Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2023 – 09:51 PM EDT

PDB ID	:	3BZ7
Title	:	Crystal Structures of (S)-(-)-Blebbistatin Analogs bound to Dictyostelium discoideum myosin II
Authors	:	Allingham, J.S.; Rayment, I.
Deposited on	:	2008-01-17
Resolution	:	2.00 Å(reported)

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

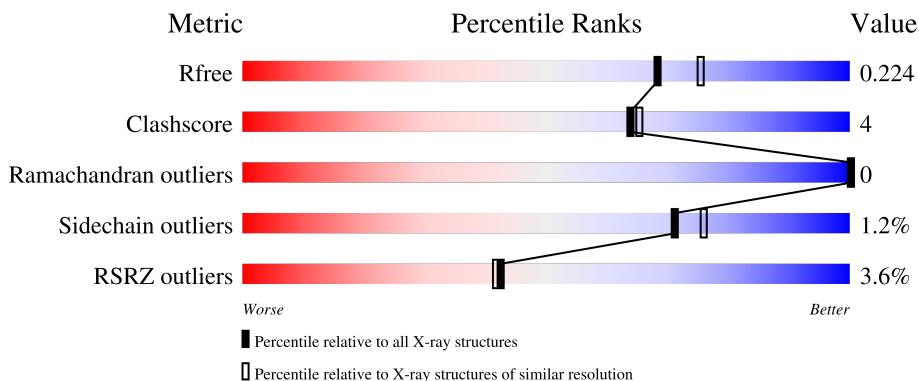|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 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 2.00 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
Rfree		0.224
Clashscore		4
Ramachandran outliers		0
Sidechain outliers		1.2%
RSRZ outliers		3.6%

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))
R$_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	762	3% 85% 7% 8%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6260 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 Myosin-2 heavy chain, non muscle.

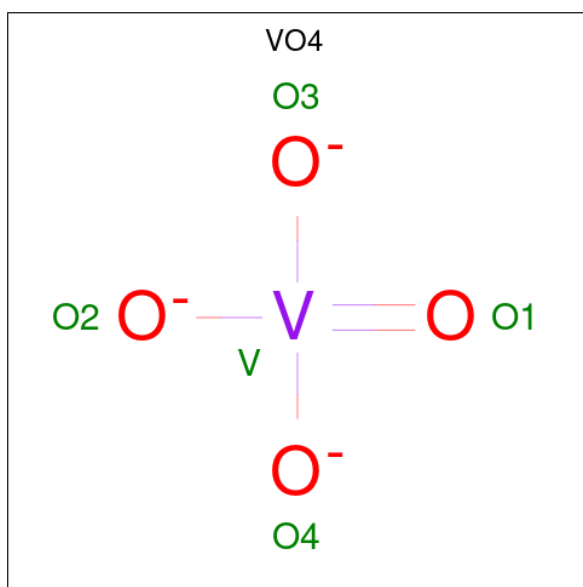| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	703	Total 5546	C 3548	N 934	O 1049	S 15	0	12	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP P08799
A	760	LEU	-	SEE REMARK 999	UNP P08799
A	761	PRO	-	SEE REMARK 999	UNP P08799
A	762	ASN	-	SEE REMARK 999	UNP P08799

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).
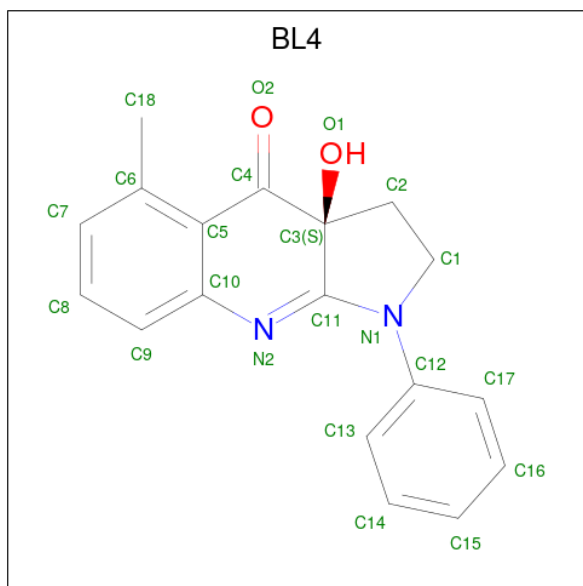
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total 2	Mg 2	0	0

- Molecule 3 is VANADATE ION (three-letter code: VO4) (formula: O_4V).

VO4

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 5	O 4	V 1	0	0

- Molecule 4 is (3aS)-3a-hydroxy-5-methyl-1-phenyl-1,2,3,3a-tetrahydro-4H-pyrrolo[2,3-b]quinolin-4-one (three-letter code: BL4) (formula: $C_{18}H_{16}N_2O_2$).

BL4

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

- Molecule 5 is A D E N O S I N E - 5' - D I P H O S P H A T E (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

ADP
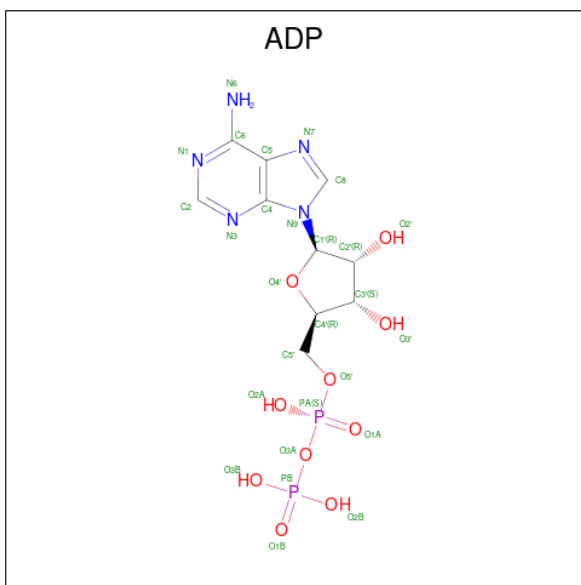
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	A	1	27	10	5	10	2	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	658	658	658	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: Myosin-2 heavy chain, non muscle
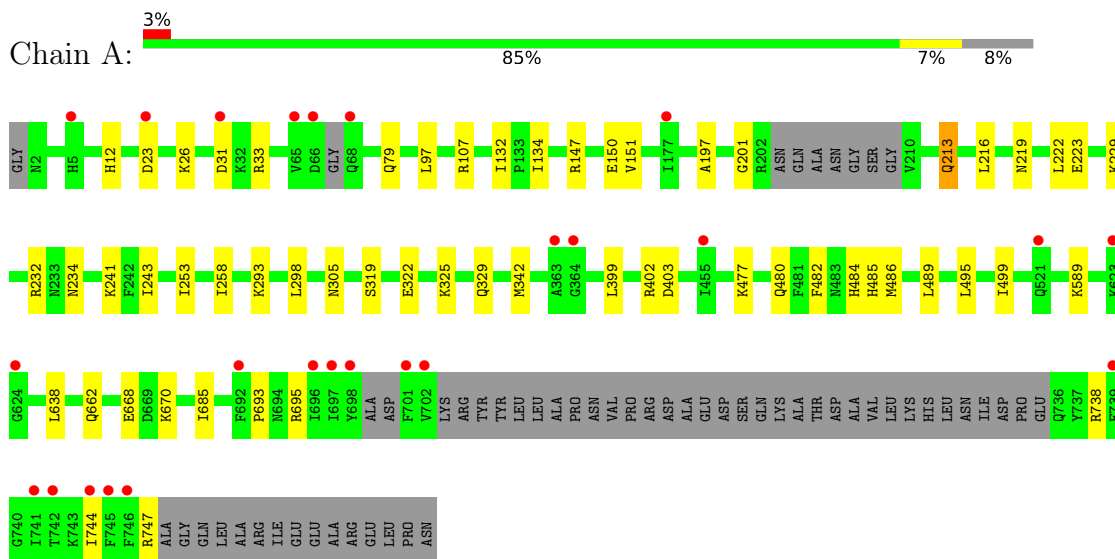
4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	88.22Å 146.00Å 153.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.51 – 2.00 35.50 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (35.51-2.00) 99.8 (35.50-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.83 (at 2.00Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.183 , 0.223 0.185 , 0.224	Depositor DCC
R_{free} test set	3376 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	23.6	Xtriage
Anisotropy	0.365	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 61.8	EDS
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.009 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.020 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	6260	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 ⓘ

5.1   Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: BL4, MG, ADP, VO4

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	0.73	1/5682 (0.0%)	0.67	4/7678 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	670	LYS	C-N	-5.05	1.22	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	402	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	A	23	ASP	CB-CG-OD2	5.21	122.99	118.30
1	A	31	ASP	CB-CG-OD2	5.21	122.99	118.30
1	A	402	ARG	NE-CZ-NH1	5.04	122.82	120.30

There are no chirality outliers.

There are no planarity outliers.

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	5546	0	5315	46	0
2	A	2	0	0	0	0
3	A	5	0	0	0	0

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W O R L D W I D E
wwPDB
PROTEIN DATA BANK

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	22	0	16	0	0
5	A	27	0	12	0	0
6	A	658	0	0	12	2
All	All	6260	0	5343	46	2

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 4.

All (46) 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:668:GLU:OE1	6:A:1207:HOH:O	1.69	1.10
1:A:107[B]:ARG:NH1	6:A:1257:HOH:O	1.84	1.05
1:A:305[B]:ASN:OD1	6:A:1284:HOH:O	1.75	1.05
1:A:485[A]:HIS:ND1	6:A:1596:HOH:O	2.03	0.90
1:A:325:LYS:O	1:A:329:GLN:HG3	1.74	0.88
1:A:97:LEU:HD11	1:A:685:ILE:HG22	1.55	0.86
1:A:97:LEU:HD11	1:A:685:ILE:CG2	2.08	0.83
1:A:293:LYS:HG2	1:A:298:LEU:HD12	1.76	0.68
1:A:232:ARG:NH1	6:A:1464:HOH:O	2.26	0.67
1:A:213:GLN:HG3	6:A:1630:HOH:O	1.96	0.66
1:A:234:ASN:H	1:A:662:GLN:HE22	1.44	0.66
1:A:97:LEU:CD1	1:A:685:ILE:HG22	2.25	0.65
1:A:241:LYS:HD2	1:A:243:ILE:HD11	1.77	0.65
1:A:33:ARG:HH21	1:A:79:GLN:HE22	1.44	0.64
1:A:499:ILE:CG1	1:A:738:ARG:HB3	2.30	0.61
1:A:484:HIS:CE1	1:A:489:LEU:HG	2.37	0.59
1:A:484:HIS:CE1	1:A:489:LEU:HD11	2.38	0.59
1:A:97:LEU:HD21	1:A:685:ILE:HG21	1.87	0.56
1:A:97:LEU:CD1	1:A:685:ILE:CG2	2.83	0.55
1:A:201:GLY:O	6:A:1448:HOH:O	2.18	0.53
1:A:484:HIS:CE1	1:A:489:LEU:CG	2.91	0.53
1:A:213:GLN:NE2	1:A:213:GLN:HA	2.24	0.53
1:A:97:LEU:HD11	1:A:685:ILE:HG21	1.90	0.51
1:A:485[A]:HIS:CE1	6:A:1596:HOH:O	2.56	0.51
1:A:26:LYS:HD2	6:A:1504:HOH:O	2.12	0.49
1:A:229:LYS:HG3	1:A:234:ASN:HD22	1.78	0.49
1:A:197:ALA:HA	1:A:253:ILE:HD12	1.94	0.48
1:A:243:ILE:HD12	1:A:258:ILE:HG12	1.95	0.48
1:A:219:ASN:ND2	1:A:223:GLU:OE2	2.46	0.48
1:A:484:HIS:CE1	1:A:489:LEU:CD1	2.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:480[A]:GLN:HA	1:A:480[A]:GLN:OE1	2.16	0.46
1:A:589[A]:LYS:NZ	6:A:1484:HOH:O	2.47	0.46
1:A:147:ARG:HB2	1:A:150:GLU:HG3	1.97	0.45
1:A:222:LEU:HD11	1:A:258:ILE:HD13	1.99	0.45
1:A:499:ILE:N	6:A:1218:HOH:O	2.48	0.45
1:A:319:SER:OG	1:A:322[B]:GLU:HG2	2.17	0.44
1:A:482:PHE:CZ	1:A:486:MET:HG3	2.54	0.43
1:A:477:LYS:HG3	1:A:638:LEU:HD21	2.01	0.42
1:A:132:ILE:HG22	1:A:134:ILE:HG23	2.00	0.42
1:A:495:LEU:CG	6:A:1636:HOH:O	2.67	0.41
1:A:399:LEU:HA	1:A:403:ASP:O	2.20	0.41
1:A:482:PHE:CE1	1:A:486:MET:HG3	2.55	0.41
1:A:693:PRO:HD2	1:A:747:ARG:HA	2.03	0.41

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	Interatomic distance (Å)	Clash overlap (Å)
6:A:1480:HOH:O	6:A:1480:HOH:O[3_655]	1.80	0.40
6:A:1170:HOH:O	6:A:1186:HOH:O[3_555]	2.14	0.06

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	702/762 (92%)	691 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	572/665 (86%)	565 (99%)	7 (1%)	71	76

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	HIS
1	A	151	VAL
1	A	213	GLN
1	A	216	LEU
1	A	342	MET
1	A	695	ARG
1	A	744	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	GLN
1	A	213	GLN
1	A	234	ASN
1	A	283	GLN
1	A	338	GLN
1	A	484	HIS
1	A	500	ASN
1	A	532	GLN
1	A	606	ASN
1	A	613	ASN
1	A	616	ASN
1	A	662	GLN

5.3.3 RNA ⓘ

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)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	#$|Z| > 2$
5	ADP	A	1000	2	24,29,29	1.15	3 (12%)	29,45,45	1.18	3 (10%)
4	BL4	A	800	-	21,25,25	2.46	5 (23%)	25,38,38	2.17	9 (36%)
3	VO4	A	998	2	1,4,4	0.95	0	-		

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
5	ADP	A	1000	2	-	3/12/32/32	0/3/3/3
4	BL4	A	800	-	-	0/4/34/34	0/3/4/4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	800	BL4	C11-N2	7.69	1.39	1.29
4	A	800	BL4	O1-C3	4.84	1.51	1.42
4	A	800	BL4	C8-C7	3.03	1.45	1.38
5	A	1000	ADP	C5-C4	2.64	1.47	1.40
5	A	1000	ADP	O4'-C1'	2.50	1.44	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	800	BL4	O2-C4	2.42	1.25	1.21
4	A	800	BL4	C5-C6	2.40	1.43	1.40
5	A	1000	ADP	C4-N3	2.32	1.38	1.35

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	800	BL4	C2-C1-N1	4.53	108.13	103.36
4	A	800	BL4	C10-C5-C6	-4.42	116.60	119.37
4	A	800	BL4	C10-N2-C11	3.71	121.73	116.28
4	A	800	BL4	C9-C10-N2	-3.20	114.34	118.59
4	A	800	BL4	C17-C12-N1	3.06	124.65	120.18
5	A	1000	ADP	N3-C2-N1	-2.91	124.12	128.68
4	A	800	BL4	C13-C12-N1	-2.90	115.94	120.18
4	A	800	BL4	C12-N1-C11	2.89	132.58	127.94
5	A	1000	ADP	C2-N1-C6	2.52	123.07	118.75
4	A	800	BL4	C1-N1-C12	-2.31	117.44	120.76
5	A	1000	ADP	O3B-PB-O1B	2.12	118.99	110.68
4	A	800	BL4	C18-C6-C7	-2.11	116.19	120.31

There are no chirality outliers.
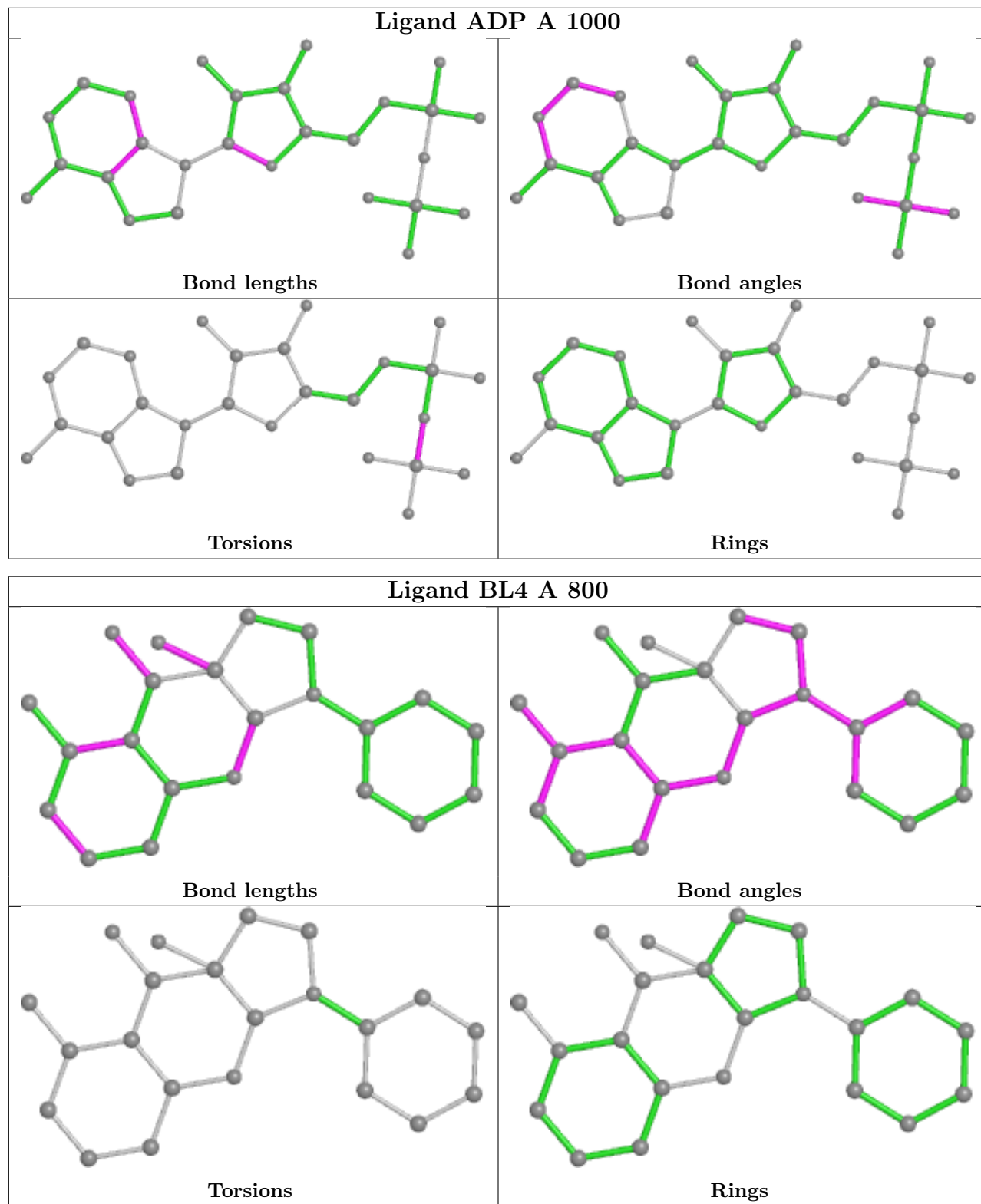
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1000	ADP	PA-O3A-PB-O3B
5	A	1000	ADP	PA-O3A-PB-O1B
5	A	1000	ADP	PA-O3A-PB-O2B

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.

Ligand ADP A 1000

Bond lengths   Bond angles

Torsions   Rings

Ligand BL4 A 800

Bond lengths   Bond angles

Torsions   Rings

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, 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(Å²)	Q<0.9
1	A	703/762 (92%)	-0.01	25 (3%)	42	42	11, 23, 44, 74	11 (1%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	65	VAL	6.6
1	A	698	TYR	5.3
1	A	697	ILE	4.7
1	A	696	ILE	4.3
1	A	702	VAL	4.2
1	A	363	ALA	4.1
1	A	624	GLY	3.4
1	A	521	GLN	3.1
1	A	744	ILE	2.8
1	A	746	PHE	2.6
1	A	31	ASP	2.5
1	A	742	THR	2.5
1	A	741	ILE	2.4
1	A	701	PHE	2.4
1	A	5	HIS	2.4
1	A	739	PHE	2.3
1	A	623	LYS	2.2
1	A	177	ILE	2.2
1	A	455	ILE	2.2
1	A	692	PHE	2.2
1	A	23	ASP	2.2
1	A	364	GLY	2.2
1	A	745	PHE	2.1
1	A	66	ASP	2.0
1	A	68	GLN	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 monosaccharides 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. The B-factors column lists the minimum, median, 95th 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.

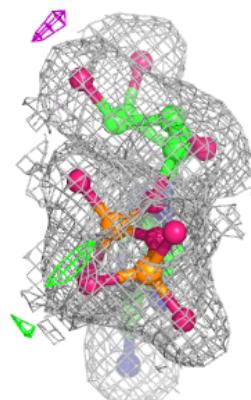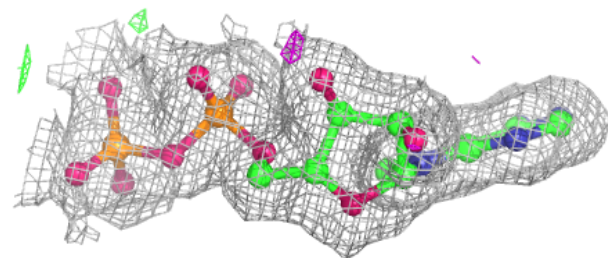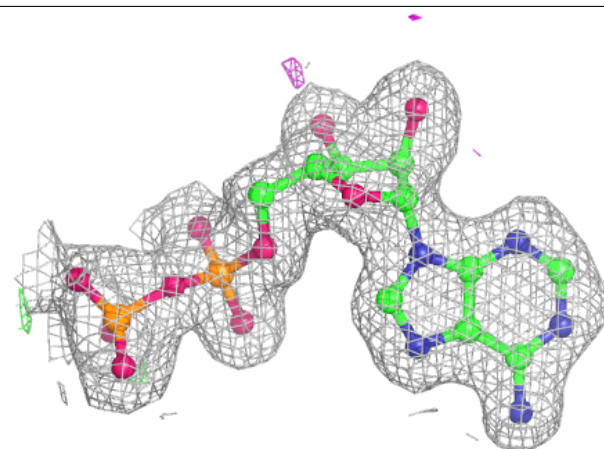| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	BL4	A	800	22/22	0.94	0.13	19,20,21,22	0
2	MG	A	999	1/1	0.97	0.05	23,23,23,23	1
3	VO4	A	998	5/5	0.99	0.16	12,12,13,15	0
2	MG	A	997	1/1	0.99	0.19	13,13,13,13	0
5	ADP	A	1000	27/27	0.99	0.11	12,16,17,19	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around BL4 A 800:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)
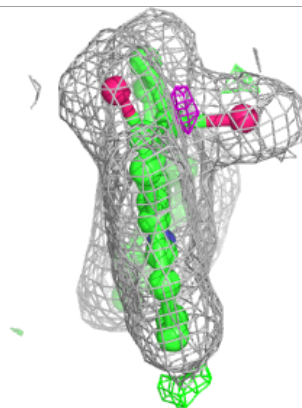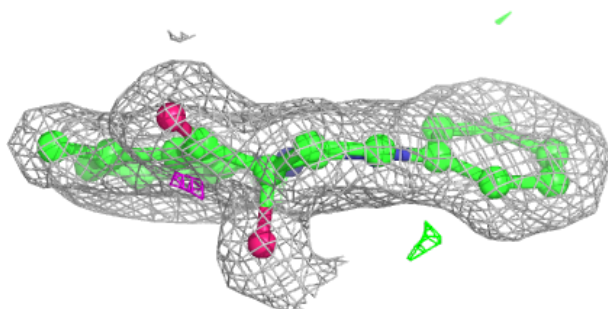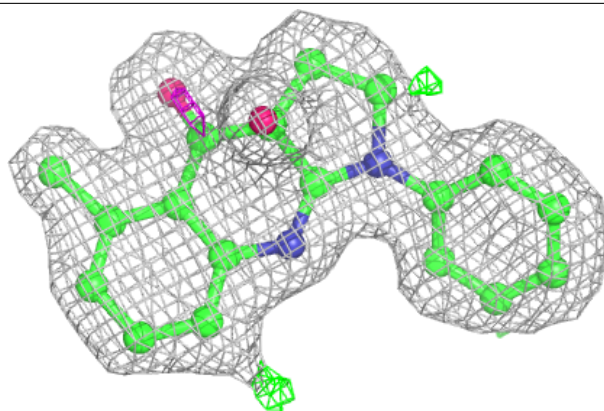
Electron density around ADP A 1000:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

6.5 Other polymers ⓘ

There are no such residues in this entry.