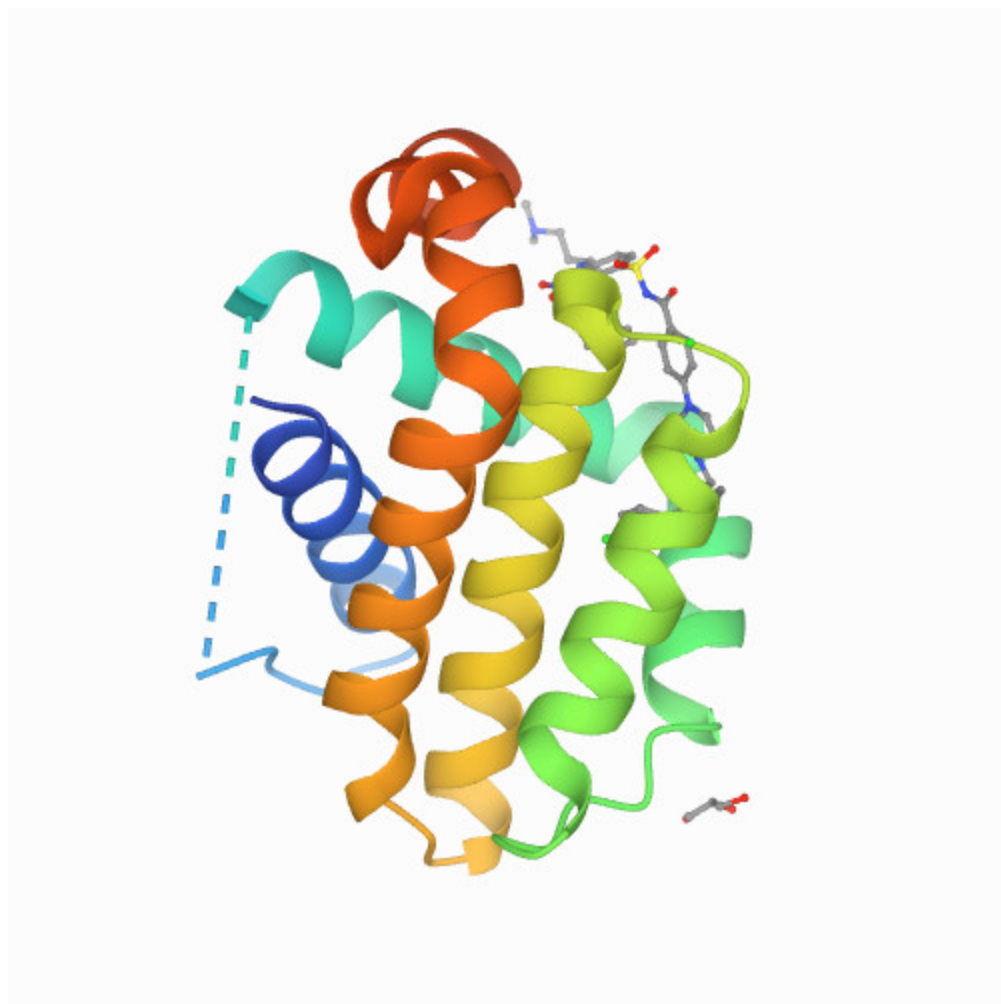


2YXJ

 rcsb.org/structure/2YXJ

Biological Assembly 1



Macromolecule Content

- Total Structure Weight: 43.36 kDa
- Atom Count: 2608
- Modelled Residue Count: 279
- Deposited Residue Count: 362
- Unique protein chains: 1

Crystal structure of Bcl-xL in complex with ABT-737

PDB DOI: [10.2210/pdb2YXJ/pdb](https://doi.org/10.2210/pdb2YXJ/pdb)

Classification: APOPTOSIS
Organism(s): Homo sapiens
Expression System: Escherichia coli
Mutation(s): No

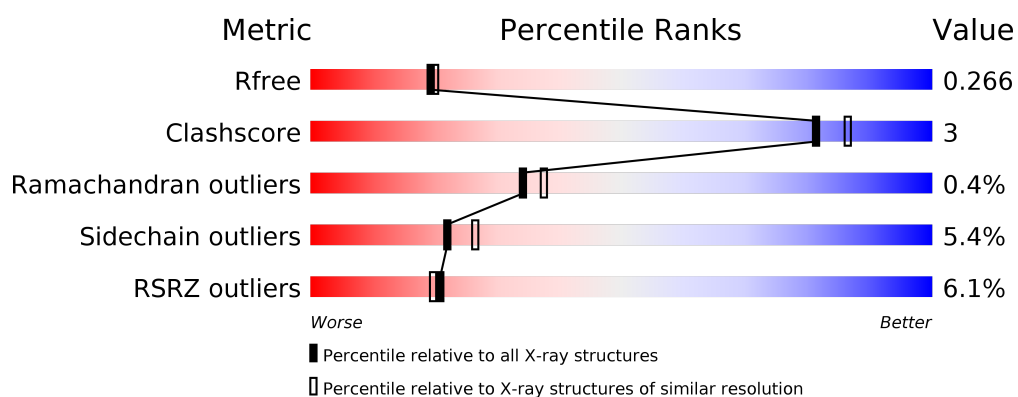
Deposited: 2007-04-26 **Released:** 2007-05-22

Deposition Author(s): Czabotar, P.E., Lee, E.F., Smith, B.J., Deshayes, K., Zobel, K., Fairlie, W.D., Colman, P.M.

wwPDB Validation

[3D Report](#) [Full Report](#)

Ligand Structure Quality Assessment



This is version 1.3
of the entry. See
complete [history](#).

Worse 0 1 Better
Ligand structure goodness of fit to experimental data

Crystal structure of ABT-737 complexed with Bcl-xL: implications for selectivity of antagonists of the Bcl-2 family

Lee, E.F., Czabotar, P.E., Smith, B.J., Deshayes, K., Zobel, K., Colman, P.M., Fairlie, W.D.
(2007) Cell Death Differ **14**: 1711-1713

PubMed: [17572662](#)

DOI: [10.1038/sj.cdd.4402178](#)

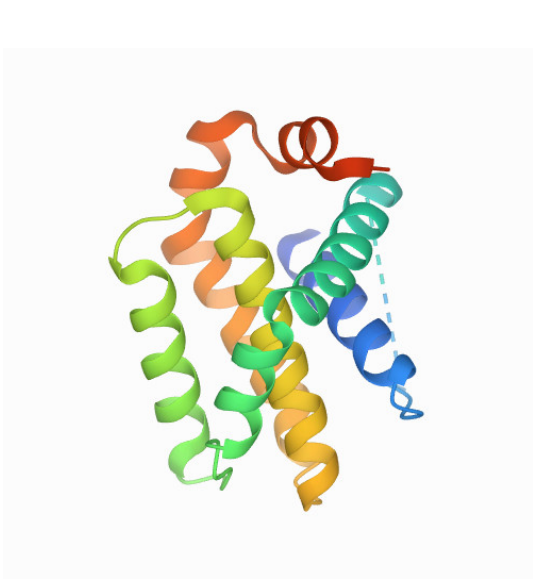
Primary Citation of Related Structures:

[2YXJ](#)

Macromolecules

Find similar proteins by:

(by identity cutoff) | [3D Structure](#)

Entity ID: 1					
Molecule					
Chains					
Sequence Length					
Organism					
Details					
Image					
Apoptosis regulator Bcl-X	A, B	181	Homo sapiens	Mutation(s): 0 Gene Names: Bcl-xL	
UniProt & NIH Common Fund Data Resources					
Find proteins for Q07817 (Homo sapiens)					
Explore Q07817					
				Go to UniProtKB: Q07817	
PHAROS: Q07817					
GTEx: ENSG00000171552					
Protein Feature View					
Expand					

Reference Sequence

2YXJ_1



PDB ENTITY 2YXJ_1

UNIPROT [Q07817](#)

UNMODELED B

UNMODELED A

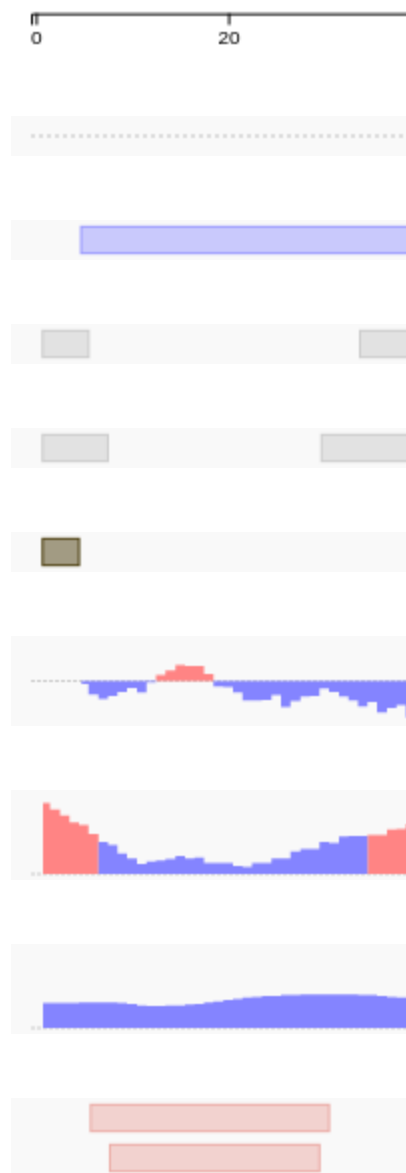
ARTIFACT

HYDROPATHY

DISORDER

DISORDERED BINDING

PFAM



Small Molecules

Ligands **3 Unique**

ID				
Chains				
Name / Formula / InChI Key				
2D Diagram				
3D Interactions				
<u>N3C</u> (Subject of Investigation/LOI)	D [auth A], F [auth B]	4-{4-[(4'-CHLOROBIPHENYL-2-YL)METHYL]PIPERAZIN-1-YL}-N-{[4-({(1R)-3-(DIMETHYLAMINO)-1-[(PHENYLTHIO)METHYL]PROPYL}AMINO)-3-NITROPHENYL]SULFONYL}BENZAMIDE C ₄₂ H ₄₅ Cl N ₆ O ₅ S ₂ HPLNQCPCUACXLM-PGUFJCEWSA-N		<u>Ligand Interacti</u>
<u>GOL</u>	E [auth A]	GLYCEROL C ₃ H ₈ O ₃ PEDCQBHIVMGVHV-UHFFFAOYSA-N		<u>Ligand Interacti</u>
<u>CL</u>	C [auth A]	CHLORIDE ION Cl VEXZGXHMUGYJMC-UHFFFAOYSA-M		<u>Ligand Interacti</u>

Binding Affinity Annotations		
ID		
Source		
Binding Affinity		
<u>N3C</u>	PDBBind: <u>2YXJ</u>	Ki: 0.5 (nM) from 1 assay(s)
	Binding MOAD: <u>2YXJ</u>	IC50: 9 (nM) from 1 assay(s)

Experimental Data & Validation

Experimental Data

Method: X-RAY DIFFRACTION

Resolution: 2.20 Å

R-Value Free: 0.249

R-Value Work: 0.199

R-Value Observed: 0.201

Space Group: P 2₁ 2₁ 2₁

Unit Cell:

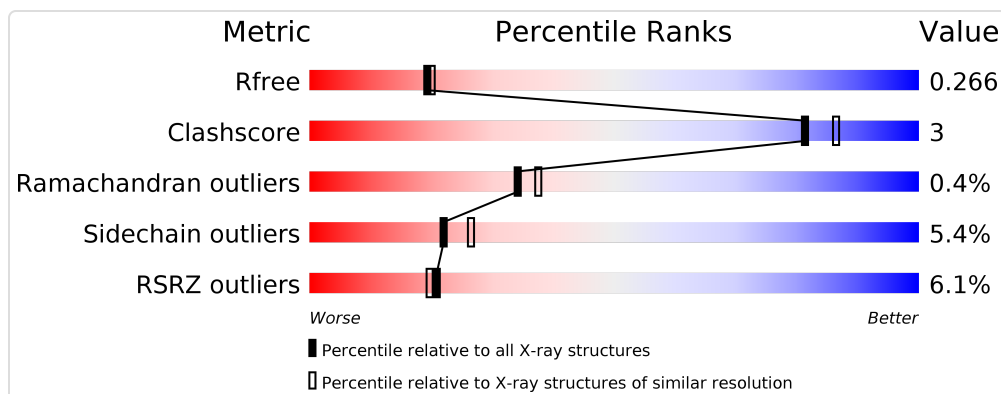
Length (Å)	Angle (°)
a = 66.321	α = 90
b = 75.37	β = 90
c = 87.778	γ = 90

Software Package:

Software Name	Purpose
REFMAC	refinement
CrystalClear	data collection
HKL-2000	data reduction
HKL-2000	data scaling
PHASER	phasing

Structure Validation

View [Full Validation Report](#)



Ligand Structure Quality Assessment

Worse 0 1 Better
Ligand structure goodness of fit to experimental data

Entry History

Deposition Data

Deposited Date: 2007-04-26

Released Date: 2007-05-22

Deposition Author(s): Czabotar, P.E., Lee, E.F., Smith, B.J., Deshayes, K., Zobel, K., Fairlie, W.D., Colman, P.M.

Revision History [\(Full details and data files\)](#)

- **Version 1.0: 2007-05-22**
Type: Initial release
- **Version 1.1: 2008-04-30**
Changes: Version format compliance
- **Version 1.2: 2011-07-13**
Changes: Non-polymer description, Version format compliance
- **Version 1.3: 2017-08-16**
Changes: Source and taxonomy