Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 04:43 AM BST

PDB ID	:	2CGL
Title	:	Crystal Structure of L-rhamnulose kinase from Escherichia coli in complex with L-fructose, ADP and a modeled ATP gamma phosphate.
Authors	:	Grueninger, D.; Schulz, G.E.
Deposited on	:	2006-03-09
Resolution	:	1.88 Å(reported)

The following versions of software and data (see references ⓘ) 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	:	2.13.1
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)	:	2.13.1

1 Overall quality at a glance (i)

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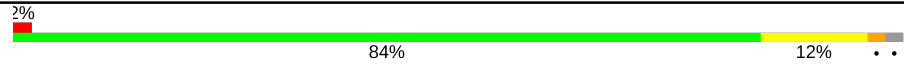*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.88 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.
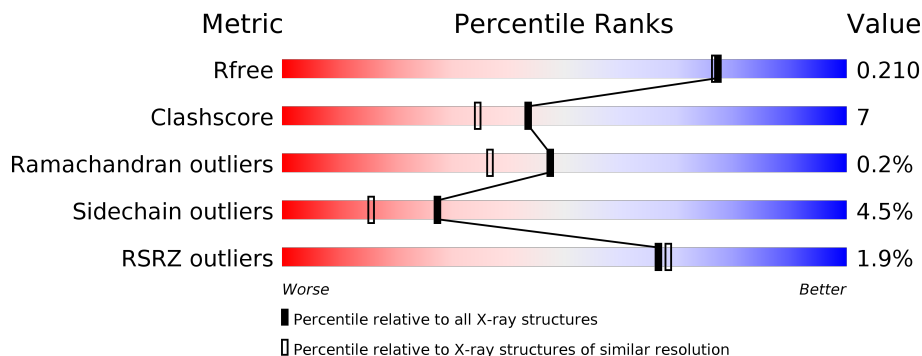
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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 >=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	489	2% 84% 12% · ·

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3958 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.
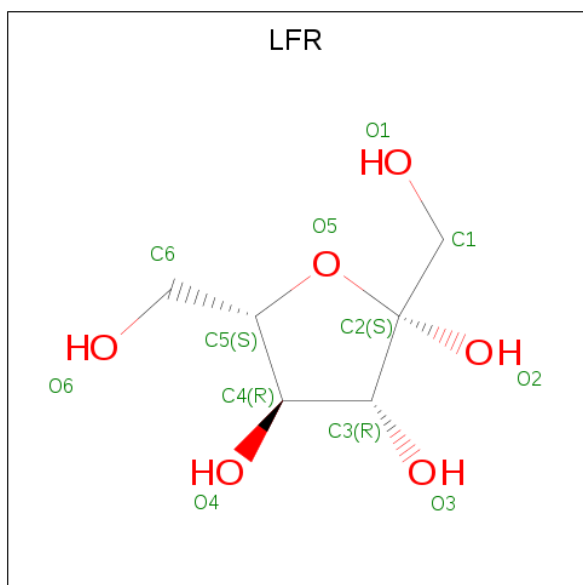
- Molecule 1 is a protein called RHAMNULOKINASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	479	3723	2336	657	710	11	9	0	4	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	69	ALA	GLU	engineered mutation	UNP Q8X899
A	70	ALA	GLU	engineered mutation	UNP Q8X899
A	73	ALA	ARG	engineered mutation	UNP Q8X899
A	320	ALA	SER	conflict	UNP Q8X899
A	343	ASP	GLU	conflict	UNP Q8X899
A	344	GLU	THR	conflict	UNP Q8X899
A	356	MSE	THR	conflict	UNP Q8X899
A	477	LEU	ARG	conflict	UNP Q8X899

- Molecule 2 is beta-L-fructofuranose (three-letter code: LFR) (formula: $C_6H_{12}O_6$).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 12	C 6	O 6	0	0

- Molecule 3 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: $C_{10}H_{15}N_5O_{10}P_2$).

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

- Molecule 4 is PHOSPHITE ION (three-letter code: PO3) (formula: O_3P).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	192	Total 192	O 192	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: RHAMNULOKINASE
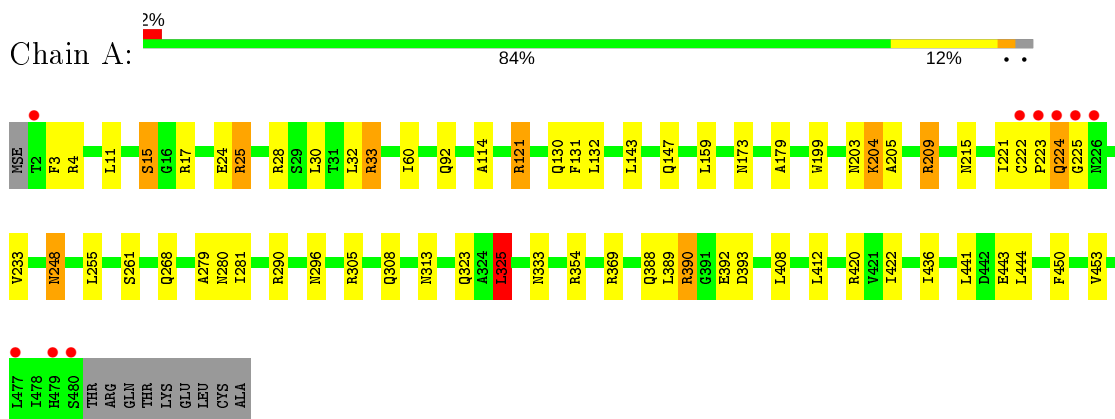
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	50.78Å 50.97Å 158.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.34 – 1.88 48.35 – 1.88	Depositor EDS
% Data completeness (in resolution range)	95.9 (48.34-1.88) 95.9 (48.35-1.88)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	4.72 (at 1.88Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.167 , 0.209 0.168 , 0.210	Depositor DCC
R_{free} test set	1645 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	22.5	Xtriage
Anisotropy	0.161	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 42.2	EDS
L-test for twinning [2]	$<|L|> = 0.46, <L^2> = 0.29$	Xtriage
Estimated twinning fraction	0.037 for k,h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	3958	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.73% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: PO3, ADP, LFR

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	0.69	0/3801	0.76	4/5165 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	33	ARG	NE-CZ-NH2	-6.39	117.11	120.30
1	A	143	LEU	CA-CB-CG	-5.39	102.91	115.30
1	A	325	LEU	CA-CB-CG	5.37	127.66	115.30
1	A	209	ARG	NE-CZ-NH1	5.11	122.86	120.30

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	3723	0	3650	50	0
2	A	12	0	12	0	0
3	A	27	0	12	0	0
4	A	4	0	0	0	0
5	A	192	0	0	6	0
All	All	3958	0	3674	50	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 7.

All (50) 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:121:ARG:HG2	1:A:121:ARG:HH11	0.89	1.06
1:A:121:ARG:NH1	1:A:121:ARG:HG2	1.68	0.99
1:A:131:PHE:H	1:A:280:ASN:HD21	1.10	0.93
1:A:121:ARG:CG	1:A:121:ARG:HH11	1.82	0.93
1:A:221:ILE:HG23	1:A:225:GLY:HA2	1.72	0.71
1:A:305:ARG:O	1:A:308:GLN:HG3	1.91	0.68
1:A:333:ASN:HB2	5:A:2115:HOH:O	1.92	0.68
1:A:222:CYS:HB2	1:A:224:GLN:OE1	1.94	0.67
1:A:204:LYS:HE2	1:A:204:LYS:H	1.61	0.63
1:A:121:ARG:CG	1:A:121:ARG:NH1	2.51	0.63
1:A:222:CYS:HB3	1:A:224:GLN:HE22	1.66	0.61
1:A:248:ASN:ND2	1:A:248:ASN:H	1.99	0.60
1:A:3:PHE:HA	1:A:24:GLU:HB3	1.86	0.58
1:A:248:ASN:HD22	1:A:248:ASN:H	1.51	0.57
1:A:130:GLN:HE22	1:A:296:ASN:H	1.51	0.57
1:A:4:ARG:HG3	1:A:443:GLU:HG3	1.88	0.55
1:A:33:ARG:HG3	5:A:2007:HOH:O	2.07	0.55
1:A:15:SER:HB2	5:A:2186:HOH:O	2.08	0.54
1:A:248:ASN:N	1:A:248:ASN:HD22	2.06	0.53
1:A:281:ILE:HD13	1:A:389:LEU:HD22	1.92	0.52
1:A:209:ARG:HG2	1:A:209:ARG:HH11	1.76	0.51
1:A:130:GLN:HG3	1:A:132:LEU:HG	1.93	0.50
1:A:25:ARG:HG3	1:A:443:GLU:O	2.11	0.50
1:A:408:LEU:HD12	5:A:2147:HOH:O	2.12	0.50
1:A:222:CYS:HB3	1:A:224:GLN:NE2	2.27	0.49
1:A:248:ASN:N	1:A:248:ASN:ND2	2.61	0.48
1:A:222:CYS:O	1:A:224:GLN:N	2.47	0.47
1:A:325:LEU:HB3	1:A:369:ARG:HD3	1.96	0.47
1:A:92:GLN:NE2	1:A:92:GLN:HA	2.30	0.46
1:A:279:ALA:HB3	1:A:281:ILE:HD12	1.97	0.46
1:A:159:LEU:HD11	1:A:179:ALA:HA	1.98	0.46
1:A:390:ARG:HD3	1:A:392:GLU:O	2.16	0.46
1:A:222:CYS:O	1:A:225:GLY:N	2.50	0.45
1:A:255:LEU:HD11	1:A:261:SER:HB3	1.98	0.45
1:A:11:LEU:HD11	1:A:60:ILE:HD11	1.99	0.45
1:A:121:ARG:HB2	5:A:2048:HOH:O	2.16	0.45
1:A:173:ASN:HD21	1:A:215:ASN:HD21	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:420:ARG:HD2	1:A:422:ILE:HD11	2.00	0.44
1:A:204:LYS:CE	1:A:204:LYS:H	2.29	0.44
1:A:233:VAL:HA	1:A:436:ILE:HG21	2.00	0.43
1:A:369:ARG:HH22	1:A:412:LEU:HD21	1.82	0.43
1:A:290:ARG:HD2	5:A:2098:HOH:O	2.19	0.42
1:A:323:GLN:HG2	1:A:408:LEU:HD13	2.01	0.42
1:A:203:ASN:HD21	1:A:205:ALA:HB3	1.85	0.42
1:A:28:ARG:HH11	1:A:453:VAL:HG23	1.85	0.41
1:A:25:ARG:HD2	1:A:443:GLU:O	2.21	0.41
1:A:305:ARG:HA	1:A:308:GLN:HG2	2.03	0.41
1:A:114:ALA:HB2	1:A:199:TRP:CH2	2.56	0.40
1:A:444:LEU:HD21	1:A:450:PHE:HB2	2.02	0.40
1:A:369:ARG:NH2	1:A:412:LEU:HD21	2.37	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	481/489 (98%)	469 (98%)	11 (2%)	1 (0%)	47	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	PRO

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	401/396 (101%)	383 (96%)	18 (4%)	27 16

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	SER
1	A	17	ARG
1	A	25	ARG
1	A	30	LEU
1	A	32	LEU
1	A	121	ARG
1	A	147	GLN
1	A	204	LYS
1	A	224	GLN
1	A	248	ASN
1	A	268	GLN
1	A	313	ASN
1	A	325	LEU
1	A	354	ARG
1	A	388	GLN
1	A	390	ARG
1	A	393	ASP
1	A	441	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	ASN
1	A	65	ASN
1	A	91	GLN
1	A	92	GLN
1	A	108	ASN
1	A	116	GLN
1	A	130	GLN
1	A	173	ASN
1	A	188	ASN
1	A	248	ASN
1	A	280	ASN
1	A	308	GLN

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Mol	Chain	Res	Type
1	A	311	GLN
1	A	388	GLN
1	A	411	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)

3 ligands are modelled in this entry.

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	LFR	A	1481	-	11,12,12	1.76	3 (27%)	10,18,18	0.87	1 (10%)
3	ADP	A	1482	4	24,29,29	1.22	4 (16%)	29,45,45	1.39	4 (13%)
4	PO3	A	1483	3	0,3,3	0.00	-	0,3,3	0.00	-

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	LFR	A	1481	-	-	1/5/24/24	0/1/1/1
3	ADP	A	1482	4	-	0/12/32/32	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1481	LFR	O5-C5	3.36	1.51	1.43
2	A	1481	LFR	C1-C2	2.88	1.57	1.52
3	A	1482	ADP	O4'-C1'	2.70	1.44	1.41
3	A	1482	ADP	C5-C4	2.60	1.47	1.40
2	A	1481	LFR	O2-C2	2.51	1.45	1.40
3	A	1482	ADP	O4'-C4'	-2.32	1.39	1.45
3	A	1482	ADP	C2-N3	2.09	1.35	1.32

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1482	ADP	N3-C2-N1	-3.67	122.94	128.68
3	A	1482	ADP	C2-N1-C6	2.53	123.08	118.75
2	A	1481	LFR	O1-C1-C2	-2.33	106.90	111.86
3	A	1482	ADP	C3'-C2'-C1'	2.15	104.21	100.98
3	A	1482	ADP	O3B-PB-O1B	2.03	118.62	110.68

There are no chirality outliers.

All (1) torsion outliers are listed below:

| Mol	Chain	Res	Type	Atoms
2	A	1481	LFR	O1-C1-C2-C3

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 1482	
Bond lengths	Bond angles
Torsions	Rings
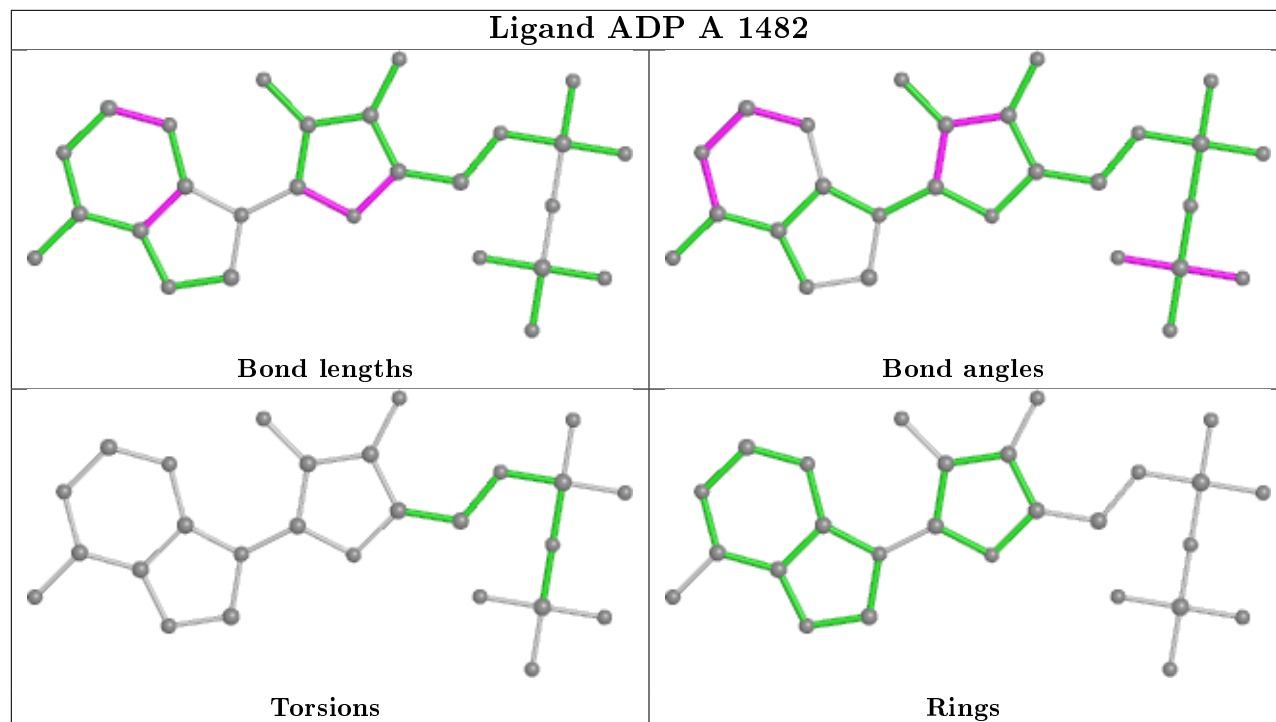
5.7 Other polymers (i)

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	470/489 (96%)	-0.25	9 (1%)	66	68	11, 22, 35, 65	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	479	HIS	4.4
1	A	224	GLN	3.2
1	A	226	ASN	3.1
1	A	477	LEU	2.7
1	A	2	THR	2.5
1	A	222	CYS	2.4
1	A	223	PRO	2.2
1	A	480	SER	2.1
1	A	225	GLY	2.1

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

There are no non-standard protein/DNA/RNA residues in this entry.
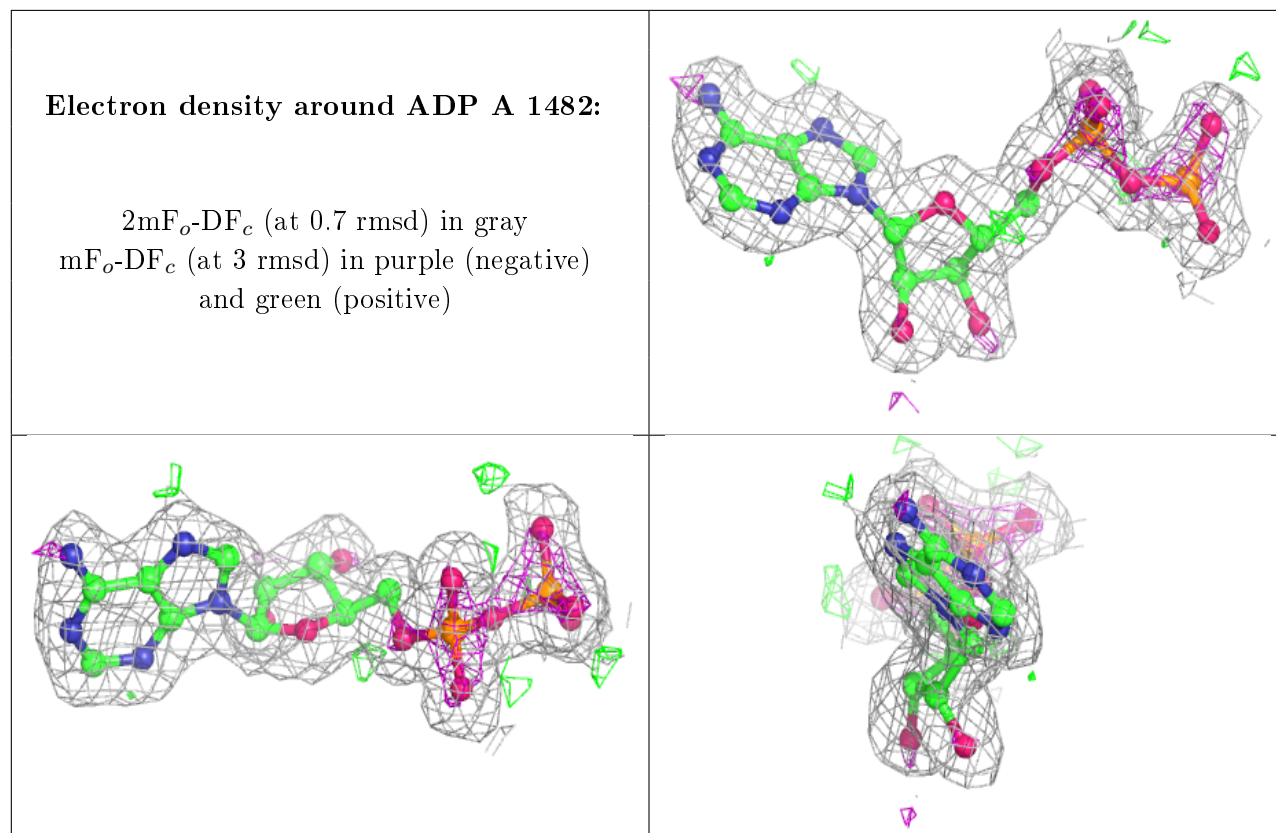
6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

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	PO3	A	1483	4/4	-	-	0,0,0,0	4
2	LFR	A	1481	12/12	0.97	0.08	12,14,18,18	0
3	ADP	A	1482	27/27	0.98	0.07	11,17,20,22	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 1482:

$2mF_o$-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.