Full wwPDB X-ray Structure Validation Report (i)

May 15, 2020 – 09:37 pm BST

PDB ID	:	6Q4M
Title	:	Crystal structure of the O-GlcNAc transferase Asn648Tyr mutation
Authors	:	Gundogdu, M.; van Aalten, D.M.F.
Deposited on	:	2018-12-06
Resolution	:	2.20 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 following versions of software and data (see references (i)) were used in the production of this report:

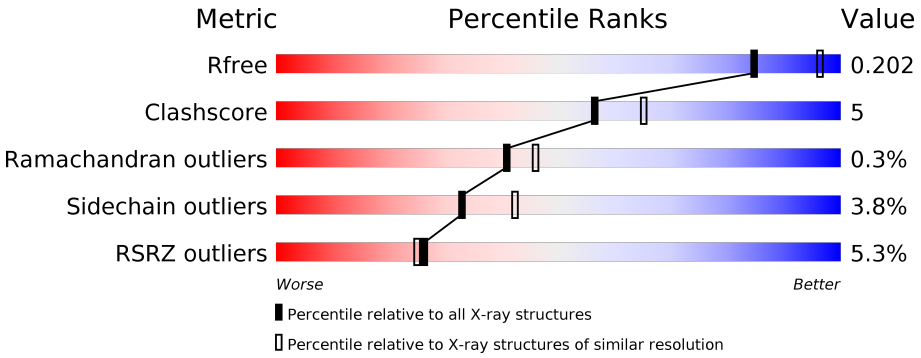
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	723	5% 84% 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5948 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.

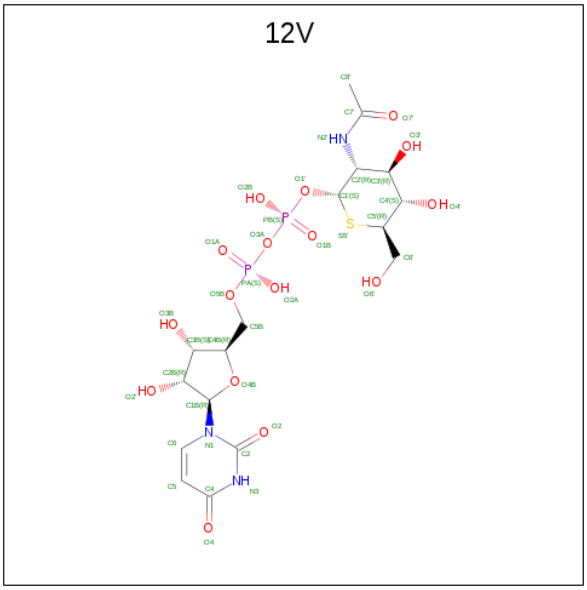
- Molecule 1 is a protein called UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	698	5529	3512	966	1013	38	0	1	0

There are 5 discrepancies between the modelled and reference sequences:

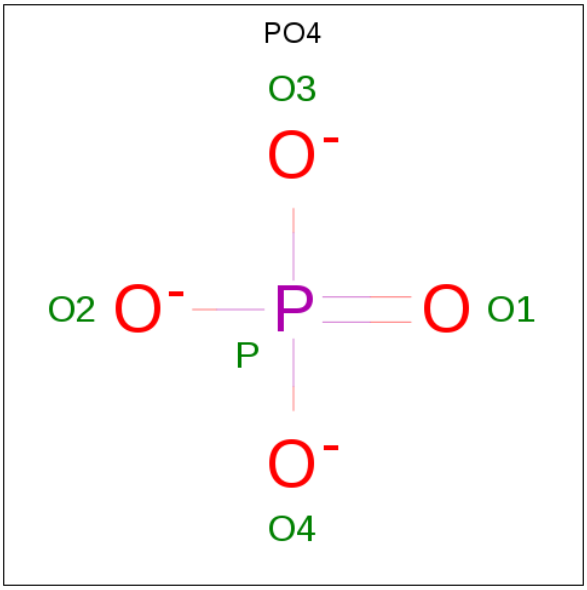
Chain	Residue	Modelled	Actual	Comment	Reference
A	319	GLY	-	expression tag	UNP O15294
A	320	PRO	-	expression tag	UNP O15294
A	321	GLY	-	expression tag	UNP O15294
A	322	SER	-	expression tag	UNP O15294
A	648	TYR	ASN	engineered mutation	UNP O15294

- Molecule 2 is (2S,3R,4R,5S,6R)-3-(acetylamino)-4,5-dihydroxy-6-(hydroxymethyl)tetrahydro-2H-thiopyran-2-yl [(2R,3S,4R,5R)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-3,4-dihydroxytetrahydrofuran-2-yl]methyl dihydrogen diphosphate (three-letter code: 12V) (formula: $C_{17}H_{27}N_3O_{16}P_2S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			39	17	3	16	2	1		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P) (labeled as "Ligand of Interest" by author).



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

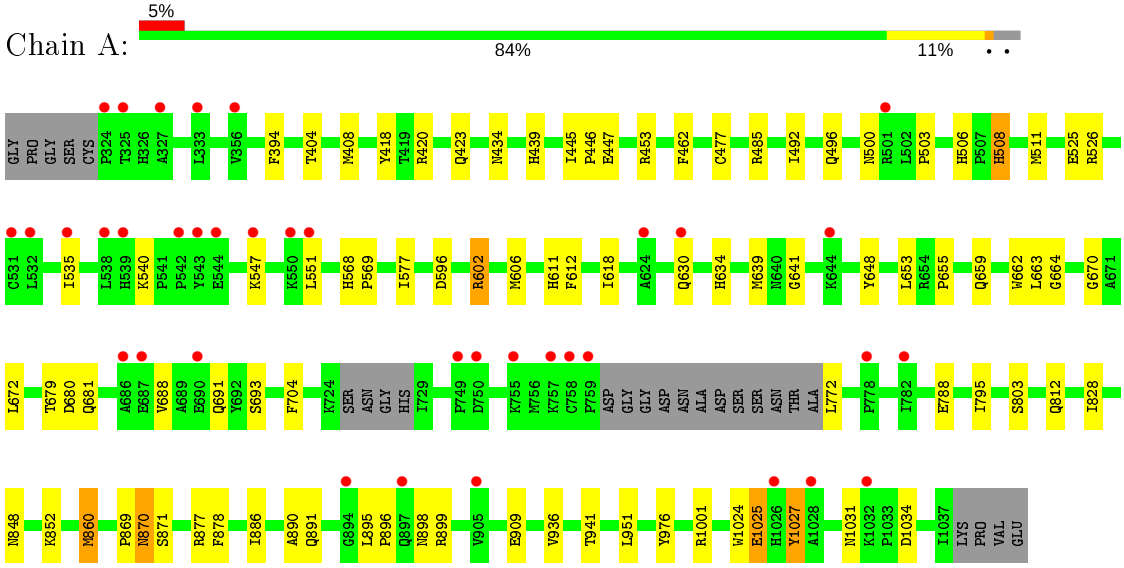
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	370	Total	O	0	0
			370	370		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit



4 Data and refinement statistics (i)

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	137.32Å 150.74Å 199.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.92 – 2.20 45.92 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (45.92-2.20) 100.0 (45.92-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.21 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.175 , 0.199 0.181 , 0.202	Depositor DCC
R_{free} test set	2638 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	42.0	Xtriage
Anisotropy	0.595	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 38.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	5948	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, 12V

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	0.75	0/5659	0.93	8/7676 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1001	ARG	CG-CD-NE	-8.27	94.44	111.80
1	A	485	ARG	NE-CZ-NH2	-6.87	116.87	120.30
1	A	602	ARG	NE-CZ-NH2	-6.64	116.98	120.30
1	A	1001	ARG	NE-CZ-NH2	-6.47	117.07	120.30
1	A	485	ARG	NE-CZ-NH1	5.59	123.10	120.30
1	A	602	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	A	860	MET	CG-SD-CE	-5.33	91.68	100.20
1	A	877	ARG	NE-CZ-NH2	-5.25	117.68	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	662	TRP	Peptide

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	5529	0	5502	54	1
2	A	39	0	25	2	0
3	A	10	0	0	1	0
4	A	370	0	0	9	3
All	All	5948	0	5527	55	4

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 5.

All (55) 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:439:HIS:ND1	4:A:1201:HOH:O	1.97	0.96
1:A:655:PRO:HD2	1:A:659:GLN:HE22	1.55	0.72
1:A:611:HIS:ND1	4:A:1203:HOH:O	2.23	0.71
1:A:860:MET:HE2	1:A:976:TYR:CD1	2.26	0.70
1:A:860:MET:HE1	1:A:976:TYR:HB3	1.72	0.70
1:A:869:PRO:O	1:A:870:ASN:CG	2.29	0.69
1:A:404:THR:HG22	1:A:408:MET:HE2	1.75	0.69
1:A:568:HIS:HB2	4:A:1467:HOH:O	1.95	0.67
1:A:420:ARG:HH11	1:A:423:GLN:HE21	1.42	0.65
1:A:506[B]:HIS:HB3	1:A:508:HIS:CE1	2.32	0.64
1:A:540:LYS:HG3	1:A:653:LEU:HD22	1.80	0.63
1:A:404:THR:HG22	1:A:408:MET:CE	2.29	0.62
1:A:655:PRO:HD2	1:A:659:GLN:NE2	2.15	0.62
2:A:1101:12V:H1'	2:A:1101:12V:O1A	2.00	0.62
1:A:691:GLN:NE2	4:A:1210:HOH:O	2.32	0.62
1:A:506[A]:HIS:HB3	1:A:508:HIS:CE1	2.36	0.60
1:A:641:GLY:HA2	1:A:648:TYR:OH	2.02	0.59
1:A:869:PRO:O	1:A:870:ASN:CB	2.51	0.58
1:A:870:ASN:HA	4:A:1441:HOH:O	2.06	0.54
1:A:568:HIS:CG	1:A:569:PRO:HD2	2.44	0.53
1:A:890:ALA:HB1	1:A:895:LEU:HD23	1.90	0.53
1:A:639:MET:O	1:A:664:GLY:HA3	2.10	0.52
1:A:496:GLN:OE1	1:A:503:PRO:HA	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:795:ILE:HD11	1:A:812:GLN:HE22	1.75	0.51
1:A:420:ARG:HH11	1:A:423:GLN:NE2	2.10	0.49
1:A:848:ASN:HB3	1:A:852:LYS:HD2	1.95	0.49
1:A:860:MET:HE1	1:A:976:TYR:CB	2.39	0.49
1:A:898:ASN:HB2	4:A:1437:HOH:O	2.12	0.49
1:A:634:HIS:HD2	1:A:1024:TRP:CH2	2.32	0.48
1:A:569:PRO:HB2	2:A:1101:12V:H6'A	1.95	0.48
1:A:606:MET:HG2	1:A:612:PHE:CD1	2.48	0.48
1:A:492:ILE:O	1:A:496:GLN:HG3	2.14	0.47
1:A:596:ASP:HA	1:A:602:ARG:HD2	1.96	0.47
1:A:688:VAL:O	1:A:691:GLN:HB3	2.15	0.47
1:A:870:ASN:OD1	1:A:871:SER:N	2.48	0.47
1:A:418:TYR:CE1	1:A:434:ASN:HB3	2.51	0.46
1:A:606:MET:HG2	1:A:612:PHE:CG	2.51	0.46
1:A:860:MET:CE	1:A:976:TYR:HB3	2.44	0.46
1:A:500:ASN:HA	1:A:526:ARG:NH1	2.31	0.45
1:A:670:GLY:HA2	1:A:693:SER:HB3	1.98	0.45
1:A:951:LEU:HD23	1:A:951:LEU:C	2.37	0.44
1:A:477:CYS:SG	1:A:886:ILE:HD11	2.57	0.44
1:A:618:ILE:HG22	1:A:618:ILE:O	2.18	0.44
1:A:828:ILE:HD11	3:A:1103:PO4:O2	2.18	0.44
1:A:447:GLU:HG2	4:A:1233:HOH:O	2.16	0.44
1:A:535:ILE:HD12	1:A:653:LEU:HD23	2.00	0.44
1:A:860:MET:CE	1:A:976:TYR:CD1	3.00	0.43
1:A:453:ARG:NH1	4:A:1223:HOH:O	2.50	0.43
1:A:795:ILE:HD11	1:A:812:GLN:NE2	2.33	0.43
1:A:895:LEU:HD12	1:A:896:PRO:HD2	2.00	0.43
1:A:679:THR:OG1	1:A:680:ASP:N	2.51	0.42
1:A:1025:GLU:OE2	1:A:1025:GLU:HA	2.19	0.41
1:A:941:THR:OG1	4:A:1202:HOH:O	2.22	0.41
1:A:445:ILE:N	1:A:446:PRO:CD	2.84	0.41
1:A:1027:TYR:CD1	1:A:1027:TYR:C	2.94	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1475:HOH:O	4:A:1475:HOH:O[8_555]	0.74	1.46
1:A:630:GLN:OE1	1:A:630:GLN:OE1[11_555]	1.54	0.66
4:A:1230:HOH:O	4:A:1454:HOH:O[3_555]	1.70	0.50
4:A:1505:HOH:O	4:A:1522:HOH:O[8_555]	2.11	0.09

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	693/723 (96%)	657 (95%)	34 (5%)	2 (0%)	41 46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	870	ASN
1	A	663	LEU

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	601/618 (97%)	578 (96%)	23 (4%)	33 42

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	394	PHE
1	A	462	PHE
1	A	508	HIS
1	A	511	MET
1	A	525	GLU
1	A	547	LYS
1	A	551	LEU
1	A	577	ILE
1	A	672	LEU

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Mol	Chain	Res	Type
1	A	681	GLN
1	A	704	PHE
1	A	772	LEU
1	A	788	GLU
1	A	803	SER
1	A	878	PHE
1	A	891	GLN
1	A	899	ARG
1	A	909	GLU
1	A	936	VAL
1	A	1025	GLU
1	A	1027	TYR
1	A	1031	ASN
1	A	1034	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	335	ASN
1	A	423	GLN
1	A	434	ASN
1	A	471	HIS
1	A	659	GLN
1	A	737	ASN
1	A	812	GLN
1	A	849	GLN
1	A	916	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 carbohydrates 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	$\#\|Z\| > 2$
3	PO4	A	1102	-	4,4,4	1.05	0	6,6,6	0.51	0
2	12V	A	1101	-	32,41,41	1.19	2 (6%)	38,62,62	1.82	6 (15%)
3	PO4	A	1103	-	4,4,4	0.94	0	6,6,6	0.77	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
2	12V	A	1101	-	-	8/23/63/63	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	12V	C4'-C5'	3.62	1.56	1.53
2	A	1101	12V	C4-N3	3.38	1.38	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1101	12V	O1'-C1'-C2'	6.09	116.67	107.47
2	A	1101	12V	C3'-C2'-N2'	5.12	120.28	110.62
2	A	1101	12V	C5-C4-N3	-3.89	114.74	123.31
2	A	1101	12V	O3'-C3'-C2'	3.40	116.51	109.66
2	A	1101	12V	O6'-C6'-C5'	2.60	116.68	110.73
2	A	1101	12V	PB-O1'-C1'	-2.20	111.25	119.74

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	12V	C2B-C1B-N1-C6
2	A	1101	12V	O4B-C1B-N1-C6
2	A	1101	12V	C4'-C5'-C6'-O6'
2	A	1101	12V	S5'-C5'-C6'-O6'
2	A	1101	12V	O4B-C4B-C5B-O5B
2	A	1101	12V	C3B-C4B-C5B-O5B
2	A	1101	12V	PA-O3A-PB-O1B
2	A	1101	12V	PA-O3A-PB-O2B

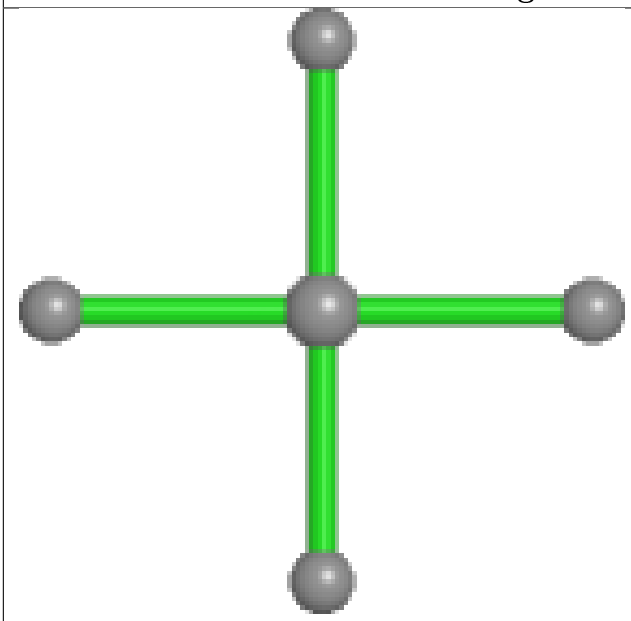
There are no ring outliers.

2 monomers are involved in 3 short contacts:

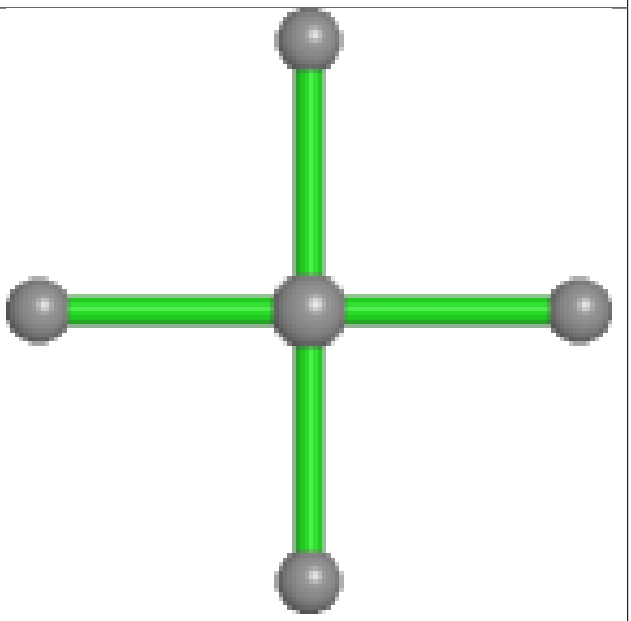
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	12V	2	0
3	A	1103	PO4	1	0

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 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.

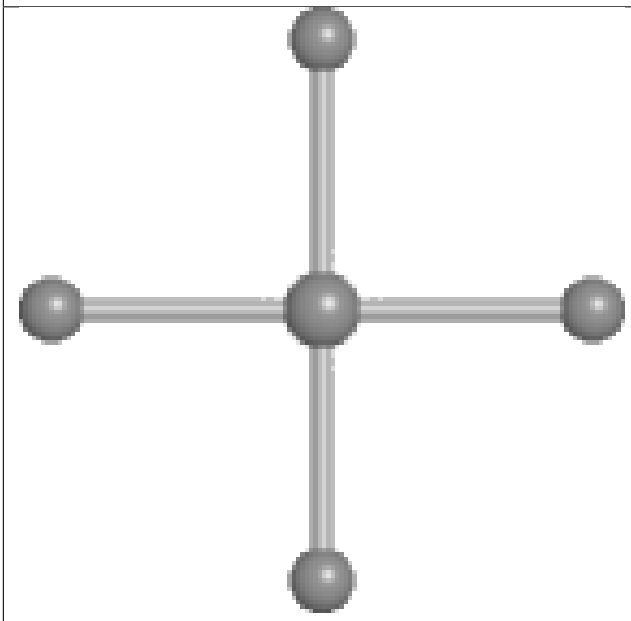
Ligand PO4 A 1102



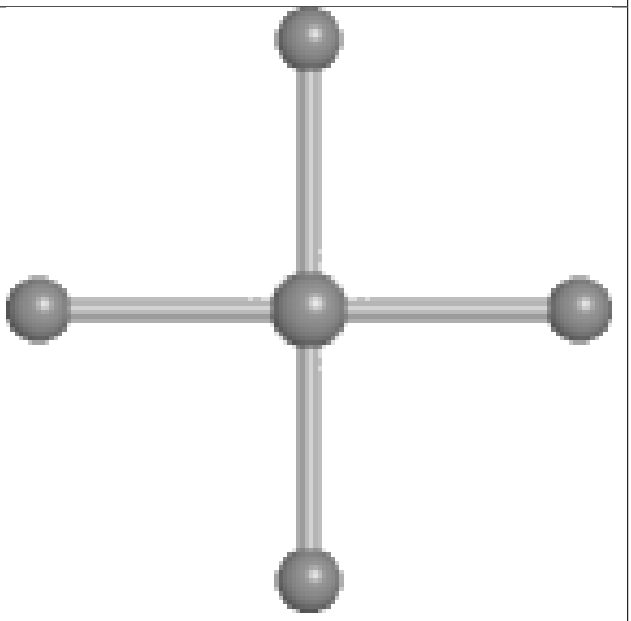
Bond lengths



Bond angles

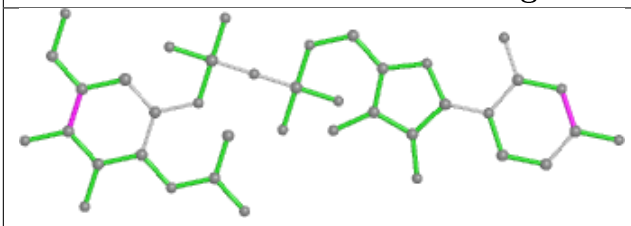


Torsions

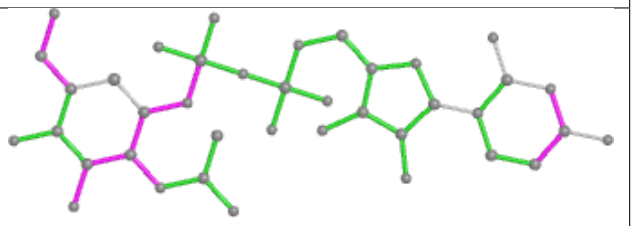


Rings

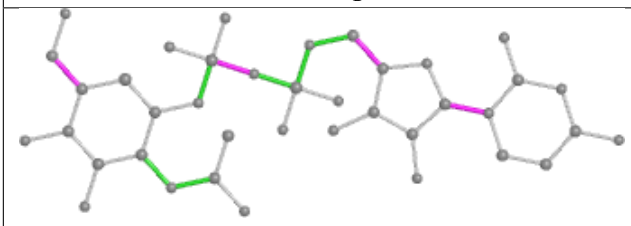
Ligand 12V A 1101



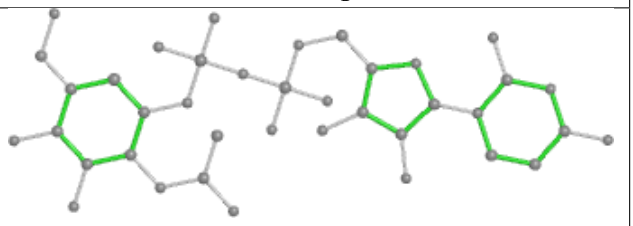
Bond lengths



Bond angles

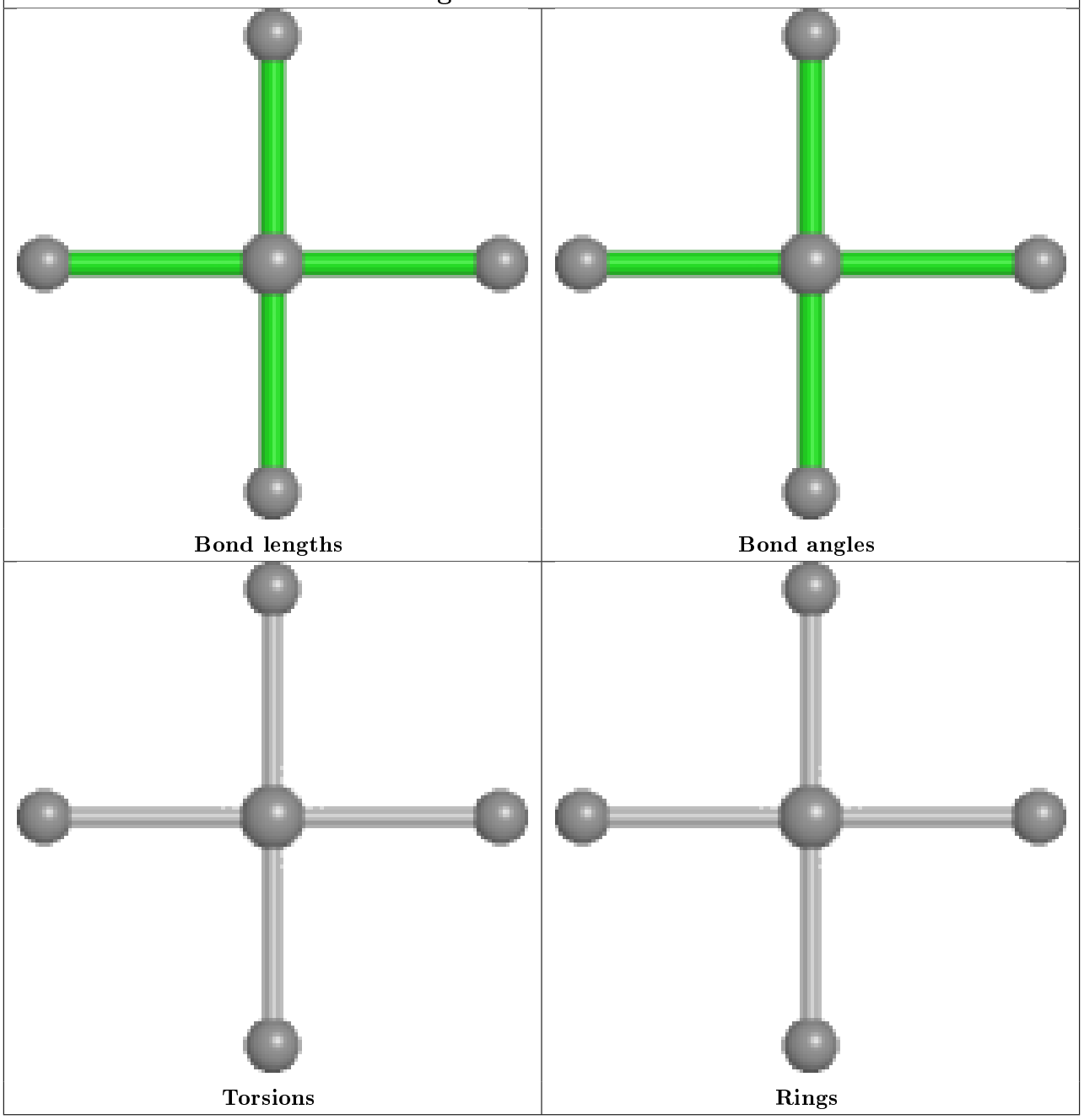


Torsions



Rings

Ligand PO4 A 1103



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

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, 95^{th} 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	698/723 (96%)	0.12	37 (5%)	26	25	30, 48, 94, 119	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	750	ASP	6.0
1	A	538	LEU	4.9
1	A	539	HIS	4.3
1	A	759	PRO	4.1
1	A	755	LYS	3.7
1	A	897	GLN	3.5
1	A	325	THR	3.4
1	A	749	PRO	3.2
1	A	758	CYS	3.2
1	A	356	VAL	3.0
1	A	686	ALA	3.0
1	A	542	PRO	3.0
1	A	327	ALA	3.0
1	A	324	PRO	2.9
1	A	630	GLN	2.9
1	A	535	ILE	2.9
1	A	1026	HIS	2.8
1	A	1028	ALA	2.7
1	A	531	CYS	2.7
1	A	782	ILE	2.7
1	A	1032	LYS	2.6
1	A	624	ALA	2.5
1	A	544	GLU	2.5
1	A	550	LYS	2.4
1	A	690	GLU	2.4
1	A	532	LEU	2.3
1	A	551	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	894	GLY	2.2
1	A	501	ARG	2.2
1	A	543	TYR	2.1
1	A	757	LYS	2.1
1	A	778	PRO	2.1
1	A	547	LYS	2.1
1	A	644	LYS	2.1
1	A	687	GLU	2.0
1	A	905	VAL	2.0
1	A	333	LEU	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 carbohydrates in this entry.

6.4 Ligands (i)

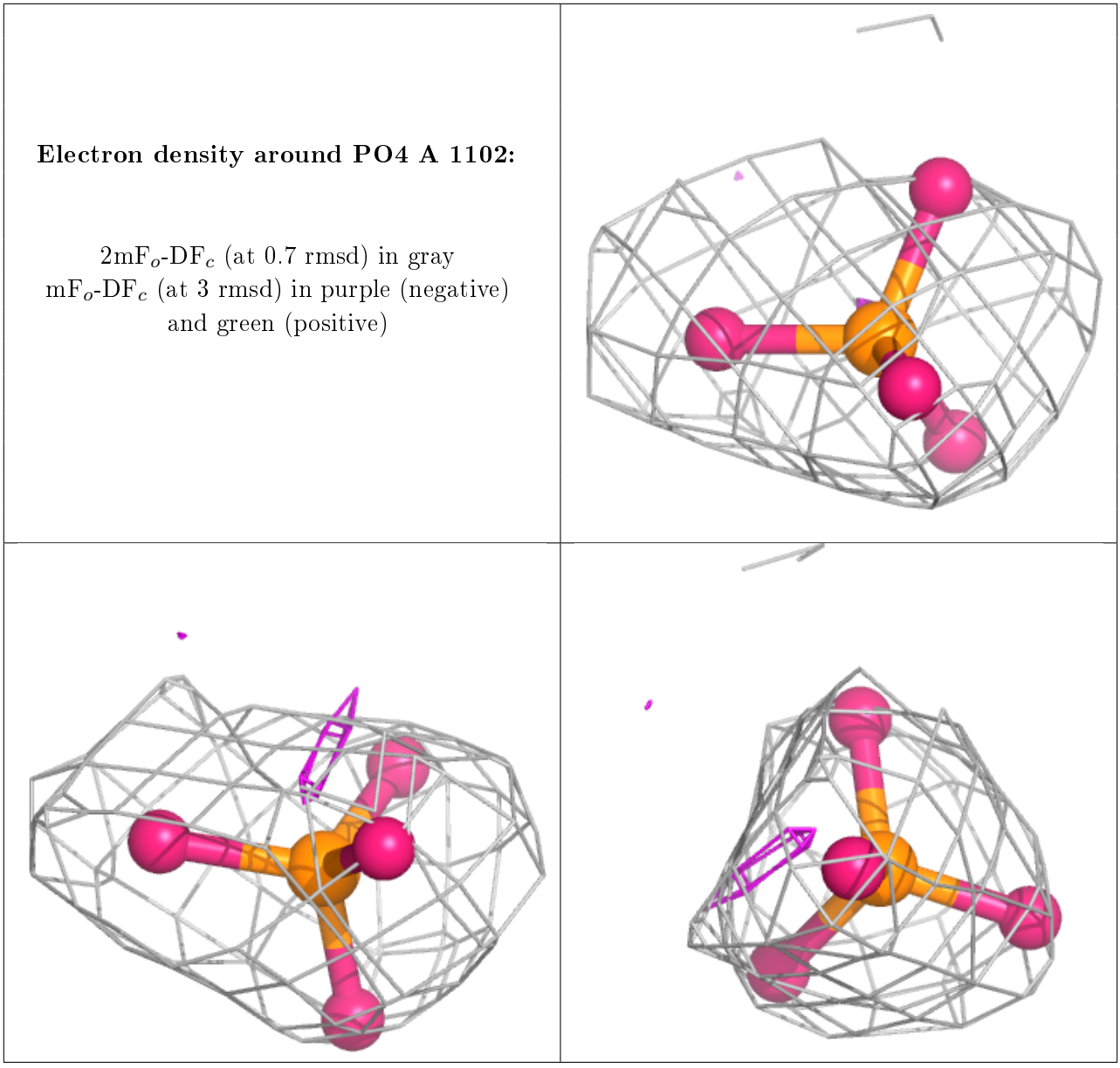
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
3	PO4	A	1102	5/5	0.92	0.23	72,80,94,103	0
3	PO4	A	1103	5/5	0.93	0.18	52,63,91,102	0
2	12V	A	1101	39/39	0.97	0.17	32,36,89,91	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.

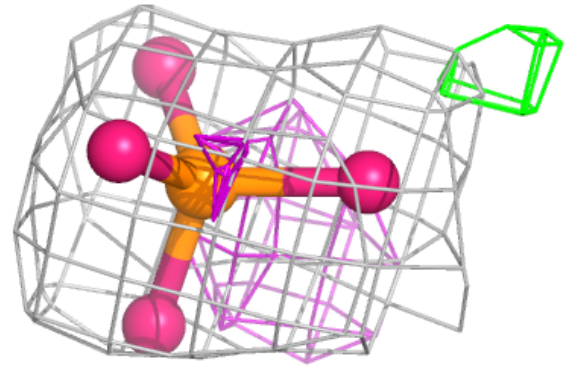
Electron density around PO4 A 1102:

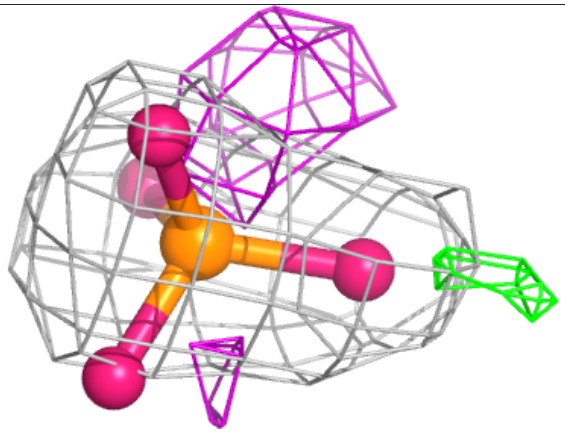
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

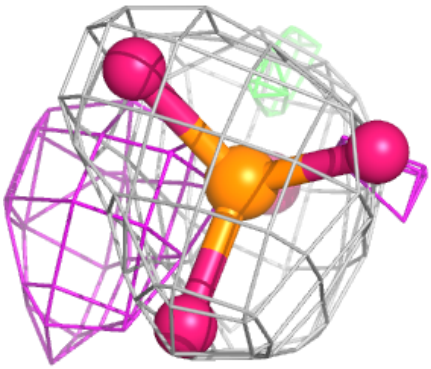


Electron density around PO4 A 1103:

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

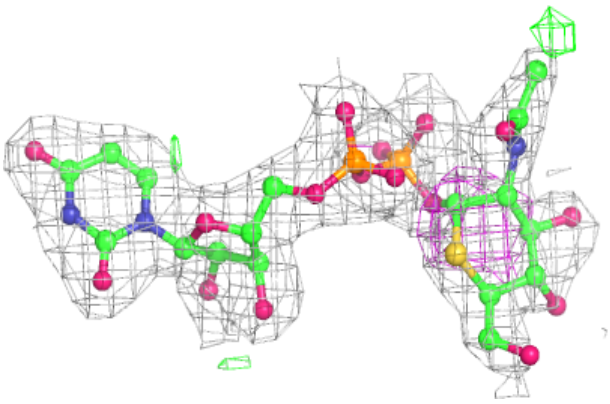


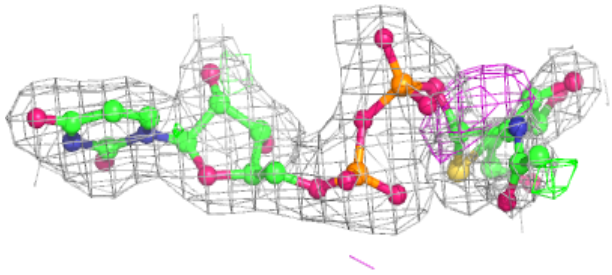


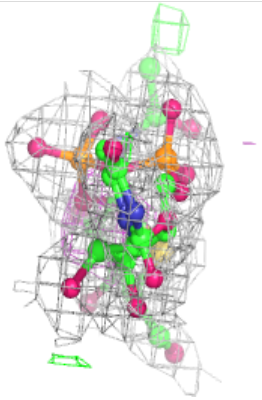


Electron density around 12V A 1101:

$2mF_o$-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.