



Full wwPDB NMR Structure Validation Report ⓘ

May 29, 2020 – 09:35 am BST

PDB ID : 6BGG
Title : Solution NMR structures of the BRD3 ET domain in complex with a CHD4 peptide
Authors : Wai, D.C.C.; Szyszka, T.N.; Campbell, A.E.; Kwong, C.; Wilkinson-White, L.; Silva, A.P.G.; Low, J.K.K.; Kwan, A.H.; Gamsjaeger, R.; Lu, B.; Vakoc, C.R.; Blobel, G.A.; Mackay, J.P.
Deposited on : 2017-10-28

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

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

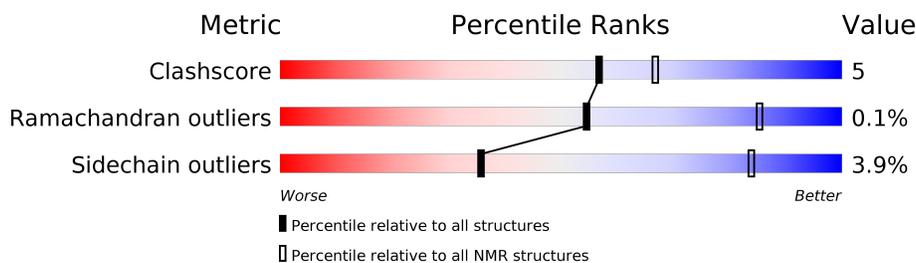
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 81%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	12	
2	B	93	

2 Ensemble composition and analysis i

This entry contains 20 models. Model 19 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	B:569-B:637 (69)	0.38	19

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 4 clusters and 6 single-model clusters were found.

Cluster number	Models
1	1, 2, 8, 15, 18
2	5, 6, 17, 19
3	3, 9, 20
4	4, 16
Single-model clusters	7; 10; 11; 12; 13; 14

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1636 atoms, of which 827 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CHD4.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
1	A	12	199	62	110	15	12	0

- Molecule 2 is a protein called Bromodomain-containing protein 3.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
2	B	88	1437	443	717	127	148	2	0

There are 5 discrepancies between the modelled and reference sequences:

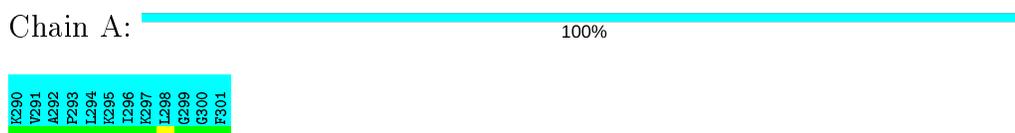
Chain	Residue	Modelled	Actual	Comment	Reference
B	552	GLY	-	expression tag	UNP Q15059
B	553	PRO	-	expression tag	UNP Q15059
B	554	LEU	-	expression tag	UNP Q15059
B	555	GLY	-	expression tag	UNP Q15059
B	556	SER	-	expression tag	UNP Q15059

4 Residue-property plots [i](#)

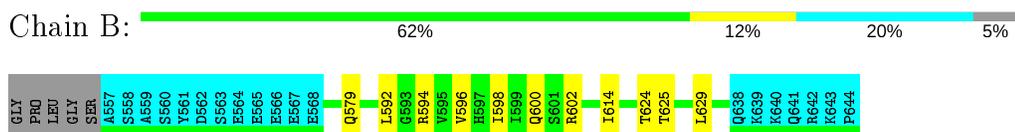
4.1 Average score per residue in the NMR ensemble

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: CHD4



- Molecule 2: Bromodomain-containing protein 3

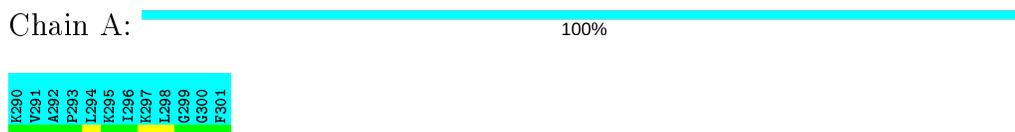


4.2 Scores per residue for each member of the ensemble

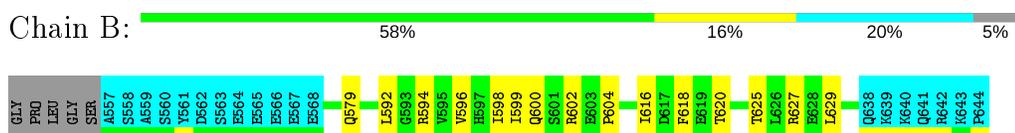
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: CHD4

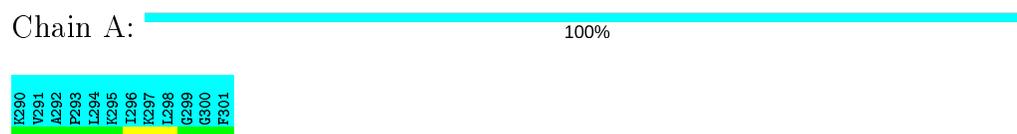


- Molecule 2: Bromodomain-containing protein 3



4.2.2 Score per residue for model 2

- Molecule 1: CHD4

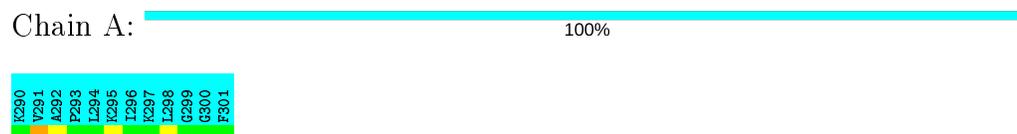


- Molecule 2: Bromodomain-containing protein 3

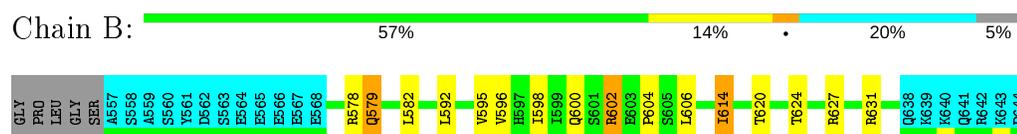


4.2.3 Score per residue for model 3

- Molecule 1: CHD4



- Molecule 2: Bromodomain-containing protein 3

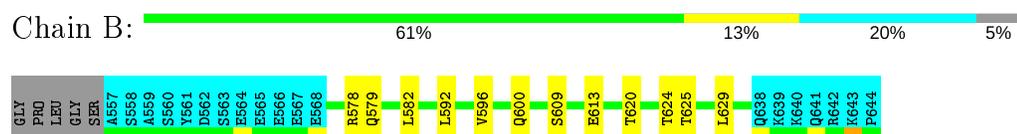


4.2.4 Score per residue for model 4

- Molecule 1: CHD4

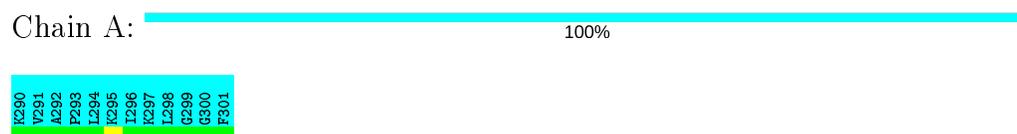


- Molecule 2: Bromodomain-containing protein 3

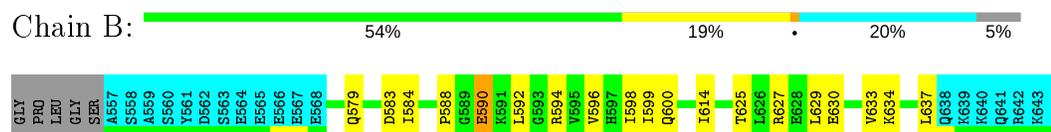


4.2.5 Score per residue for model 5

- Molecule 1: CHD4

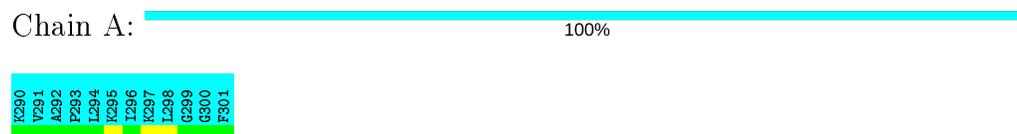


- Molecule 2: Bromodomain-containing protein 3



4.2.6 Score per residue for model 6

- Molecule 1: CHD4



- Molecule 2: Bromodomain-containing protein 3

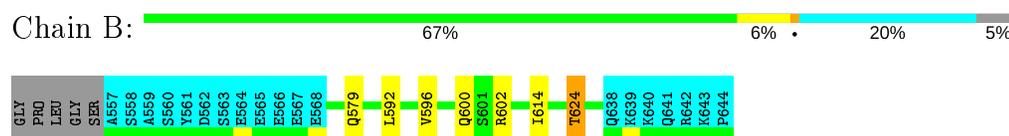


4.2.7 Score per residue for model 7

- Molecule 1: CHD4

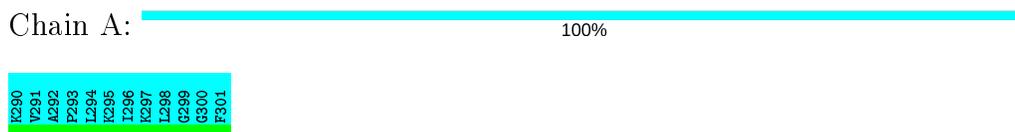


- Molecule 2: Bromodomain-containing protein 3

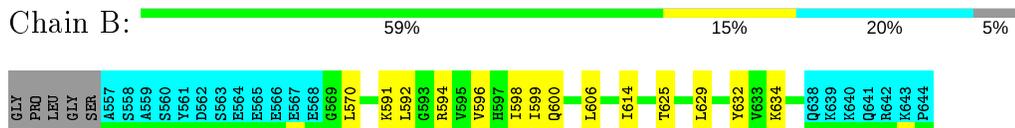


4.2.8 Score per residue for model 8

- Molecule 1: CHD4



- Molecule 2: Bromodomain-containing protein 3

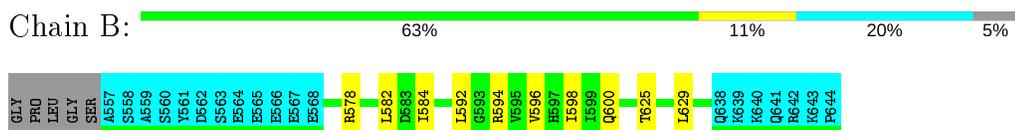


4.2.9 Score per residue for model 9

- Molecule 1: CHD4

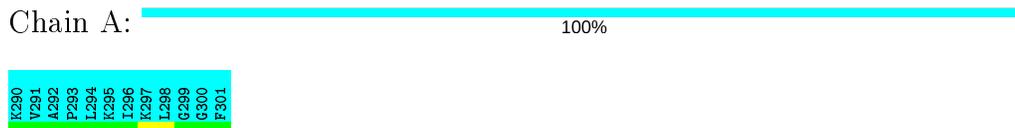


- Molecule 2: Bromodomain-containing protein 3



4.2.10 Score per residue for model 10

- Molecule 1: CHD4

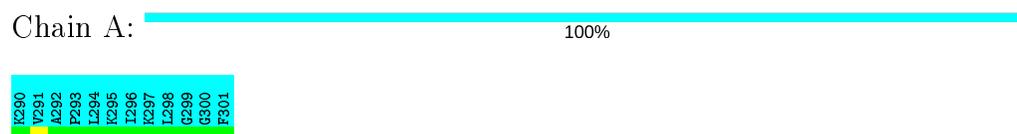


- Molecule 2: Bromodomain-containing protein 3

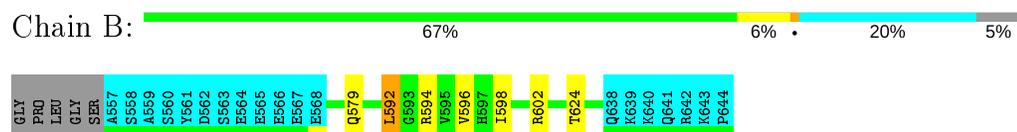


4.2.11 Score per residue for model 11

- Molecule 1: CHD4

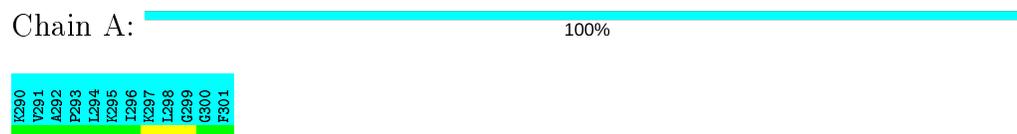


- Molecule 2: Bromodomain-containing protein 3



4.2.12 Score per residue for model 12

- Molecule 1: CHD4



- Molecule 2: Bromodomain-containing protein 3

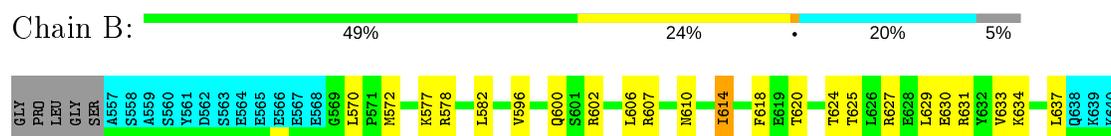


4.2.13 Score per residue for model 13

- Molecule 1: CHD4



- Molecule 2: Bromodomain-containing protein 3



K641
K642
K643
P644

4.2.14 Score per residue for model 14

- Molecule 1: CHD4

Chain A:  100%

K290
V291
A292
P293
L294
K295
L296
K297
L298
G299
G300
F301

- Molecule 2: Bromodomain-containing protein 3

Chain B:  55% 17% 20% 5%

GLY PRD LEU GLY SER A557 S558 A559 S560 Y561 D562 S563 S564 E565 E566 E567 E568 Q579 L580 K591 L592 G593 R594 V595 H597 I598 I599 Q600 L606 E613 I614 D617 T620 T624 T625 L629 C636 L637 Q638 K639 K640 Q641 K642 K643 P644

4.2.15 Score per residue for model 15

- Molecule 1: CHD4

Chain A:  100%

K290
V291
A292
P293
L294
K295
L296
K297
L298
G299
G300
F301

- Molecule 2: Bromodomain-containing protein 3

Chain B:  59% 15% 20% 5%

GLY PRD LEU GLY SER A557 S558 A559 S560 Y561 D562 S563 S564 E565 E566 E567 E568 Q579 L582 G593 R594 V595 H597 I598 I599 Q600 L606 I614 T620 L621 K622 T625 L626 R627 E628 L629 E630 R631 Q638 K639 K640 Q641 K642 K643 P644

4.2.16 Score per residue for model 16

- Molecule 1: CHD4

Chain A:  100%

K290
V291
A292
P293
L294
K295
L296
K297
L298
G299
G300
F301

- Molecule 2: Bromodomain-containing protein 3

Chain B:  67% 8% 20% 5%



4.2.17 Score per residue for model 17

- Molecule 1: CHD4

Chain A: 100%



- Molecule 2: Bromodomain-containing protein 3

Chain B: 58% 16% 20% 5%



4.2.18 Score per residue for model 18

- Molecule 1: CHD4

Chain A: 100%



- Molecule 2: Bromodomain-containing protein 3

Chain B: 54% 20% 20% 5%



4.2.19 Score per residue for model 19 (medoid)

- Molecule 1: CHD4

Chain A: 100%



- Molecule 2: Bromodomain-containing protein 3

Chain B: 59% 15% 20% 5%



4.2.20 Score per residue for model 20

- Molecule 1: CHD4

Chain A: 100%



- Molecule 2: Bromodomain-containing protein 3

Chain B: 59% 15% 20% 5%



5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CYANA	structure calculation	3.97
CNS	refinement	1.2

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1039
Number of shifts mapped to atoms	1039
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	81%

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](#)

There are no covalent bond-length or bond-angle outliers.

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
2	B	0.0±0.0	0.5±0.5
All	All	0	10

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
2	B	602	ARG	Sidechain	6
2	B	627	ARG	Sidechain	1
2	B	607	ARG	Sidechain	1
2	B	594	ARG	Sidechain	1
2	B	631	ARG	Sidechain	1

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	0	0	0	0±0
2	B	563	574	574	6±2
All	All	11260	11480	11480	115

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:600:GLN:HG2	2:B:606:LEU:HD23	0.61	1.72	8	1
2:B:625:THR:O	2:B:629:LEU:HG	0.61	1.95	13	15
2:B:578:ARG:O	2:B:582:LEU:HG	0.60	1.97	19	9
2:B:600:GLN:HG2	2:B:606:LEU:HD12	0.59	1.74	10	5
2:B:592:LEU:O	2:B:596:VAL:HG23	0.56	2.01	2	18
2:B:596:VAL:O	2:B:600:GLN:HG3	0.55	2.02	7	17
2:B:633:VAL:O	2:B:637:LEU:HG	0.54	2.02	18	3
2:B:572:MET:SD	2:B:626:LEU:HB3	0.52	2.44	12	2
2:B:591:LYS:HE2	2:B:632:TYR:OH	0.51	2.05	8	2
2:B:600:GLN:HG2	2:B:606:LEU:HD22	0.50	1.82	18	2
2:B:627:ARG:O	2:B:631:ARG:HG3	0.50	2.07	3	2
2:B:630:GLU:HA	2:B:633:VAL:HG22	0.49	1.84	13	3
2:B:594:ARG:O	2:B:598:ILE:HG13	0.49	2.08	9	11
2:B:599:ILE:HD12	2:B:614:ILE:HD11	0.49	1.83	5	2
2:B:633:VAL:O	2:B:637:LEU:HB2	0.48	2.08	13	1
2:B:584:ILE:HG23	2:B:592:LEU:HD21	0.48	1.85	5	1
2:B:596:VAL:HA	2:B:614:ILE:HD12	0.47	1.85	14	2
2:B:627:ARG:O	2:B:631:ARG:HB2	0.46	2.11	13	1
2:B:599:ILE:HD13	2:B:614:ILE:HD11	0.45	1.86	8	2
2:B:602:ARG:NH1	2:B:621:LEU:HA	0.45	2.27	10	1
2:B:579:GLN:HE21	2:B:579:GLN:HA	0.44	1.71	3	1
2:B:590:GLU:OE1	2:B:591:LYS:HG2	0.44	2.13	20	1
2:B:588:PRO:HG2	2:B:590:GLU:OE1	0.43	2.13	5	1
2:B:599:ILE:HG21	2:B:615:GLU:O	0.43	2.13	12	1
2:B:602:ARG:O	2:B:604:PRO:HD3	0.43	2.13	3	2
2:B:591:LYS:HG2	2:B:636:CYS:SG	0.43	2.53	14	1
2:B:583:ASP:OD2	2:B:637:LEU:HG	0.42	2.14	5	1
2:B:584:ILE:HG23	2:B:592:LEU:HD11	0.42	1.90	9	1
2:B:599:ILE:HD13	2:B:616:ILE:HG12	0.42	1.90	1	1
2:B:631:ARG:HA	2:B:634:LYS:HE2	0.42	1.92	17	1
2:B:595:VAL:HA	2:B:598:ILE:HD12	0.41	1.91	3	1
2:B:600:GLN:NE2	2:B:607:ARG:HA	0.41	2.30	18	1
2:B:572:MET:O	2:B:577:LYS:HE3	0.41	2.15	13	1
2:B:573:SER:OG	2:B:576:GLU:HG3	0.41	2.16	18	1

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	0	-	-	-	-	
2	B	69/93 (74%)	68±1 (99±1%)	1±1 (1±1%)	0±0 (0±0%)	54	85
All	All	1380/2100 (66%)	1366 (99%)	13 (1%)	1 (0%)	54	85

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
2	B	609	SER	1

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	0	-	-	-	
2	B	66/86 (77%)	63±2 (96±3%)	3±2 (4±3%)	36	84
All	All	1320/1900 (69%)	1269 (96%)	51 (4%)	36	84

All 16 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	579	GLN	14
2	B	620	THR	8
2	B	624	THR	6
2	B	634	LYS	4
2	B	614	ILE	3
2	B	610	ASN	3
2	B	602	ARG	3
2	B	592	LEU	2

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Mol	Chain	Res	Type	Models (Total)
2	B	580	LEU	1
2	B	628	GLU	1
2	B	627	ARG	1
2	B	608	ASP	1
2	B	590	GLU	1
2	B	606	LEU	1
2	B	591	LYS	1
2	B	585	ASN	1

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](#)

There are no ligands in this entry.

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](#)

The completeness of assignment taking into account all chemical shift lists is 81% for the well-defined parts and 71% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *BRD3-CHD4_NMRSTAR_3L.txt*

7.1.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1039
Number of shifts mapped to atoms	1039
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	84	-0.24 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	80	0.15 ± 0.04	None needed (< 0.5 ppm)
$^{13}\text{C}'$	84	-0.22 ± 0.11	None needed (< 0.5 ppm)
^{15}N	76	0.05 ± 0.28	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 81%, i.e. 730 atoms were assigned a chemical shift out of a possible 906. 10 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	326/335 (97%)	129/133 (97%)	136/138 (99%)	61/64 (95%)
Sidechain	394/539 (73%)	236/318 (74%)	154/192 (80%)	4/29 (14%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	10/32 (31%)	7/17 (41%)	3/14 (21%)	0/1 (0%)
Overall	730/906 (81%)	372/468 (79%)	293/344 (85%)	65/94 (69%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 71%, i.e. 925 atoms were assigned a chemical shift out of a possible 1301. 10 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	418/486 (86%)	174/193 (90%)	168/200 (84%)	76/93 (82%)
Sidechain	490/766 (64%)	307/454 (68%)	177/272 (65%)	6/40 (15%)
Aromatic	17/49 (35%)	12/26 (46%)	5/22 (23%)	0/1 (0%)
Overall	925/1301 (71%)	493/673 (73%)	350/494 (71%)	82/134 (61%)

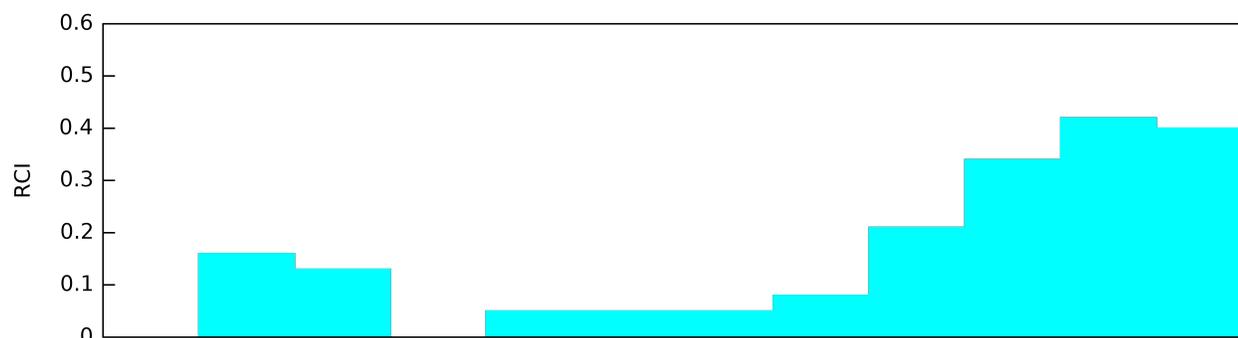
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots [i](#)

The images below report *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:



Random coil index (RCI) for chain B:

