WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Mar 23, 2024 – 10:08 PM EDT

PDB ID	:	2DVR
Title	:	Crystal structure analysis of the N-terminal bromodomain of human BRD2 complexed with acetylated histone H4 peptide
Authors	:	Nakamura, Y.; Umehara, T.; Shirouzu, M.; Padmanabhan, B.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on	:	2006-08-01
Resolution	:	2.30 Å(reported)

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

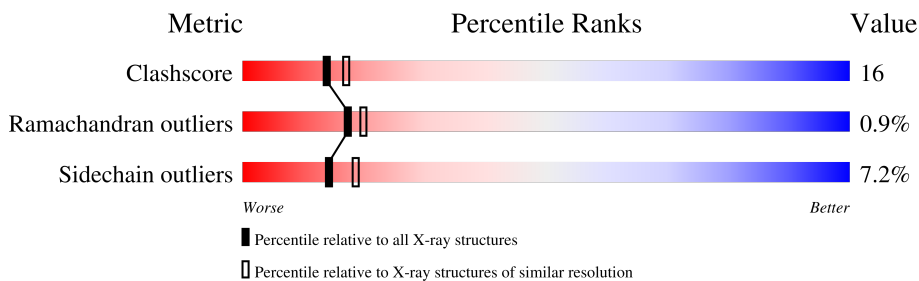|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.1

1   Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

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	Percentile Ranks	Value
Clashscore		16
Ramachandran outliers		0.9%
Sidechain outliers		7.2%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	122	61% 27% 5% 7%
1	B	122	70% 19% • 8%
1	C	122	68% 16% • 12%
2	P	15	13% 33% 7% 47%
2	Q	15	33% 20% 13% 33%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ALY	Q	12	-	X	-	-

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 3137 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called bromodomain-containing protein 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	114	Total	C	N	O	S	Se	0	0	0
			953	615	161	168	2	7			
1	B	112	Total	C	N	O	S	Se	0	0	0
			935	605	158	163	2	7			
1	C	107	Total	C	N	O	S	Se	0	0	0
			895	582	150	154	2	7			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	MSE	MET	modified residue	UNP P25440
A	55	MSE	MET	modified residue	UNP P25440
A	57	MSE	MET	modified residue	UNP P25440
A	76	MSE	MET	modified residue	UNP P25440
A	82	MSE	MET	modified residue	UNP P25440
A	99	MSE	MET	modified residue	UNP P25440
A	114	MSE	MET	modified residue	UNP P25440
B	21	MSE	MET	modified residue	UNP P25440
B	55	MSE	MET	modified residue	UNP P25440
B	57	MSE	MET	modified residue	UNP P25440
B	76	MSE	MET	modified residue	UNP P25440
B	82	MSE	MET	modified residue	UNP P25440
B	99	MSE	MET	modified residue	UNP P25440
B	114	MSE	MET	modified residue	UNP P25440
C	21	MSE	MET	modified residue	UNP P25440
C	55	MSE	MET	modified residue	UNP P25440
C	57	MSE	MET	modified residue	UNP P25440
C	76	MSE	MET	modified residue	UNP P25440
C	82	MSE	MET	modified residue	UNP P25440
C	99	MSE	MET	modified residue	UNP P25440
C	114	MSE	MET	modified residue	UNP P25440

- Molecule 2 is a protein called histone H4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	8	Total 46	C 28	N 9	O 9	0	0	0
2	Q	10	Total 58	C 35	N 12	O 11	0	0	0

• Molecule 3 is water.

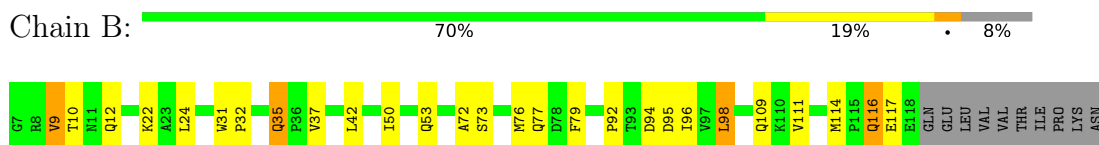| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	72	Total 72	O 72	0	0
3	B	85	Total 85	O 85	0	0
3	C	66	Total 66	O 66	0	0
3	P	12	Total 12	O 12	0	0
3	Q	15	Total 15	O 15	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-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 outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

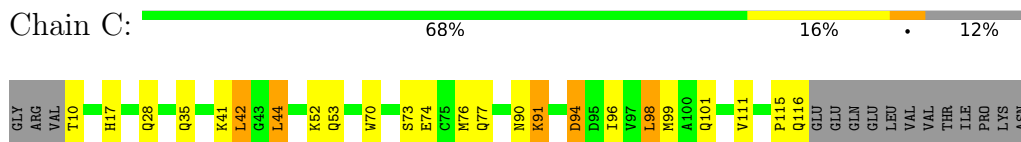- Molecule 1: bromodomain-containing protein 2
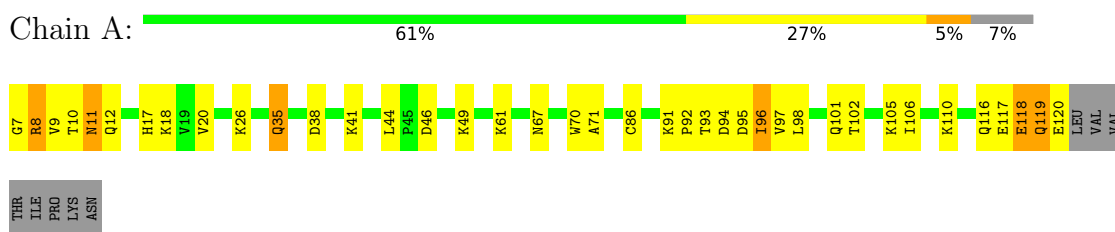
Chain A:

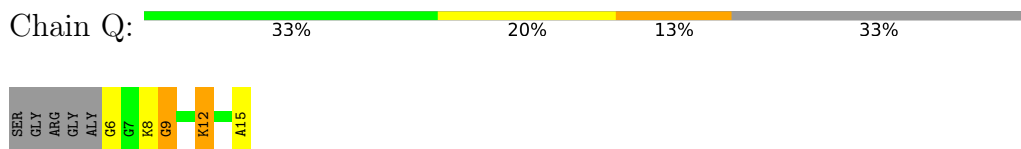- Molecule 1: bromodomain-containing protein 2

Chain B:

- Molecule 1: bromodomain-containing protein 2

Chain C:

- Molecule 2: histone H4

Chain P:

- Molecule 2: histone H4

Chain Q:

4 Data and refinement statistics ⓘ

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	113.53Å 55.24Å 67.73Å 90.00° 93.92° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30	Depositor
% Data completeness (in resolution range)	99.8 (20.00-2.30)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.180 , 0.243	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3137	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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 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	0.86	0/971	0.83	2/1301 (0.2%)
1	B	0.90	0/953	0.87	1/1277 (0.1%)
1	C	0.85	0/913	0.82	1/1224 (0.1%)
2	P	0.79	0/32	1.37	0/39
2	Q	0.93	0/44	1.31	0/53
All	All	0.87	0/2913	0.86	4/3894 (0.1%)

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 outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	94	ASP	CB-CG-OD2	6.29	123.96	118.30
1	A	94	ASP	CB-CG-OD2	5.96	123.67	118.30
1	C	94	ASP	CB-CG-OD1	5.70	123.43	118.30
1	A	38	ASP	CB-CG-OD1	5.03	122.83	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119	GLN	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	953	0	946	39	0
1	B	935	0	932	30	0
1	C	895	0	895	16	0
2	P	46	0	42	8	0
2	Q	58	0	59	11	0
3	A	72	0	0	19	0
3	B	85	0	0	9	1
3	C	66	0	0	5	0
3	P	12	0	0	4	1
3	Q	15	0	0	6	0
All	All	3137	0	2874	91	1

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.

The worst 5 of 91 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:ILE:HG12	3:Q:136:HOH:O	1.36	1.21
1:C:10:THR:HA	3:C:138:HOH:O	1.48	1.09
1:B:77:GLN:HG3	3:B:209:HOH:O	1.54	1.02
1:A:26:LYS:HG2	3:A:198:HOH:O	1.68	0.92
1:A:102:THR:HG22	3:A:196:HOH:O	1.72	0.90

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:141:HOH:O	3:P:27:HOH:O[4_556]	1.50	0.70

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	112/122 (92%)	111 (99%)	0	1 (1%)	17	20
1	B	110/122 (90%)	107 (97%)	2 (2%)	1 (1%)	17	20
1	C	105/122 (86%)	104 (99%)	1 (1%)	0	100	100
2	P	5/15 (33%)	4 (80%)	1 (20%)	0	100	100
2	Q	7/15 (47%)	4 (57%)	2 (29%)	1 (14%)	0	0
All	All	339/396 (86%)	330 (97%)	6 (2%)	3 (1%)	17	20

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Q	9	GLY
1	A	118	GLU
1	B	9	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	104/105 (99%)	96 (92%)	8 (8%)	13	16
1	B	102/105 (97%)	96 (94%)	6 (6%)	19	27
1	C	98/105 (93%)	90 (92%)	8 (8%)	11	14
2	P	1/4 (25%)	1 (100%)	0	100	100
2	Q	2/4 (50%)	2 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	307/323 (95%)	285 (93%)	22 (7%)	14 18

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	17	HIS
1	C	42	LEU
1	C	35	GLN
1	C	44	LEU
1	A	44	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	28	GLN
1	C	35	GLN
1	C	101	GLN
1	A	101	GLN
1	B	12	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or 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 length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
2	ALY	P	12	2	10,11,12	3.56	3 (30%)	7,12,14	2.90	3 (42%)
2	ALY	Q	12	2	10,11,12	3.46	3 (30%)	7,12,14	5.20	5 (71%)

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	ALY	P	12	2	-	7/9/10/12	-
2	ALY	Q	12	2	-	6/9/10/12	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	12	ALY	OH-CH	8.76	1.43	1.23
2	Q	12	ALY	OH-CH	8.16	1.41	1.23
2	P	12	ALY	O-C	5.32	1.41	1.19
2	Q	12	ALY	O-C	5.09	1.40	1.19
2	Q	12	ALY	CH-NZ	4.65	1.47	1.34

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Q	12	ALY	CE-NZ-CH	-8.32	109.77	122.56
2	Q	12	ALY	OH-CH-CH3	-8.12	106.97	122.06
2	P	12	ALY	OH-CH-CH3	-6.73	109.55	122.06
2	Q	12	ALY	CD-CE-NZ	4.80	125.93	112.21
2	Q	12	ALY	CH3-CH-NZ	4.70	124.41	116.09

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	P	12	ALY	CH3-CH-NZ-CE
2	P	12	ALY	N-CA-CB-CG
2	P	12	ALY	C-CA-CB-CG
2	Q	12	ALY	N-CA-CB-CG
2	Q	12	ALY	C-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	12	ALY	1	0
2	Q	12	ALY	3	0

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.