Full wwPDB X-ray Structure Validation Report (i)

Sep 25, 2023 – 06:17 PM EDT

PDB ID	:	6BCD
Title	:	Crystal structure of Rev7-K44A/R124A/A135D in complex with Rev3-RBM2 (residues 1988-2014)
Authors	:	Rizzo, A.A.; Hao, B.; Li, Y.; Korzhnev, D.M.
Deposited on	:	2017-10-20
Resolution	:	1.43 Å(reported)

This is a Full wwPDB X-ray 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/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

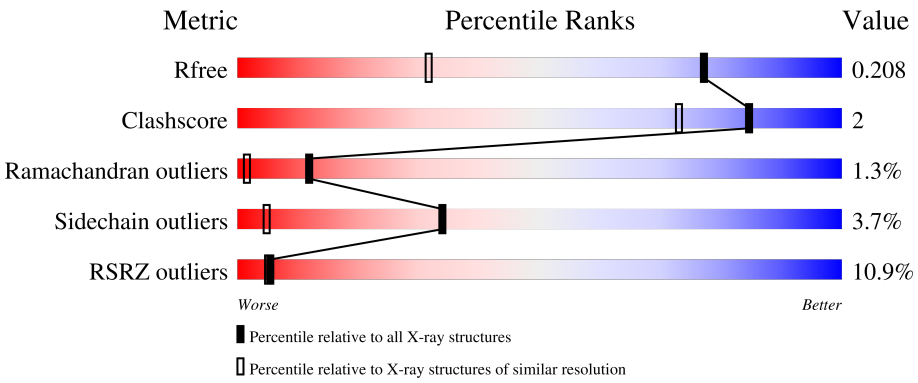
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.43 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2021 (1.46-1.42)
Clashscore	141614	2086 (1.46-1.42)
Ramachandran outliers	138981	2047 (1.46-1.42)
Sidechain outliers	138945	2047 (1.46-1.42)
RSRZ outliers	127900	1993 (1.46-1.42)

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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	227	10%; 74%; 15%; • ; 10%
2	B	28	7%; 86%; • ; 11%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2086 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 Mitotic spindle assembly checkpoint protein MAD2B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	205	1700	1090	285	314	11	0	6	0

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	initiating methionine	UNP Q9UI95
A	-14	GLY	-	expression tag	UNP Q9UI95
A	-13	SER	-	expression tag	UNP Q9UI95
A	-12	SER	-	expression tag	UNP Q9UI95
A	-11	HIS	-	expression tag	UNP Q9UI95
A	-10	HIS	-	expression tag	UNP Q9UI95
A	-9	HIS	-	expression tag	UNP Q9UI95
A	-8	HIS	-	expression tag	UNP Q9UI95
A	-7	HIS	-	expression tag	UNP Q9UI95
A	-6	HIS	-	expression tag	UNP Q9UI95
A	-5	SER	-	expression tag	UNP Q9UI95
A	-4	GLN	-	expression tag	UNP Q9UI95
A	-3	ASP	-	expression tag	UNP Q9UI95
A	-2	PRO	-	expression tag	UNP Q9UI95
A	-1	ASN	-	expression tag	UNP Q9UI95
A	0	SER	-	expression tag	UNP Q9UI95
A	44	ALA	LYS	engineered mutation	UNP Q9UI95
A	124	ALA	ARG	engineered mutation	UNP Q9UI95
A	135	ASP	ALA	engineered mutation	UNP Q9UI95

- Molecule 2 is a protein called DNA polymerase zeta catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	25	199	129	36	31	3	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1987	MET	-	initiating methionine	UNP O60673

- Molecule 3 is water.

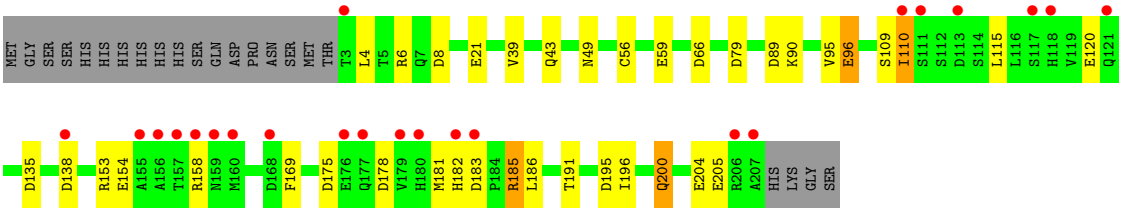
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	157	157	157	0	0
			Total	O		
3	B	30	30	30	0	0

3 Residue-property plots (i)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

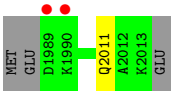
• Molecule 1: Mitotic spindle assembly checkpoint protein MAD2B

Chain A:



• Molecule 2: DNA polymerase zeta catalytic subunit

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	64.58Å 64.58Å 116.55Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	116.55 – 1.43 32.29 – 1.43	Depositor EDS
% Data completeness (in resolution range)	98.5 (116.55-1.43) 98.5 (32.29-1.43)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.01 (at 1.43Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.175 , 0.197 0.183 , 0.208	Depositor DCC
R_{free} test set	2521 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å^2)	20.0	Xtriage
Anisotropy	0.617	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 47.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	2086	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.65% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	1.27	7/1739 (0.4%)	1.29	15/2367 (0.6%)
2	B	1.22	0/202	1.17	0/271
All	All	1.27	7/1941 (0.4%)	1.28	15/2638 (0.6%)

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

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	59	GLU	CD-OE1	8.23	1.34	1.25
1	A	96	GLU	CB-CG	-7.10	1.38	1.52
1	A	154	GLU	CA-C	-5.55	1.38	1.52
1	A	21	GLU	CG-CD	5.47	1.60	1.51
1	A	205	GLU	CD-OE1	5.18	1.31	1.25
1	A	21	GLU	CD-OE2	-5.11	1.20	1.25
1	A	154	GLU	CD-OE2	-5.09	1.20	1.25

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	66	ASP	CB-CG-OD2	-11.66	107.80	118.30
1	A	153	ARG	NE-CZ-NH1	10.62	125.61	120.30
1	A	79	ASP	CB-CG-OD1	10.10	127.39	118.30
1	A	181	MET	CG-SD-CE	-9.65	84.76	100.20
1	A	195	ASP	CB-CG-OD1	6.99	124.59	118.30
1	A	185	ARG	NE-CZ-NH1	6.93	123.77	120.30
1	A	89	ASP	CB-CG-OD1	6.74	124.36	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	178	ASP	CB-CG-OD2	6.55	124.19	118.30
1	A	8	ASP	CB-CG-OD2	-5.79	113.09	118.30
1	A	200	GLN	CA-CB-CG	5.54	125.59	113.40
1	A	153	ARG	NE-CZ-NH2	-5.33	117.64	120.30
1	A	66	ASP	OD1-CG-OD2	5.26	133.29	123.30
1	A	169	PHE	CB-CG-CD2	-5.22	117.15	120.80
1	A	6	ARG	CG-CD-NE	-5.08	101.12	111.80
1	A	154	GLU	CA-C-N	-5.07	106.06	117.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	109	SER	Peptide

5.2 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 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	1700	0	1715	9	0
2	B	199	0	221	0	0
3	A	157	0	0	2	0
3	B	30	0	0	0	0
All	All	2086	0	1936	9	0

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 2.

All (9) 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:A:191:THR:HG22	1:A:200:GLN:HG3	1.51	0.92
1:A:175[B]:ASP:OD1	3:A:301:HOH:O	2.04	0.76
1:A:49[B]:ASN:ND2	1:A:120:GLU:OE1	2.32	0.62
1:A:138:ASP:OD2	1:A:185:ARG:NH2	2.34	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:LEU:HB3	1:A:196:ILE:HD11	1.88	0.54
1:A:43:GLN:CD	1:A:56[B]:CYS:SG	2.90	0.50
1:A:39:VAL:HG12	3:A:389:HOH:O	2.16	0.46
1:A:186:LEU:CD2	1:A:204:GLU:HG2	2.49	0.43
1:A:185:ARG:HH11	1:A:185:ARG:HB2	1.85	0.41

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 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 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	209/227 (92%)	204 (98%)	2 (1%)	3 (1%)	11 1
2	B	23/28 (82%)	23 (100%)	0	0	100 100
All	All	232/255 (91%)	227 (98%)	2 (1%)	3 (1%)	12 1

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	110	ILE
1	A	182	HIS
1	A	158	ARG

5.3.2 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 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	199/213 (93%)	191 (96%)	8 (4%)	31	4
2	B	23/26 (88%)	22 (96%)	1 (4%)	29	3
All	All	222/239 (93%)	213 (96%)	9 (4%)	34	4

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	90	LYS
1	A	95	VAL
1	A	96	GLU
1	A	110	ILE
1	A	135[A]	ASP
1	A	135[B]	ASP
1	A	183	ASP
2	B	2011	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	205/227 (90%)	0.39	23 (11%)	5	4	17, 24, 55, 102	0
2	B	25/28 (89%)	0.25	2 (8%)	12	13	18, 26, 51, 56	0
All	All	230/255 (90%)	0.37	25 (10%)	5	5	17, 24, 55, 102	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	179	VAL	10.2
1	A	158	ARG	10.2
1	A	182	HIS	7.7
1	A	159	ASN	6.9
1	A	110	ILE	6.2
1	A	183	ASP	5.7
1	A	207	ALA	4.6
2	B	1989	ASP	4.1
1	A	180	HIS	4.1
1	A	111	SER	3.6
1	A	155	ALA	3.6
1	A	157	THR	3.4
1	A	206	ARG	3.0
1	A	113	ASP	2.9
1	A	3	THR	2.9
2	B	1990	LYS	2.9
1	A	156	ALA	2.8
1	A	121	GLN	2.7
1	A	160	MET	2.7
1	A	118	HIS	2.6
1	A	176	GLU	2.6
1	A	177	GLN	2.4
1	A	117	SER	2.4
1	A	168	ASP	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	138	ASP	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.