Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2O21
Title	:	Solution structure of the anti-apoptotic protein Bcl-2 in complex with an acyl-sulfonamide-based ligand
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Deposited on	:	2006-11-29

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

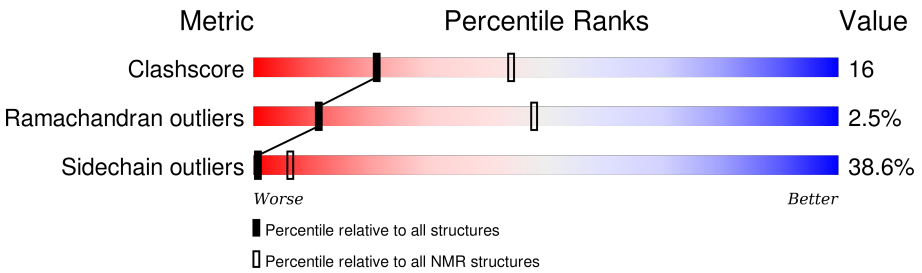
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	164	48% 41% 10% •

2 Ensemble composition and analysis (i)

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

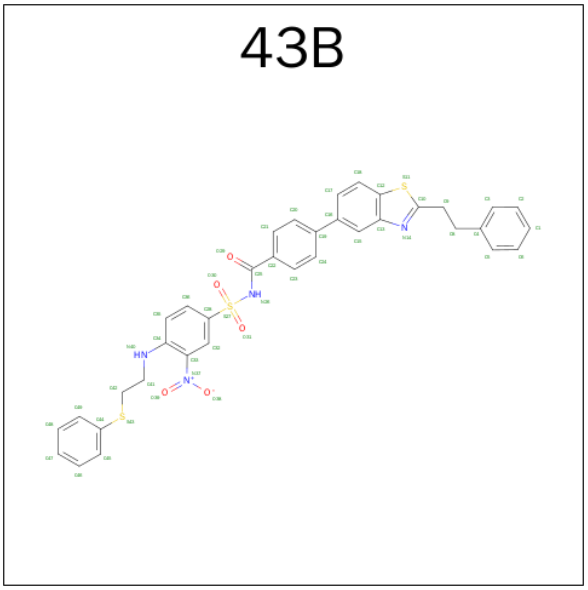
3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2689 atoms, of which 1291 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Apoptosis regulator Bcl-2.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	164	2611	847	1261	242	254	7	0

- Molecule 2 is 3-NITRO-N-{4-[2-(2-PHENYLETHYL)-1,3-BENZOTHIAZOL-5-YL]BENZOYL}-4-{[2-(PHENYLSULFANYL)ETHYL]AMINO}BENZENESULFONAMIDE (three-letter code: 43B) (formula: $C_{36}H_{30}N_4O_5S_3$).



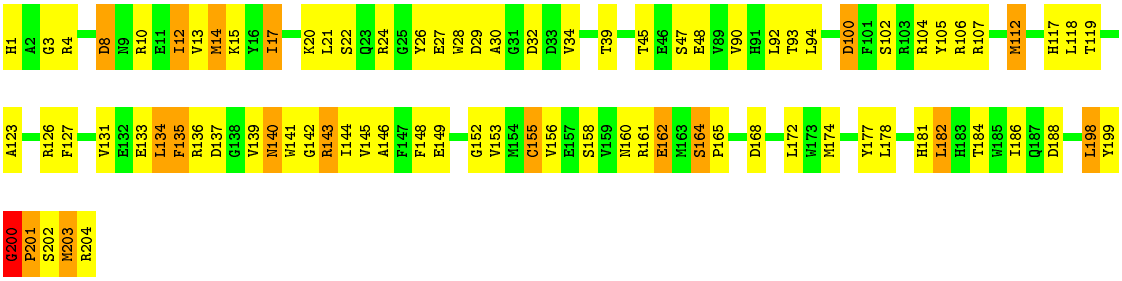
Mol	Chain	Residues	Atoms					
			Total	C	H	N	O	S
2	A	1	78	36	30	4	5	3

4 Residue-property plots (i)

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Apoptosis regulator Bcl-2

Chain A: 48% 41% 10%



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *simulated annealing*.

Of the ? calculated structures, 1 were deposited, based on the following criterion: *?*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CNS	refinement	

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality (i)

6.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 43B

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.50	2/1385 (0.1%)	0.95	7/1872 (0.4%)
All	All	1.50	2/1385 (0.1%)	0.95	7/1872 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0	2
All	All	0	2

All bond outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	200	GLY	C-O	53.19	2.08	1.23
1	A	200	GLY	C-N	-12.99	1.09	1.34

All angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	200	GLY	CA-C-O	-21.29	82.28	120.60
1	A	200	GLY	O-C-N	-19.55	83.95	121.10
1	A	200	GLY	C-N-CD	-14.89	87.84	120.60
1	A	200	GLY	N-CA-C	12.66	144.75	113.10
1	A	200	GLY	CA-C-N	10.48	146.44	117.10
1	A	200	GLY	C-N-CA	7.42	153.15	122.00
1	A	141	TRP	CD1-NE1-CE2	-5.70	103.87	109.00

There are no chirality outliers.

All planar outliers are listed below.

Mol	Chain	Res	Type	Group
1	A	200	GLY	Mainchain,Peptide

6.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1350	1261	1261	42
2	A	48	30	30	12
All	All	1398	1291	1291	42

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

All clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:200:GLY:C	1:A:200:GLY:O	0.91	2.08
1:A:146:ALA:HB1	2:A:1000:43B:HC2	0.84	1.48
1:A:145:VAL:HG21	2:A:1000:43B:HQ2	0.76	1.58
1:A:94:LEU:HD22	1:A:148:PHE:CE2	0.74	2.17
1:A:12:ILE:HD11	1:A:148:PHE:CZ	0.73	2.17
1:A:200:GLY:CA	1:A:200:GLY:O	0.70	2.39
1:A:152:GLY:O	1:A:156:VAL:HG22	0.70	1.86
1:A:200:GLY:O	1:A:201:PRO:N	0.69	2.25
1:A:14:MET:CE	1:A:30:ALA:HB1	0.67	2.20
1:A:142:GLY:O	1:A:145:VAL:HG22	0.66	1.90
1:A:21:LEU:HD11	1:A:155:CYS:SG	0.61	2.34
1:A:145:VAL:CG2	2:A:1000:43B:HQ2	0.60	2.26
1:A:119:THR:O	1:A:123:ALA:HB2	0.60	1.96
1:A:198:LEU:HD12	1:A:199:TYR:CE1	0.60	2.31
1:A:146:ALA:HB1	2:A:1000:43B:C5	0.59	2.27
1:A:144:ILE:HG22	1:A:182:LEU:HD11	0.59	1.73
1:A:149:GLU:O	1:A:153:VAL:HG23	0.59	1.96
1:A:14:MET:HE2	1:A:30:ALA:HB1	0.56	1.76
1:A:17:ILE:HD12	1:A:174:MET:CE	0.56	2.30
1:A:142:GLY:O	2:A:1000:43B:HJ2	0.56	1.99
1:A:118:LEU:N	1:A:118:LEU:HD12	0.55	2.16

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:134:LEU:HD12	1:A:135:PHE:CE2	0.54	2.38
1:A:178:LEU:HD11	1:A:182:LEU:HD22	0.52	1.80
1:A:134:LEU:HD23	2:A:1000:43B:N14	0.51	2.21
1:A:21:LEU:HD22	1:A:28:TRP:HB2	0.51	1.82
1:A:178:LEU:CD1	1:A:182:LEU:HD22	0.51	2.36
1:A:17:ILE:HD12	1:A:174:MET:HE1	0.50	1.82
1:A:100:ASP:CB	2:A:1000:43B:S43	0.49	3.01
1:A:34:VAL:HG13	1:A:34:VAL:O	0.49	2.06
1:A:145:VAL:CB	2:A:1000:43B:HQ2	0.49	2.37
1:A:127:PHE:O	1:A:131:VAL:HG22	0.46	2.10
1:A:10:ARG:O	1:A:13:VAL:HG12	0.46	2.11
1:A:100:ASP:HB2	2:A:1000:43B:S43	0.45	2.51
1:A:164:SER:N	1:A:165:PRO:CD	0.45	2.79
1:A:112:MET:CE	2:A:1000:43B:HC1	0.44	2.42
1:A:142:GLY:HA2	2:A:1000:43B:HK	0.44	1.88
1:A:145:VAL:HG21	2:A:1000:43B:C48	0.44	2.39
1:A:135:PHE:N	1:A:135:PHE:CD1	0.44	2.85
1:A:8:ASP:O	1:A:12:ILE:HG22	0.43	2.12
1:A:105:TYR:N	1:A:105:TYR:CD1	0.42	2.87
1:A:143:ARG:N	1:A:143:ARG:CD	0.41	2.83
1:A:139:VAL:HG12	1:A:140:ASN:N	0.40	2.32

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	162/164 (99%)	132 (81%)	26 (16%)	4 (2%)	11 48
All	All	162/164 (99%)	132 (81%)	26 (16%)	4 (2%)	11 48

All 4 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	201	PRO
1	A	203	MET

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Mol	Chain	Res	Type
1	A	3	GLY
1	A	162	GLU

6.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	140/140 (100%)	86 (61%)	54 (39%)	1 6
All	All	140/140 (100%)	86 (61%)	54 (39%)	1 6

All 54 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	48	GLU
1	A	158	SER
1	A	184	THR
1	A	12	ILE
1	A	133	GLU
1	A	92	LEU
1	A	15	LYS
1	A	161	ARG
1	A	39	THR
1	A	188	ASP
1	A	90	VAL
1	A	14	MET
1	A	164	SER
1	A	168	ASP
1	A	27	GLU
1	A	47	SER
1	A	182	LEU
1	A	107	ARG
1	A	32	ASP
1	A	29	ASP
1	A	135	PHE
1	A	17	ILE
1	A	181	HIS

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Mol	Chain	Res	Type
1	A	24	ARG
1	A	45	THR
1	A	204	ARG
1	A	8	ASP
1	A	102	SER
1	A	172	LEU
1	A	140	ASN
1	A	160	ASN
1	A	155	CYS
1	A	117	HIS
1	A	22	SER
1	A	93	THR
1	A	20	LYS
1	A	136	ARG
1	A	198	LEU
1	A	134	LEU
1	A	112	MET
1	A	186	ILE
1	A	1	HIS
1	A	100	ASP
1	A	177	TYR
1	A	137	ASP
1	A	143	ARG
1	A	203	MET
1	A	106	ARG
1	A	104	ARG
1	A	202	SER
1	A	4	ARG
1	A	126	ARG
1	A	162	GLU
1	A	26	TYR

6.3.3 RNA (i)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates (i)

There are no carbohydrates in this entry.

6.6 Ligand geometry (i)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	43B	A	1000	-	49,53,53	1.54	2 (4%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	43B	A	1000	-	61,74,74	1.66	1 (1%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	43B	A	1000	-	-	0,33,35,35	0,6,6,6

All bond outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1000	43B	S27-N26	5.82	1.76	1.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1000	43B	C28-S27	5.37	1.84	1.76

All angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1000	43B	O31-S27-O30	8.02	108.91	119.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

No chemical shift data were provided