



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 12:37 PM UTC

PDB ID : 2GK6 / pdb_00002gk6
Title : Structural and Functional insights into the human Upf1 helicase core
Authors : Cheng, Z.; Muhlrاد, D.; Parker, R.; Song, H.
Deposited on : 2006-03-31
Resolution : 2.40 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

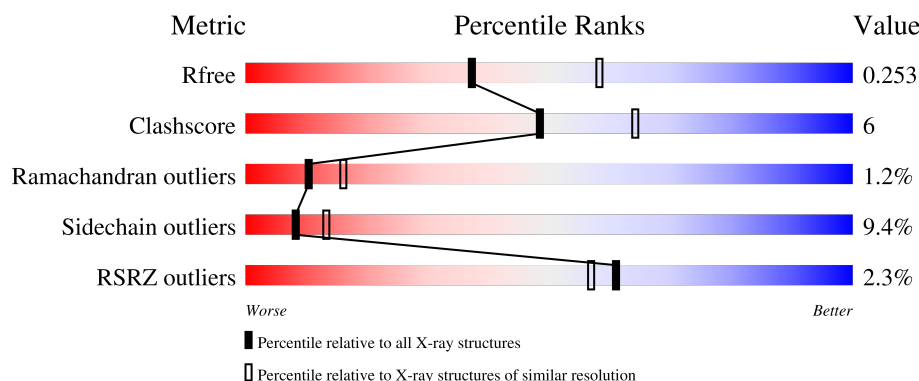
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

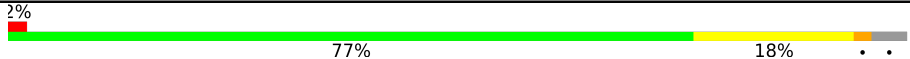
The reported resolution of this entry is 2.40 Å.

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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 $\leq 5\%$. 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	624	
1	B	624	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PO4	A	990	-	-	X	-
3	PO4	B	1990	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9795 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 Regulator of nonsense transcripts 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	602	Total	C	N	O	S	0	0	0
			4748	3022	829	874	23			
1	B	602	Total	C	N	O	S	0	0	0
			4748	3022	829	874	23			

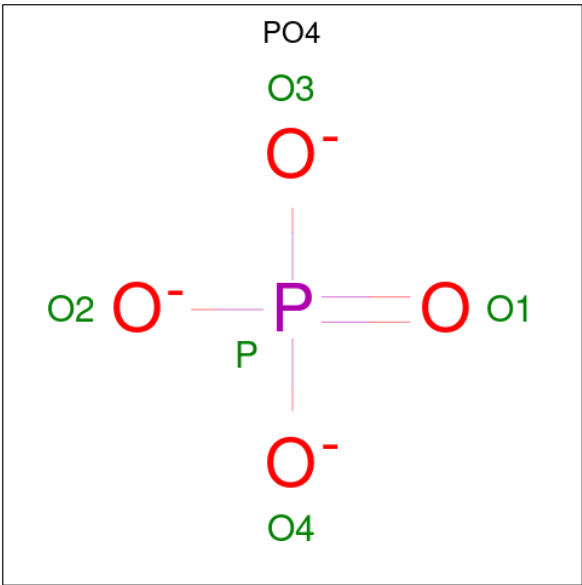
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	291	PRO	-	cloning artifact	UNP Q92900
A	292	LEU	-	cloning artifact	UNP Q92900
A	293	GLY	-	cloning artifact	UNP Q92900
A	294	SER	-	cloning artifact	UNP Q92900
B	291	PRO	-	cloning artifact	UNP Q92900
B	292	LEU	-	cloning artifact	UNP Q92900
B	293	GLY	-	cloning artifact	UNP Q92900
B	294	SER	-	cloning artifact	UNP Q92900

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

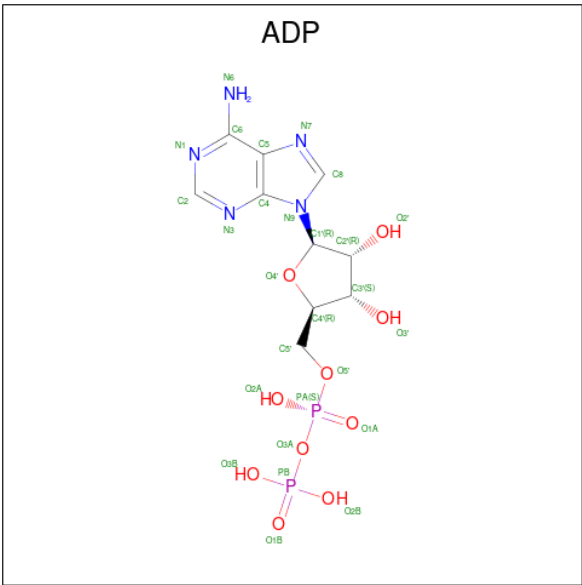
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



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

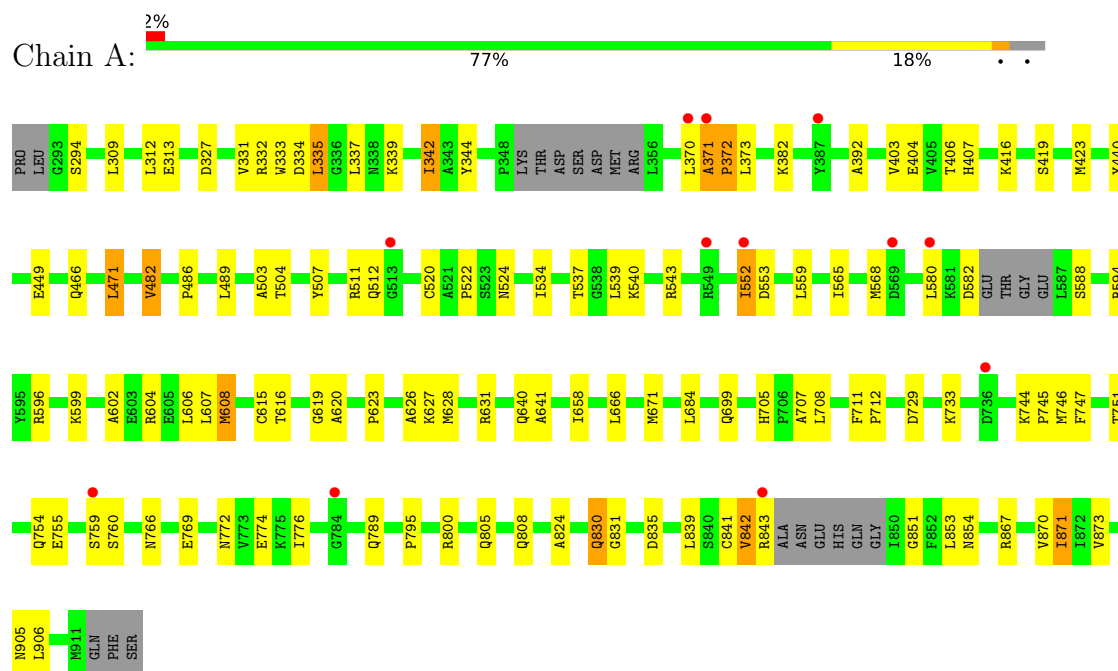
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	115	Total 115	O 115	0	0
5	B	118	Total 118	O 118	0	0

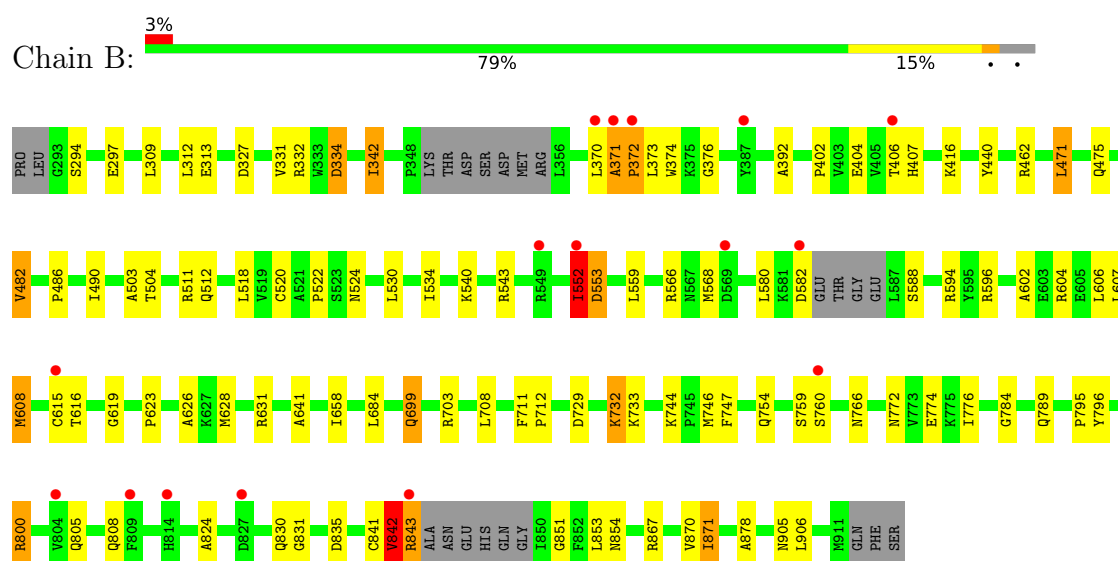
3 Residue-property plots

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: Regulator of nonsense transcripts 1



• Molecule 1: Regulator of nonsense transcripts 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	63.28Å 67.84Å 87.25Å 114.41° 90.13° 110.22°	Depositor
Resolution (Å)	20.00 – 2.40 20.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	90.9 (20.00-2.40) 90.7 (20.00-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.235 , 0.272 0.239 , 0.253	Depositor DCC
R_{free} test set	2171 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	38.4	Xtriage
Anisotropy	0.345	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9795	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, MG, PO4

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	0.52	0/4839	0.81	0/6545
1	B	0.55	1/4839 (0.0%)	0.82	1/6545 (0.0%)
All	All	0.54	1/9678 (0.0%)	0.81	1/13090 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	842	VAL	C-N	12.35	1.50	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	842	VAL	O-C-N	9.76	133.18	122.06

There are no chirality outliers.

There are no planarity outliers.

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	4748	0	4828	51	0
1	B	4748	0	4827	54	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	5	0	0	2	0
3	B	5	0	0	2	0
4	A	27	0	12	1	0
4	B	27	0	12	2	0
5	A	115	0	0	1	0
5	B	118	0	0	2	0
All	All	9795	0	9679	106	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 6.

All (106) 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:524:ASN:HD22	1:A:543:ARG:HH22	1.23	0.85
1:A:708:LEU:HD22	1:A:870:VAL:HG12	1.68	0.74
1:B:843:ARG:C	1:B:853:LEU:HD22	2.15	0.72
1:B:843:ARG:C	1:B:853:LEU:CD2	2.64	0.71
1:B:524:ASN:HD22	1:B:543:ARG:HH22	1.37	0.70
1:B:843:ARG:O	1:B:853:LEU:HD21	1.92	0.70
1:B:616:THR:HG23	1:B:619:GLY:H	1.58	0.68
1:A:747:PHE:CZ	1:A:871:ILE:HD12	2.29	0.67
1:B:482:VAL:HG13	1:B:658:ILE:HG12	1.77	0.66
1:B:747:PHE:CZ	1:B:871:ILE:HD12	2.31	0.65
1:A:520:CYS:HA	1:A:615:CYS:O	1.97	0.64
1:B:708:LEU:HD22	1:B:870:VAL:HG12	1.79	0.64
1:A:568:MET:HE1	1:A:602:ALA:HB1	1.80	0.64
1:A:482:VAL:HG13	1:A:658:ILE:HG12	1.80	0.64
1:A:616:THR:HG23	1:A:619:GLY:H	1.64	0.62
1:B:568:MET:HE1	1:B:602:ALA:HB1	1.81	0.62
3:B:1990:PO4:O1	4:B:1820:ADP:O2B	2.19	0.60
1:B:795:PRO:HB3	1:B:851:GLY:HA3	1.84	0.59
1:A:795:PRO:HB3	1:A:851:GLY:HA3	1.84	0.58
1:A:746:MET:HA	1:A:870:VAL:O	2.03	0.58
1:B:608:MET:HE3	1:B:628:MET:HE3	1.86	0.57
1:B:746:MET:HA	1:B:870:VAL:O	2.04	0.57
1:B:482:VAL:HG21	1:B:490:ILE:HD11	1.87	0.57
1:B:518:LEU:HD11	1:B:615:CYS:SG	2.46	0.56
1:B:772:ASN:O	1:B:776:ILE:HG12	2.06	0.55
1:B:342:ILE:HD11	1:B:392:ALA:HB1	1.90	0.54
1:B:800:ARG:HD2	1:B:824:ALA:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:608:MET:HE3	1:A:628:MET:HE3	1.89	0.53
1:B:905:ASN:C	1:B:905:ASN:HD22	2.17	0.53
1:B:520:CYS:HA	1:B:615:CYS:O	2.09	0.53
1:B:371:ALA:N	1:B:372:PRO:CD	2.73	0.52
1:A:342:ILE:HD11	1:A:392:ALA:HB1	1.93	0.51
1:B:331:VAL:O	1:B:406:THR:OG1	2.27	0.51
1:A:482:VAL:CG1	1:A:658:ILE:HG12	2.40	0.51
1:B:766:ASN:HB2	1:B:842:VAL:HB	1.93	0.51
1:B:482:VAL:CG1	1:B:658:ILE:HG12	2.40	0.51
1:A:331:VAL:O	1:A:406:THR:OG1	2.29	0.50
1:A:371:ALA:N	1:A:372:PRO:CD	2.74	0.50
1:A:449:GLU:HB2	5:A:236:HOH:O	2.11	0.50
1:A:772:ASN:O	1:A:776:ILE:HG12	2.11	0.50
1:B:843:ARG:O	1:B:853:LEU:CD2	2.59	0.50
1:B:843:ARG:C	1:B:853:LEU:HD21	2.33	0.50
1:A:522:PRO:HG3	1:A:641:ALA:HB2	1.94	0.49
3:A:990:PO4:O3	4:A:1001:ADP:O2B	2.30	0.49
1:B:374:TRP:CZ2	1:B:376:GLY:HA3	2.48	0.48
1:B:440:TYR:CE2	1:B:486:PRO:HG2	2.47	0.48
1:A:666:LEU:HD12	1:A:830:GLN:HG3	1.95	0.48
4:B:1820:ADP:H1'	5:B:178:HOH:O	2.11	0.48
1:A:831:GLY:HA2	3:A:990:PO4:O2	2.14	0.47
1:A:471:LEU:HD21	1:A:504:THR:HG21	1.96	0.47
1:B:471:LEU:HA	1:B:475:GLN:NE2	2.29	0.47
1:B:503:ALA:HA	1:B:534:ILE:HD11	1.95	0.47
1:A:507:TYR:HA	1:A:539:LEU:HD11	1.96	0.47
1:A:568:MET:HE2	1:A:606:LEU:HD11	1.95	0.47
1:B:471:LEU:HD21	1:B:504:THR:HG21	1.97	0.47
1:B:566:ARG:HD2	5:B:112:HOH:O	2.14	0.47
1:A:705:HIS:ND1	1:A:745:PRO:HG2	2.30	0.47
1:B:503:ALA:HA	1:B:534:ILE:CD1	2.45	0.46
1:A:800:ARG:HD2	1:A:824:ALA:HA	1.95	0.46
1:B:623:PRO:O	1:B:626:ALA:HB2	2.16	0.46
1:A:766:ASN:HB2	1:A:842:VAL:HB	1.97	0.46
1:A:769:GLU:HG2	1:A:873:VAL:HG12	1.98	0.46
1:B:703:ARG:O	1:B:867:ARG:HG2	2.16	0.46
1:A:337:LEU:HB3	1:B:784:GLY:HA3	1.97	0.46
1:B:699:GLN:HE21	1:B:699:GLN:HB2	1.55	0.46
1:B:796:TYR:CE1	1:B:842:VAL:HG22	2.51	0.46
1:A:776:ILE:HG21	1:A:871:ILE:HD13	1.98	0.45
1:B:711:PHE:HB3	1:B:712:PRO:HD3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:530:LEU:O	1:B:534:ILE:HG12	2.16	0.45
1:A:331:VAL:HG12	1:A:332:ARG:N	2.31	0.45
1:A:800:ARG:HB3	1:A:800:ARG:CZ	2.47	0.45
1:B:370:LEU:C	1:B:372:PRO:HD2	2.42	0.45
1:A:623:PRO:O	1:A:626:ALA:HB2	2.17	0.45
1:A:419:SER:O	1:A:423:MET:HG3	2.17	0.44
1:A:332:ARG:HB2	1:A:344:TYR:HB2	1.99	0.44
1:A:565:ILE:HA	1:A:568:MET:HE3	2.00	0.44
1:B:371:ALA:N	1:B:372:PRO:HD3	2.33	0.43
1:B:334:ASP:HB3	1:B:342:ILE:HG22	2.00	0.43
1:B:522:PRO:HG3	1:B:641:ALA:HB2	1.99	0.43
1:A:751:THR:HG21	1:A:769:GLU:HA	2.00	0.43
1:A:776:ILE:CG2	1:A:871:ILE:HD13	2.48	0.43
1:A:371:ALA:N	1:A:372:PRO:HD3	2.33	0.43
1:A:711:PHE:HB3	1:A:712:PRO:HD3	2.01	0.43
1:B:843:ARG:HG3	1:B:878:ALA:HB1	2.00	0.43
1:B:374:TRP:CD2	1:B:402:PRO:HD3	2.53	0.43
1:B:789:GLN:HB3	1:B:835:ASP:HB2	2.00	0.43
1:A:905:ASN:HD22	1:A:905:ASN:C	2.27	0.42
1:A:337:LEU:HD11	1:B:732:LYS:HG2	2.00	0.42
1:B:552:ILE:HD13	1:B:553:ASP:H	1.85	0.42
1:B:747:PHE:CE1	1:B:871:ILE:HD12	2.54	0.42
1:A:335:LEU:HD22	1:A:339:LYS:HA	2.02	0.42
1:A:440:TYR:CE2	1:A:486:PRO:HG2	2.55	0.42
1:B:776:ILE:HG21	1:B:871:ILE:HD13	2.02	0.42
1:A:705:HIS:HD2	1:A:707:ALA:H	1.66	0.42
1:A:466:GLN:O	1:A:537:THR:HA	2.20	0.41
1:A:382:LYS:HB3	1:A:392:ALA:HB3	2.01	0.41
1:B:370:LEU:C	1:B:372:PRO:CD	2.93	0.41
1:B:568:MET:HE2	1:B:606:LEU:HD11	2.03	0.41
1:B:331:VAL:HG12	1:B:332:ARG:N	2.35	0.41
1:A:503:ALA:HA	1:A:534:ILE:HD11	2.02	0.41
1:A:503:ALA:HA	1:A:534:ILE:CD1	2.51	0.41
1:A:789:GLN:HB3	1:A:835:ASP:HB2	2.03	0.41
1:A:333:TRP:CB	1:A:403:VAL:HG13	2.51	0.41
1:A:843:ARG:O	1:A:843:ARG:NE	2.53	0.40
1:B:831:GLY:HA2	3:B:1990:PO4:O4	2.21	0.40
1:A:615:CYS:SG	1:A:620:ALA:HB2	2.61	0.40

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	594/624 (95%)	540 (91%)	47 (8%)	7 (1%)	10	16
1	B	594/624 (95%)	545 (92%)	42 (7%)	7 (1%)	10	16
All	All	1188/1248 (95%)	1085 (91%)	89 (8%)	14 (1%)	10	16

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	372	PRO
1	A	759	SER
1	B	372	PRO
1	B	808	GLN
1	A	808	GLN
1	B	760	SER
1	A	760	SER
1	B	371	ALA
1	B	373	LEU
1	B	759	SER
1	A	373	LEU
1	B	552	ILE
1	A	371	ALA
1	A	552	ILE

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	521/540 (96%)	469 (90%)	52 (10%)	7	11
1	B	521/540 (96%)	475 (91%)	46 (9%)	9	15
All	All	1042/1080 (96%)	944 (91%)	98 (9%)	8	13

All (98) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	294	SER
1	A	309	LEU
1	A	312	LEU
1	A	313	GLU
1	A	327	ASP
1	A	334	ASP
1	A	335	LEU
1	A	342	ILE
1	A	370	LEU
1	A	404	GLU
1	A	407	HIS
1	A	416	LYS
1	A	471	LEU
1	A	482	VAL
1	A	489	LEU
1	A	511	ARG
1	A	512	GLN
1	A	540	LYS
1	A	552	ILE
1	A	553	ASP
1	A	559	LEU
1	A	580	LEU
1	A	582	ASP
1	A	588	SER
1	A	594	ARG
1	A	596	ARG
1	A	599	LYS
1	A	604	ARG
1	A	607	LEU
1	A	608	MET
1	A	627	LYS
1	A	631	ARG
1	A	640	GLN
1	A	671	MET
1	A	684	LEU

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Mol	Chain	Res	Type
1	A	699	GLN
1	A	729	ASP
1	A	733	LYS
1	A	744	LYS
1	A	754	GLN
1	A	755	GLU
1	A	774	GLU
1	A	805	GLN
1	A	830	GLN
1	A	839	LEU
1	A	841	CYS
1	A	842	VAL
1	A	853	LEU
1	A	854	ASN
1	A	867	ARG
1	A	871	ILE
1	A	906	LEU
1	B	294	SER
1	B	297	GLU
1	B	309	LEU
1	B	312	LEU
1	B	313	GLU
1	B	327	ASP
1	B	334	ASP
1	B	342	ILE
1	B	404	GLU
1	B	407	HIS
1	B	416	LYS
1	B	462	ARG
1	B	471	LEU
1	B	482	VAL
1	B	511	ARG
1	B	512	GLN
1	B	540	LYS
1	B	552	ILE
1	B	553	ASP
1	B	559	LEU
1	B	580	LEU
1	B	582	ASP
1	B	588	SER
1	B	594	ARG
1	B	596	ARG

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Mol	Chain	Res	Type
1	B	604	ARG
1	B	607	LEU
1	B	608	MET
1	B	631	ARG
1	B	684	LEU
1	B	699	GLN
1	B	729	ASP
1	B	732	LYS
1	B	733	LYS
1	B	744	LYS
1	B	754	GLN
1	B	774	GLU
1	B	800	ARG
1	B	805	GLN
1	B	830	GLN
1	B	841	CYS
1	B	842	VAL
1	B	843	ARG
1	B	854	ASN
1	B	871	ILE
1	B	906	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	301	GLN
1	A	324	GLN
1	A	328	ASN
1	A	358	GLN
1	A	408	ASN
1	A	410	GLN
1	A	466	GLN
1	A	475	GLN
1	A	524	ASN
1	A	536	GLN
1	A	578	GLN
1	A	699	GLN
1	A	705	HIS
1	A	738	GLN
1	A	772	ASN
1	A	805	GLN
1	A	830	GLN

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Mol	Chain	Res	Type
1	A	875	ASN
1	A	886	ASN
1	A	887	HIS
1	A	895	GLN
1	A	904	ASN
1	A	905	ASN
1	B	304	ASN
1	B	324	GLN
1	B	328	ASN
1	B	358	GLN
1	B	408	ASN
1	B	410	GLN
1	B	475	GLN
1	B	524	ASN
1	B	535	HIS
1	B	536	GLN
1	B	640	GLN
1	B	665	GLN
1	B	699	GLN
1	B	738	GLN
1	B	805	GLN
1	B	830	GLN
1	B	890	ASN
1	B	905	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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
3	PO4	B	1990	-	4,4,4	1.19	0	6,6,6	0.66	0
3	PO4	A	990	-	4,4,4	1.28	0	6,6,6	0.59	0
4	ADP	A	1001	2	28,29,29	1.10	3 (10%)	43,45,45	1.90	10 (23%)
4	ADP	B	1820	2	28,29,29	1.09	4 (14%)	43,45,45	1.88	11 (25%)

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
4	ADP	B	1820	2	-	2/16/32/32	0/3/3/3
4	ADP	A	1001	2	-	2/16/32/32	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1820	ADP	C2-N1	2.86	1.39	1.33
4	A	1001	ADP	C2-N1	2.64	1.38	1.33
4	B	1820	ADP	C2-N3	2.54	1.38	1.33
4	A	1001	ADP	C2-N3	2.48	1.38	1.33
4	A	1001	ADP	C8-N7	2.14	1.35	1.31
4	B	1820	ADP	C8-N7	2.09	1.35	1.31
4	B	1820	ADP	C5-N7	-2.08	1.35	1.39

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1820	ADP	N3-C2-N1	-5.80	119.80	128.58
4	A	1001	ADP	N3-C2-N1	-5.71	119.93	128.58
4	A	1001	ADP	C5-C4-N3	-4.06	121.13	126.72
4	B	1820	ADP	C5-C4-N3	-3.95	121.28	126.72
4	B	1820	ADP	N9-C8-N7	-3.93	108.36	113.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1001	ADP	N9-C8-N7	-3.84	108.49	113.94
4	A	1001	ADP	C5-N7-C8	3.37	108.75	103.45
4	B	1820	ADP	C5-N7-C8	3.31	108.66	103.45
4	A	1001	ADP	C2-N3-C4	3.31	119.90	111.83
4	B	1820	ADP	C2-N3-C4	3.24	119.75	111.83
4	A	1001	ADP	O3'-C3'-C2'	3.12	121.82	111.82
4	B	1820	ADP	O3'-C3'-C2'	3.03	121.52	111.82
4	B	1820	ADP	N3-C4-N9	2.66	131.69	127.17
4	A	1001	ADP	N3-C4-N9	2.54	131.50	127.17
4	B	1820	ADP	O4'-C4'-C5'	2.54	117.48	109.33
4	A	1001	ADP	C4-C5-N7	-2.46	107.77	110.58
4	A	1001	ADP	O4'-C4'-C5'	2.46	117.22	109.33
4	B	1820	ADP	C4-C5-N7	-2.28	107.97	110.58
4	B	1820	ADP	O4'-C1'-N9	2.15	112.21	108.09
4	B	1820	ADP	C4-N9-C8	2.14	107.98	105.74
4	A	1001	ADP	O4'-C1'-N9	2.04	112.00	108.09

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1001	ADP	C5'-O5'-PA-O1A
4	A	1001	ADP	C5'-O5'-PA-O3A
4	B	1820	ADP	C5'-O5'-PA-O3A
4	B	1820	ADP	C5'-O5'-PA-O1A

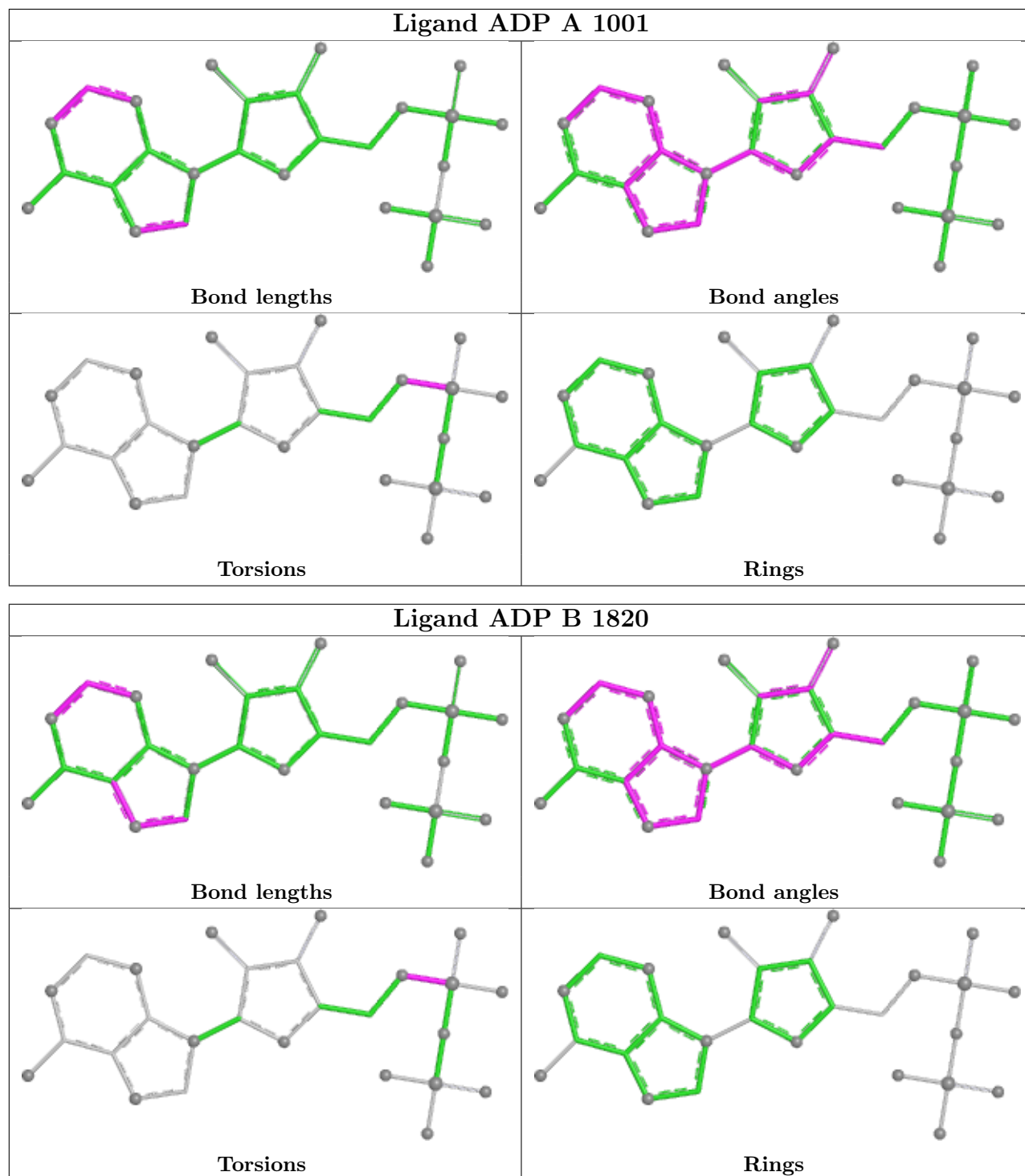
There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1990	PO4	2	0
3	A	990	PO4	2	0
4	A	1001	ADP	1	0
4	B	1820	ADP	2	0

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 than 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.



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(Å ²)	Q<0.9
1	A	602/624 (96%)	-0.00	12 (1%) 65 60	12, 33, 53, 62	0
1	B	602/624 (96%)	-0.00	16 (2%) 56 52	13, 33, 53, 62	0
All	All	1204/1248 (96%)	-0.00	28 (2%) 61 57	12, 33, 53, 62	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	843	ARG	5.1
1	A	843	ARG	4.5
1	A	370	LEU	3.8
1	B	370	LEU	3.7
1	A	387	TYR	3.5
1	B	371	ALA	3.2
1	B	809	PHE	3.1
1	B	552	ILE	3.0
1	B	569	ASP	2.9
1	A	371	ALA	2.9
1	A	513	GLY	2.9
1	A	569	ASP	2.8
1	A	549	ARG	2.7
1	A	580	LEU	2.6
1	B	406	THR	2.5
1	B	760	SER	2.5
1	B	372	PRO	2.4
1	A	784	GLY	2.4
1	A	736	ASP	2.4
1	A	759	SER	2.4
1	B	814	HIS	2.3
1	B	615	CYS	2.3
1	B	827	ASP	2.2
1	A	552	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	387	TYR	2.1
1	B	804	VAL	2.1
1	B	582	ASP	2.1
1	B	549	ARG	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

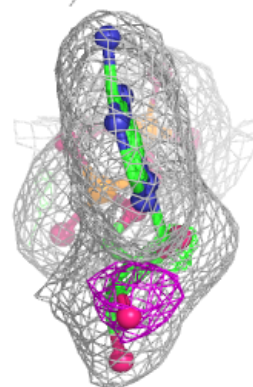
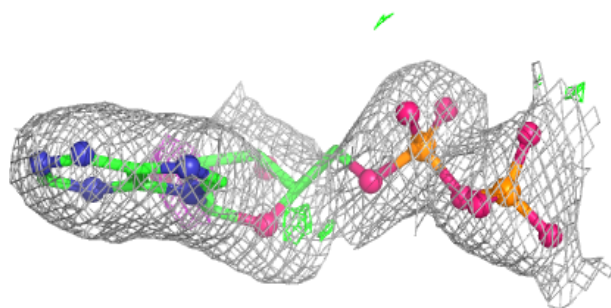
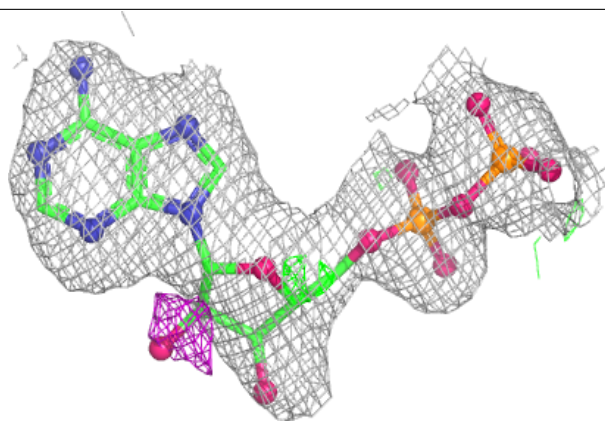
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MG	A	1000	1/1	0.72	0.24	55,55,55,55	0
2	MG	B	2000	1/1	0.76	0.16	50,50,50,50	0
4	ADP	A	1001	27/27	0.90	0.11	41,52,54,56	0
4	ADP	B	1820	27/27	0.91	0.12	42,51,54,55	0
3	PO4	A	990	5/5	0.96	0.07	39,40,40,41	0
3	PO4	B	1990	5/5	0.97	0.09	41,41,42,42	0

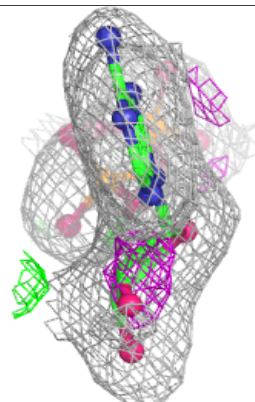
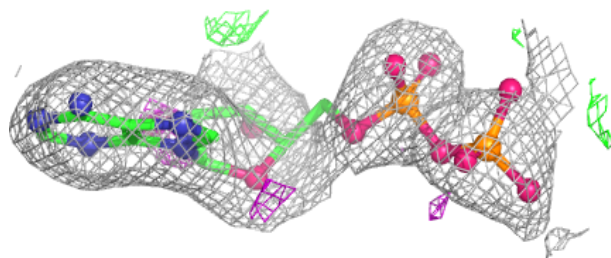
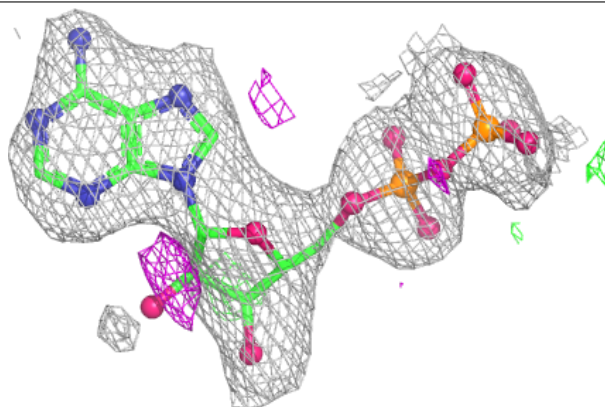
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ADP A 1001:

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

**Electron density around ADP B 1820:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.