

14 4 18 ar

15 5 9 1

16 5 10 1

17 5 48 1

18 12 17 ar

19 14 19 ar

20 15 16 ar

21 15 18 ar

22 15 20 ar

23 15 21 ar

24 17 20 ar

25 17 22 1

26 19 21 ar

27 19 23 1

28 22 24 1

29 22 25 1

30 22 26 1

31 23 27 1

32 23 28 1

33 23 29 1

34 30 31 1

35 30 35 1

36 30 49 1

37 30 50 1

38 31 32 1

39 31 51 1

40 31 52 1

41 32 33 1

42 32 47 1

43 32 53 1

44 33 34 1
45 33 54 1
46 33 55 1
47 34 35 1
48 34 56 1
49 34 57 1
50 35 40 1
51 36 45 1
52 36 58 1
53 36 59 1
54 37 38 ar
55 37 42 ar
56 37 46 ar
57 38 39 ar
58 38 60 1
59 39 40 ar
60 39 61 1
61 40 41 ar
62 41 42 ar
63 41 62 1
64 42 43 ar
65 43 44 ar

66 43 63 1
67 44 45 ar
68 44 64 1
69 45 46 ar
70 46 65 1
71 47 48 1
72 47 66 1
73 47 67 1
74 48 68 1
75 48 69 1
76 11 70 1
77 11 71 1
78 12 72 1
79 12 73 1
80 13 74 1
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82 14 76 1
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88 20 82 1

89 20 83 1

90 21 84 1

91 21 85 1

@<TRIPOS>SUBSTRUCTURE

1 **** 1

@<TRIPOS>SET

LONE_PAIRS STATIC ATOMS <user> **** ""

16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

DONOR_HYDROGENS STATIC ATOMS <user> **** ""

4 53 58 59 65

ATOM\$BLUE STATIC ATOMS COLORGROUP SYSTEM

16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

ATOM\$RED STATIC ATOMS COLORGROUP SYSTEM

4 53 58 59 65

@<TRIPOS>COMMENT

> <Gold.Version>

5.7.2

> <Gold.Id.Protein>

unknown|gold_protein|mol2

><Gold.Protein.RotatedTorsions>

[614 603 602 601] final -113.50 input 2.31 | X-H torsion

[841 836 835 832] final 78.73 input 27.02 | X-H torsion

[172 163 162 160] final -21.43 input 178.05 | X-H torsion

[876 867 866 864] final -86.52 input 173.38 | X-H torsion

><Gold.Protein.ActiveResidues>

TYR19 ILE22 HIS23 ASP25 ASP26 HIS41 GLY42 GLU43 TRP44 LYS46
PHE57 PRO59 SER60 ASN61 TYR62

><Gold.Protein.RotatedAtoms>

20.6822 -0.5482 -29.3807 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 172 bound_to 163
14.2583 -0.2864 -22.9358 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 614 bound_to 603
12.8958 -1.2201 -22.5412 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 615 bound_to 603
12.8731 0.4618 -22.3055 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 616 bound_to 603
17.1972 -13.8310 -27.5030 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 841 bound_to 836
24.9208 -6.8326 -34.6930 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 876 bound_to 867
18.0808 -14.1223 -28.8096 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 987 bound_to 836
16.4643 -14.3528 -28.8309 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 988 bound_to 836
20.5685 -1.8628 -30.2937 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 998 bound_to 163
21.5201 -0.6158 -30.7475 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 999 bound_to 163
24.8438 -5.3519 -34.0800 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1000 bound_to 867

23.4861 -6.1291 -34.5482 LP 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1001 bound_to 867

><Gold.Score>

Score	S(PLP)	S(hbond)	S(cho)	S(metal)	DE(clash)	DE(tors)	intcor
78.99	-60.05	7.23	0.00	0.00	0.00	1.49	0.22

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78.9906

><Gold.PLP.PLP>

-60.0518

><Gold.PLP.part.hbond>

-4.9100

><Gold.PLP.part.metal>

0.0000

><Gold.PLP.part.buried>

-6.5257

><Gold.PLP.part.nonpolar>

-50.5650

> <Gold.PLP.part.repulsive>

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> <Gold.PLP.ligand.clash>

0.0000

> <Gold.PLP.ligand.torsion>

1.4869

> <Gold.PLP.Chemscore.Hbond>

7.2320

> <Gold.PLP.Chemscore.CHOScore>

0.0000

> <Gold.PLP.Chemscore.Metal>

0.0000

> <Gold.Chemscore.Hbonds>

donor molecule, donor type, donor heavy atom, donor atom, acceptor molecule, acceptor atom, score

L1 H 36 59 P1 261 1.76

L1 H 46 65 P1 261 1.89

P1 H 603 615 L1 20 1.66

P1 H 603 616 L1 21 1.92

><Gold.PLP.Chemscore.Internal.Correction>

0.2167

Name: *****

Creating user name zbl

Creation time: Thu Jun 13 10:31:09 2019

File generated by GOLD software.

#

@<TRIPOS>MOLECULE

*****|pRh-6|mol2|1|dock2

85 91 1

SMALL

USER_CHARGES

@<TRIPOS>ATOM

1 Cr	13.0456	-7.8803	-33.9882	Cr.oh	1 <1>	0.0000
2 C	15.4365	-7.4003	-35.5127	C.2	1 <1>	0.0000
3 C	16.8883	-7.4479	-35.8341	C.3	1 <1>	0.0000
4 C	12.8458	-5.0195	-34.0961	C.2	1 <1>	0.0000
5 C	12.7980	-3.6420	-33.5256	C.3	1 <1>	0.0000
6 H	16.9994	-7.8317	-36.6352	H	1 <1>	0.0000
7 H	17.3461	-7.7366	-35.2454	H	1 <1>	0.0000
8 H	17.2556	-6.5901	-36.0946	H	1 <1>	0.0000
9 H	12.1606	-2.9884	-34.1779	H	1 <1>	0.0000
10 H	13.2754	-2.9229	-34.2425	H	1 <1>	0.0000
11 O	15.0341	-7.8251	-34.3926	O.co2	1 <1>	0.0000
12 O	11.0317	-7.9297	-33.7307	O.co2	1 <1>	0.0000
13 O	13.0653	-5.9880	-33.3117	O.co2	1 <1>	0.0000
14 O	13.0197	-9.7139	-34.7893	O.co2	1 <1>	0.0000
15 Cr	12.6359	-6.9902	-36.1375	Cr.oh	1 <1>	0.0000
16 O	14.6498	-6.9408	-36.3949	O.co2	1 <1>	0.0000
17 C	10.2450	-7.4702	-34.6129	C.2	1 <1>	0.0000
18 O	12.6618	-5.1565	-35.3364	O.co2	1 <1>	0.0000
19 C	12.8357	-9.8510	-36.0296	C.2	1 <1>	0.0000
20 O	10.6474	-7.0454	-35.7331	O.co2	1 <1>	0.0000
21 O	12.6162	-8.8824	-36.8140	O.co2	1 <1>	0.0000

22 C	8.7932 -7.4226 -34.2916 C.3	1 <1>	0.0000
23 C	12.8835 -11.2285 -36.6000 C.3	1 <1>	0.0000
24 H	8.6821 -7.0387 -33.4905 H	1 <1>	0.0000
25 H	8.3354 -7.1338 -34.8802 H	1 <1>	0.0000
26 H	8.4259 -8.2803 -34.0311 H	1 <1>	0.0000
27 H	13.3214 -11.2171 -37.3783 H	1 <1>	0.0000
28 H	13.1422 -11.8252 -36.0252 H	1 <1>	0.0000
29 H	12.1132 -11.3512 -36.9053 H	1 <1>	0.0000
30 C	11.8232 0.2478 -29.3426 C.3	1 <1>	0.0000
31 C	12.2598 -1.0344 -30.0642 C.3	1 <1>	0.0000
32 N	13.7785 -1.1511 -30.1422 N.4	1 <1>	0.0000
33 C	14.5558 -0.7443 -28.8898 C.3	1 <1>	0.0000
34 C	13.9950 0.5357 -28.2536 C.3	1 <1>	0.0000
35 N	12.5653 0.1928 -28.0558 N.pl3	1 <1>	0.0000
36 N	8.8775 -2.9128 -22.4401 N.pl3	1 <1>	0.0000
37 C	11.0001 -1.3015 -24.6021 C.ar	1 <1>	0.0000
38 C	12.1285 -0.5708 -24.6152 C.ar	1 <1>	0.0000
39 C	12.6545 -0.1029 -25.7595 C.ar	1 <1>	0.0000
40 C	12.0964 -0.3129 -26.9718 C.ar	1 <1>	0.0000
41 C	10.9774 -1.0724 -26.9276 C.ar	1 <1>	0.0000
42 C	10.4368 -1.5645 -25.7946 C.ar	1 <1>	0.0000
43 C	9.3198 -2.3147 -25.8218 C.ar	1 <1>	0.0000

44 C	8.7988 -2.7738 -24.6766 C.ar	1 <1>	0.0000
45 C	9.3941 -2.4684 -23.5112 C.ar	1 <1>	0.0000
46 N	10.4784 -1.7388 -23.4806 N.pl3	1 <1>	0.0000
47 C	14.3028 -2.4976 -30.6032 C.3	1 <1>	0.0000
48 C	13.0268 -3.1688 -31.7919 C.3	1 <1>	0.0000
49 H	10.7223 0.3515 -29.2601 H	1 <1>	0.0000
50 H	12.1270 1.1403 -29.9368 H	1 <1>	0.0000
51 H	11.8333 -1.0463 -31.0943 H	1 <1>	0.0000
52 H	11.8222 -1.8648 -29.4686 H	1 <1>	0.0000
53 H	14.0663 -0.4608 -30.8769 H	1 <1>	0.0000
54 H	15.6248 -0.5805 -29.1648 H	1 <1>	0.0000
55 H	14.5070 -1.5577 -28.1284 H	1 <1>	0.0000
56 H	14.5539 0.8528 -27.3517 H	1 <1>	0.0000
57 H	14.1043 1.3940 -28.9564 H	1 <1>	0.0000
58 H	8.0084 -3.5036 -22.4573 H	1 <1>	0.0000
59 H	9.3160 -2.6873 -21.5116 H	1 <1>	0.0000
60 H	12.6315 -0.3271 -23.6641 H	1 <1>	0.0000
61 H	13.5608 0.5086 -25.6276 H	1 <1>	0.0000
62 H	10.4272 -1.3178 -27.8477 H	1 <1>	0.0000
63 H	8.8198 -2.5693 -26.7717 H	1 <1>	0.0000
64 H	7.8891 -3.3985 -24.7056 H	1 <1>	0.0000
65 H	10.9177 -1.5201 -22.5760 H	1 <1>	0.0000

66 H	14.3153	-3.2439	-29.7720 H	1 <1>	0.0000
67 H	15.2701	-2.6257	-31.1506 H	1 <1>	0.0000
68 H	12.4034	-3.9029	-31.2281 H	1 <1>	0.0000
69 H	12.3736	-2.2563	-31.8376 H	1 <1>	0.0000
70 ****	14.0589	-7.8073	-34.1721 LP	1 <1>	0.0000
71 ****	15.6909	-8.1790	-33.7267 LP	1 <1>	0.0000
72 ****	12.0151	-7.9665	-33.9081 LP	1 <1>	0.0000
73 ****	10.6686	-8.2552	-32.8577 LP	1 <1>	0.0000
74 ****	13.1000	-6.9218	-33.6678 LP	1 <1>	0.0000
75 ****	13.2041	-5.8195	-32.3358 LP	1 <1>	0.0000
76 ****	12.9960	-8.8027	-34.3780 LP	1 <1>	0.0000
77 ****	13.1892	-10.5164	-34.2173 LP	1 <1>	0.0000
78 ****	13.6663	-6.9039	-36.2176 LP	1 <1>	0.0000
79 ****	15.0129	-6.6153	-37.2680 LP	1 <1>	0.0000
80 ****	12.6855	-6.0677	-35.7477 LP	1 <1>	0.0000
81 ****	12.4923	-4.3540	-35.9084 LP	1 <1>	0.0000
82 ****	11.6226	-7.0632	-35.9536 LP	1 <1>	0.0000
83 ****	9.9906	-6.6914	-36.3989 LP	1 <1>	0.0000
84 ****	12.5815	-7.9486	-36.4579 LP	1 <1>	0.0000
85 ****	12.4774	-9.0509	-37.7898 LP	1 <1>	0.0000

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2 1 12 ar

3 1 13 ar

4 1 14 ar

5 1 15 1

6 2 3 1

7 2 11 ar

8 2 16 ar

9 3 6 1

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11 3 8 1

12 4 5 1

13 4 13 ar

14 4 18 ar

15 5 9 1

16 5 10 1

17 5 48 1

18 12 17 ar

19 14 19 ar

20 15 16 ar

21 15 18 ar

22 15 20 ar

23 15 21 ar

24 17 20 ar

25 17 22 1

26 19 21 ar

27 19 23 1

28 22 24 1

29 22 25 1

30 22 26 1

31 23 27 1

32 23 28 1

33 23 29 1

34 30 31 1

35 30 35 1

36 30 49 1

37 30 50 1

38 31 32 1

39 31 51 1

40 31 52 1

41 32 33 1

42 32 47 1

43 32 53 1

44 33 34 1

45 33 54 1

46 33 55 1
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49 34 57 1
50 35 40 1
51 36 45 1
52 36 58 1
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54 37 38 ar
55 37 42 ar
56 37 46 ar
57 38 39 ar
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64 42 43 ar
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69 45 46 ar
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71 47 48 1
72 47 66 1
73 47 67 1
74 48 68 1
75 48 69 1
76 11 70 1
77 11 71 1
78 12 72 1
79 12 73 1
80 13 74 1
81 13 75 1
82 14 76 1
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87 18 81 1
88 20 82 1
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90 21 84 1

91 21 85 1

@<TRIPOS>SUBSTRUCTURE

1 **** 1

@<TRIPOS>SET

LONE_PAIRS STATIC ATOMS <user> **** ""

16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

DONOR_HYDROGENS STATIC ATOMS <user> **** ""

4 53 58 59 65

ATOM\$BLUE STATIC ATOMS COLORGROUP SYSTEM

16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

ATOM\$RED STATIC ATOMS COLORGROUP SYSTEM

4 53 58 59 65

@<TRIPOS>COMMENT

><Gold.Version>

5.7.2

><Gold.Id.Protein>

unknown|gold_protein|mol2

><Gold.Protein.RotatedTorsions>

[614 603 602 601] final 133.44 input 2.31 | X-H torsion

S110

[841 836 835 832] final -73.76 input 27.02 | X-H torsion

[172 163 162 160] final 87.56 input 178.05 | X-H torsion

[876 867 866 864] final 131.20 input 173.38 | X-H torsion

><Gold.Protein.ActiveResidues>

TYR19 ILE22 HIS23 ASP25 ASP26 HIS41 GLY42 GLU43 TRP44 LYS46

PHE57 PRO59 SER60 ASN61 TYR62

><Gold.Protein.RotatedAtoms>

21.5318 -0.5093 -30.6012 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 172 bound_to 163

12.9697 0.5201 -22.3335 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 614 bound_to 603

14.2537 -0.4044 -22.9502 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 615 bound_to 603

12.8010 -1.1593 -22.4976 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 616 bound_to 603

17.7016 -14.2285 -29.1559 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 841 bound_to 836

24.4856 -5.2933 -34.0373 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 876 bound_to 867

16.3166 -14.2364 -28.3469 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 987 bound_to 836

17.7122 -13.8318 -27.6018 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 988 bound_to 836

20.5441 -0.6604 -29.3455 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 998 bound_to 163

20.6758 -1.8579 -30.4479 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 999 bound_to 163

23.5758 -6.4462 -34.6833 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1000 bound_to 867

25.1992 -6.6088 -34.6154 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1001 bound_to 867

> <Gold.Score>

Score	S(PLP)	S(hbond)	S(cho)	S(metal)	DE(clash)	DE(tors)	intcor
54.92	-53.89	1.00	0.00	0.00	0.00	1.07	0.17

> <Gold.PLP.Fitness>

54.9235

> <Gold.PLP.PLP>

-53.8877

> <Gold.PLP.part.hbond>

-3.0000

> <Gold.PLP.part.metal>

0.0000

> <Gold.PLP.part.buried>

0.7209

> <Gold.PLP.part.nonpolar>

-52.7134

> <Gold.PLP.part.repulsive>

0.2165

> <Gold.PLP.ligand.clash>

0.0000

> <Gold.PLP.ligand.torsion>

1.0692

> <Gold.PLP.Chemscore.Hbond>

1.0000

> <Gold.PLP.Chemscore.CHOScore>

0.0000

> <Gold.PLP.Chemscore.Metal>

0.0000

> <Gold.Chemscore.Hbonds>

donor molecule, donor type, donor heavy atom, donor atom, acceptor molecule, acceptor atom, score

P1 H 557 566 L1 11 1.00

><Gold.PLP.Chemscore.Internal.Correction>

0.1743

Name: *****

Creating user name zb1

Creation time: Thu Jun 13 10:31:10 2019

File generated by GOLD software.

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@<TRIPOS>MOLECULE

*****|pRh-6|mol2|1|dock3

85 91 1

SMALL

USER_CHARGES

@<TRIPOS>ATOM

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2 C	8.3729	3.7788	-30.5000	C.2	1 <1>	0.0000
3 C	6.9565	3.3963	-30.2536	C.3	1 <1>	0.0000
4 C	11.2869	2.8601	-32.7477	C.2	1 <1>	0.0000

S114

5 C	11.5924	1.8698	-33.8206	C.3	1 <1>	0.0000
6 H	6.4650	4.1379	-30.1544	H	1 <1>	0.0000
7 H	6.8600	2.8389	-29.6884	H	1 <1>	0.0000
8 H	6.4946	3.0888	-31.0477	H	1 <1>	0.0000
9 H	11.8562	2.4120	-34.7668	H	1 <1>	0.0000
10 H	10.8376	1.9661	-34.6452	H	1 <1>	0.0000
11 O	9.2892	3.2439	-29.8134	O.co2	1 <1>	0.0000
12 O	13.0854	4.5720	-30.3544	O.co2	1 <1>	0.0000
13 O	11.5053	2.5310	-31.5454	O.co2	1 <1>	0.0000
14 O	10.8630	5.2370	-28.6588	O.co2	1 <1>	0.0000
15 Cr	10.4765	5.3758	-31.6944	Cr.oh	1 <1>	0.0000
16 O	8.6042	4.6489	-31.3933	O.co2	1 <1>	0.0000
17 C	13.3167	5.4421	-31.2476	C.2	1 <1>	0.0000
18 O	10.8266	3.9838	-33.0888	O.co2	1 <1>	0.0000
19 C	10.4028	6.3608	-28.9999	C.2	1 <1>	0.0000
20 O	12.4004	5.9770	-31.9342	O.co2	1 <1>	0.0000
21 O	10.1843	6.6899	-30.2022	O.co2	1 <1>	0.0000
22 C	14.7331	5.8246	-31.4940	C.3	1 <1>	0.0000
23 C	10.0973	7.3511	-27.9271	C.3	1 <1>	0.0000
24 H	15.2247	5.0830	-31.5932	H	1 <1>	0.0000
25 H	14.8296	6.3820	-32.0593	H	1 <1>	0.0000
26 H	15.1950	6.1320	-30.6999	H	1 <1>	0.0000

27 H	9.3282	7.7664	-28.1106 H	1 <1>	0.0000
28 H	10.1710	7.0198	-27.1282 H	1 <1>	0.0000
29 H	10.6127	7.9919	-28.0863 H	1 <1>	0.0000
30 C	15.4264	-2.1695	-31.7880 C.3	1 <1>	0.0000
31 C	14.8110	-1.3730	-32.9465 C.3	1 <1>	0.0000
32 N	13.6440	-2.1165	-33.5878 N.4	1 <1>	0.0000
33 C	12.6866	-2.8302	-32.6326 C.3	1 <1>	0.0000
34 C	13.4333	-3.5601	-31.5068 C.3	1 <1>	0.0000
35 N	14.2602	-2.4776	-30.9194 N.pl3	1 <1>	0.0000
36 N	10.9964	1.4093	-25.5322 N.pl3	1 <1>	0.0000
37 C	13.0278	-0.0789	-27.8635 C.ar	1 <1>	0.0000
38 C	14.2863	-0.0420	-28.3350 C.ar	1 <1>	0.0000
39 C	14.6944	-0.8535	-29.3248 C.ar	1 <1>	0.0000
40 C	13.8849	-1.7512	-29.9283 C.ar	1 <1>	0.0000
41 C	12.6335	-1.7818	-29.4144 C.ar	1 <1>	0.0000
42 C	12.2030	-0.9877	-28.4134 C.ar	1 <1>	0.0000
43 C	10.9427	-1.0701	-27.9487 C.ar	1 <1>	0.0000
44 C	10.5418	-0.2547	-26.9648 C.ar	1 <1>	0.0000
45 C	11.4031	0.6456	-26.4613 C.ar	1 <1>	0.0000
46 N	12.6276	0.7298	-26.9112 N.pl3	1 <1>	0.0000
47 C	12.8143	-1.3035	-34.5632 C.3	1 <1>	0.0000
48 C	12.1901	0.1734	-33.6036 C.3	1 <1>	0.0000

49 H	16.2699	-1.6454	-31.2946 H	1 <1>	0.0000
50 H	15.8900	-3.1061	-32.1750 H	1 <1>	0.0000
51 H	15.5914	-1.1721	-33.7170 H	1 <1>	0.0000
52 H	14.4774	-0.4143	-32.4933 H	1 <1>	0.0000
53 H	14.0866	-2.8818	-34.1512 H	1 <1>	0.0000
54 H	12.0814	-3.5679	-33.2112 H	1 <1>	0.0000
55 H	11.9929	-2.0929	-32.1648 H	1 <1>	0.0000
56 H	12.7560	-4.0937	-30.8119 H	1 <1>	0.0000
57 H	14.0763	-4.3656	-31.9312 H	1 <1>	0.0000
58 H	10.0147	1.3444	-25.1627 H	1 <1>	0.0000
59 H	11.6440	2.1279	-25.1207 H	1 <1>	0.0000
60 H	15.0039	0.6845	-27.9178 H	1 <1>	0.0000
61 H	15.7382	-0.6986	-29.6398 H	1 <1>	0.0000
62 H	11.8764	-2.4705	-29.8172 H	1 <1>	0.0000
63 H	10.2252	-1.8025	-28.3560 H	1 <1>	0.0000
64 H	9.5105	-0.3346	-26.5793 H	1 <1>	0.0000
65 H	13.2698	1.4257	-26.5080 H	1 <1>	0.0000
66 H	11.8830	-1.8422	-34.8641 H	1 <1>	0.0000
67 H	13.2310	-0.8558	-35.4999 H	1 <1>	0.0000
68 H	11.5861	-0.2177	-32.7505 H	1 <1>	0.0000
69 H	13.1637	0.4583	-33.1219 H	1 <1>	0.0000
70 ****	10.2432	3.5029	-29.9644 LP	1 <1>	0.0000

71	****	9.0602	2.5616	-29.1191 LP	1 <1>	0.0000
72	****	12.1462	4.2828	-30.1694 LP	1 <1>	0.0000
73	****	13.8423	4.1752	-29.8350 LP	1 <1>	0.0000
74	****	11.3116	3.1770	-30.8071 LP	1 <1>	0.0000
75	****	11.8716	1.6249	-31.3337 LP	1 <1>	0.0000
76	****	11.0753	4.5514	-29.3551 LP	1 <1>	0.0000
77	****	11.0157	5.0318	-27.6921 LP	1 <1>	0.0000
78	****	9.5434	4.9381	-31.5783 LP	1 <1>	0.0000
79	****	7.8473	5.0457	-31.9126 LP	1 <1>	0.0000
80	****	10.6144	4.6695	-32.3926 LP	1 <1>	0.0000
81	****	10.6739	4.1891	-34.0556 LP	1 <1>	0.0000
82	****	11.4465	5.7180	-31.7832 LP	1 <1>	0.0000
83	****	12.6294	6.6593	-32.6285 LP	1 <1>	0.0000
84	****	10.3781	6.0439	-30.9406 LP	1 <1>	0.0000
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- 2 1 12 ar
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- 4 1 14 ar
- 5 1 15 1
- 6 2 3 1

7 2 11 ar

8 2 16 ar

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10 3 7 1

11 3 8 1

12 4 5 1

13 4 13 ar

14 4 18 ar

15 5 9 1

16 5 10 1

17 5 48 1

18 12 17 ar

19 14 19 ar

20 15 16 ar

21 15 18 ar

22 15 20 ar

23 15 21 ar

24 17 20 ar

25 17 22 1

26 19 21 ar

27 19 23 1

28 22 24 1

29 22 25 1

30 22 26 1

31 23 27 1

32 23 28 1

33 23 29 1

34 30 31 1

35 30 35 1

36 30 49 1

37 30 50 1

38 31 32 1

39 31 51 1

40 31 52 1

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47 34 35 1

48 34 56 1

49 34 57 1

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@<TRIPOS>SUBSTRUCTURE

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DONOR_HYDROGENS STATIC ATOMS <user> **** ""

4 53 58 59 65

ATOM\$BLUE STATIC ATOMS COLORGROUP SYSTEM

16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

ATOM\$RED STATIC ATOMS COLORGROUP SYSTEM

4 53 58 59 65

@<TRIPOS>COMMENT

> <Gold.Version>

5.7.2

> <Gold.Id.Protein>

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> <Gold.Protein.RotatedTorsions>

[614 603 602 601] final 147.39 input 2.31 | X-H torsion

[841 836 835 832] final 87.01 input 27.02 | X-H torsion

[172 163 162 160] final -75.59 input 178.05 | X-H torsion

[876 867 866 864] final -58.42 input 173.38 | X-H torsion

> <Gold.Protein.ActiveResidues>

TYR19 ILE22 HIS23 ASP25 ASP26 HIS41 GLY42 GLU43 TRP44 LYS46
PHE57 PRO59 SER60 ASN61 TYR62

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13.1825 0.5999 -22.4041 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 614 bound_to 603
14.2035 -0.6368 -22.9625 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 615 bound_to 603
12.6388 -1.0064 -22.4148 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 616 bound_to 603
17.0677 -13.8520 -27.5139 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 841 bound_to 836
24.5039 -6.9535 -34.7837 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 876 bound_to 867
18.1327 -14.0816 -28.6910 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 987 bound_to 836
16.5449 -14.3720 -28.9384 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 988 bound_to 836
21.1201 -1.5554 -30.8721 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 998 bound_to 163
21.2990 -0.1465 -30.0662 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 999 bound_to 163
25.1885 -5.6352 -34.1777 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1000 bound_to 867
23.5678 -5.7221 -34.3577 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1001 bound_to 867

><Gold.Score>

Score	S(PLP)	S(hbond)	S(cho)	S(metal)	DE(clash)	DE(tors)	intcor
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> <Gold.PLP.part.hbond>

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> <Gold.PLP.part.metal>

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0.0000

> <Gold.PLP.Chemscore.Metal>

0.0000

> <Gold.Chemscore.Hbonds>

donor molecule, donor type, donor heavy atom, donor atom, acceptor molecule, acceptor atom, score

L1 H 36 59 P1 249 0.19

L1 H 46 65 P1 249 2.00

> <Gold.PLP.Chemscore.Internal.Correction>

0.1743

Name: *****

Creating user name zbl

Creation time: Thu Jun 13 10:31:11 2019

File generated by GOLD software.

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@<TRIPOS>MOLECULE

*****|pRh-6|mol2|1|dock4

85 91 1

SMALL

USER_CHARGES

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2 C	20.7845	-3.6487	-33.0400	C.2	1 <1>	0.0000
3 C	21.2741	-4.8984	-32.3983	C.3	1 <1>	0.0000
4 C	17.5356	-1.8353	-33.7771	C.2	1 <1>	0.0000
5 C	16.0721	-2.0626	-33.5990	C.3	1 <1>	0.0000
6 H	21.9838	-4.7076	-31.8871	H	1 <1>	0.0000
7 H	21.3655	-5.5128	-32.9021	H	1 <1>	0.0000
8 H	20.7165	-5.2022	-31.6667	H	1 <1>	0.0000

S127

9 H	15.7564	-2.9572	-34.1981	H	1 <1>	0.0000
10 H	15.5496	-1.9274	-34.5827	H	1 <1>	0.0000
11 O	20.5800	-3.6298	-34.2869	O.co2	1 <1>	0.0000
12 O	19.5344	-0.0947	-35.9836	O.co2	1 <1>	0.0000
13 O	18.0848	-2.2548	-34.8372	O.co2	1 <1>	0.0000
14 O	21.9777	-1.4984	-35.4210	O.co2	1 <1>	0.0000
15 Cr	20.1071	-0.8308	-33.0889	Cr.oh	1 <1>	0.0000
16 O	20.6029	-2.6352	-32.2996	O.co2	1 <1>	0.0000
17 C	19.3528	0.9188	-35.2432	C.2	1 <1>	0.0000
18 O	18.1596	-1.2316	-32.8622	O.co2	1 <1>	0.0000
19 C	22.6017	-0.8946	-34.5062	C.2	1 <1>	0.0000
20 O	19.5574	0.8999	-33.9963	O.co2	1 <1>	0.0000
21 O	22.0525	-0.4751	-33.4460	O.co2	1 <1>	0.0000
22 C	18.8632	2.1685	-35.8849	C.3	1 <1>	0.0000
23 C	24.0652	-0.6674	-34.6842	C.3	1 <1>	0.0000
24 H	18.1535	1.9777	-36.3961	H	1 <1>	0.0000
25 H	18.7718	2.7829	-35.3812	H	1 <1>	0.0000
26 H	19.4208	2.4723	-36.6165	H	1 <1>	0.0000
27 H	24.4888	-0.8131	-33.9115	H	1 <1>	0.0000
28 H	24.3896	-1.0728	-35.3797	H	1 <1>	0.0000
29 H	24.1431	0.1665	-34.7004	H	1 <1>	0.0000
30 C	12.3929	0.9091	-29.1585	C.3	1 <1>	0.0000

31 C	12.8522	-0.2540	-30.0481	C.3	1 <1>	0.0000
32 N	14.2883	-0.6671	-29.7433	N.4	1 <1>	0.0000
33 C	14.6845	-0.7063	-28.2668	C.3	1 <1>	0.0000
34 C	14.1348	0.4988	-27.4903	C.3	1 <1>	0.0000
35 N	12.6818	0.4293	-27.7816	N.pl3	1 <1>	0.0000
36 N	8.5108	-2.8071	-22.5940	N.pl3	1 <1>	0.0000
37 C	10.0800	-1.6183	-25.4048	C.ar	1 <1>	0.0000
38 C	10.0685	-1.7399	-26.7437	C.ar	1 <1>	0.0000
39 C	10.9110	-1.0426	-27.5241	C.ar	1 <1>	0.0000
40 C	11.8335	-0.1844	-27.0368	C.ar	1 <1>	0.0000
41 C	11.8025	-0.0650	-25.6893	C.ar	1 <1>	0.0000
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43 C	10.9812	-0.5769	-23.5499	C.ar	1 <1>	0.0000
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45 C	9.2933	-2.1513	-23.3487	C.ar	1 <1>	0.0000
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57 H	14.5745	1.4438	-27.8854 H	1 <1>	0.0000
58 H	8.5211	-2.6761	-21.5513 H	1 <1>	0.0000
59 H	7.8391	-3.5012	-23.0088 H	1 <1>	0.0000
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63 H	11.6750	0.1335	-23.0693 H	1 <1>	0.0000
64 H	10.1557	-1.1299	-21.6844 H	1 <1>	0.0000
65 H	8.6098	-2.9890	-25.0593 H	1 <1>	0.0000
66 H	13.9174	-2.7205	-30.4150 H	1 <1>	0.0000
67 H	15.6594	-2.5191	-30.0696 H	1 <1>	0.0000
68 H	14.0714	-1.3010	-32.6400 H	1 <1>	0.0000
69 H	15.5491	-0.5730	-32.0314 H	1 <1>	0.0000
70 ****	20.2615	-2.7911	-34.7287 LP	1 <1>	0.0000
71 ****	20.7366	-4.4535	-34.8319 LP	1 <1>	0.0000
72 ****	19.8524	-0.9548	-35.5846 LP	1 <1>	0.0000
73 ****	19.3597	-0.0339	-36.9663 LP	1 <1>	0.0000
74 ****	19.0640	-2.1133	-34.9828 LP	1 <1>	0.0000

75 ****	17.5396	-2.7277	-35.5294 LP	1 <1>	0.0000
76 ****	20.9965	-1.6677	-35.3293 LP	1 <1>	0.0000
77 ****	22.4643	-1.8077	-36.2381 LP	1 <1>	0.0000
78 ****	20.2849	-1.7751	-32.6986 LP	1 <1>	0.0000
79 ****	20.7777	-2.6960	-31.3169 LP	1 <1>	0.0000
80 ****	19.1409	-1.0622	-32.9539 LP	1 <1>	0.0000
81 ****	17.6730	-0.9222	-32.0451 LP	1 <1>	0.0000
82 ****	19.8759	0.0612	-33.5545 LP	1 <1>	0.0000
83 ****	19.4007	1.7236	-33.4513 LP	1 <1>	0.0000
84 ****	21.0733	-0.6166	-33.3004 LP	1 <1>	0.0000
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@<TRIPOS>BOND

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- 10 3 7 1

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81 13 75 1

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89 20 83 1

90 21 84 1

91 21 85 1

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4 53 58 59 65

ATOM\$BLUE STATIC ATOMS COLORGROUP SYSTEM

16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

ATOM\$RED STATIC ATOMS COLORGROUP SYSTEM

4 53 58 59 65

@<TRIPOS>COMMENT

> <Gold.Version>

5.7.2

> <Gold.Id.Protein>

unknown|gold_protein|mol2

> <Gold.Protein.RotatedTorsions>

[614 603 602 601] final 160.93 input 2.31 | X-H torsion

[841 836 835 832] final -90.20 input 27.02 | X-H torsion

[172 163 162 160] final -177.98 input 178.05 | X-H torsion

[876 867 866 864] final -48.41 input 173.38 | X-H torsion

> <Gold.Protein.ActiveResidues>

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PHE57 PRO59 SER60 ASN61 TYR62

> <Gold.Protein.RotatedAtoms>

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 13.3982 0.6239 -22.4834 H 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 614 bound_to 603
 14.1062 -0.8463 -22.9536 H 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 615 bound_to 603
 12.5208 -0.8207 -22.3446 H 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 616 bound_to 603
 17.4621 -14.2861 -29.2421 H 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 841 bound_to 836
 24.3450 -6.9493 -34.7956 H 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 876 bound_to 867
 16.3517 -14.1593 -28.0916 LP 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 987 bound_to 836
 17.9222 -13.8499 -27.7688 LP 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 988 bound_to 836
 21.4260 -0.2328 -30.3185 LP 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 998 bound_to 163
 20.3672 -1.0437 -29.3761 LP 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 999 bound_to 163
 25.2707 -5.7673 -34.2300 LP 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1000 bound_to 867
 23.6481 -5.5944 -34.2932 LP 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1001 bound_to 867

><Gold.Score>

Score	S(PLP)	S(hbond)	S(cho)	S(metal)	DE(clash)	DE(tors)	intcor
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61.1772

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-60.1569

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1.0759

> <Gold.PLP.Chemscore.Hbond>

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donor molecule, donor type, donor heavy atom, donor atom, acceptor molecule, acceptor atom, score

P1 H 163 172 L1 16 1.00

> <Gold.PLP.Chemscore.Internal.Correction>

0.1721

Name: *****

Creating user name zbl

Creation time: Thu Jun 13 10:31:13 2019

File generated by GOLD software.

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@<TRIPOS>MOLECULE

*****|pRh-6|mol2|1|dock5

85 91 1

SMALL

USER_CHARGES

@<TRIPOS>ATOM

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2 C	11.3959	-0.3707	-25.9378	C.2	1 <1>	0.0000
3 C	12.8065	-0.1080	-26.3306	C.3	1 <1>	0.0000
4 C	8.5655	-2.7807	-26.6913	C.2	1 <1>	0.0000
5 C	8.3038	-3.9384	-27.5948	C.3	1 <1>	0.0000
6 H	13.2883	0.0662	-25.5964	H	1 <1>	0.0000
7 H	12.8890	0.4141	-26.9306	H	1 <1>	0.0000
8 H	13.2969	-0.9080	-26.5712	H	1 <1>	0.0000
9 H	7.4377	-3.7004	-28.2672	H	1 <1>	0.0000
10 H	7.2876	-4.3612	-27.3773	H	1 <1>	0.0000
11 O	10.4620	0.2402	-26.5309	O.co2	1 <1>	0.0000
12 O	6.6746	-0.3207	-25.1856	O.co2	1 <1>	0.0000
13 O	8.3102	-1.6163	-27.1163	O.co2	1 <1>	0.0000

S140

14 O	8.8343	1.4959	-24.6450	O.co2	1 <1>	0.0000
15 Cr	9.3196	-1.5044	-24.2628	Cr.oh	1 <1>	0.0000
16 O	11.1869	-1.1993	-25.0007	O.co2	1 <1>	0.0000
17 C	6.4657	-1.1493	-24.2485	C.2	1 <1>	0.0000
18 O	9.0273	-3.0159	-25.5414	O.co2	1 <1>	0.0000
19 C	9.2961	1.2607	-23.4951	C.2	1 <1>	0.0000
20 O	7.3996	-1.7602	-23.6555	O.co2	1 <1>	0.0000
21 O	9.5513	0.0963	-23.0700	O.co2	1 <1>	0.0000
22 C	5.0550	-1.4120	-23.8558	C.3	1 <1>	0.0000
23 C	9.5577	2.4184	-22.5915	C.3	1 <1>	0.0000
24 H	4.5732	-1.5861	-24.5899	H	1 <1>	0.0000
25 H	4.9725	-1.9341	-23.2557	H	1 <1>	0.0000
26 H	4.5646	-0.6119	-23.6151	H	1 <1>	0.0000
27 H	10.3290	2.2942	-22.1586	H	1 <1>	0.0000
28 H	9.4605	3.1855	-22.9858	H	1 <1>	0.0000
29 H	9.0426	2.2934	-21.9430	H	1 <1>	0.0000
30 C	10.8736	-1.9884	-31.0483	C.3	1 <1>	0.0000
31 C	10.7546	-3.0307	-29.9283	C.3	1 <1>	0.0000
32 N	10.6187	-4.4449	-30.4829	N.4	1 <1>	0.0000
33 C	11.5029	-4.7919	-31.6813	C.3	1 <1>	0.0000
34 C	11.5558	-3.6514	-32.7080	C.3	1 <1>	0.0000
35 N	11.9933	-2.4995	-31.8818	N.pl3	1 <1>	0.0000

36 N	19.2436	-1.0241	-32.0767	N.pl3	1 <1>	0.0000
37 C	15.9217	-1.5347	-31.3838	C.ar	1 <1>	0.0000
38 C	15.0441	-1.4961	-30.3660	C.ar	1 <1>	0.0000
39 C	13.7448	-1.7897	-30.5413	C.ar	1 <1>	0.0000
40 C	13.2219	-2.1545	-31.7324	C.ar	1 <1>	0.0000
41 C	14.1243	-2.1588	-32.7406	C.ar	1 <1>	0.0000
42 C	15.4300	-1.8560	-32.5935	C.ar	1 <1>	0.0000
43 C	16.2752	-1.8799	-33.6406	C.ar	1 <1>	0.0000
44 C	17.5699	-1.5905	-33.4572	C.ar	1 <1>	0.0000
45 C	18.0110	-1.2904	-32.2238	C.ar	1 <1>	0.0000
46 N	17.1935	-1.2677	-31.2040	N.pl3	1 <1>	0.0000
47 C	10.7546	-5.5581	-29.4616	C.3	1 <1>	0.0000
48 C	9.4925	-5.1955	-28.1322	C.3	1 <1>	0.0000
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50 H	9.9273	-1.9524	-31.6359	H	1 <1>	0.0000
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52 H	11.6852	-2.9203	-29.3304	H	1 <1>	0.0000
53 H	9.6363	-4.5014	-30.8445	H	1 <1>	0.0000
54 H	11.1025	-5.7105	-32.1723	H	1 <1>	0.0000
55 H	12.5447	-4.9981	-31.3409	H	1 <1>	0.0000
56 H	12.1820	-3.8900	-33.5896	H	1 <1>	0.0000
57 H	10.5423	-3.4716	-33.1355	H	1 <1>	0.0000

58 H	19.9058	-1.0362	-32.8927 H	1 <1>	0.0000
59 H	19.6212	-0.7907	-31.1238 H	1 <1>	0.0000
60 H	15.3950	-1.2372	-29.3527 H	1 <1>	0.0000
61 H	13.1412	-1.7524	-29.6210 H	1 <1>	0.0000
62 H	13.8259	-2.4372	-33.7619 H	1 <1>	0.0000
63 H	15.9259	-2.1280	-34.6572 H	1 <1>	0.0000
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66 H	11.7329	-5.5102	-28.9244 H	1 <1>	0.0000
67 H	10.5848	-6.6373	-29.7028 H	1 <1>	0.0000
68 H	8.9976	-6.1617	-27.8736 H	1 <1>	0.0000
69 H	10.2123	-5.0388	-27.2845 H	1 <1>	0.0000
70 ****	9.5113	0.0783	-26.2661 LP	1 <1>	0.0000
71 ****	10.6736	0.8855	-27.2649 LP	1 <1>	0.0000
72 ****	7.6096	-0.1278	-25.4833 LP	1 <1>	0.0000
73 ****	5.9044	0.1399	-25.6268 LP	1 <1>	0.0000
74 ****	8.4741	-0.8229	-26.5300 LP	1 <1>	0.0000
75 ****	7.9447	-1.4895	-28.0384 LP	1 <1>	0.0000
76 ****	8.6509	0.7407	-25.2742 LP	1 <1>	0.0000
77 ****	8.6515	2.4376	-24.9274 LP	1 <1>	0.0000
78 ****	10.2519	-1.3922	-24.7030 LP	1 <1>	0.0000
79 ****	11.9571	-1.6598	-24.5595 LP	1 <1>	0.0000

80 ****	9.2107 -2.2607 -24.9121 LP	1 <1>	0.0000
81 ****	9.2101 -3.9576 -25.2590 LP	1 <1>	0.0000
82 ****	8.3502 -1.5983 -23.9202 LP	1 <1>	0.0000
83 ****	7.1880 -2.4054 -22.9214 LP	1 <1>	0.0000
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85 ****	9.9168 -0.0304 -22.1479 LP	1 <1>	0.0000

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@<TRIPOS>SUBSTRUCTURE

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@<TRIPOS>SET

LONE_PAIRS STATIC ATOMS <user> **** ""

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DONOR_HYDROGENS STATIC ATOMS <user> **** ""

4 53 58 59 65

ATOM\$BLUE STATIC ATOMS COLORGROUP SYSTEM

16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

ATOM\$RED STATIC ATOMS COLORGROUP SYSTEM

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@<TRIPOS>COMMENT

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5.7.2

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[841 836 835 832] final -72.43 input 27.02 | X-H torsion

[172 163 162 160] final -56.35 input 178.05 | X-H torsion

[876 867 866 864] final -1.15 input 173.38 | X-H torsion

><Gold.Protein.ActiveResidues>

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14.1562 -0.7528 -22.9600 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 614 bound_to 603

12.5700 -0.9121 -22.3748 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 615 bound_to 603

13.3010 0.6193 -22.4479 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 616 bound_to 603

17.7196 -14.2232 -29.1460 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 841 bound_to 836

23.7020 -6.6123 -34.6997 H 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 876 bound_to 867
16.3171 -14.2423 -28.3679 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 987 bound_to 836
17.6933 -13.8314 -27.5909 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 988 bound_to 836
20.9194 -1.7430 -30.7191 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 998 bound_to 163
21.4326 -0.2412 -30.3346 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 999 bound_to 163
25.2905 -6.4552 -34.5383 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1000 bound_to 867
24.2857 -5.2510 -34.0831 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1001 bound_to 867

><Gold.Score>

Score	S(PLP)	S(hbond)	S(cho)	S(metal)	DE(clash)	DE(tors)	intcor
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-56.6550

><Gold.PLP.part.hbond>

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0.0000

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donor molecule, donor type, donor heavy atom, donor atom, acceptor molecule, acceptor atom, score

L1 H 36 59 P1 261 1.82

L1 H 46 65 P1 261 1.89

><Gold.PLP.Chemscore.Internal.Correction>

0.1396

Name: *****

Creating user name zbl

Creation time: Thu Jun 13 10:31:14 2019

File generated by GOLD software.

#

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85 91 1

SMALL

USER_CHARGES

@<TRIPOS>ATOM

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2 C	6.1772 -9.8186 -30.1434 C.2	1 <1>	0.0000
3 C	5.4160 -9.1228 -29.0711 C.3	1 <1>	0.0000
4 C	9.4835 -9.5827 -31.9873 C.2	1 <1>	0.0000
5 C	10.6738 -8.6843 -32.0221 C.3	1 <1>	0.0000
6 H	5.0596 -9.7325 -28.5209 H	1 <1>	0.0000
7 H	4.9133 -8.5604 -29.3367 H	1 <1>	0.0000
8 H	5.9805 -8.7145 -28.3980 H	1 <1>	0.0000
9 H	11.5842 -9.2562 -31.7012 H	1 <1>	0.0000
10 H	11.0807 -8.5613 -30.9838 H	1 <1>	0.0000
11 O	5.9708 -9.5106 -31.3515 O.co2	1 <1>	0.0000
12 O	7.8746 -11.6708 -34.2111 O.co2	1 <1>	0.0000
13 O	8.5071 -9.3173 -32.7475 O.co2	1 <1>	0.0000
14 O	5.3733 -11.8160 -32.8045 O.co2	1 <1>	0.0000
15 Cr	7.9680 -11.8502 -31.1767 Cr.oh	1 <1>	0.0000
16 O	7.0044 -10.7149 -29.7957 O.co2	1 <1>	0.0000
17 C	8.7018 -12.5671 -33.8634 C.2	1 <1>	0.0000

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18 O	9.5057 -10.5697 -31.2023 O.co2	1 <1>	0.0000
19 C	5.3955 -12.8030 -32.0195 C.2	1 <1>	0.0000
20 O	8.9082 -12.8751 -32.6553 O.co2	1 <1>	0.0000
21 O	6.3719 -13.0684 -31.2593 O.co2	1 <1>	0.0000
22 C	9.4630 -13.2628 -34.9357 C.3	1 <1>	0.0000
23 C	4.2052 -13.7014 -31.9847 C.3	1 <1>	0.0000
24 H	9.8194 -12.6532 -35.4859 H	1 <1>	0.0000
25 H	9.9657 -13.8252 -34.6701 H	1 <1>	0.0000
26 H	8.8985 -13.6711 -35.6088 H	1 <1>	0.0000
27 H	4.0240 -13.9287 -31.1402 H	1 <1>	0.0000
28 H	3.5380 -13.3990 -32.4502 H	1 <1>	0.0000
29 H	4.4998 -14.4426 -32.2407 H	1 <1>	0.0000
30 C	12.1269 -3.1700 -30.7788 C.3	1 <1>	0.0000
31 C	12.3079 -4.5782 -31.3613 C.3	1 <1>	0.0000
32 N	11.8061 -4.6651 -32.7989 N.4	1 <1>	0.0000
33 C	12.1327 -3.4772 -33.7049 C.3	1 <1>	0.0000
34 C	11.9374 -2.1340 -32.9870 C.3	1 <1>	0.0000
35 N	12.7861 -2.2916 -31.7806 N.pl3	1 <1>	0.0000
36 N	19.9334 -0.5267 -32.5441 N.pl3	1 <1>	0.0000
37 C	16.7186 -1.2399 -31.5786 C.ar	1 <1>	0.0000
38 C	15.9535 -1.3512 -30.4786 C.ar	1 <1>	0.0000
39 C	14.6511 -1.6725 -30.5529 C.ar	1 <1>	0.0000

40 C	14.0142 -1.9190 -31.7186 C.ar	1 <1>	0.0000
41 C	14.8041 -1.7739 -32.8076 C.ar	1 <1>	0.0000
42 C	16.1096 -1.4399 -32.7608 C.ar	1 <1>	0.0000
43 C	16.8389 -1.3120 -33.8846 C.ar	1 <1>	0.0000
44 C	18.1378 -0.9959 -33.8023 C.ar	1 <1>	0.0000
45 C	18.6996 -0.8216 -32.5941 C.ar	1 <1>	0.0000
46 N	17.9949 -0.9466 -31.5002 N.pl3	1 <1>	0.0000
47 C	12.1764 -5.9359 -33.5395 C.3	1 <1>	0.0000
48 C	10.8998 -7.2094 -33.0495 C.3	1 <1>	0.0000
49 H	12.4961 -3.0752 -29.7375 H	1 <1>	0.0000
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71 ****	5.3085	-8.7968	-31.5794 LP	1 <1>	0.0000
72 ****	7.3534	-11.1749	-33.5165 LP	1 <1>	0.0000
73 ****	7.7435	-11.4600	-35.1798 LP	1 <1>	0.0000
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75 ****	8.5449	-8.5201	-33.3501 LP	1 <1>	0.0000
76 ****	6.1553	-11.1943	-32.8485 LP	1 <1>	0.0000
77 ****	4.5736	-11.6551	-33.3829 LP	1 <1>	0.0000
78 ****	7.5256	-11.2108	-30.4903 LP	1 <1>	0.0000
79 ****	7.1355	-10.9256	-28.8270 LP	1 <1>	0.0000
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81 ****	10.3054	-10.7306	-30.6239 LP	1 <1>	0.0000
82 ****	8.4092	-12.4050	-31.9272 LP	1 <1>	0.0000
83 ****	9.5705	-13.5888	-32.4274 LP	1 <1>	0.0000

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85 ****	6.3341 -13.8656 -30.6568 LP	1 <1>	0.0000

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DONOR_HYDROGENS STATIC ATOMS <user> **** ""

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ATOM\$BLUE STATIC ATOMS COLORGROUP SYSTEM

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ATOM\$RED STATIC ATOMS COLORGROUP SYSTEM

4 53 58 59 65

@<TRIPOS>COMMENT

> <Gold.Version>

5.7.2

> <Gold.Id.Protein>

unknown|gold_protein|mol2

><Gold.Protein.RotatedTorsions>

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[841 836 835 832] final 76.35 input 27.02 | X-H torsion

[172 163 162 160] final -81.97 input 178.05 | X-H torsion

[876 867 866 864] final -124.18 input 173.38 | X-H torsion

><Gold.Protein.ActiveResidues>

TYR19 ILE22 HIS23 ASP25 ASP26 HIS41 GLY42 GLU43 TRP44 LYS46

PHE57 PRO59 SER60 ASN61 TYR62

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20.3513 -1.3938 -29.5355 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 172 bound_to 163

12.8300 0.4311 -22.2921 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 614 bound_to 603

14.2566 -0.2351 -22.9284 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 615 bound_to 603

12.9375 -1.2399 -22.5608 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 616 bound_to 603

17.2348 -13.8258 -27.5033 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 841 bound_to 836

25.2801 -6.4188 -34.4753 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 876 bound_to 867

18.0626 -14.1340 -28.8421 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 987 bound_to 836

16.4440 -14.3463 -28.7981 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 988 bound_to 836

21.1826 -1.4782 -30.9054 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 998 bound_to 163

21.2442 -0.1359 -29.9775 LP 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 999 bound_to 163

24.2442 -5.2561 -34.0890 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1000 bound_to 867

23.7182 -6.6480 -34.7618 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1001 bound_to 867

><Gold.Score>

Score	S(PLP)	S(hbond)	S(cho)	S(metal)	DE(clash)	DE(tors)	intcor
59.03	-49.16	3.95	0.00	0.00	0.00	1.06	0.14

><Gold.PLP.Fitness>

59.0256

><Gold.PLP.PLP>

-49.1628

><Gold.PLP.part.hbond>

-3.0000

><Gold.PLP.part.metal>

0.0000

><Gold.PLP.part.buried>

-7.5353

> <Gold.PLP.part.nonpolar>

-41.4689

> <Gold.PLP.part.repulsive>

0.8701

> <Gold.PLP.ligand.clash>

0.0000

> <Gold.PLP.ligand.torsion>

1.0634

> <Gold.PLP.Chemscore.Hbond>

3.9500

> <Gold.PLP.Chemscore.CHOScore>

0.0000

> <Gold.PLP.Chemscore.Metal>

0.0000

><Gold.Chemscore.Hbonds>

donor molecule, donor type, donor heavy atom, donor atom, acceptor molecule, acceptor atom, score

L1 H 36 59 P1 163 0.95

L1 H 46 65 P1 261 2.00

P1 H 532 541 L1 18 1.00

><Gold.PLP.Chemscore.Internal.Correction>

0.1396

Name: *****

Creating user name zb1

Creation time: Thu Jun 13 10:31:15 2019

File generated by GOLD software.

#

@<TRIPOS>MOLECULE

*****|pRh-6|mol2|1|dock7

85 91 1

SMALL

USER_CHARGES

@<TRIPOS>ATOM

1 Cr	17.9568	-8.5540	-35.1891	Cr.oh	1 <1>	0.0000
2 C	19.5194	-6.2523	-34.4602	C.2	1 <1>	0.0000
3 C	20.4598	-5.4382	-33.6440	C.3	1 <1>	0.0000
4 C	15.7976	-6.6679	-35.0623	C.2	1 <1>	0.0000
5 C	14.5186	-6.1054	-34.5397	C.3	1 <1>	0.0000
6 H	21.1412	-5.1715	-34.1597	H	1 <1>	0.0000
7 H	20.6635	-5.7720	-32.9464	H	1 <1>	0.0000
8 H	20.1357	-4.5449	-33.4557	H	1 <1>	0.0000
9 H	14.6007	-5.9559	-33.4307	H	1 <1>	0.0000
10 H	14.0468	-6.8397	-33.8347	H	1 <1>	0.0000
11 O	19.1413	-7.3796	-34.0322	O.co2	1 <1>	0.0000
12 O	16.8172	-9.6493	-36.4643	O.co2	1 <1>	0.0000
13 O	16.2907	-7.6795	-34.4834	O.co2	1 <1>	0.0000
14 O	19.6296	-9.3186	-35.9776	O.co2	1 <1>	0.0000
15 Cr	18.0015	-6.8748	-36.8498	Cr.oh	1 <1>	0.0000
16 O	19.1411	-5.7796	-35.5746	O.co2	1 <1>	0.0000
17 C	16.4389	-9.1766	-37.5787	C.2	1 <1>	0.0000
18 O	16.3286	-6.1103	-36.0612	O.co2	1 <1>	0.0000
19 C	20.1607	-8.7609	-36.9766	C.2	1 <1>	0.0000
20 O	16.8170	-8.0492	-38.0067	O.co2	1 <1>	0.0000

21 O	19.6675 -7.7494 -37.5555 O.co2	1 <1>	0.0000
22 C	15.4985 -9.9907 -38.3949 C.3	1 <1>	0.0000
23 C	21.4396 -9.3234 -37.4992 C.3	1 <1>	0.0000
24 H	14.8170 -10.2574 -37.8792 H	1 <1>	0.0000
25 H	15.2947 -9.6569 -39.0924 H	1 <1>	0.0000
26 H	15.8226 -10.8840 -38.5832 H	1 <1>	0.0000
27 H	21.9944 -8.6583 -37.7171 H	1 <1>	0.0000
28 H	21.7698 -9.9450 -36.9911 H	1 <1>	0.0000
29 H	21.2518 -9.5733 -38.2763 H	1 <1>	0.0000
30 C	11.9055 -4.2658 -31.5352 C.3	1 <1>	0.0000
31 C	12.0473 -4.9124 -32.9198 C.3	1 <1>	0.0000
32 N	11.2370 -4.1699 -33.9771 N.4	1 <1>	0.0000
33 C	11.2626 -2.6427 -33.9034 C.3	1 <1>	0.0000
34 C	11.1426 -2.1332 -32.4600 C.3	1 <1>	0.0000
35 N	12.2541 -2.8415 -31.7790 N.pl3	1 <1>	0.0000
36 N	19.2090 -0.3332 -32.1247 N.pl3	1 <1>	0.0000
37 C	16.0474 -1.4156 -31.3445 C.ar	1 <1>	0.0000
38 C	15.2539 -1.6630 -30.2877 C.ar	1 <1>	0.0000
39 C	13.9952 -2.1080 -30.4377 C.ar	1 <1>	0.0000
40 C	13.4342 -2.3523 -31.6422 C.ar	1 <1>	0.0000
41 C	14.2485 -2.0693 -32.6852 C.ar	1 <1>	0.0000
42 C	15.5101 -1.6099 -32.5619 C.ar	1 <1>	0.0000

43 C	16.2673	-1.3481	-33.6434	C.ar	1 <1>	0.0000
44 C	17.5228	-0.9091	-33.4859	C.ar	1 <1>	0.0000
45 C	18.0147	-0.7465	-32.2459	C.ar	1 <1>	0.0000
46 N	17.2829	-1.0012	-31.1931	N.pl3	1 <1>	0.0000
47 C	11.5166	-4.5753	-35.4117	C.3	1 <1>	0.0000
48 C	13.3028	-5.1223	-35.4546	C.3	1 <1>	0.0000
49 H	12.4958	-4.7788	-30.7490	H	1 <1>	0.0000
50 H	10.8543	-4.3604	-31.1776	H	1 <1>	0.0000
51 H	11.7103	-5.9742	-32.8718	H	1 <1>	0.0000
52 H	13.1350	-4.8752	-33.1464	H	1 <1>	0.0000
53 H	10.2399	-4.4344	-33.7901	H	1 <1>	0.0000
54 H	10.4170	-2.2371	-34.5082	H	1 <1>	0.0000
55 H	12.2186	-2.2554	-34.3275	H	1 <1>	0.0000
56 H	11.1467	-1.0281	-32.3882	H	1 <1>	0.0000
57 H	10.1587	-2.4296	-32.0281	H	1 <1>	0.0000
58 H	19.8017	-0.1223	-32.9665	H	1 <1>	0.0000
59 H	19.6252	-0.2008	-31.1685	H	1 <1>	0.0000
60 H	15.6451	-1.5190	-29.2664	H	1 <1>	0.0000
61 H	13.4651	-2.3024	-29.4922	H	1 <1>	0.0000
62 H	13.9111	-2.2236	-33.7206	H	1 <1>	0.0000
63 H	15.8761	-1.4809	-34.6663	H	1 <1>	0.0000
64 H	18.1354	-0.6847	-34.3763	H	1 <1>	0.0000

65 H	17.6809 -0.8667 -30.2536 H	1 <1>	0.0000
66 H	11.4868 -3.6984 -36.1032 H	1 <1>	0.0000
67 H	10.9723 -5.4016 -35.9339 H	1 <1>	0.0000
68 H	13.5718 -5.2895 -36.5247 H	1 <1>	0.0000
69 H	13.7675 -4.1262 -35.2239 H	1 <1>	0.0000
70 ****	18.5180 -7.9387 -34.5790 LP	1 <1>	0.0000
71 ****	19.4654 -7.7127 -33.1467 LP	1 <1>	0.0000
72 ****	17.4404 -9.1247 -35.8843 LP	1 <1>	0.0000
73 ****	16.4922 -10.5466 -36.1655 LP	1 <1>	0.0000
74 ****	17.1459 -8.0779 -34.8150 LP	1 <1>	0.0000
75 ****	15.8253 -8.0804 -33.6943 LP	1 <1>	0.0000
76 ****	18.7734 -8.9630 -35.6030 LP	1 <1>	0.0000
77 ****	20.0649 -10.1164 -35.5603 LP	1 <1>	0.0000
78 ****	18.5178 -6.3042 -36.1545 LP	1 <1>	0.0000
79 ****	19.4661 -4.8823 -35.8733 LP	1 <1>	0.0000
80 ****	17.1849 -6.4659 -36.4359 LP	1 <1>	0.0000
81 ****	15.8934 -5.3125 -36.4786 LP	1 <1>	0.0000
82 ****	17.4402 -7.4902 -37.4599 LP	1 <1>	0.0000
83 ****	16.4929 -7.7162 -38.8922 LP	1 <1>	0.0000
84 ****	18.8123 -7.3510 -37.2239 LP	1 <1>	0.0000
85 ****	20.1330 -7.3485 -38.3445 LP	1 <1>	0.0000

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- 2 1 12 ar
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- 4 1 14 ar
- 5 1 15 1
- 6 2 3 1
- 7 2 11 ar
- 8 2 16 ar
- 9 3 6 1
- 10 3 7 1
- 11 3 8 1
- 12 4 5 1
- 13 4 13 ar
- 14 4 18 ar
- 15 5 9 1
- 16 5 10 1
- 17 5 48 1
- 18 12 17 ar
- 19 14 19 ar
- 20 15 16 ar
- 21 15 18 ar
- 22 15 20 ar

23 15 21 ar

24 17 20 ar

25 17 22 1

26 19 21 ar

27 19 23 1

28 22 24 1

29 22 25 1

30 22 26 1

31 23 27 1

32 23 28 1

33 23 29 1

34 30 31 1

35 30 35 1

36 30 49 1

37 30 50 1

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40 31 52 1

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69 45 46 ar

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77 11 71 1

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79 12 73 1

80 13 74 1

81 13 75 1

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DONOR_HYDROGENS STATIC ATOMS <user> **** ""

4 53 58 59 65

ATOM\$BLUE STATIC ATOMS COLORGROUP SYSTEM

16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

ATOM\$RED STATIC ATOMS COLORGROUP SYSTEM

4 53 58 59 65

@<TRIPOS>COMMENT

> <Gold.Version>

5.7.2

> <Gold.Id.Protein>

unknown|gold_protein|mol2

> <Gold.Protein.RotatedTorsions>

[614 603 602 601] final 14.03 input 2.31 | X-H torsion
[841 836 835 832] final 176.02 input 27.02 | X-H torsion
[172 163 162 160] final -114.09 input 178.05 | X-H torsion
[876 867 866 864] final -21.97 input 173.38 | X-H torsion

><Gold.Protein.ActiveResidues>

TYR19 ILE22 HIS23 ASP25 ASP26 HIS41 GLY42 GLU43 TRP44 LYS46
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20.4236 -1.7353 -29.9010 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 172 bound_to 163
12.7953 -1.1558 -22.4939 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 614 bound_to 603
12.9783 0.5251 -22.3362 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 615 bound_to 603
14.2511 -0.4162 -22.9517 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 616 bound_to 603
16.3529 -14.2317 -28.5052 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 841 bound_to 836
23.9486 -6.8197 -34.7717 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 876 bound_to 867
17.5612 -13.8322 -27.5289 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 987 bound_to 836
17.8481 -14.2328 -29.0858 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 988 bound_to 836
21.4316 -1.0218 -30.9255 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 998 bound_to 163
20.9213 -0.2431 -29.5838 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 999 bound_to 163
25.3593 -6.1538 -34.3965 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1000 bound_to 867
23.9648 -5.3403 -34.1512 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1001 bound_to 867

> <Gold.Score>

Score	S(PLP)	S(hbond)	S(cho)	S(metal)	DE(clash)	DE(tors)	intcor
55.70	-47.76	4.12	0.00	0.00	0.00	2.28	0.14

> <Gold.PLP.Fitness>

55.7000

> <Gold.PLP.PLP>

-47.7624

> <Gold.PLP.part.hbond>

-4.0000

> <Gold.PLP.part.metal>

0.0000

> <Gold.PLP.part.buried>

-2.3435

> <Gold.PLP.part.nonpolar>

-42.1360

> <Gold.PLP.part.repulsive>

0.1127

> <Gold.PLP.ligand.clash>

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> <Gold.PLP.ligand.torsion>

2.2799

> <Gold.PLP.Chemscore.Hbond>

4.1193

> <Gold.PLP.Chemscore.CHOScore>

0.0000

> <Gold.PLP.Chemscore.Metal>

0.0000

> <Gold.Chemscore.Hbonds>

donor molecule, donor type, donor heavy atom, donor atom, acceptor molecule, acceptor atom, score

L1 H 36 59 P1 261 1.66

L1 H 46 65 P1 261 1.98

P1 H 557 566 L1 13 0.47

><Gold.PLP.Chemscore.Internal.Correction>

0.1396

Name: *****

Creating user name zbl

Creation time: Thu Jun 13 10:31:17 2019

File generated by GOLD software.

#

@<TRIPOS>MOLECULE

*****|pRh-6|mol2|1|dock8

85 91 1

SMALL

USER_CHARGES

@<TRIPOS>ATOM

1 Cr 20.9625 -0.7128 -33.5525 Cr.oh 1 <1> 0.0000

S178

2 C	19.7011	0.9419	-35.5379	C.2	1 <1>	0.0000
3 C	19.4130	2.1854	-36.3021	C.3	1 <1>	0.0000
4 C	18.2493	-1.1478	-32.7250	C.2	1 <1>	0.0000
5 C	17.0946	-1.0919	-31.7822	C.3	1 <1>	0.0000
6 H	19.5526	2.0338	-37.1733	H	1 <1>	0.0000
7 H	19.7600	2.8418	-36.0050	H	1 <1>	0.0000
8 H	18.4671	2.3726	-36.3948	H	1 <1>	0.0000
9 H	17.1016	-0.1100	-31.2393	H	1 <1>	0.0000
10 H	17.4742	-1.0325	-30.7281	H	1 <1>	0.0000
11 O	20.4627	0.9942	-34.5308	O.co2	1 <1>	0.0000
12 O	21.4235	-2.4959	-32.6965	O.co2	1 <1>	0.0000
13 O	19.3341	-0.5943	-32.3809	O.co2	1 <1>	0.0000
14 O	22.5043	-0.8854	-34.8165	O.co2	1 <1>	0.0000
15 Cr	19.6340	-1.9207	-35.0872	Cr.oh	1 <1>	0.0000
16 O	19.1730	-0.1376	-35.9432	O.co2	1 <1>	0.0000
17 C	20.8954	-3.5754	-33.1018	C.2	1 <1>	0.0000
18 O	18.0922	-1.7481	-33.8231	O.co2	1 <1>	0.0000
19 C	22.3473	-1.4857	-35.9147	C.2	1 <1>	0.0000
20 O	20.1339	-3.6277	-34.1089	O.co2	1 <1>	0.0000
21 O	21.2625	-2.0392	-36.2588	O.co2	1 <1>	0.0000
22 C	21.1835	-4.8188	-32.3376	C.3	1 <1>	0.0000
23 C	23.5019	-1.5416	-36.8575	C.3	1 <1>	0.0000

24 H	21.0439	-4.6673	-31.4664 H	1 <1>	0.0000
25 H	20.8366	-5.4752	-32.6347 H	1 <1>	0.0000
26 H	22.1295	-5.0060	-32.2449 H	1 <1>	0.0000
27 H	23.2152	-1.4095	-37.6929 H	1 <1>	0.0000
28 H	24.1725	-1.0531	-36.6023 H	1 <1>	0.0000
29 H	23.6731	-2.3588	-36.9244 H	1 <1>	0.0000
30 C	11.2051	-0.1303	-29.6900 C.3	1 <1>	0.0000
31 C	11.8120	-1.3844	-30.3334 C.3	1 <1>	0.0000
32 N	13.3176	-1.2460	-30.5335 N.4	1 <1>	0.0000
33 C	14.0962	-0.5881	-29.3936 C.3	1 <1>	0.0000
34 C	13.3617	0.6340	-28.8239 C.3	1 <1>	0.0000
35 N	12.0342	0.0724	-28.4730 N.pl3	1 <1>	0.0000
36 N	9.2825	-2.8512	-22.2551 N.pl3	1 <1>	0.0000
37 C	11.0284	-1.3004	-24.7697 C.ar	1 <1>	0.0000
38 C	12.1275	-0.5549	-24.9788 C.ar	1 <1>	0.0000
39 C	12.4686	-0.1271	-26.2058 C.ar	1 <1>	0.0000
40 C	11.7414	-0.3948	-27.3125 C.ar	1 <1>	0.0000
41 C	10.6569	-1.1677	-27.0730 C.ar	1 <1>	0.0000
42 C	10.3001	-1.6203	-25.8540 C.ar	1 <1>	0.0000
43 C	9.2067	-2.3868	-25.6856 C.ar	1 <1>	0.0000
44 C	8.8705	-2.8057	-24.4587 C.ar	1 <1>	0.0000
45 C	9.6257	-2.4441	-23.4076 C.ar	1 <1>	0.0000

46 N	10.6875	-1.6984	-23.5670	N.p13	1 <1>	0.0000
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48 C	15.5272	-1.9900	-31.9198	C.3	1 <1>	0.0000
49 H	10.1120	-0.2094	-29.5209	H	1 <1>	0.0000
50 H	11.3012	0.7368	-30.3833	H	1 <1>	0.0000
51 H	11.3227	-1.5728	-31.3174	H	1 <1>	0.0000
52 H	11.5735	-2.2135	-29.6324	H	1 <1>	0.0000
53 H	13.4244	-0.5939	-31.3474	H	1 <1>	0.0000
54 H	15.0964	-0.2718	-29.7741	H	1 <1>	0.0000
55 H	14.2479	-1.3172	-28.5634	H	1 <1>	0.0000
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57 H	13.2654	1.4233	-29.6050	H	1 <1>	0.0000
58 H	8.4326	-3.4545	-22.1200	H	1 <1>	0.0000
59 H	9.8491	-2.5814	-21.4117	H	1 <1>	0.0000
60 H	12.7608	-0.2650	-24.1233	H	1 <1>	0.0000
61 H	13.3719	0.5021	-26.2341	H	1 <1>	0.0000
62 H	9.9814	-1.4586	-27.8907	H	1 <1>	0.0000
63 H	8.5768	-2.6874	-26.5399	H	1 <1>	0.0000
64 H	7.9794	-3.4439	-24.3278	H	1 <1>	0.0000
65 H	11.2516	-1.4364	-22.7470	H	1 <1>	0.0000
66 H	13.4417	-3.1369	-31.6354	H	1 <1>	0.0000
67 H	14.4646	-3.2387	-30.1733	H	1 <1>	0.0000

68 H	15.7493	-2.8094	-32.6441 H	1 <1>	0.0000
69 H	15.0112	-1.2187	-32.5523 H	1 <1>	0.0000
70 ****	20.6709	0.1616	-34.0175 LP	1 <1>	0.0000
71 ****	20.8571	1.8682	-34.2470 LP	1 <1>	0.0000
72 ****	21.2431	-1.6389	-33.1793 LP	1 <1>	0.0000
73 ****	22.0203	-2.5016	-31.8941 LP	1 <1>	0.0000
74 ****	20.1243	-0.6192	-32.9931 LP	1 <1>	0.0000
75 ****	19.4010	-0.1320	-31.4967 LP	1 <1>	0.0000
76 ****	21.7479	-0.8291	-34.1649 LP	1 <1>	0.0000
77 ****	23.3852	-0.4659	-34.5975 LP	1 <1>	0.0000
78 ****	19.3535	-0.9946	-35.4604 LP	1 <1>	0.0000
79 ****	18.5762	-0.1319	-36.7456 LP	1 <1>	0.0000
80 ****	18.8487	-1.8044	-34.4748 LP	1 <1>	0.0000
81 ****	17.2113	-2.1676	-34.0422 LP	1 <1>	0.0000
82 ****	19.9257	-2.7951	-34.6222 LP	1 <1>	0.0000
83 ****	19.7394	-4.5017	-34.3927 LP	1 <1>	0.0000
84 ****	20.4722	-2.0143	-35.6466 LP	1 <1>	0.0000
85 ****	21.1955	-2.5015	-37.1430 LP	1 <1>	0.0000

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2 1 12 ar

3 1 13 ar

4 1 14 ar
5 1 15 1
6 2 3 1
7 2 11 ar
8 2 16 ar
9 3 6 1
10 3 7 1
11 3 8 1
12 4 5 1
13 4 13 ar
14 4 18 ar
15 5 9 1
16 5 10 1
17 5 48 1
18 12 17 ar
19 14 19 ar
20 15 16 ar
21 15 18 ar
22 15 20 ar
23 15 21 ar
24 17 20 ar
25 17 22 1

26 19 21 ar

27 19 23 1

28 22 24 1

29 22 25 1

30 22 26 1

31 23 27 1

32 23 28 1

33 23 29 1

34 30 31 1

35 30 35 1

36 30 49 1

37 30 50 1

38 31 32 1

39 31 51 1

40 31 52 1

41 32 33 1

42 32 47 1

43 32 53 1

44 33 34 1

45 33 54 1

46 33 55 1

47 34 35 1

48 34 56 1
49 34 57 1
50 35 40 1
51 36 45 1
52 36 58 1
53 36 59 1
54 37 38 ar
55 37 42 ar
56 37 46 ar
57 38 39 ar
58 38 60 1
59 39 40 ar
60 39 61 1
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62 41 42 ar
63 41 62 1
64 42 43 ar
65 43 44 ar
66 43 63 1
67 44 45 ar
68 44 64 1
69 45 46 ar

70 46 65 1

71 47 48 1

72 47 66 1

73 47 67 1

74 48 68 1

75 48 69 1

76 11 70 1

77 11 71 1

78 12 72 1

79 12 73 1

80 13 74 1

81 13 75 1

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88 20 82 1

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91 21 85 1

@<TRIPOS>SUBSTRUCTURE

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@<TRIPOS>SET

LONE_PAIRS STATIC ATOMS <user> **** ""

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DONOR_HYDROGENS STATIC ATOMS <user> **** ""

4 53 58 59 65

ATOM\$BLUE STATIC ATOMS COLORGROUP SYSTEM

16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

ATOM\$RED STATIC ATOMS COLORGROUP SYSTEM

4 53 58 59 65

@<TRIPOS>COMMENT

><Gold.Version>

5.7.2

><Gold.Id.Protein>

unknown|gold_protein|mol2

><Gold.Protein.RotatedTorsions>

[614 603 602 601] final -161.52 input 2.31 | X-H torsion

[841 836 835 832] final 119.87 input 27.02 | X-H torsion

[172 163 162 160] final 161.69 input 178.05 | X-H torsion

S187

[876 867 866 864] final -98.25 input 173.38 | X-H torsion

><Gold.Protein.ActiveResidues>

TYR19 ILE22 HIS23 ASP25 ASP26 HIS41 GLY42 GLU43 TRP44 LYS46

PHE57 PRO59 SER60 ASN61 TYR62

><Gold.Protein.RotatedAtoms>

21.1751 -1.5224 -30.8451 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 172 bound_to 163
13.9441 0.4144 -22.7206 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 614 bound_to 603
13.6390 -1.2526 -22.8299 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 615 bound_to 603
12.4432 -0.2053 -22.2315 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 616 bound_to 603
16.6141 -13.9756 -27.7279 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 841 bound_to 836
25.0647 -6.7294 -34.6340 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 876 bound_to 867
18.1525 -13.9343 -28.1799 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 987 bound_to 836
16.9894 -14.3929 -29.2304 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 988 bound_to 836
21.2801 -0.1415 -30.0346 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 998 bound_to 163
20.3045 -1.3411 -29.5094 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 999 bound_to 163
24.6648 -5.2836 -34.0648 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1000 bound_to 867
23.5180 -6.3030 -34.6237 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1001 bound_to 867

><Gold.Score>

Score	S(PLP)	S(hbond)	S(cho)	S(metal)	DE(clash)	DE(tors)	intcor
-------	--------	----------	--------	----------	-----------	----------	--------

S188

64.65 -62.48 0.99 0.00 0.00 0.00 0.47 0.13

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64.6503

><Gold.PLP.PLP>

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><Gold.PLP.part.hbond>

-3.0000

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> <Gold.PLP.ligand.clash>

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> <Gold.PLP.ligand.torsion>

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> <Gold.PLP.Chemscore.Hbond>

0.9913

> <Gold.PLP.Chemscore.CHOScore>

0.0000

> <Gold.PLP.Chemscore.Metal>

0.0000

> <Gold.Chemscore.Hbonds>

donor molecule, donor type, donor heavy atom, donor atom, acceptor molecule, acceptor atom, score

P1 H 163 172 L1 12 0.99

> <Gold.PLP.Chemscore.Internal.Correction>

0.1263

Name: *****
Creating user name zbl
Creation time: Thu Jun 13 10:31:21 2019

File generated by GOLD software.

#

@<TRIPOS>MOLECULE

*****|pRh-6|mol2|1|dock9

85 91 1

SMALL

USER_CHARGES

@<TRIPOS>ATOM

1 Cr	19.6967	-2.1118	-35.1775	Cr.oh	1 <1>	0.0000
2 C	20.5016	-3.6612	-32.8922	C.2	1 <1>	0.0000
3 C	21.1993	-4.7452	-32.1496	C.3	1 <1>	0.0000
4 C	17.0685	-2.8186	-34.2673	C.2	1 <1>	0.0000
5 C	15.7256	-3.4599	-34.3704	C.3	1 <1>	0.0000
6 H	21.7148	-4.3814	-31.5145	H	1 <1>	0.0000

S191

7 H	21.5564	-5.2869	-32.6171 H	1 <1>	0.0000
8 H	20.6250	-5.2248	-31.5343 H	1 <1>	0.0000
9 H	15.8225	-4.4505	-34.8884 H	1 <1>	0.0000
10 H	15.4413	-3.5621	-35.4510 H	1 <1>	0.0000
11 O	20.5389	-3.6501	-34.1554 O.co2	1 <1>	0.0000
12 O	18.8618	-0.4923	-36.0746 O.co2	1 <1>	0.0000
13 O	17.9044	-3.0206	-35.1957 O.co2	1 <1>	0.0000
14 O	21.4535	-1.1645	-35.0318 O.co2	1 <1>	0.0000
15 Cr	19.0656	-1.1530	-33.1130 Cr.oh	1 <1>	0.0000
16 O	19.9006	-2.7725	-32.2160 O.co2	1 <1>	0.0000
17 C	18.2607	0.3965	-35.3983 C.2	1 <1>	0.0000
18 O	17.3089	-2.1002	-33.2588 O.co2	1 <1>	0.0000
19 C	21.6939	-0.4462	-34.0233 C.2	1 <1>	0.0000
20 O	18.2234	0.3854	-34.1351 O.co2	1 <1>	0.0000
21 O	20.8579	-0.2442	-33.0949 O.co2	1 <1>	0.0000
22 C	17.5630	1.4804	-36.1409 C.3	1 <1>	0.0000
23 C	23.0367	0.1952	-33.9201 C.3	1 <1>	0.0000
24 H	17.0476	1.1167	-36.7761 H	1 <1>	0.0000
25 H	17.2060	2.0222	-35.6735 H	1 <1>	0.0000
26 H	18.1373	1.9600	-36.7562 H	1 <1>	0.0000
27 H	23.3308	0.1445	-33.0784 H	1 <1>	0.0000
28 H	23.5887	-0.0724	-34.5342 H	1 <1>	0.0000

29 H	22.8736	1.0166	-33.9337 H	1 <1>	0.0000
30 C	12.4191	0.1724	-30.1749 C.3	1 <1>	0.0000
31 C	12.3753	-1.1744	-30.9092 C.3	1 <1>	0.0000
32 N	13.7592	-1.8062	-31.0167 N.4	1 <1>	0.0000
33 C	14.6499	-1.7044	-29.7778 C.3	1 <1>	0.0000
34 C	14.5750	-0.3160	-29.1265 C.3	1 <1>	0.0000
35 N	13.1182	-0.1476	-28.9027 N.pl3	1 <1>	0.0000
36 N	8.7580	-2.2748	-23.3129 N.pl3	1 <1>	0.0000
37 C	11.1523	-1.0629	-25.4518 C.ar	1 <1>	0.0000
38 C	12.3053	-0.3714	-25.4529 C.ar	1 <1>	0.0000
39 C	12.9628	-0.0952	-26.5914 C.ar	1 <1>	0.0000
40 C	12.5219	-0.4717	-27.8117 C.ar	1 <1>	0.0000
41 C	11.3740	-1.1872	-27.7748 C.ar	1 <1>	0.0000
42 C	10.7021	-1.4887	-26.6453 C.ar	1 <1>	0.0000
43 C	9.5637	-2.2058	-26.6797 C.ar	1 <1>	0.0000
44 C	8.9114	-2.4733	-25.5410 C.ar	1 <1>	0.0000
45 C	9.3980	-2.0106	-24.3770 C.ar	1 <1>	0.0000
46 N	10.5025	-1.3123	-24.3397 N.pl3	1 <1>	0.0000
47 C	13.7799	-3.2462	-31.4925 C.3	1 <1>	0.0000
48 C	14.2995	-3.1895	-33.2865 C.3	1 <1>	0.0000
49 H	11.4228	0.6480	-30.0710 H	1 <1>	0.0000
50 H	13.0018	0.9116	-30.7715 H	1 <1>	0.0000

51 H	11.9536	-1.0285	-31.9311 H	1 <1>	0.0000
52 H	11.6884	-1.8093	-30.3084 H	1 <1>	0.0000
53 H	14.2549	-1.2499	-31.7542 H	1 <1>	0.0000
54 H	15.7051	-1.9160	-30.0725 H	1 <1>	0.0000
55 H	14.3365	-2.4588	-29.0186 H	1 <1>	0.0000
56 H	15.2238	-0.2198	-28.2342 H	1 <1>	0.0000
57 H	14.9615	0.4592	-29.8280 H	1 <1>	0.0000
58 H	7.8717	-2.8392	-23.3347 H	1 <1>	0.0000
59 H	9.1094	-1.9228	-22.3867 H	1 <1>	0.0000
60 H	12.7191	0.0004	-24.5003 H	1 <1>	0.0000
61 H	13.8754	0.5060	-26.4560 H	1 <1>	0.0000
62 H	10.9099	-1.5548	-28.7016 H	1 <1>	0.0000
63 H	9.1522	-2.5882	-27.6292 H	1 <1>	0.0000
64 H	7.9845	-3.0719	-25.5738 H	1 <1>	0.0000
65 H	10.8569	-0.9708	-23.4359 H	1 <1>	0.0000
66 H	12.7538	-3.6871	-31.5231 H	1 <1>	0.0000
67 H	14.4422	-4.0307	-31.0480 H	1 <1>	0.0000
68 H	13.4302	-3.5374	-33.8937 H	1 <1>	0.0000
69 H	14.2728	-2.0739	-33.4124 H	1 <1>	0.0000
70 ****	20.0822	-2.9194	-34.6627 LP	1 <1>	0.0000
71 ****	21.0252	-4.3722	-34.6476 LP	1 <1>	0.0000
72 ****	19.3322	-1.2419	-35.6090 LP	1 <1>	0.0000

73	****	18.8652	-0.4434	-37.0734 LP	1 <1>	0.0000
74	****	18.8109	-2.6005	-35.1525 LP	1 <1>	0.0000
75	****	17.6585	-3.6003	-35.9725 LP	1 <1>	0.0000
76	****	20.5632	-1.6097	-35.1278 LP	1 <1>	0.0000
77	****	22.1532	-1.2888	-35.7353 LP	1 <1>	0.0000
78	****	19.4301	-2.0228	-32.6816 LP	1 <1>	0.0000
79	****	19.8971	-2.8213	-31.2172 LP	1 <1>	0.0000
80	****	18.1991	-1.6551	-33.1627 LP	1 <1>	0.0000
81	****	16.6092	-1.9759	-32.5552 LP	1 <1>	0.0000
82	****	18.6801	-0.3454	-33.6278 LP	1 <1>	0.0000
83	****	17.7372	1.1074	-33.6429 LP	1 <1>	0.0000
84	****	19.9514	-0.6642	-33.1381 LP	1 <1>	0.0000
85	****	21.1038	0.3355	-32.3180 LP	1 <1>	0.0000

@<TRIPOS>BOND

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- 2 1 12 ar
- 3 1 13 ar
- 4 1 14 ar
- 5 1 15 1
- 6 2 3 1
- 7 2 11 ar
- 8 2 16 ar

9 3 6 1
10 3 7 1
11 3 8 1
12 4 5 1
13 4 13 ar
14 4 18 ar
15 5 9 1
16 5 10 1
17 5 48 1
18 12 17 ar
19 14 19 ar
20 15 16 ar
21 15 18 ar
22 15 20 ar
23 15 21 ar
24 17 20 ar
25 17 22 1
26 19 21 ar
27 19 23 1
28 22 24 1
29 22 25 1
30 22 26 1

31 23 27 1

32 23 28 1

33 23 29 1

34 30 31 1

35 30 35 1

36 30 49 1

37 30 50 1

38 31 32 1

39 31 51 1

40 31 52 1

41 32 33 1

42 32 47 1

43 32 53 1

44 33 34 1

45 33 54 1

46 33 55 1

47 34 35 1

48 34 56 1

49 34 57 1

50 35 40 1

51 36 45 1

52 36 58 1

53 36 59 1
54 37 38 ar
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68 44 64 1
69 45 46 ar
70 46 65 1
71 47 48 1
72 47 66 1
73 47 67 1
74 48 68 1

75 48 69 1

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77 11 71 1

78 12 72 1

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80 13 74 1

81 13 75 1

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88 20 82 1

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90 21 84 1

91 21 85 1

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S199

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16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

ATOM\$RED STATIC ATOMS COLORGROUP SYSTEM

4 53 58 59 65

@<TRIPOS>COMMENT

> <Gold.Version>

5.7.2

> <Gold.Id.Protein>

unknown|gold_protein|mol2

> <Gold.Protein.RotatedTorsions>

[614 603 602 601] final -102.73 input 2.31 | X-H torsion

[841 836 835 832] final 125.78 input 27.02 | X-H torsion

[172 163 162 160] final -173.99 input 178.05 | X-H torsion

[876 867 866 864] final 104.19 input 173.38 | X-H torsion

> <Gold.Protein.ActiveResidues>

TYR19 ILE22 HIS23 ASP25 ASP26 HIS41 GLY42 GLU43 TRP44 LYS46

PHE57 PRO59 SER60 ASN61 TYR62

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20.9297 -1.7540 -30.6598 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 172 bound_to 163
14.2449 -0.4688 -22.9554 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 614 bound_to 603
12.7540 -1.1240 -22.4739 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 615 bound_to 603
13.0284 0.5478 -22.3533 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 616 bound_to 603
16.5506 -14.0024 -27.7917 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 841 bound_to 836
24.0659 -5.3423 -34.0958 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 876 bound_to 867
18.1240 -13.9127 -28.0899 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 987 bound_to 836
17.0829 -14.3869 -29.2551 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 988 bound_to 836
21.4476 -0.2625 -30.3728 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 998 bound_to 163
20.3879 -0.9833 -29.3607 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 999 bound_to 163
23.8516 -6.7662 -34.8035 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1000 bound_to 867
25.3525 -6.2387 -34.4353 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1001 bound_to 867

><Gold.Score>

Score	S(PLP)	S(hbond)	S(cho)	S(metal)	DE(clash)	DE(tors)	intcor
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><Gold.PLP.Fitness>

60.8179

> <Gold.PLP.PLP>

-61.2462

> <Gold.PLP.part.hbond>

-1.4449

> <Gold.PLP.part.metal>

0.0000

> <Gold.PLP.part.buried>

-4.5743

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0.3093

> <Gold.PLP.ligand.clash>

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> <Gold.PLP.ligand.torsion>

1.6911

> <Gold.PLP.Chemscore.Hbond>

0.9425

> <Gold.PLP.Chemscore.CHOScore>

0.0000

> <Gold.PLP.Chemscore.Metal>

0.0000

> <Gold.Chemscore.Hbonds>

donor molecule, donor type, donor heavy atom, donor atom, acceptor molecule, acceptor atom, score

P1 H 163 172 L1 16 0.94

> <Gold.PLP.Chemscore.Internal.Correction>

0.1263

Name: *****

Creating user name zbl

Creation time: Thu Jun 13 10:31:23 2019

File generated by GOLD software.

#

@<TRIPOS>MOLECULE

*****|pRh-6|mol2|1|dock10

85 91 1

SMALL

USER_CHARGES

@<TRIPOS>ATOM

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3 C	13.1024	-0.0992	-26.4186	C.3	1 <1>	0.0000
4 C	9.4532	-2.9384	-28.3890	C.2	1 <1>	0.0000
5 C	9.6071	-4.2493	-29.0839	C.3	1 <1>	0.0000
6 H	13.1625	0.2220	-25.5852	H	1 <1>	0.0000
7 H	13.5059	0.3078	-26.9764	H	1 <1>	0.0000
8 H	13.5968	-0.9121	-26.2366	H	1 <1>	0.0000
9 H	8.5956	-4.6448	-29.3659	H	1 <1>	0.0000
10 H	9.1259	-5.0568	-28.4713	H	1 <1>	0.0000
11 O	11.1985	0.1253	-27.8269	O.co2	1 <1>	0.0000

S204

12 O	7.2194	-0.3129	-28.4926	O.co2	1 <1>	0.0000
13 O	9.5172	-1.8801	-29.0801	O.co2	1 <1>	0.0000
14 O	8.9274	1.6455	-27.2663	O.co2	1 <1>	0.0000
15 Cr	8.9701	-1.2169	-26.1759	Cr.oh	1 <1>	0.0000
16 O	10.9710	-0.9863	-25.9159	O.co2	1 <1>	0.0000
17 C	6.5193	-0.9643	-27.6595	C.2	1 <1>	0.0000
18 O	9.2630	-2.9446	-27.1422	O.co2	1 <1>	0.0000
19 C	8.7372	1.6392	-26.0194	C.2	1 <1>	0.0000
20 O	6.9919	-1.4245	-26.5816	O.co2	1 <1>	0.0000
21 O	8.6732	0.5809	-25.3283	O.co2	1 <1>	0.0000
22 C	5.0880	-1.2000	-27.9898	C.3	1 <1>	0.0000
23 C	8.5833	2.9502	-25.3245	C.3	1 <1>	0.0000
24 H	5.0279	-1.5212	-28.8232	H	1 <1>	0.0000
25 H	4.6845	-1.6070	-27.4320	H	1 <1>	0.0000
26 H	4.5936	-0.3871	-28.1718	H	1 <1>	0.0000
27 H	9.0256	2.9335	-24.5488	H	1 <1>	0.0000
28 H	8.7438	3.6290	-25.8410	H	1 <1>	0.0000
29 H	7.8064	2.9272	-25.0123	H	1 <1>	0.0000
30 C	14.3906	-1.4632	-30.3132	C.3	1 <1>	0.0000
31 C	13.7772	-2.8696	-30.2824	C.3	1 <1>	0.0000
32 N	12.6159	-3.0025	-31.2621	N.4	1 <1>	0.0000
33 C	12.8013	-2.3411	-32.6283	C.3	1 <1>	0.0000

34 C	13.4512	-0.9547	-32.5142	C.3	1 <1>	0.0000
35 N	14.6906	-1.2459	-31.7528	N.pl3	1 <1>	0.0000
36 N	20.6325	-3.6746	-35.4375	N.pl3	1 <1>	0.0000
37 C	18.2890	-2.1903	-33.4173	C.ar	1 <1>	0.0000
38 C	18.1830	-1.3274	-32.3918	C.ar	1 <1>	0.0000
39 C	16.9918	-0.9995	-31.8641	C.ar	1 <1>	0.0000
40 C	15.8208	-1.5101	-32.3037	C.ar	1 <1>	0.0000
41 C	15.9588	-2.3545	-33.3520	C.ar	1 <1>	0.0000
42 C	17.1407	-2.6897	-33.9078	C.ar	1 <1>	0.0000
43 C	17.2069	-3.5373	-34.9511	C.ar	1 <1>	0.0000
44 C	18.3984	-3.8630	-35.4689	C.ar	1 <1>	0.0000
45 C	19.5159	-3.3463	-34.9303	C.ar	1 <1>	0.0000
46 N	19.4557	-2.5240	-33.9159	N.pl3	1 <1>	0.0000
47 C	12.1173	-4.4169	-31.4892	C.3	1 <1>	0.0000
48 C	11.0498	-4.8310	-30.0125	C.3	1 <1>	0.0000
49 H	15.2467	-1.3428	-29.6188	H	1 <1>	0.0000
50 H	13.6485	-0.7171	-29.9466	H	1 <1>	0.0000
51 H	13.4207	-3.0986	-29.2511	H	1 <1>	0.0000
52 H	14.6107	-3.5546	-30.5507	H	1 <1>	0.0000
53 H	11.8225	-2.4837	-30.8144	H	1 <1>	0.0000
54 H	11.8045	-2.2409	-33.1199	H	1 <1>	0.0000
55 H	13.4525	-2.9750	-33.2748	H	1 <1>	0.0000

56 H	13.5819	-0.4549	-33.4937 H	1 <1>	0.0000
57 H	12.7872	-0.2646	-31.9437 H	1 <1>	0.0000
58 H	20.6883	-4.3318	-36.2557 H	1 <1>	0.0000
59 H	21.5254	-3.2919	-35.0358 H	1 <1>	0.0000
60 H	19.0944	-0.8878	-31.9525 H	1 <1>	0.0000
61 H	17.0474	-0.3091	-31.0079 H	1 <1>	0.0000
62 H	15.0807	-2.8378	-33.8047 H	1 <1>	0.0000
63 H	16.2971	-3.9708	-35.3998 H	1 <1>	0.0000
64 H	18.4461	-4.5494	-36.3321 H	1 <1>	0.0000
65 H	20.3252	-2.1392	-33.5221 H	1 <1>	0.0000
66 H	12.9481	-5.1621	-31.4384 H	1 <1>	0.0000
67 H	11.4872	-4.7130	-32.3648 H	1 <1>	0.0000
68 H	10.9714	-5.9432	-29.9626 H	1 <1>	0.0000
69 H	11.8020	-4.5888	-29.2144 H	1 <1>	0.0000
70 ****	10.2349	-0.0187	-28.0520 LP	1 <1>	0.0000
71 ****	11.7881	0.6334	-28.4547 LP	1 <1>	0.0000
72 ****	8.1879	-0.1450	-28.3085 LP	1 <1>	0.0000
73 ****	6.8030	0.0328	-29.3334 LP	1 <1>	0.0000
74 ****	9.4148	-0.9883	-28.6395 LP	1 <1>	0.0000
75 ****	9.6701	-1.9358	-30.0668 LP	1 <1>	0.0000
76 ****	9.0367	0.7826	-27.7597 LP	1 <1>	0.0000
77 ****	8.9690	2.5133	-27.7614 LP	1 <1>	0.0000

78 ****	10.0025	-1.1542	-26.0999 LP	1 <1>	0.0000
79 ****	11.3874	-1.3320	-25.0750 LP	1 <1>	0.0000
80 ****	9.1537	-2.0818	-26.6487 LP	1 <1>	0.0000
81 ****	9.2215	-3.8125	-26.6471 LP	1 <1>	0.0000
82 ****	7.9556	-1.2805	-26.3564 LP	1 <1>	0.0000
83 ****	6.4023	-1.9326	-25.9538 LP	1 <1>	0.0000
84 ****	8.7756	-0.3109	-25.7689 LP	1 <1>	0.0000
85 ****	8.5203	0.6366	-24.3417 LP	1 <1>	0.0000

@<TRIPOS>BOND

1 1 11 ar
2 1 12 ar
3 1 13 ar
4 1 14 ar
5 1 15 1
6 2 3 1
7 2 11 ar
8 2 16 ar
9 3 6 1
10 3 7 1
11 3 8 1
12 4 5 1
13 4 13 ar

14 4 18 ar

15 5 9 1

16 5 10 1

17 5 48 1

18 12 17 ar

19 14 19 ar

20 15 16 ar

21 15 18 ar

22 15 20 ar

23 15 21 ar

24 17 20 ar

25 17 22 1

26 19 21 ar

27 19 23 1

28 22 24 1

29 22 25 1

30 22 26 1

31 23 27 1

32 23 28 1

33 23 29 1

34 30 31 1

35 30 35 1

36 30 49 1
37 30 50 1
38 31 32 1
39 31 51 1
40 31 52 1
41 32 33 1
42 32 47 1
43 32 53 1
44 33 34 1
45 33 54 1
46 33 55 1
47 34 35 1
48 34 56 1
49 34 57 1
50 35 40 1
51 36 45 1
52 36 58 1
53 36 59 1
54 37 38 ar
55 37 42 ar
56 37 46 ar
57 38 39 ar

58 38 60 1
59 39 40 ar
60 39 61 1
61 40 41 ar
62 41 42 ar
63 41 62 1
64 42 43 ar
65 43 44 ar
66 43 63 1
67 44 45 ar
68 44 64 1
69 45 46 ar
70 46 65 1
71 47 48 1
72 47 66 1
73 47 67 1
74 48 68 1
75 48 69 1
76 11 70 1
77 11 71 1
78 12 72 1
79 12 73 1

80 13 74 1

81 13 75 1

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@<TRIPOS>SUBSTRUCTURE

1 **** 1

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LONE_PAIRS STATIC ATOMS <user> **** ""

16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

DONOR_HYDROGENS STATIC ATOMS <user> **** ""

4 53 58 59 65

ATOM\$BLUE STATIC ATOMS COLORGROUP SYSTEM

16 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85

ATOM\$RED STATIC ATOMS COLORGROUP SYSTEM

4 53 58 59 65

@<TRIPOS>COMMENT

><Gold.Version>

5.7.2

><Gold.Id.Protein>

unknown|gold_protein|mol2

><Gold.Protein.RotatedTorsions>

[614 603 602 601] final -162.48 input 2.31 | X-H torsion

[841 836 835 832] final 168.07 input 27.02 | X-H torsion

[172 163 162 160] final 168.19 input 178.05 | X-H torsion

[876 867 866 864] final 116.13 input 173.38 | X-H torsion

><Gold.Protein.ActiveResidues>

TYR19 ILE22 HIS23 ASP25 ASP26 HIS41 GLY42 GLU43 TRP44 LYS46

PHE57 PRO59 SER60 ASN61 TYR62

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21.1119 -1.5951 -30.8072 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 172 bound_to 163

13.9324 0.4244 -22.7148 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 614 bound_to 603

13.6535 -1.2464 -22.8346 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 615 bound_to 603

S213

12.4404 -0.2214 -22.2326 H 0 0 0 0 0 0 0 0 0 0 0 0 0 # atno 616 bound_to 603
16.3393 -14.1992 -28.3836 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 841 bound_to 836
24.2471 -5.2982 -34.0602 H 0 0 0 0 0 0 0 0 0 0 0 0 # atno 876 bound_to 867
17.6798 -13.8311 -27.5834 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 987 bound_to 836
17.7435 -14.2671 -29.1558 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 988 bound_to 836
21.3328 -0.1593 -30.1256 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 998 bound_to 163
20.3165 -1.2489 -29.4572 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 999 bound_to 163
23.7100 -6.6390 -34.7585 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1000 bound_to 867
25.3088 -6.4110 -34.5168 LP 0 0 0 0 0 0 0 0 0 0 0 0 # atno 1001 bound_to 867

><Gold.Score>

Score	S(PLP)	S(hbond)	S(cho)	S(metal)	DE(clash)	DE(tors)	intcor
47.00	-49.19	0.00	0.00	0.00	0.00	1.16	0.13

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46.9973

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-49.1946

><Gold.PLP.part.hbond>

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> <Gold.PLP.Chemscore.Metal>

0.0000

> <Gold.PLP.Chemscore.Internal.Correction>

0.1263

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