Full wwPDB X-ray Structure Validation Report (i)

Dec 16, 2023 – 08:43 pm GMT

PDB ID	:	4A8W
Title	:	Non-Catalytic Ions Direct the RNA-Dependent RNA Polymerase of Bacterial dsRNA virus phi6 from De Novo Initiation to Elongation
Authors	:	Wright, S.; Poranen, M.M.; Bamford, D.H.; Stuart, D.I.; Grimes, J.M.
Deposited on	:	2011-11-21
Resolution	:	3.04 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 (i) 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 (i)) were used in the production of this report:

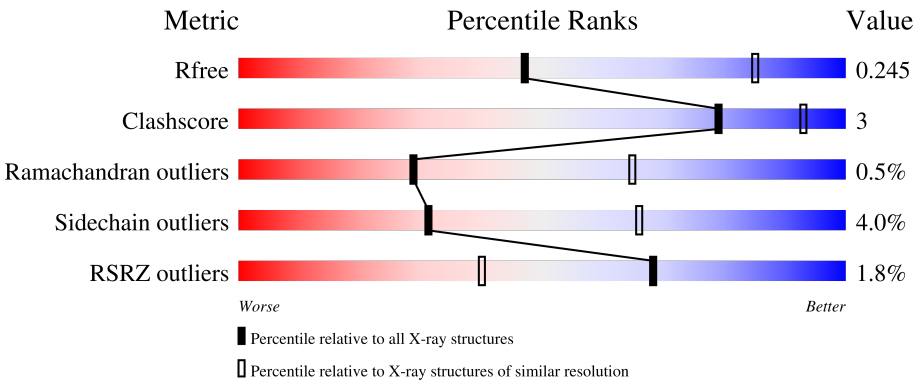
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.04 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	2752 (3.08-3.00)
Clashscore	141614	3096 (3.08-3.00)
Ramachandran outliers	138981	2986 (3.08-3.00)
Sidechain outliers	138945	2988 (3.08-3.00)
RSRZ outliers	127900	2636 (3.08-3.00)

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	665	91% 9%
1	B	665	90% 9% •
1	C	665	4% 86% 9% • •
2	F	12	17% 17% 83%
2	G	12	25% 17% 8% 75%

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Mol	Chain	Length	Quality of chain
2	H	12	8% 25% 25% 50%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 15890 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 RNA-DIRECTED RNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	664	5265	3342	915	976	32	0	0	0
1	B	664	5265	3342	915	976	32	0	0	0
1	C	643	5101	3241	884	944	32	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	456	MET	ILE	SEE REMARK 999	UNP P11124
A	634	GLN	GLU	engineered mutation	UNP P11124
B	456	MET	ILE	SEE REMARK 999	UNP P11124
B	634	GLN	GLU	engineered mutation	UNP P11124
C	456	MET	ILE	SEE REMARK 999	UNP P11124
C	634	GLN	GLU	engineered mutation	UNP P11124

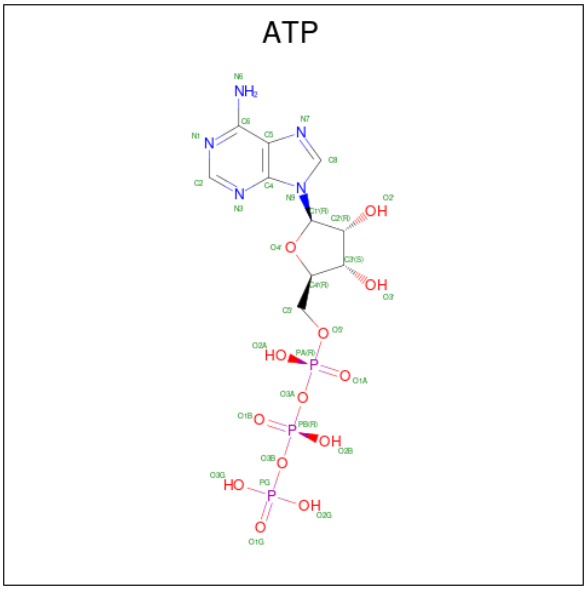
- Molecule 2 is a DNA chain called 5'-D(*TP*TP*CP*GP*CP*GP*TP*AP*AP*GP*CP*GP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	F	2	38	19	8	10	1	0	0	0
2	G	3	60	29	13	16	2	0	0	0
2	H	6	119	58	20	36	5	0	0	0

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

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

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



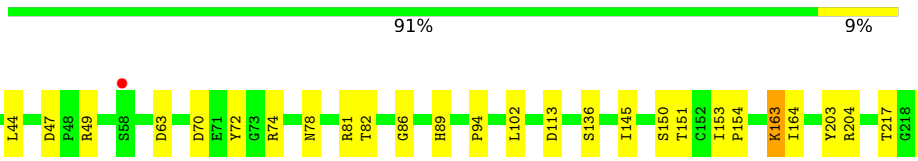
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
4	A	1	13	10	3	0	0
			Total	O	P		
4	B	1	13	10	3	0	0
			Total	O	P		
4	C	1	13	10	3	0	0

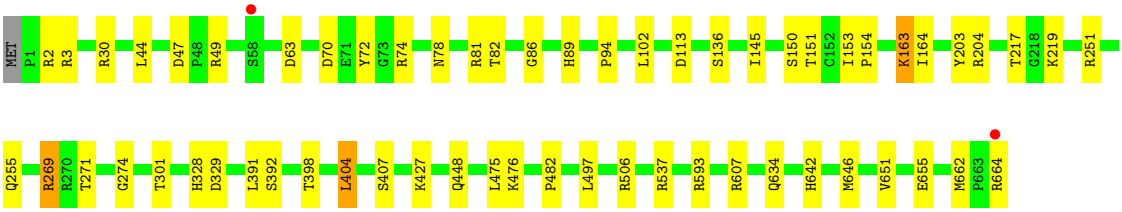
3 Residue-property plots (i)

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: RNA-DIRECTED RNA POLYMERASE

Chain A:



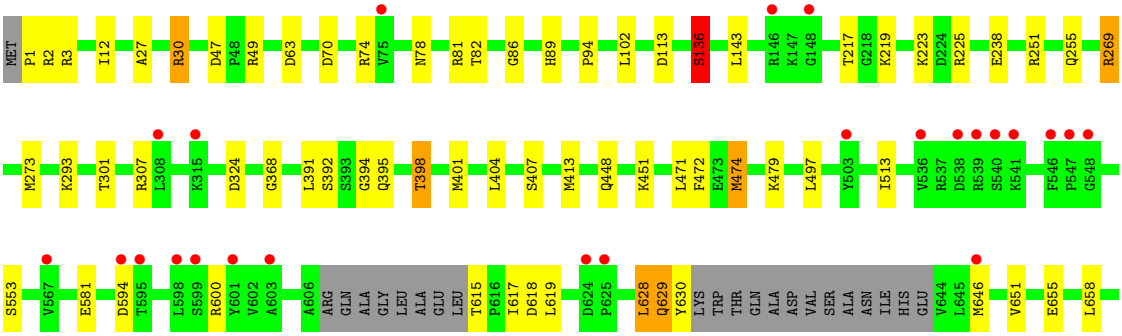


• Molecule 1: RNA-DIRECTED RNA POLYMERASE

Chain B:

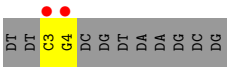
• Molecule 1: RNA-DIRECTED RNA POLYMERASE

Chain C:



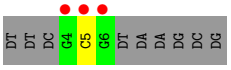
• Molecule 2: 5'-D(*TP*TP*CP*GP*CP*GP*TP*AP*AP*GP*CP*GP)-3'

Chain F:



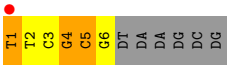
• Molecule 2: 5'-D(*TP*TP*CP*GP*CP*GP*TP*AP*AP*GP*CP*GP)-3'

Chain G:



• Molecule 2: 5'-D(*TP*TP*CP*GP*CP*GP*TP*AP*AP*GP*CP*GP)-3'

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	106.91Å 91.43Å 141.57Å 90.00° 101.92° 90.00°	Depositor
Resolution (Å)	44.51 – 3.04 104.60 – 3.04	Depositor EDS
% Data completeness (in resolution range)	99.0 (44.51-3.04) 99.1 (104.60-3.04)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.92 (at 3.01Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.9.2	Depositor
R, R_{free}	0.209 , 0.243 0.220 , 0.245	Depositor DCC
R_{free} test set	2600 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	62.6	Xtriage
Anisotropy	0.887	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 37.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	15890	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: MG, ATP

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	0.41	0/5396	0.63	1/7297 (0.0%)
1	B	0.41	0/5396	0.64	0/7297
1	C	0.42	0/5227	0.66	0/7064
2	F	1.17	0/42	2.21	1/63 (1.6%)
2	G	0.98	0/67	1.68	1/102 (1.0%)
2	H	1.41	0/132	2.76	13/202 (6.4%)
All	All	0.44	0/16260	0.71	16/22025 (0.1%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	1	DT	P-O3'-C3'	13.12	135.45	119.70
2	H	1	DT	O4'-C1'-N1	11.62	116.13	108.00
2	H	3	DC	P-O3'-C3'	10.02	131.72	119.70
2	H	4	DG	O4'-C1'-N9	9.14	114.40	108.00
2	H	3	DC	O4'-C1'-N1	8.65	114.05	108.00
2	F	3	DC	O4'-C4'-C3'	-7.59	101.45	106.00
2	H	5	DC	O4'-C1'-N1	7.47	113.23	108.00
2	G	5	DC	O4'-C1'-N1	7.14	113.00	108.00
2	H	3	DC	O4'-C4'-C3'	-6.81	101.78	104.50
2	H	4	DG	C1'-O4'-C4'	-6.64	103.45	110.10
2	H	3	DC	N1-C2-O2	6.14	122.58	118.90
2	H	2	DT	N3-C2-O2	-6.07	118.66	122.30
2	H	5	DC	C6-N1-C2	-5.35	118.16	120.30
2	H	3	DC	N3-C2-O2	-5.32	118.17	121.90
1	A	404	LEU	CA-CB-CG	5.07	126.96	115.30
2	H	6	DG	O4'-C1'-N9	5.04	111.53	108.00

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	5265	0	5167	30	0
1	B	5265	0	5167	32	0
1	C	5101	0	5007	30	0
2	F	38	0	24	2	0
2	G	60	0	35	0	0
2	H	119	0	70	6	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
4	A	13	0	0	0	0
4	B	13	0	0	0	0
4	C	13	0	0	0	0
All	All	15890	0	15470	88	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 3.

All (88) 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:C:392:SER:O	1:C:398:THR:HG21	1.87	0.74
1:B:251:ARG:HH11	1:B:255:GLN:HE22	1.37	0.70
1:C:391:LEU:HG	1:C:398:THR:HG22	1.74	0.69
1:A:251:ARG:HH11	1:A:255:GLN:HE22	1.41	0.69
1:B:413:MET:HE2	1:B:488:ILE:HG13	1.74	0.68
1:C:251:ARG:HH11	1:C:255:GLN:HE22	1.40	0.68
1:C:553:SER:HB2	1:C:619:LEU:HG	1.77	0.66
1:A:427:LYS:HE3	1:C:12:ILE:HG21	1.78	0.65
1:C:30:ARG:HD2	2:H:1:DT:H5"	1.78	0.64
1:C:629:GLN:HB3	2:H:5:DC:O2	1.98	0.62
1:C:223:LYS:HE3	1:C:225:ARG:NH2	2.19	0.58
1:C:664:ARG:HD3	1:C:664:ARG:H	1.68	0.57
1:A:203:TYR:HE1	1:A:271:THR:HG22	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:THR:HG22	1:A:163:LYS:HG3	1.86	0.55
1:A:392:SER:O	1:A:398:THR:HG21	2.06	0.55
1:C:273:MET:O	1:C:394:GLY:HA3	2.07	0.54
1:C:629:GLN:HB3	2:H:5:DC:C2	2.42	0.53
1:A:47:ASP:OD1	1:A:49:ARG:HD3	2.08	0.53
1:A:150:SER:H	2:F:4:DG:H5'	1.74	0.53
1:C:628:LEU:HB3	2:H:5:DC:C6	2.44	0.53
1:C:471:LEU:HD12	1:C:474:MET:HE3	1.92	0.52
1:A:651:VAL:O	1:A:655:GLU:HB2	2.10	0.52
1:B:70:ASP:OD2	1:B:74:ARG:HD2	2.09	0.52
1:B:606:ALA:HB3	1:B:609:ALA:HB2	1.91	0.51
1:B:651:VAL:O	1:B:655:GLU:HB2	2.10	0.51
1:A:70:ASP:OD2	1:A:74:ARG:HD2	2.10	0.51
1:A:407:SER:HA	1:A:448:GLN:HE22	1.76	0.51
1:B:407:SER:HA	1:B:448:GLN:HE22	1.76	0.51
1:C:651:VAL:O	1:C:655:GLU:HB2	2.11	0.51
1:A:203:TYR:CE1	1:A:271:THR:HG22	2.45	0.51
1:C:407:SER:HA	1:C:448:GLN:HE22	1.76	0.51
1:B:506:ARG:NH1	1:B:511:SER:HB2	2.26	0.50
1:B:413:MET:CE	1:B:488:ILE:HG13	2.42	0.50
1:C:70:ASP:OD2	1:C:74:ARG:HD2	2.11	0.50
1:B:47:ASP:OD1	1:B:49:ARG:HD3	2.11	0.49
1:A:72:TYR:CE2	1:A:476:LYS:HD3	2.48	0.49
1:A:145:ILE:HD12	1:A:164:ILE:HD13	1.95	0.49
1:A:94:PRO:HB3	1:A:269:ARG:HG3	1.95	0.48
1:C:47:ASP:OD1	1:C:49:ARG:HD3	2.13	0.48
1:A:392:SER:O	1:A:398:THR:CG2	2.62	0.48
1:A:593:ARG:HG2	1:B:42:GLY:HA2	1.95	0.47
1:A:634:GLN:HE21	1:A:642:HIS:CE1	2.32	0.47
1:C:94:PRO:HB3	1:C:269:ARG:HG3	1.96	0.47
1:C:136:SER:OG	1:C:293:LYS:NZ	2.48	0.47
1:A:163:LYS:HE3	1:A:163:LYS:HB2	1.65	0.47
1:A:328:HIS:HD2	1:A:329:ASP:OD1	1.98	0.47
1:B:145:ILE:HD12	1:B:164:ILE:HD13	1.96	0.47
1:B:140:PRO:HB3	1:B:658:LEU:HD13	1.97	0.47
1:C:86:GLY:O	1:C:89:HIS:HD2	1.98	0.46
1:B:72:TYR:CE2	1:B:476:LYS:HD3	2.50	0.46
1:A:217:THR:HG23	1:A:219:LYS:H	1.80	0.45
1:B:94:PRO:HB3	1:B:269:ARG:HG3	1.97	0.45
1:B:217:THR:HG23	1:B:219:LYS:H	1.82	0.45
1:A:274:GLY:HA2	2:F:4:DG:H1'	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:204:ARG:HH12	1:B:626:ASN:HD21	1.65	0.45
1:B:414:GLN:HG2	1:B:459:TRP:CZ2	2.52	0.45
1:A:44:LEU:HD21	1:B:257:GLY:HA3	1.98	0.44
1:A:427:LYS:HE3	1:C:12:ILE:CG2	2.47	0.44
2:H:4:DG:H2"	2:H:5:DC:H5'	1.98	0.44
1:C:94:PRO:CB	1:C:269:ARG:HG3	2.48	0.44
1:C:395:GLN:HB3	1:C:398:THR:HG23	1.99	0.44
1:B:301:THR:HG23	1:B:448:GLN:HG3	2.00	0.44
1:A:153:ILE:HA	1:A:154:PRO:HA	1.87	0.44
1:C:1:PRO:HG2	1:C:238:GLU:OE2	2.17	0.44
1:C:217:THR:HG23	1:C:219:LYS:H	1.83	0.44
1:C:301:THR:HG23	1:C:448:GLN:HG3	1.99	0.44
1:B:418:THR:HG21	1:B:459:TRP:CZ2	2.53	0.43
1:B:94:PRO:CB	1:B:269:ARG:HG3	2.49	0.43
1:A:94:PRO:CB	1:A:269:ARG:HG3	2.49	0.43
1:A:537:ARG:HD2	1:B:49:ARG:HG3	2.00	0.43
1:A:301:THR:HG23	1:A:448:GLN:HG3	2.01	0.43
1:B:607:ARG:H	1:B:607:ARG:HG3	1.68	0.43
1:B:136:SER:OG	1:B:293:LYS:NZ	2.52	0.42
1:B:413:MET:HB2	1:B:413:MET:HE3	1.84	0.42
1:B:606:ALA:O	1:B:608:GLN:N	2.52	0.42
1:A:642:HIS:CE1	1:A:646:MET:HG3	2.54	0.42
1:A:86:GLY:O	1:A:89:HIS:HD2	2.02	0.42
1:C:27:ALA:HA	2:H:1:DT:H5'	2.02	0.41
1:C:391:LEU:HD11	1:C:401:MET:CB	2.50	0.41
1:B:153:ILE:HA	1:B:154:PRO:HA	1.84	0.41
1:B:475:LEU:HD21	1:B:482:PRO:HG3	2.02	0.41
1:B:642:HIS:CE1	1:B:646:MET:HG3	2.55	0.41
1:C:251:ARG:HH11	1:C:255:GLN:NE2	2.14	0.41
1:B:204:ARG:HH12	1:B:626:ASN:ND2	2.19	0.41
1:A:475:LEU:HD21	1:A:482:PRO:HG3	2.03	0.40
1:B:634:GLN:HE21	1:B:642:HIS:CE1	2.39	0.40
1:C:451:LYS:HB3	1:C:497:LEU:HD21	2.02	0.40
1:B:395:GLN:HB3	1:B:398:THR:HG22	2.02	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	662/665 (100%)	642 (97%)	17 (3%)	3 (0%)	29	65
1	B	662/665 (100%)	636 (96%)	23 (4%)	3 (0%)	29	65
1	C	637/665 (96%)	611 (96%)	22 (4%)	4 (1%)	25	60
All	All	1961/1995 (98%)	1889 (96%)	62 (3%)	10 (0%)	29	65

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	607	ARG
1	A	607	ARG
1	B	136	SER
1	A	136	SER
1	B	2	ARG
1	A	2	ARG
1	C	2	ARG
1	C	136	SER
1	C	474	MET
1	C	368	GLY

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	557/558 (100%)	540 (97%)	17 (3%)	40	73
1	B	557/558 (100%)	540 (97%)	17 (3%)	40	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	541/558 (97%)	509 (94%)	32 (6%)	19	51
All	All	1655/1674 (99%)	1589 (96%)	66 (4%)	31	66

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	30	ARG
1	A	63	ASP
1	A	78	ASN
1	A	81	ARG
1	A	82	THR
1	A	102	LEU
1	A	113	ASP
1	A	163	LYS
1	A	204	ARG
1	A	269	ARG
1	A	391	LEU
1	A	404	LEU
1	A	497	LEU
1	A	506	ARG
1	A	662	MET
1	A	664	ARG
1	B	3	ARG
1	B	30	ARG
1	B	63	ASP
1	B	78	ASN
1	B	81	ARG
1	B	82	THR
1	B	102	LEU
1	B	113	ASP
1	B	269	ARG
1	B	273	MET
1	B	391	LEU
1	B	404	LEU
1	B	474	MET
1	B	497	LEU
1	B	658	LEU
1	B	662	MET
1	B	664	ARG
1	C	3	ARG
1	C	30	ARG

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Mol	Chain	Res	Type
1	C	63	ASP
1	C	78	ASN
1	C	81	ARG
1	C	82	THR
1	C	102	LEU
1	C	113	ASP
1	C	136	SER
1	C	143	LEU
1	C	269	ARG
1	C	307	ARG
1	C	324	ASP
1	C	398	THR
1	C	404	LEU
1	C	413	MET
1	C	472	PHE
1	C	479	LYS
1	C	513	ILE
1	C	581	GLU
1	C	594	ASP
1	C	600	ARG
1	C	615	THR
1	C	617	ILE
1	C	618	ASP
1	C	628	LEU
1	C	629	GLN
1	C	630	TYR
1	C	646	MET
1	C	658	LEU
1	C	662	MET
1	C	664	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	26	GLN
1	A	78	ASN
1	A	89	HIS
1	A	91	ASN
1	A	255	GLN
1	A	309	ASN
1	A	328	HIS

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Mol	Chain	Res	Type
1	A	448	GLN
1	A	525	GLN
1	A	626	ASN
1	A	634	GLN
1	A	642	HIS
1	B	15	GLN
1	B	26	GLN
1	B	78	ASN
1	B	89	HIS
1	B	255	GLN
1	B	309	ASN
1	B	328	HIS
1	B	448	GLN
1	B	469	HIS
1	B	525	GLN
1	B	626	ASN
1	B	634	GLN
1	B	642	HIS
1	C	15	GLN
1	C	26	GLN
1	C	78	ASN
1	C	89	HIS
1	C	91	ASN
1	C	255	GLN
1	C	288	GLN
1	C	309	ASN
1	C	448	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)

Of 6 ligands modelled in this entry, 3 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	$\#\|Z\| > 2$
4	ATP	B	1666	-	8,12,33	1.11	0	15,20,52	0.95	0
4	ATP	A	1666	3	8,12,33	0.99	0	15,20,52	1.03	1 (6%)
4	ATP	C	1665	-	8,12,33	1.03	1 (12%)	15,20,52	0.98	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
4	ATP	B	1666	-	-	0/12/12/38	-
4	ATP	A	1666	3	-	0/12/12/38	-
4	ATP	C	1665	-	-	0/12/12/38	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1665	ATP	PA-O5'	2.00	1.62	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1666	ATP	O3G-PG-O3B	2.33	112.45	104.64

There are no chirality outliers.

There are no torsion outliers.

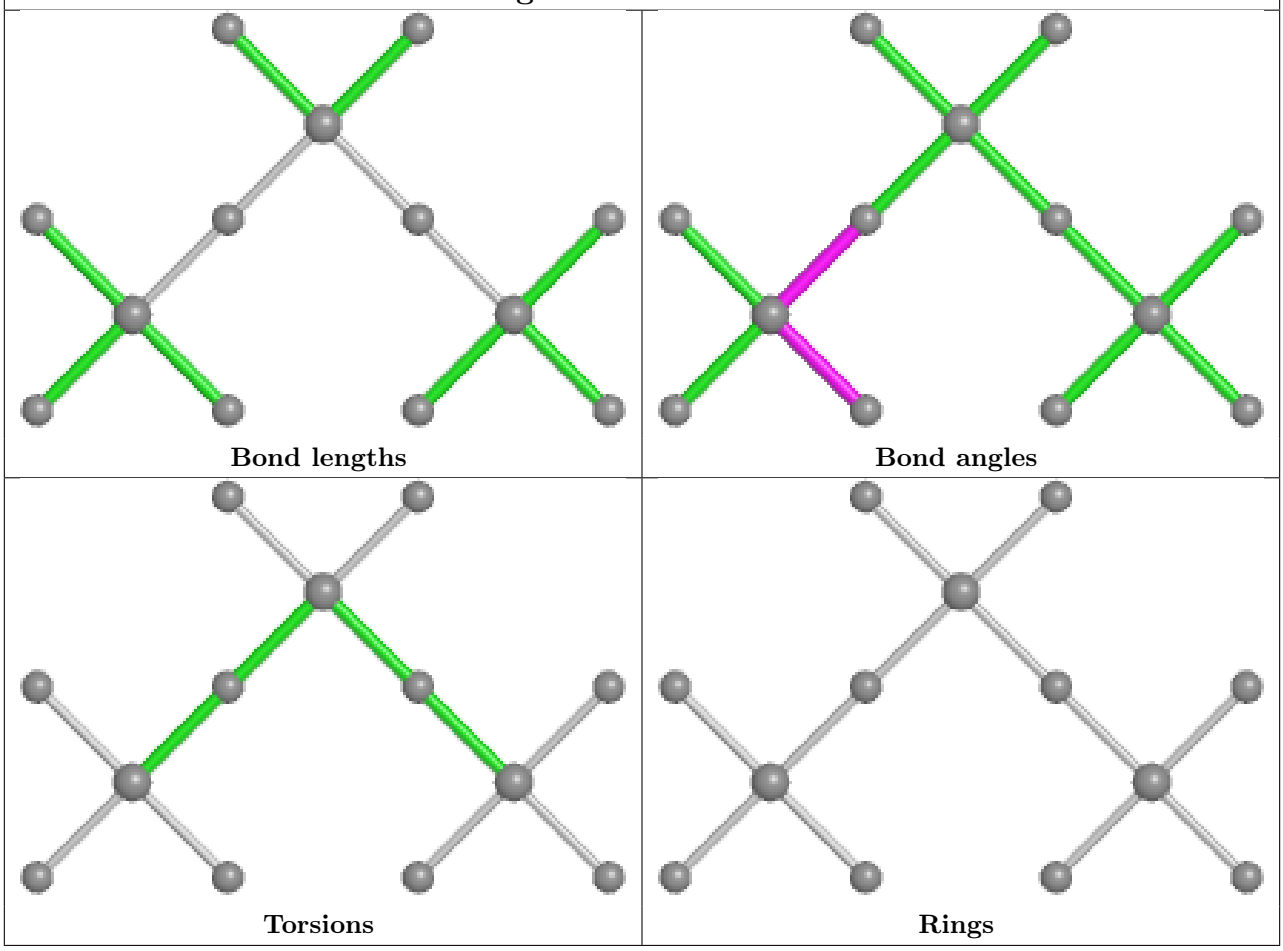
There are no ring outliers.

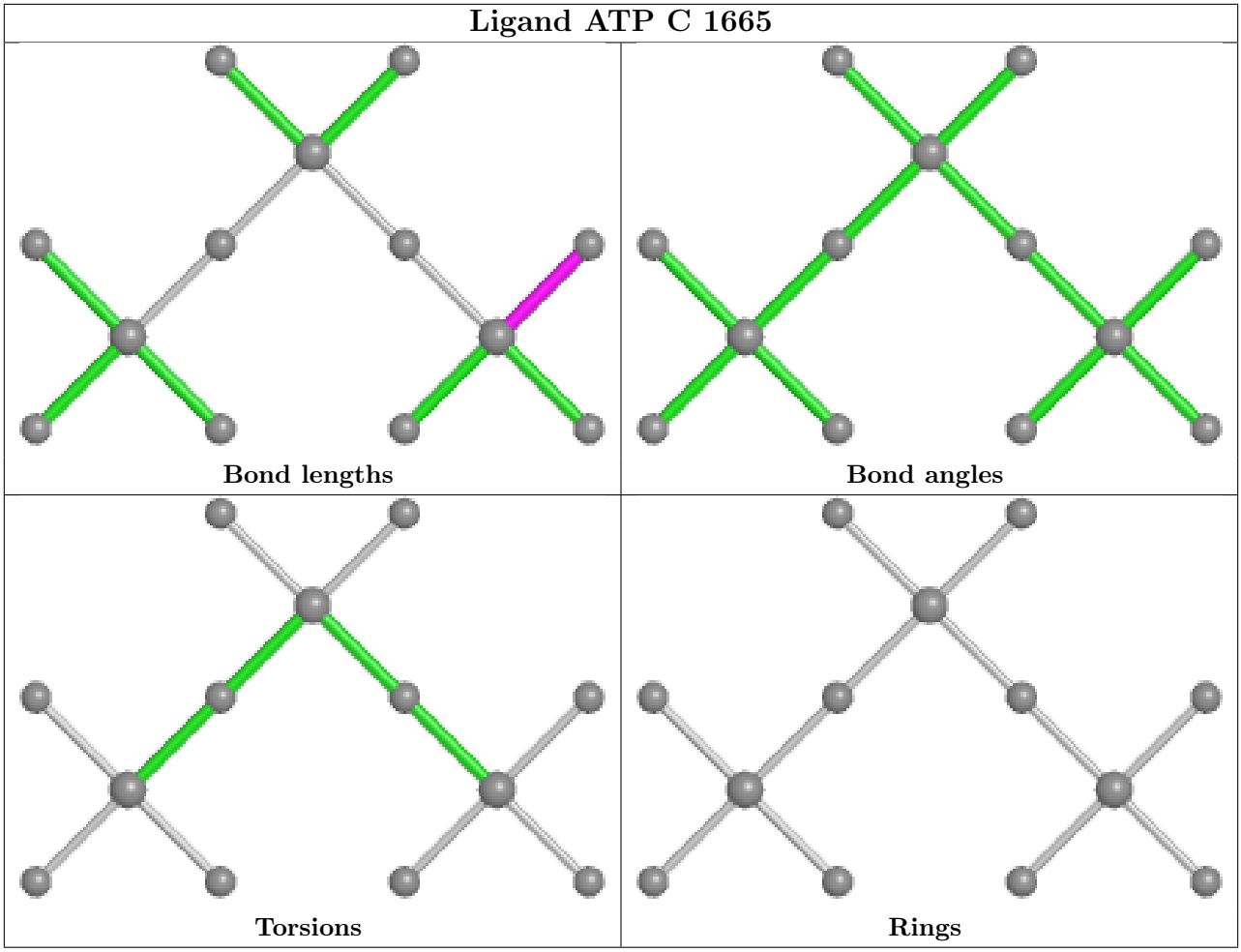
No monomer is involved in short contacts.

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 ATP A 1666





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	664/665 (99%)	-0.02	2 (0%)	94	83	38, 61, 84, 117	0
1	B	664/665 (99%)	0.14	3 (0%)	91	75	47, 67, 96, 152	0
1	C	643/665 (96%)	0.34	24 (3%)	41	17	44, 83, 133, 165	0
2	F	2/12 (16%)	5.07	2 (100%)	0	0	167, 167, 167, 167	0
2	G	3/12 (25%)	6.68	3 (100%)	0	0	183, 183, 183, 183	0
2	H	6/12 (50%)	1.25	1 (16%)	1	0	110, 119, 126, 126	0
All	All	1982/2031 (97%)	0.17	35 (1%)	68	40	38, 68, 121, 183	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	6	DG	8.8
1	C	601	TYR	6.3
2	G	5	DC	5.8
1	B	608	GLN	5.6
2	G	4	DG	5.5
1	C	594	ASP	5.4
2	F	3	DC	5.1
2	F	4	DG	5.0
1	C	646	MET	4.1
1	C	599	SER	3.5
1	C	315	LYS	3.3
1	C	547	PRO	3.3
1	C	541	LYS	3.3
1	C	567	VAL	2.9
1	C	503	TYR	2.7
1	C	603	ALA	2.7
1	C	540	SER	2.7
1	C	536	VAL	2.6
1	C	546	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
2	H	1	DT	2.5
1	B	601	TYR	2.4
1	A	58	SER	2.3
1	C	598	LEU	2.3
1	C	624	ASP	2.3
1	C	625	PRO	2.3
1	C	595	THR	2.3
1	C	548	GLY	2.2
1	C	75	VAL	2.2
1	C	146	ARG	2.1
1	C	148	GLY	2.1
1	C	538	ASP	2.1
1	A	664	ARG	2.0
1	B	453	ASP	2.0
1	C	308	LEU	2.0
1	C	539	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 monosaccharides in this entry.

6.4 Ligands (i)

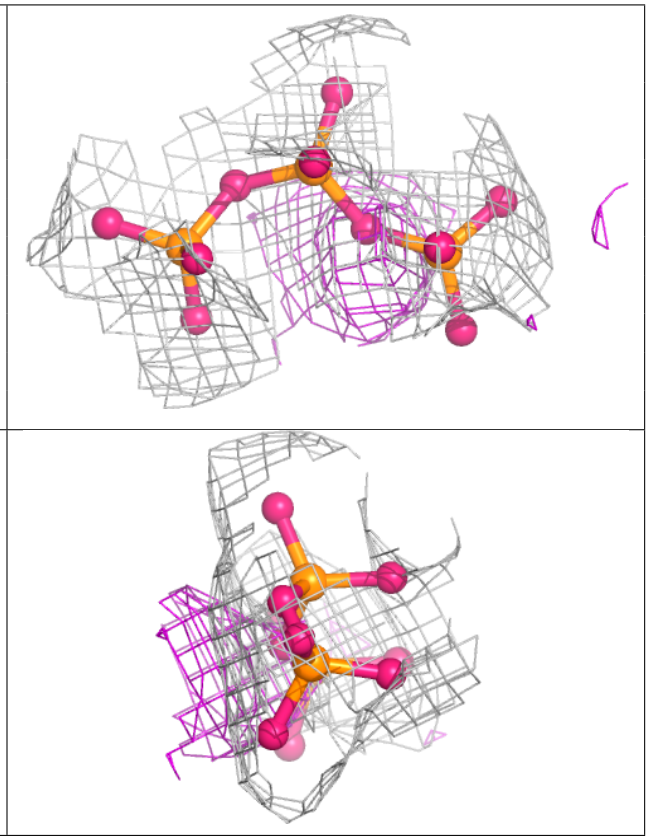
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

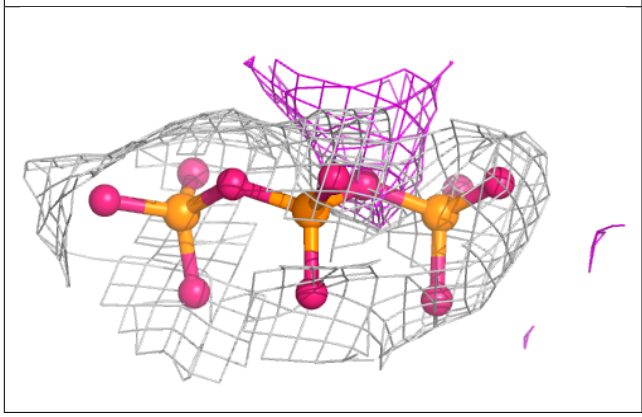
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	ATP	A	1666	13/31	0.61	0.22	176,179,182,183	0
4	ATP	C	1665	13/31	0.74	0.20	173,177,182,183	0
4	ATP	B	1666	13/31	0.77	0.19	141,144,147,148	0
3	MG	A	1667	1/1	0.86	0.18	69,69,69,69	0
3	MG	B	1665	1/1	0.95	0.07	63,63,63,63	0
3	MG	A	1665	1/1	0.95	0.11	55,55,55,55	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 ATP A 1666:

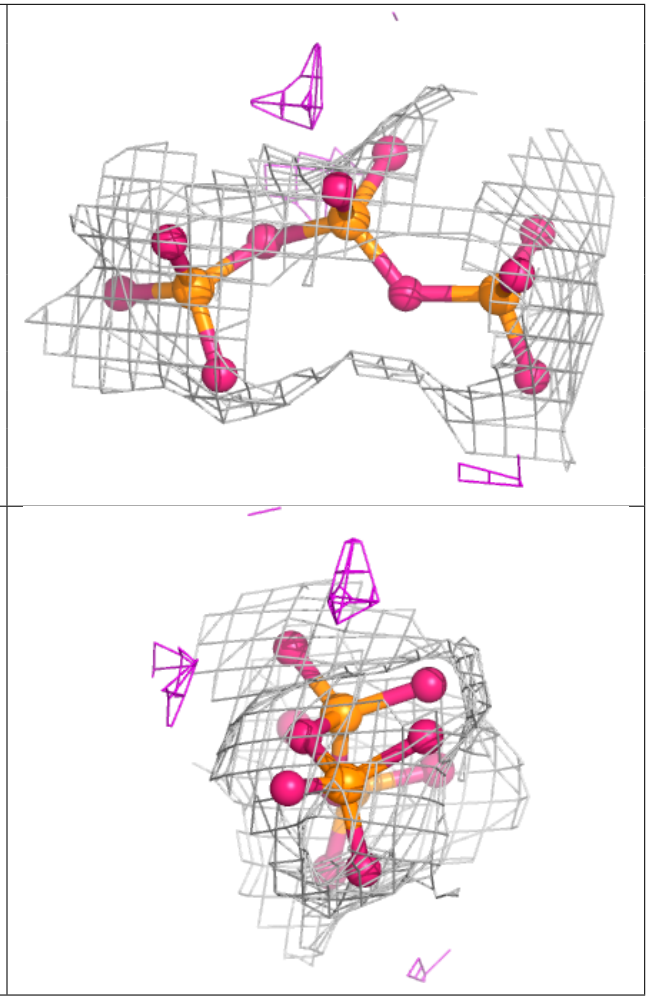
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around ATP C 1665:

$2mF_o$-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.