WORLDWIDE PDB

PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Jun 13, 2024 – 12:15 AM EDT

PDB ID	:	3RRM
Title	:	S. cerevisiae dbp5 l327v bound to nup159, gle1 h337r, ip6 and adp
Authors	:	Montpetit, B.; Thomsen, N.D.; Helmke, K.J.; Seeliger, M.A.; Berger, J.M.; Weis, K.
Deposited on	:	2011-04-29
Resolution	:	2.90 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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

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 2.90 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.
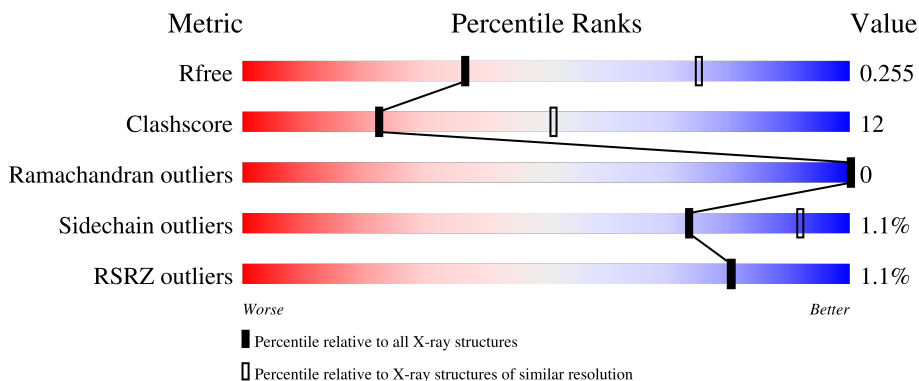
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	395	2% — 70% — 25% — • 5%
2	B	297	72% — 27% — •
3	C	388	% — 68% — 28% — 5%

2 Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 8323 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 ATP-dependent RNA helicase DBP5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	375	Total 2948	C 1869	N 512	O 553	S 14	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	88	GLY	-	expression tag	UNP P20449
A	89	ALA	-	expression tag	UNP P20449
A	90	MET	-	expression tag	UNP P20449
A	327	VAL	LEU	engineered mutation	UNP P20449

- Molecule 2 is a protein called Nucleoporin GLE1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	295	Total 2406	C 1551	N 418	O 427	S 10	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	242	GLY	-	expression tag	UNP Q12315
B	243	ALA	-	expression tag	UNP Q12315
B	337	ARG	HIS	engineered mutation	UNP Q12315

- Molecule 3 is a protein called Nucleoporin NUP159.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	370	Total 2905	C 1852	N 463	O 585	S 5	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	GLY	-	expression tag	UNP P40477
C	1	ALA	-	expression tag	UNP P40477

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).
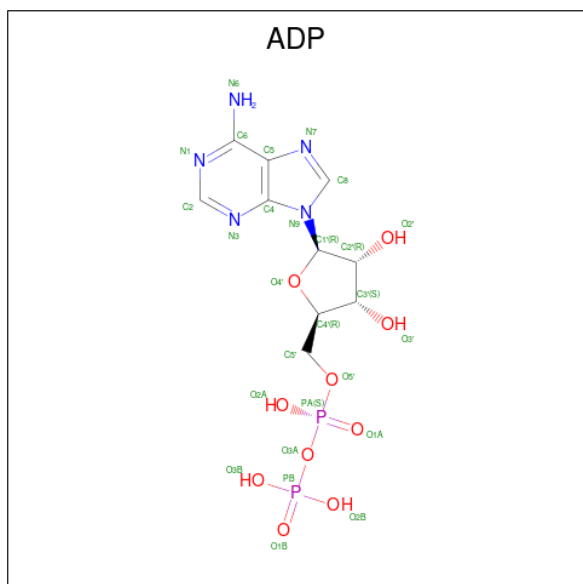
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	27	10	5	10	2	0	0

- Molecule 5 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$).
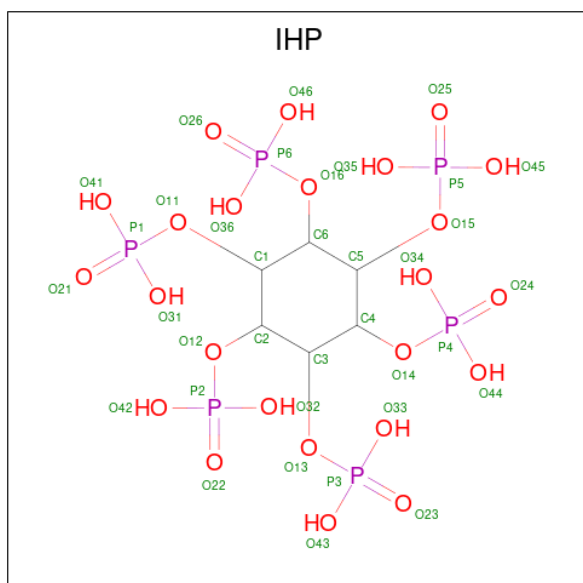
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total 36	C 6	O 24	P 6	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

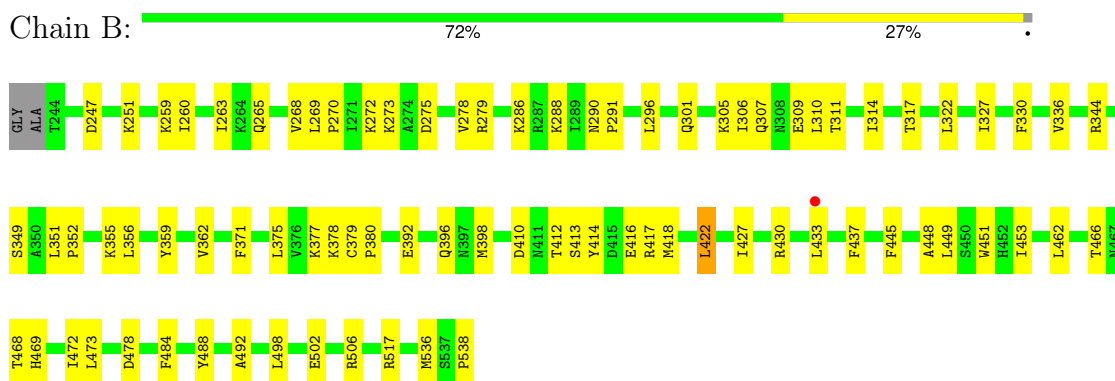| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total 1	Mg 1	0	0

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 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: ATP-dependent RNA helicase DBP5
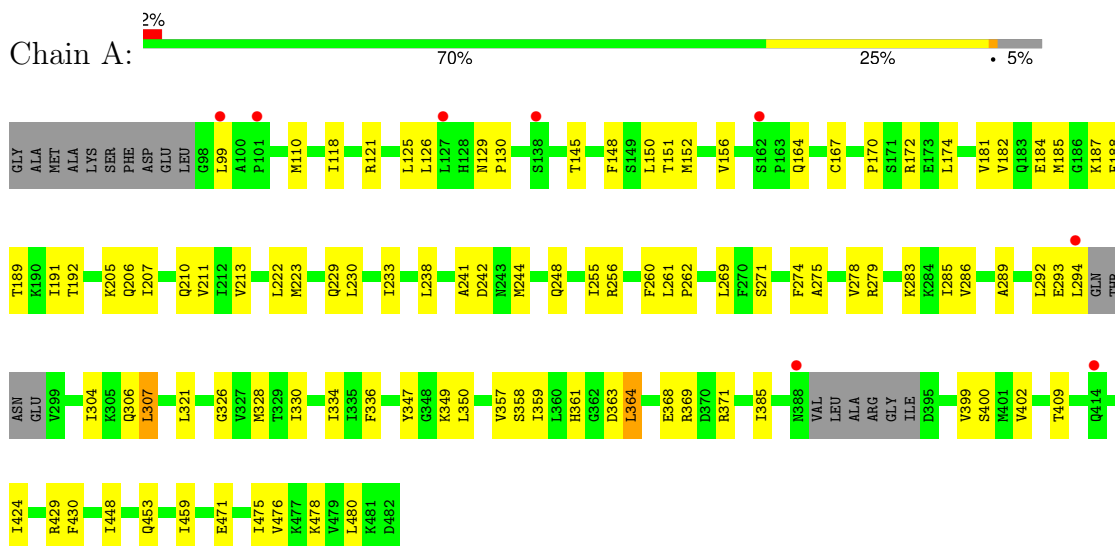
• Molecule 2: Nucleoporin GLE1

• Molecule 3: Nucleoporin NUP159

L141 N142 S443 V144 N145 A149 L160 V164 F167 D168 V169 L174 A175 V176 L177 R181 A187 W188 R189 M193 P202 L205 E211 P215 L216 S217 V218 L221 V229 E240 V241 Q245 K246 M247 Y248 K251 H252 I253 S256 E261

T266 P267 P268 V273 R274 S284 I287 E288 P289 D290 A291 N292 S298 S301 S302 W307 D308 S309 P315 S316 Q317 D318 S319 E320 R321 A322 V323 L324 P325 D333 T334 N335 P336 V344 G347 T348 ILE LEU GLU PRO CYS SER GLY VAL ASP THR ILE GLU R361

N369 S373 V377 H381 VAL ALA ALA ILE LYS SER

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	186.91Å 67.98Å 132.39Å 90.00° 127.52° 90.00°	Depositor
Resolution (Å)	48.27 – 2.90 48.27 – 2.88	Depositor EDS
% Data completeness (in resolution range)	98.8 (48.27-2.90) 98.6 (48.27-2.88)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.71 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.6.4_486, ELVES	Depositor
R, R_{free}	0.229 , 0.261 0.223 , 0.255	Depositor DCC
R_{free} test set	1516 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å²)	54.7	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent k_{sol}(e/Å³), B_{sol}(Å²)	0.30 , 22.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	8323	wwPDB-VP
Average B, all atoms (Å²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.68% 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: ADP, IHP, MG

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	0.21	0/2991	0.38	0/4034
2	B	0.21	0/2460	0.36	0/3328
3	C	0.22	0/2962	0.38	0/4026
All	All	0.21	0/8413	0.37	0/11388

There are no bond length outliers.

There are no bond angle outliers.

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	2948	0	3043	75	0
2	B	2406	0	2454	52	0
3	C	2905	0	2863	71	0
4	A	27	0	12	0	0
5	B	36	0	6	0	0
6	B	1	0	0	0	0
All	All	8323	0	8378	194	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 12.

The worst 5 of 194 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)
3:C:266:THR:HG21	3:C:298:SER:HB3	1.41	0.99
1:A:241:ALA:HB2	1:A:269:LEU:HD11	1.50	0.90
3:C:284:SER:HA	3:C:292:ASN:HB3	1.54	0.89
3:C:251:LYS:HE3	3:C:253:ILE:HD11	1.57	0.86
2:B:379:CYS:HA	2:B:418:MET:HE1	1.58	0.84

There are no symmetry-related clashes.

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	369/395 (93%)	360 (98%)	9 (2%)	0	100	100
2	B	293/297 (99%)	289 (99%)	4 (1%)	0	100	100
3	C	366/388 (94%)	345 (94%)	21 (6%)	0	100	100
All	All	1028/1080 (95%)	994 (97%)	34 (3%)	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	328/343 (96%)	324 (99%)	4 (1%)	71	91

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	263/263 (100%)	261 (99%)	2 (1%)	81	94
3	C	339/354 (96%)	335 (99%)	4 (1%)	71	91
All	All	930/960 (97%)	920 (99%)	10 (1%)	73	92

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	240	GLU
3	C	335	ASN
3	C	369	ASN
1	A	364	LEU
2	B	412	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	355	HIS
3	C	142	ASN
3	C	375	GLN
1	A	229	GLN
1	A	210	GLN

5.3.3   RNA ⓘ

There are no RNA molecules 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 monosaccharides 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	$\#\|Z\| > 2$
5	IHP	B	1	6	36,36,36	1.34	5 (13%)	60,60,60	1.96	16 (26%)
4	ADP	A	1	-	24,29,29	0.93	0	29,45,45	1.19	2 (6%)

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	IHP	B	1	6	-	2/30/54/54	0/1/1/1
4	ADP	A	1	-	-	6/12/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1	IHP	C4-C3	2.58	1.57	1.52
5	B	1	IHP	C5-C4	2.56	1.57	1.52
5	B	1	IHP	C6-C5	2.41	1.57	1.52
5	B	1	IHP	C3-C2	2.19	1.56	1.52
5	B	1	IHP	P2-O22	2.06	1.56	1.50

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	1	IHP	O14-C4-C5	4.64	118.63	108.76
5	B	1	IHP	O12-C2-C3	4.56	118.47	108.76
5	B	1	IHP	O15-C5-C4	4.21	117.73	108.76
5	B	1	IHP	O12-C2-C1	4.04	117.36	108.76
5	B	1	IHP	C6-C5-C4	3.92	119.03	110.43

There are no chirality outliers.

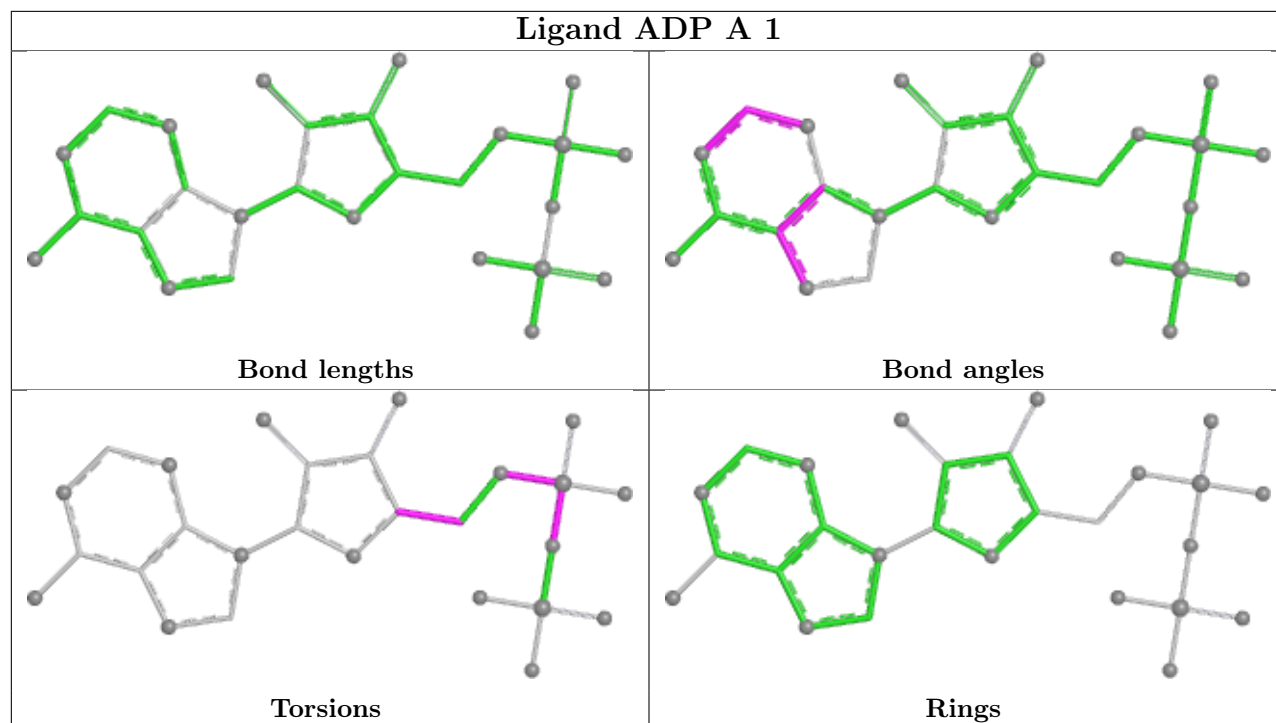5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1	ADP	C5'-O5'-PA-O1A
4	A	1	ADP	C5'-O5'-PA-O2A
4	A	1	ADP	C5'-O5'-PA-O3A
4	A	1	ADP	PB-O3A-PA-O2A
5	B	1	IHP	C5-O15-P5-O35

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 IHP B 1

Bond lengths

Bond angles

Torsions

Rings

Ligand ADP A 1

Bond lengths

Bond angles

Torsions

Rings
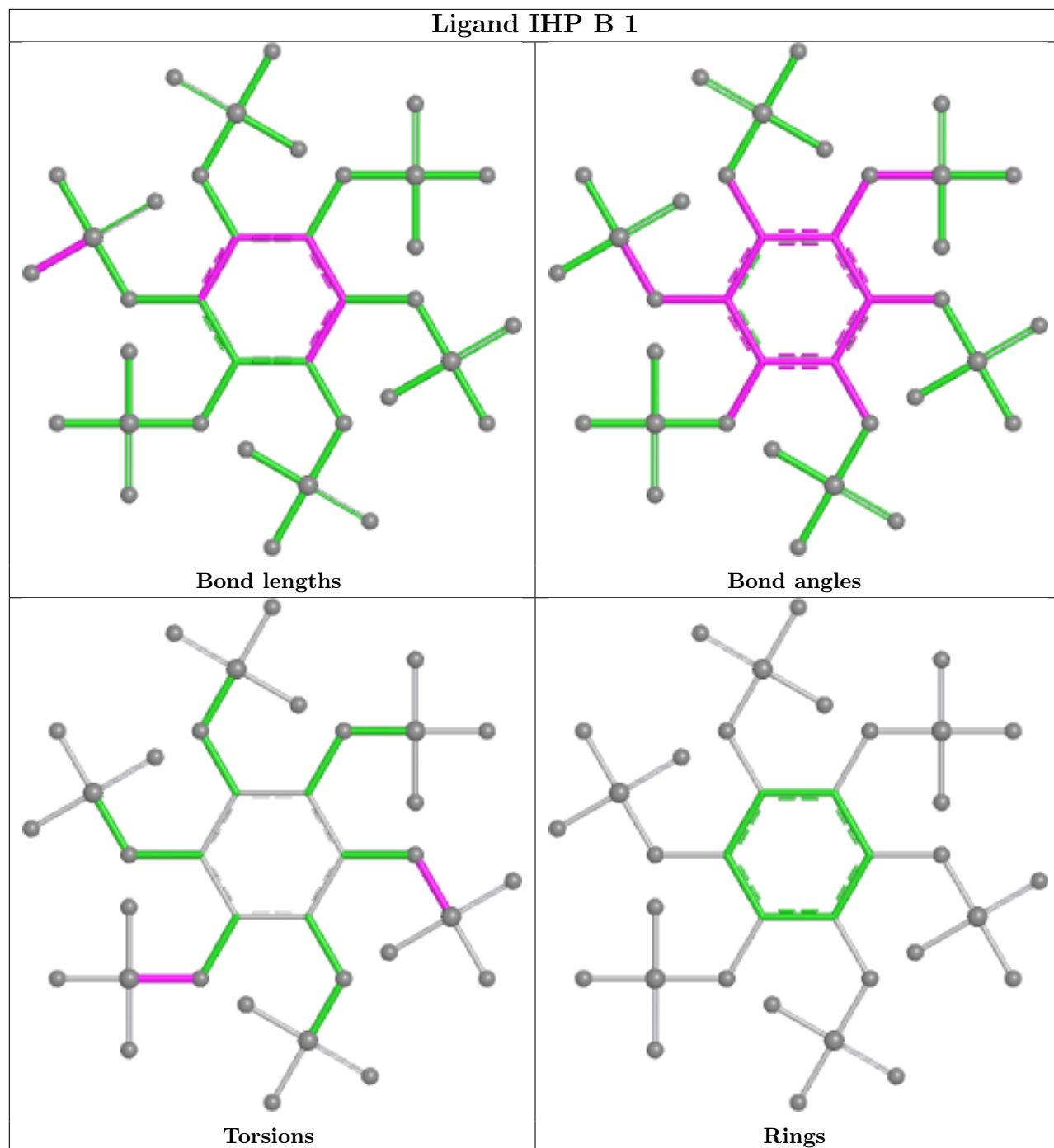
5.7 Other polymers ⓘ

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	375/395 (94%)	-0.00	8 (2%)	63	61	40, 62, 92, 110	0
2	B	295/297 (99%)	-0.23	1 (0%)	94	94	35, 56, 83, 108	0
3	C	370/388 (95%)	-0.23	2 (0%)	91	91	35, 55, 83, 102	0
All	All	1040/1080 (96%)	-0.15	11 (1%)	80	80	35, 58, 88, 110	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	294	LEU	2.9
1	A	162	SER	2.5
3	C	290	ASP	2.5
1	A	388	ASN	2.4
1	A	414	GLN	2.2

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

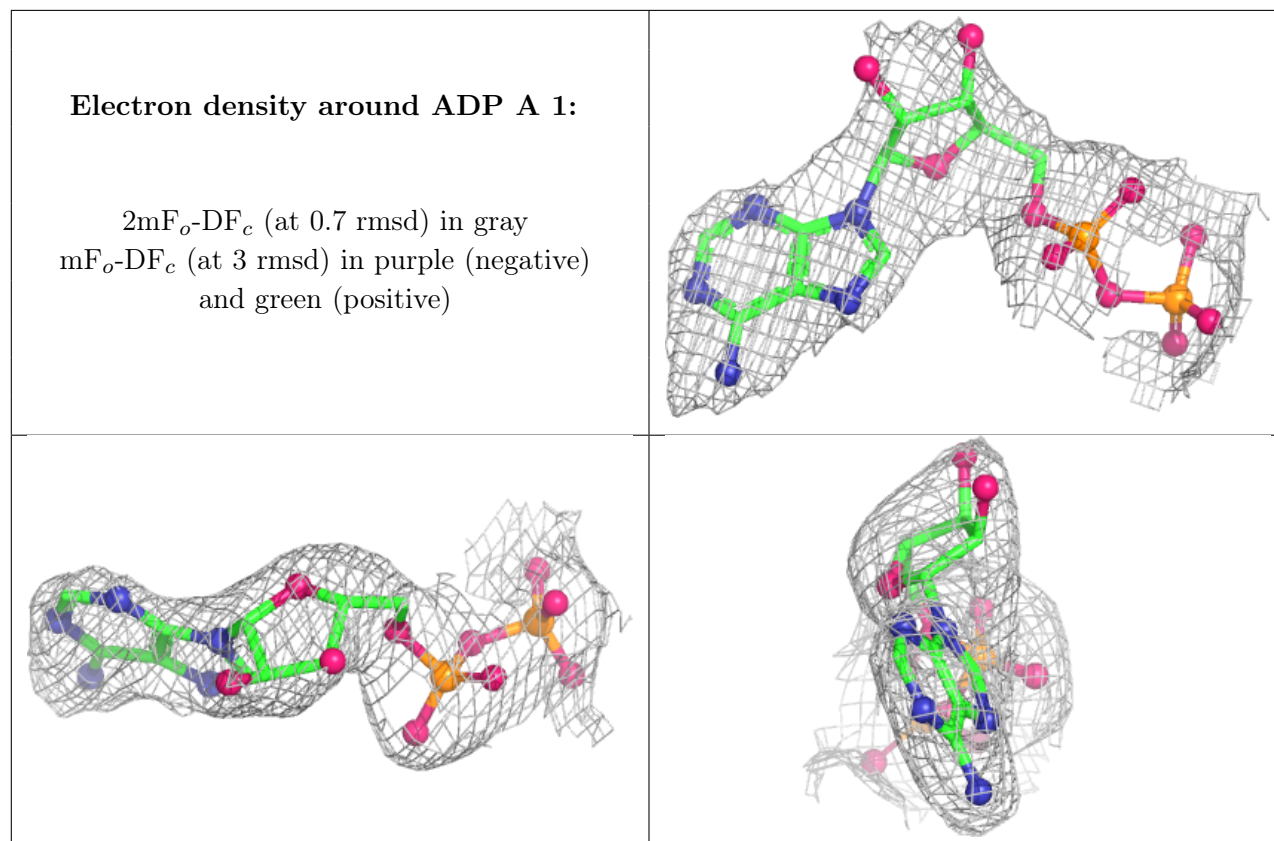There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

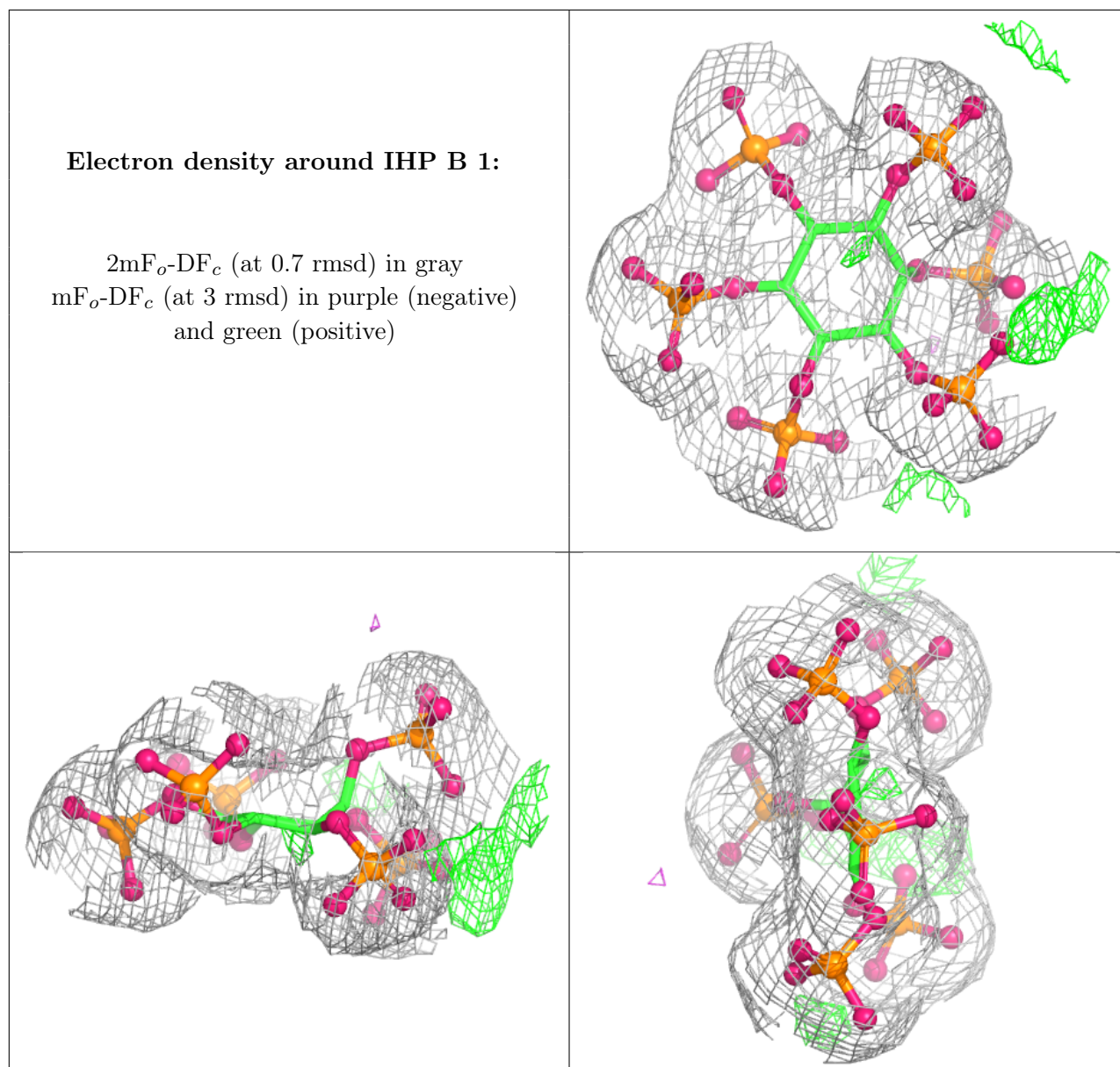## 6.4 Ligands ⓘ

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	ADP	A	1	27/27	0.90	0.17	111,114,123,126	0
6	MG	B	2	1/1	0.95	0.31	51,51,51,51	0
5	IHP	B	1	36/36	0.97	0.13	53,57,77,119	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 ADP A 1:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around IHP B 1:

$2mF_o$-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.