



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 05:31 PM GMT

PDB ID : 3MJX  
Title : Crystal structure of myosin-2 motor domain in complex with ADP-Metavanadate and blebbistatin  
Authors : Fedorov, R.; Baruch, P.; Bauer, S.; Manstein, D.J.  
Deposited on : 2010-04-13  
Resolution : 2.20 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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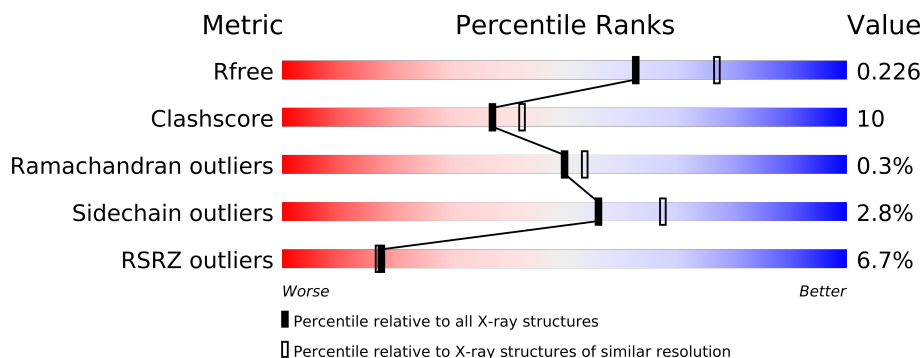
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.20 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))
$R_{free}$	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	788	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	MG	A	901	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6089 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Myosin-2 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	690	Total	C	N	O	S	9	0	0
			5535	3520	950	1049	16			

There are 28 discrepancies between the modelled and reference sequences:

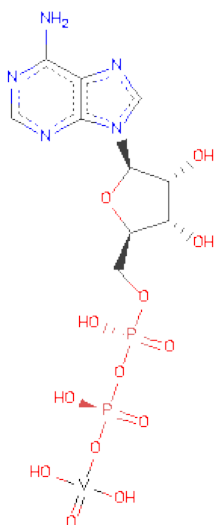
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	EXPRESSION TAG	UNP P08799
A	-9	HIS	-	EXPRESSION TAG	UNP P08799
A	-8	HIS	-	EXPRESSION TAG	UNP P08799
A	-7	HIS	-	EXPRESSION TAG	UNP P08799
A	-6	HIS	-	EXPRESSION TAG	UNP P08799
A	-5	HIS	-	EXPRESSION TAG	UNP P08799
A	-4	HIS	-	EXPRESSION TAG	UNP P08799
A	-3	HIS	-	EXPRESSION TAG	UNP P08799
A	-2	ASP	-	EXPRESSION TAG	UNP P08799
A	-1	GLY	-	EXPRESSION TAG	UNP P08799
A	0	THR	-	EXPRESSION TAG	UNP P08799
A	1	GLU	-	EXPRESSION TAG	UNP P08799
A	762	LEU	-	EXPRESSION TAG	UNP P08799
A	763	GLU	-	EXPRESSION TAG	UNP P08799
A	764	SER	-	EXPRESSION TAG	UNP P08799
A	765	ASN	-	EXPRESSION TAG	UNP P08799
A	766	GLU	-	EXPRESSION TAG	UNP P08799
A	767	PRO	-	EXPRESSION TAG	UNP P08799
A	768	PRO	-	EXPRESSION TAG	UNP P08799
A	769	MET	-	EXPRESSION TAG	UNP P08799
A	770	ASP	-	EXPRESSION TAG	UNP P08799
A	771	PHE	-	EXPRESSION TAG	UNP P08799
A	772	ASP	-	EXPRESSION TAG	UNP P08799
A	773	ASP	-	EXPRESSION TAG	UNP P08799
A	774	ASP	-	EXPRESSION TAG	UNP P08799
A	775	ILE	-	EXPRESSION TAG	UNP P08799
A	776	PRO	-	EXPRESSION TAG	UNP P08799

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Chain	Residue	Modelled	Actual	Comment	Reference
A	777	PHE	-	EXPRESSION TAG	UNP P08799

- Molecule 2 is ADP METAVANADATE (three-letter code: AD9) (formula:  $C_{10}H_{16}N_5O_{13}P_2V$ ).

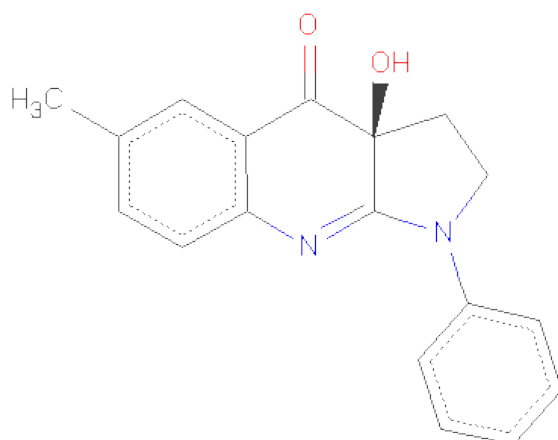


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	V		
2	A	1	31	10	5	13	2	1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is (-)-1-PHENYL-1,2,3,4-TETRAHYDRO-4-HYDROXYPYRROLO[2,3-B]-7-METHYLQUINOLIN-4-ONE (three-letter code: BIT) (formula:  $C_{18}H_{16}N_2O_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			22	18	2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	500	Total	O	0	0
			500	500		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Myosin-2 heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.31Å 147.03Å 154.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 24.86 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.20) 99.9 (24.86-2.20)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.91 (at 2.19Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.204 , 0.226 0.198 , 0.226	Depositor DCC
$R_{free}$ test set	2592 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.8	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 73.9	EDS
Estimated twinning fraction	0.021 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.028 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 51830 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6089	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, BIT, AD9

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	0.33	0/5643	0.56	1/7613 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	498	LYS	N-CA-C	6.77	129.28	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5535	0	5499	112	0
2	A	31	0	14	0	0
3	A	1	0	0	0	0
4	A	22	0	16	5	0
5	A	500	0	0	8	2
All	All	6089	0	5529	112	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including



hydrogens) of the entry. The overall clashscore for this entry is 10.

All (112) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:622:LYS:H	1:A:622:LYS:HE2	1.23	1.03
1:A:465:SER:H	1:A:468:GLN:HE21	1.20	0.90
1:A:461:PHE:H	1:A:464:ASN:HD21	1.17	0.89
1:A:343:SER:HA	1:A:346:LYS:HD3	1.58	0.85
1:A:499:ILE:HD12	1:A:499:ILE:N	1.91	0.85
1:A:499:ILE:H	1:A:499:ILE:HD12	1.42	0.84
1:A:291:GLU:HA	1:A:294:LYS:HD2	1.59	0.84
1:A:622:LYS:H	1:A:622:LYS:CE	1.90	0.83
1:A:68:GLN:HG2	1:A:69:ASP:H	1.48	0.78
1:A:622:LYS:HE2	1:A:622:LYS:N	2.00	0.76
1:A:497:GLU:HB3	1:A:499:ILE:HD11	1.70	0.74
1:A:262:LEU:H	1:A:637:GLN:HE22	1.37	0.72
1:A:33:ARG:HH21	1:A:79:GLN:HE22	1.38	0.71
1:A:293:LYS:HE3	5:A:1363:HOH:O	1.90	0.70
1:A:248:ASN:HD21	1:A:252:PHE:HB2	1.56	0.69
1:A:291:GLU:O	1:A:294:LYS:HG2	1.92	0.69
1:A:499:ILE:H	1:A:499:ILE:CD1	2.08	0.67
1:A:548:HIS:CE1	1:A:560:GLU:HG3	2.32	0.65
1:A:305:ASN:H	1:A:356:ASN:HD21	1.45	0.65
1:A:68:GLN:HG2	1:A:69:ASP:N	2.11	0.65
1:A:609:THR:HG23	1:A:613:ASN:ND2	2.13	0.64
1:A:465:SER:H	1:A:468:GLN:NE2	1.96	0.63
1:A:518:ASP:OD1	1:A:635:LYS:HD2	1.99	0.62
1:A:107:ARG:HD3	5:A:1471:HOH:O	2.01	0.61
1:A:499:ILE:O	1:A:499:ILE:HG22	2.01	0.61
1:A:610:LYS:HE3	1:A:614:ASP:OD2	2.01	0.60
1:A:553:LYS:HE2	1:A:553:LYS:HA	1.83	0.60
1:A:248:ASN:ND2	1:A:252:PHE:HB2	2.16	0.60
1:A:160:ASP:O	1:A:164:ARG:HG2	2.02	0.59
1:A:246:GLN:HB3	1:A:446:LYS:HB3	1.83	0.59
1:A:197:ALA:HA	1:A:253:ILE:CD1	2.34	0.58
1:A:467:GLU:HG3	4:A:902:BIT:H16	1.85	0.58
1:A:222:LEU:HD11	1:A:258:ILE:HD13	1.86	0.57
1:A:300:GLY:HA3	1:A:302:GLU:OE2	2.04	0.57
1:A:4:ILE:HD12	1:A:146:ARG:NH2	2.20	0.57
1:A:305:ASN:H	1:A:356:ASN:ND2	2.03	0.56
1:A:697:ILE:HG12	1:A:698:TYR:N	2.20	0.56
1:A:135:TYR:CD1	1:A:191:LYS:HD3	2.42	0.55
1:A:609:THR:HG23	1:A:613:ASN:HD22	1.72	0.55
1:A:289:THR:OG1	1:A:292:GLU:HG3	2.07	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:145:GLY:N	1:A:164:ARG:HH21	2.06	0.54
1:A:4:ILE:HD12	1:A:146:ARG:HH22	1.72	0.54
1:A:461:PHE:H	1:A:464:ASN:ND2	1.98	0.54
1:A:402:ARG:NH1	5:A:1371:HOH:O	2.43	0.52
1:A:531:GLU:O	1:A:534:VAL:HG22	2.10	0.51
1:A:634:TYR:CD1	4:A:902:BIT:H9	2.46	0.51
1:A:342:MET:HE3	1:A:345:PHE:HB2	1.93	0.51
1:A:48:GLU:OE1	1:A:65:VAL:HG11	2.12	0.50
1:A:609:THR:CG2	1:A:613:ASN:HD22	2.24	0.50
1:A:145:GLY:H	1:A:164:ARG:HH21	1.58	0.50
1:A:210:VAL:O	1:A:214:GLN:HG3	2.11	0.50
1:A:695:ARG:HG2	1:A:695:ARG:O	2.11	0.49
1:A:533:SER:O	1:A:589:LYS:HE2	2.13	0.49
1:A:22:SER:O	1:A:26:LYS:HG3	2.13	0.48
1:A:304:PHE:HA	1:A:356:ASN:HD21	1.78	0.48
1:A:467:GLU:CG	4:A:902:BIT:H16	2.43	0.48
1:A:296:LEU:HB2	1:A:298:LEU:HG	1.95	0.48
1:A:296:LEU:HD11	1:A:342:MET:HE1	1.96	0.48
1:A:289:THR:O	1:A:293:LYS:HG3	2.13	0.48
1:A:144:LYS:HD3	1:A:199:VAL:HG12	1.95	0.48
1:A:187:GLU:O	1:A:191:LYS:HG2	2.14	0.48
1:A:259:GLN:HG2	5:A:1035:HOH:O	2.14	0.48
1:A:20:GLY:HA3	1:A:24:LEU:HD23	1.96	0.47
1:A:7:ARG:HD3	1:A:7:ARG:H	1.80	0.47
1:A:520:ARG:HD3	1:A:521:GLN:N	2.29	0.47
1:A:499:ILE:CD1	1:A:499:ILE:N	2.61	0.46
1:A:246:GLN:HB3	1:A:446:LYS:CB	2.46	0.46
1:A:623:LYS:N	1:A:626:ASN:O	2.48	0.46
1:A:438:ASN:O	1:A:442:CYS:HB3	2.15	0.46
1:A:316:LYS:HD2	5:A:1194:HOH:O	2.16	0.46
1:A:147:ARG:HB2	1:A:150:GLU:CD	2.37	0.46
1:A:493:GLU:HG2	1:A:695:ARG:NH2	2.32	0.45
1:A:302:GLU:H	1:A:302:GLU:CD	2.20	0.45
1:A:212:GLU:O	1:A:216:LEU:HG	2.17	0.45
1:A:484:HIS:CD2	1:A:488:LYS:HD2	2.52	0.45
1:A:395:GLU:HA	1:A:407:GLN:O	2.16	0.45
1:A:162:ALA:O	1:A:173:GLN:HG3	2.17	0.44
1:A:306:TYR:O	1:A:307:LEU:HD23	2.17	0.44
1:A:497:GLU:O	1:A:498:LYS:HG2	2.17	0.44
1:A:467:GLU:HG3	4:A:902:BIT:C16	2.46	0.44
1:A:642:MET:O	1:A:646:GLU:HG2	2.17	0.44
1:A:21:ASP:OD1	1:A:23:ASP:HB2	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:532:GLN:HE21	1:A:543:LEU:CA	2.31	0.43
1:A:695:ARG:C	1:A:696:ILE:HD12	2.38	0.43
1:A:241:LYS:NZ	1:A:454:ASP:OD2	2.49	0.43
1:A:684:GLY:O	1:A:687:ILE:HG22	2.18	0.43
1:A:294:LYS:HG2	1:A:295:ALA:N	2.34	0.43
1:A:239:PHE:HA	4:A:902:BIT:O1	2.18	0.43
1:A:646:GLU:HA	1:A:646:GLU:OE1	2.18	0.43
1:A:138:GLU:O	1:A:142:ILE:HG13	2.18	0.43
1:A:622:LYS:H	1:A:622:LYS:CD	2.31	0.43
1:A:63:LYS:HA	1:A:68:GLN:O	2.18	0.43
1:A:697:ILE:HG12	1:A:698:TYR:H	1.84	0.42
1:A:615:PRO:O	1:A:619:SER:OG	2.35	0.42
1:A:327:THR:HG22	1:A:331:MET:CE	2.49	0.42
1:A:482:PHE:CZ	1:A:486:MET:HG3	2.54	0.42
1:A:520:ARG:HD3	1:A:521:GLN:CB	2.49	0.42
1:A:2:ASN:ND2	1:A:4:ILE:H	2.18	0.42
1:A:244:GLU:O	1:A:256:ALA:HA	2.20	0.41
1:A:132:ILE:HG22	1:A:134:ILE:HG23	2.02	0.41
1:A:248:ASN:OD1	1:A:250:ALA:HB3	2.20	0.41
1:A:7:ARG:HA	1:A:12:HIS:CG	2.55	0.41
1:A:234:ASN:ND2	5:A:1030:HOH:O	2.54	0.41
1:A:532:GLN:HE21	1:A:543:LEU:HA	1.85	0.41
1:A:390:GLU:HG3	1:A:394:MET:CE	2.51	0.41
1:A:446:LYS:HB3	5:A:1511:HOH:O	2.21	0.41
1:A:534:VAL:O	1:A:536:PRO:HD3	2.21	0.40
1:A:129:PHE:CZ	1:A:662:GLN:HA	2.55	0.40
1:A:264:GLU:HG2	1:A:264:GLU:O	2.21	0.40
1:A:688:THR:HA	5:A:1447:HOH:O	2.21	0.40
1:A:222:LEU:O	1:A:226:GLY:N	2.48	0.40
1:A:247:PHE:HA	1:A:252:PHE:O	2.22	0.40

All (2) 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	Distance(Å)	Clash(Å)
5:A:1389:HOH:O	5:A:1389:HOH:O[3_555]	1.39	0.81
5:A:1380:HOH:O	5:A:1380:HOH:O[3_655]	1.80	0.40

## 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	686/788 (87%)	655 (96%)	29 (4%)	2 (0%)	50 53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	ARG
1	A	499	ILE

### 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	606/691 (88%)	589 (97%)	17 (3%)	56 67

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	7	ARG
1	A	12	HIS
1	A	17	VAL
1	A	69	ASP
1	A	314	ASP
1	A	360	GLU
1	A	446	LYS
1	A	497	GLU
1	A	498	LYS
1	A	520	ARG
1	A	535	PHE

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Mol	Chain	Res	Type
1	A	622	LYS
1	A	635	LYS
1	A	669	ASP
1	A	694	ASN
1	A	695	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	ASN
1	A	71	GLN
1	A	79	GLN
1	A	171	GLN
1	A	194	GLN
1	A	234	ASN
1	A	283	GLN
1	A	305	ASN
1	A	338	GLN
1	A	356	ASN
1	A	407	GLN
1	A	439	ASN
1	A	443	GLN
1	A	464	ASN
1	A	468	GLN
1	A	484	HIS
1	A	500	ASN
1	A	521	GLN
1	A	532	GLN
1	A	613	ASN
1	A	616	ASN
1	A	637	GLN
1	A	679	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	AD9	A	900	3,5	33,33,33	1.85	8 (24%)	45,52,52	1.36	4 (8%)
4	BIT	A	902	-	25,25,25	1.69	2 (8%)	38,38,38	3.72	14 (36%)

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	AD9	A	900	3,5	-	0/16/38/38	0/1/3/3
4	BIT	A	902	-	1/1/4/4	0/4/34/34	0/1/4/4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	902	BIT	C5-C10	5.29	1.48	1.40
2	A	900	AD9	PB-O1B	4.85	1.69	1.51
2	A	900	AD9	PA-O3A	4.00	1.67	1.59
2	A	900	AD9	O4'-C1'	3.90	1.47	1.41
4	A	902	BIT	C11-N2	3.71	1.33	1.29
2	A	900	AD9	PA-O2A	3.50	1.70	1.55
2	A	900	AD9	C8-N9	3.15	1.41	1.36
2	A	900	AD9	PB-O3A	3.14	1.65	1.59
2	A	900	AD9	C2-N3	2.24	1.36	1.32
2	A	900	AD9	C2'-C1'	2.18	1.56	1.53

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	902	BIT	C2-C3-C11	-11.05	88.60	102.91
4	A	902	BIT	C3-C11-N2	-10.19	117.47	126.24
4	A	902	BIT	O1-C3-C2	-9.50	86.39	109.79
4	A	902	BIT	C2-C3-C4	-7.26	93.54	112.67
4	A	902	BIT	O1-C3-C11	6.57	126.98	109.18
2	A	900	AD9	O3B-PB-O3A	4.64	112.11	102.03
4	A	902	BIT	O1-C3-C4	4.06	123.63	108.32
4	A	902	BIT	O2-C4-C3	3.87	127.29	119.93
4	A	902	BIT	C1-N1-C11	-3.64	106.82	112.67
4	A	902	BIT	C3-C4-C5	-3.23	108.03	116.88
4	A	902	BIT	N1-C11-N2	3.16	130.86	125.78
2	A	900	AD9	N3-C2-N1	-2.85	126.32	128.71
2	A	900	AD9	O2B-PB-O3B	2.83	117.43	105.35
4	A	902	BIT	C3-C11-N1	2.71	111.66	108.69
4	A	902	BIT	C1-N1-C12	2.61	125.11	120.61
2	A	900	AD9	O3B-PB-O1B	-2.47	99.06	109.49
4	A	902	BIT	C10-N2-C11	2.19	120.23	116.26
4	A	902	BIT	C9-C10-N2	2.11	121.83	118.51

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	902	BIT	C3

There are no torsion outliers.

There are no ring outliers.

## 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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	688/788 (87%)	0.10	46 (6%) 17 17	18, 41, 76, 108	6 (0%)

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	698	TYR	8.4
1	A	697	ILE	7.2
1	A	696	ILE	6.8
1	A	170	ARG	5.6
1	A	535	PHE	5.6
1	A	536	PRO	5.2
1	A	469	LEU	4.5
1	A	623	LYS	4.3
1	A	365	GLU	4.3
1	A	65	VAL	4.2
1	A	521	GLN	3.9
1	A	496	LYS	3.9
1	A	348	ILE	3.7
1	A	442	CYS	3.7
1	A	3	PRO	3.5
1	A	443	GLN	3.4
1	A	44	ARG	3.2
1	A	147	ARG	3.2
1	A	4	ILE	3.1
1	A	363	ALA	3.1
1	A	520	ARG	3.0
1	A	280	ILE	3.0
1	A	124	VAL	2.9
1	A	299	ALA	2.8
1	A	8	THR	2.7
1	A	364	GLY	2.5
1	A	294	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	517	ILE	2.4
1	A	525	ILE	2.3
1	A	291	GLU	2.3
1	A	499	ILE	2.3
1	A	537	ASN	2.2
1	A	347	ILE	2.2
1	A	106	LEU	2.2
1	A	290	ALA	2.2
1	A	66	ASP	2.2
1	A	526	LEU	2.2
1	A	5	HIS	2.2
1	A	329	GLN	2.2
1	A	624	GLY	2.1
1	A	497	GLU	2.1
1	A	362	GLY	2.1
1	A	626	ASN	2.1
1	A	498	LYS	2.0
1	A	681	VAL	2.0
1	A	125	ALA	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	A	901	1/1	0.10	2.01	26,26,26,26	0
4	BIT	A	902	22/22	0.15	1.04	32,36,43,49	0
2	AD9	A	900	31/31	0.10	0.36	21,30,39,48	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.