



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 18, 2022 – 04:16 pm BST

PDB ID : 7P5O
Title : Crystal structure of *Aspergillus fumigatus* phosphoglucomutase in complex with the reaction intermediate
Authors : Raimi, O.G.; Yan, K.; van Aalten, D.M.F.
Deposited on : 2021-07-14
Resolution : 2.48 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.29
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.29

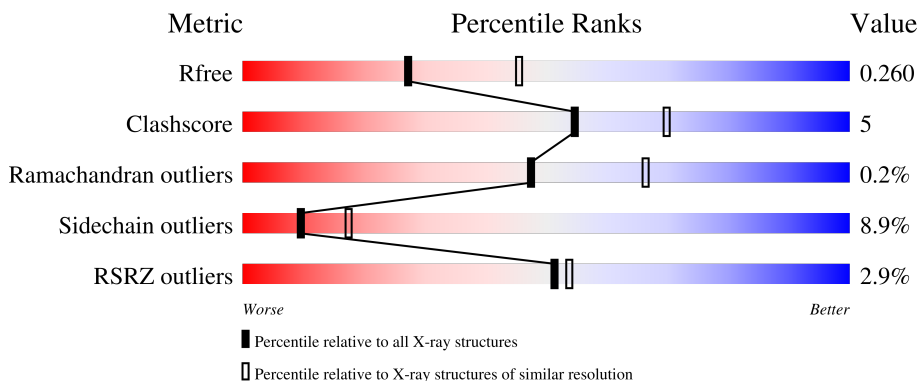
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

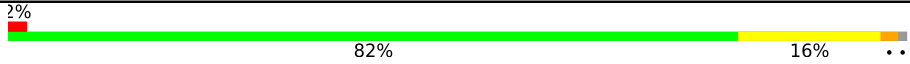
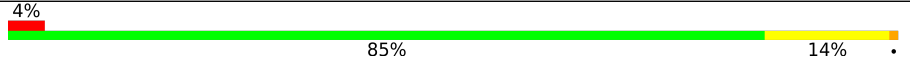
The reported resolution of this entry is 2.48 Å.

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	5857 (2.50-2.46)
Clashscore	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)
RSRZ outliers	127900	5738 (2.50-2.46)

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	560	 2% 82% 16% ..
1	B	560	 4% 85% 14% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9110 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.

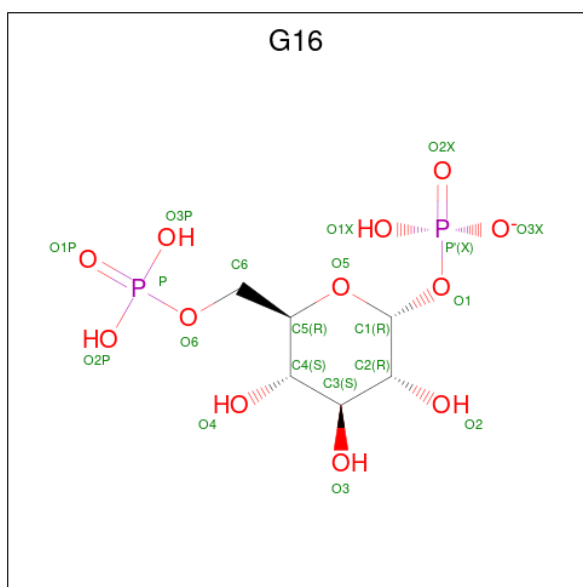
- Molecule 1 is a protein called Phosphoglucomutase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	556	4274	2722	714	826	12	0	1	0
1	B	558	4284	2731	715	826	12	0	2	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP A0A229WAX6
A	-3	PRO	-	expression tag	UNP A0A229WAX6
A	-2	LEU	-	expression tag	UNP A0A229WAX6
A	-1	GLY	-	cloning artifact	UNP A0A229WAX6
A	0	SER	-	cloning artifact	UNP A0A229WAX6
B	-4	GLY	-	expression tag	UNP A0A229WAX6
B	-3	PRO	-	expression tag	UNP A0A229WAX6
B	-2	LEU	-	expression tag	UNP A0A229WAX6
B	-1	GLY	-	cloning artifact	UNP A0A229WAX6
B	0	SER	-	cloning artifact	UNP A0A229WAX6

- Molecule 2 is 1,6-di-O-phosphono-alpha-D-glucopyranose (three-letter code: G16) (formula: $C_6H_{13}O_{12}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
2	A	1	Total	C	O	P	0	0
			20	6	12	2		
2	B	1	Total	C	O	P	0	0
			20	6	12	2		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

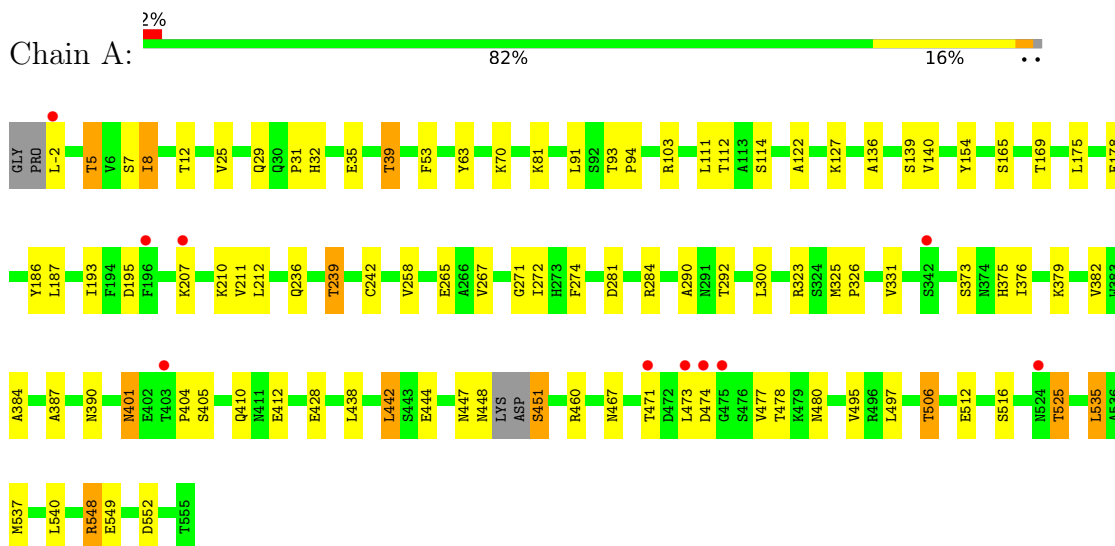
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	268	Total	O	0	0
			268	268		
4	B	242	Total	O	0	0
			242	242		

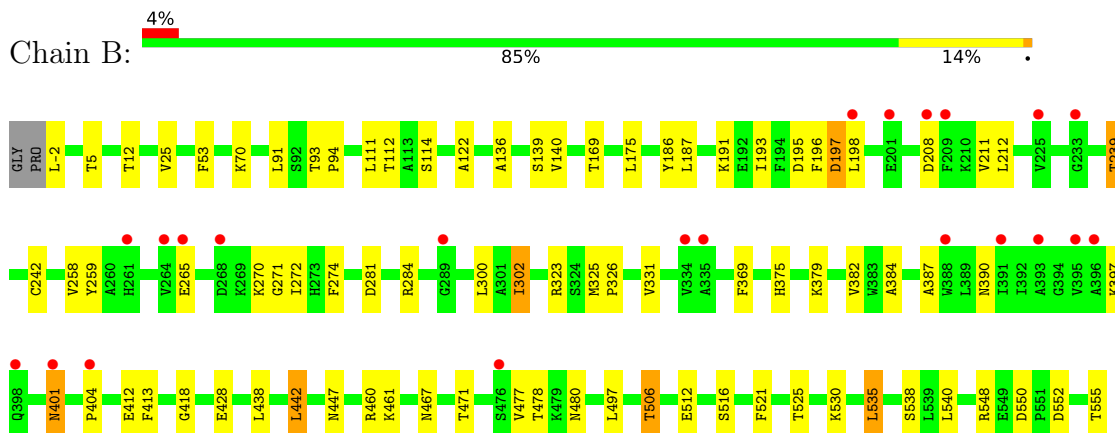
3 Residue-property plots [i](#)

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: Phosphoglucosyltransferase



- Molecule 1: Phosphoglucosyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	98.57Å 209.61Å 61.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	89.20 – 2.48 89.20 – 2.48	Depositor EDS
% Data completeness (in resolution range)	98.4 (89.20-2.48) 98.4 (89.20-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.48Å)	Xtrriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.201 , 0.258 0.206 , 0.260	Depositor DCC
R_{free} test set	2250 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	40.4	Xtrriage
Anisotropy	0.542	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9110	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% 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: MG, G16

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	0.72	0/4371	0.86	0/5916
1	B	0.72	0/4385	0.86	0/5937
All	All	0.72	0/8756	0.86	0/11853

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
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	271	GLY	Peptide
1	B	271	GLY	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	4274	0	4221	43	0
1	B	4284	0	4237	45	0
2	A	20	0	10	2	0
2	B	20	0	10	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	268	0	0	10	0
4	B	242	0	0	4	0
All	All	9110	0	8478	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 5.

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:B:195:ASP:CB	1:B:198[B]:LEU:HD13	1.96	0.95
1:B:-2:LEU:HD11	4:B:942:HOH:O	1.79	0.83
1:A:242:CYS:SG	4:A:847:HOH:O	2.36	0.82
1:B:302:ILE:HG22	1:B:413:PHE:CD1	2.24	0.71
1:B:428:GLU:HA	1:B:506:THR:HB	1.73	0.70
1:B:471:THR:HG22	1:B:477:VAL:HG22	1.75	0.69
1:A:428:GLU:HA	1:A:506:THR:HB	1.76	0.67
1:A:8:ILE:HD11	1:A:32:HIS:CG	2.30	0.66
1:A:290:ALA:O	1:A:292:THR:HG22	1.95	0.66
1:B:114:SER:OG	2:B:601:G16:P	2.54	0.65
1:A:267:VAL:HA	1:A:272:ILE:HD12	1.77	0.65
1:B:369:PHE:HZ	1:B:555:THR:HG21	1.62	0.65
1:A:114:SER:OG	2:A:601:G16:P	2.55	0.65
1:A:548:ARG:NH2	1:A:552:ASP:OD1	2.29	0.64
1:B:548:ARG:NH2	1:B:552:ASP:OD1	2.30	0.64
1:B:302:ILE:CG2	1:B:413:PHE:CG	2.81	0.63
1:B:196:PHE:O	1:B:197:ASP:HB2	1.99	0.62
1:A:39:THR:HG21	1:A:154:TYR:HB2	1.81	0.62
1:A:404:PRO:HA	4:A:702:HOH:O	2.01	0.60
1:B:195:ASP:CB	1:B:198[B]:LEU:HD22	2.31	0.60
1:B:191:LYS:NZ	4:B:704:HOH:O	2.36	0.59
1:A:136:ALA:HB1	1:A:140:VAL:HG22	1.85	0.59
1:B:198[B]:LEU:H	1:B:198[B]:LEU:HD12	1.69	0.58
1:A:467:ASN:HD21	1:A:480:ASN:HD22	1.51	0.57
1:B:467:ASN:HD21	1:B:480:ASN:HD22	1.53	0.57
1:A:284:ARG:HD2	2:A:601:G16:O3P	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:302:ILE:HG22	1:B:413:PHE:CG	2.39	0.56
1:A:35:GLU:O	1:A:39:THR:HG23	2.06	0.56
1:A:448:ASN:HD21	1:A:451:SER:CB	2.18	0.56
1:A:525:THR:HG21	4:A:930:HOH:O	2.06	0.55
1:B:136:ALA:HB1	1:B:140:VAL:HG22	1.87	0.55
1:B:195:ASP:CB	1:B:198[B]:LEU:CD1	2.79	0.54
1:A:405:SER:N	4:A:702:HOH:O	2.22	0.54
1:A:410:GLN:NE2	4:A:708:HOH:O	2.41	0.54
1:A:112:THR:HG23	1:A:127:LYS:HD2	1.90	0.53
1:B:442:LEU:HG	1:B:540:LEU:CD2	2.39	0.52
1:A:442:LEU:HG	1:A:540:LEU:HD22	1.92	0.51
1:B:302:ILE:CG2	1:B:413:PHE:CD1	2.92	0.51
1:A:5:THR:HG22	4:A:749:HOH:O	2.11	0.50
1:B:369:PHE:CZ	1:B:555:THR:HG21	2.46	0.49
1:A:506:THR:HG23	4:A:869:HOH:O	2.11	0.49
1:A:103:ARG:NH2	1:A:178:GLU:OE2	2.47	0.47
1:A:193:ILE:HD11	1:A:375:HIS:HB2	1.97	0.47
1:B:186:TYR:OH	1:B:382:VAL:HB	2.15	0.47
1:B:401:ASN:ND2	1:B:401:ASN:H	2.14	0.46
1:B:384:ALA:O	1:B:387:ALA:HB3	2.15	0.46
1:A:186:TYR:OH	1:A:382:VAL:HB	2.16	0.46
1:B:438:LEU:HD23	1:B:438:LEU:C	2.36	0.46
1:A:5:THR:CG2	4:A:749:HOH:O	2.64	0.46
1:B:284:ARG:HD2	2:B:601:G16:O3P	2.15	0.45
1:B:369:PHE:HZ	1:B:555:THR:CG2	2.29	0.45
1:A:401:ASN:H	1:A:401:ASN:ND2	2.14	0.45
1:B:196:PHE:O	1:B:197:ASP:CB	2.64	0.45
1:B:198[B]:LEU:H	1:B:198[B]:LEU:CD1	2.30	0.45
1:A:384:ALA:O	1:A:387:ALA:HB3	2.17	0.45
1:A:239:THR:HG23	1:A:242:CYS:HB3	1.98	0.45
1:A:535:LEU:C	1:A:535:LEU:HD13	2.37	0.45
1:A:473:LEU:N	1:A:473:LEU:HD23	2.31	0.44
1:B:535:LEU:C	1:B:535:LEU:HD13	2.38	0.44
1:B:239:THR:HG23	1:B:242:CYS:HB3	2.00	0.44
1:A:535:LEU:C	1:A:535:LEU:CD1	2.86	0.44
1:B:535:LEU:C	1:B:535:LEU:CD1	2.86	0.44
1:B:404:PRO:HB3	4:B:876:HOH:O	2.18	0.43
1:A:211:VAL:HA	1:A:274:PHE:O	2.18	0.43
1:A:447:ASN:OD1	4:A:701:HOH:O	2.20	0.43
1:A:325:MET:N	1:A:326:PRO:CD	2.82	0.43
1:A:438:LEU:C	1:A:438:LEU:HD23	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:193:ILE:HD11	1:B:375:HIS:HB2	2.01	0.43
1:B:404:PRO:CB	4:B:876:HOH:O	2.66	0.42
1:B:418:GLY:HA2	1:B:521:PHE:CZ	2.54	0.42
1:A:195:ASP:H	1:A:390:ASN:ND2	2.18	0.42
1:B:325:MET:N	1:B:326:PRO:CD	2.82	0.42
1:B:25:VAL:HG23	1:B:122:ALA:O	2.20	0.41
1:B:259:TYR:OH	1:B:428:GLU:OE1	2.35	0.41
1:A:29:GLN:HG2	1:A:63:TYR:CE1	2.55	0.41
1:B:211:VAL:HA	1:B:274:PHE:O	2.20	0.41
1:A:112:THR:OG1	1:A:281:ASP:HB3	2.21	0.41
1:B:195:ASP:H	1:B:390:ASN:ND2	2.19	0.41
1:A:93:THR:HB	1:A:94:PRO:HD3	2.01	0.41
1:A:471:THR:OG1	1:A:477:VAL:HG22	2.21	0.41
1:A:537:MET:CE	1:A:549:GLU:HA	2.50	0.41
1:B:112:THR:OG1	1:B:281:ASP:HB3	2.19	0.41
1:B:270:LYS:HB2	1:B:272:ILE:CD1	2.51	0.41
1:A:25:VAL:HG23	1:A:122:ALA:O	2.20	0.41
1:B:93:THR:HB	1:B:94:PRO:HD3	2.02	0.40
1:B:93:THR:N	1:B:94:PRO:CD	2.84	0.40
1:A:506:THR:CG2	4:A:869:HOH:O	2.69	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	553/560 (99%)	535 (97%)	17 (3%)	1 (0%)	47 66
1	B	558/560 (100%)	542 (97%)	15 (3%)	1 (0%)	47 66
All	All	1111/1120 (99%)	1077 (97%)	32 (3%)	2 (0%)	47 66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	197	ASP
1	A	376	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	463/465 (100%)	418 (90%)	45 (10%)	8	14
1	B	463/465 (100%)	426 (92%)	37 (8%)	12	21
All	All	926/930 (100%)	844 (91%)	82 (9%)	9	17

All (82) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-2	LEU
1	A	5	THR
1	A	7	SER
1	A	8	ILE
1	A	12	THR
1	A	31	PRO
1	A	39	THR
1	A	53	PHE
1	A	70	LYS
1	A	81	LYS
1	A	91	LEU
1	A	111	LEU
1	A	139	SER
1	A	165	SER
1	A	169	THR
1	A	175	LEU
1	A	187	LEU
1	A	207	LYS
1	A	210	LYS
1	A	212	LEU
1	A	236	GLN
1	A	239	THR

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Mol	Chain	Res	Type
1	A	258	VAL
1	A	265	GLU
1	A	300	LEU
1	A	323	ARG
1	A	331	VAL
1	A	373	SER
1	A	379	LYS
1	A	401	ASN
1	A	412	GLU
1	A	442	LEU
1	A	444	GLU
1	A	451	SER
1	A	460	ARG
1	A	474	ASP
1	A	478	THR
1	A	495	VAL
1	A	497	LEU
1	A	506	THR
1	A	512	GLU
1	A	516	SER
1	A	525	THR
1	A	535	LEU
1	A	548	ARG
1	B	5	THR
1	B	12	THR
1	B	53	PHE
1	B	70	LYS
1	B	91	LEU
1	B	111	LEU
1	B	139	SER
1	B	169	THR
1	B	175	LEU
1	B	187	LEU
1	B	208	ASP
1	B	212	LEU
1	B	239	THR
1	B	258	VAL
1	B	265	GLU
1	B	300	LEU
1	B	302	ILE
1	B	323	ARG
1	B	331	VAL

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Mol	Chain	Res	Type
1	B	379	LYS
1	B	397	LYS
1	B	401	ASN
1	B	412	GLU
1	B	442	LEU
1	B	447	ASN
1	B	460	ARG
1	B	461	LYS
1	B	478	THR
1	B	497	LEU
1	B	506	THR
1	B	512	GLU
1	B	516	SER
1	B	525	THR
1	B	530	LYS
1	B	535	LEU
1	B	538	SER
1	B	550	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	273	HIS
1	A	305	HIS
1	A	390	ASN
1	A	401	ASN
1	A	410	GLN
1	A	411	ASN
1	A	448	ASN
1	A	480	ASN
1	A	532	ASN
1	B	236	GLN
1	B	273	HIS
1	B	285	ASN
1	B	305	HIS
1	B	341	GLN
1	B	390	ASN
1	B	401	ASN
1	B	410	GLN
1	B	411	ASN
1	B	480	ASN
1	B	532	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	G16	B	601	3	19,20,20	1.75	4 (21%)	30,31,31	1.88	9 (30%)
2	G16	A	601	3	19,20,20	1.44	2 (10%)	30,31,31	1.76	9 (30%)

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	G16	B	601	3	-	3/11/31/31	0/1/1/1
2	G16	A	601	3	-	3/11/31/31	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	G16	P-O6	3.58	1.71	1.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	G16	O5-C5	3.23	1.52	1.44
2	A	601	G16	P-O6	3.15	1.70	1.60
2	A	601	G16	O2-C2	3.15	1.50	1.43
2	B	601	G16	O2-C2	2.48	1.48	1.43
2	B	601	G16	P'-O3X	-2.12	1.46	1.54

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	G16	O1-P'-O2X	-4.27	92.91	109.39
2	B	601	G16	C1-O5-C5	3.91	121.35	113.69
2	A	601	G16	O3X-P'-O1	-3.23	91.54	105.99
2	A	601	G16	O3X-P'-O1X	3.17	119.75	107.64
2	A	601	G16	O5-C1-O1	-2.99	107.46	111.36
2	B	601	G16	O3X-P'-O1	-2.97	92.69	105.99
2	B	601	G16	O3X-P'-O1X	2.97	118.98	107.64
2	A	601	G16	O1-C1-C2	2.97	113.82	108.38
2	B	601	G16	P-O6-C6	2.93	126.36	118.30
2	A	601	G16	O3P-P-O6	-2.87	99.11	106.73
2	B	601	G16	O5-C5-C6	2.83	112.37	106.67
2	A	601	G16	O1-P'-O2X	-2.68	99.05	109.39
2	B	601	G16	O3X-P'-O2X	2.47	120.35	110.68
2	B	601	G16	O3-C3-C2	-2.43	104.73	110.35
2	A	601	G16	O6-C6-C5	2.30	116.90	108.99
2	A	601	G16	O3P-P-O2P	2.27	116.32	107.64
2	A	601	G16	C1-O5-C5	2.25	118.10	113.69
2	B	601	G16	O3P-P-O2P	2.08	115.58	107.64

There are no chirality outliers.

All (6) torsion outliers are listed below:

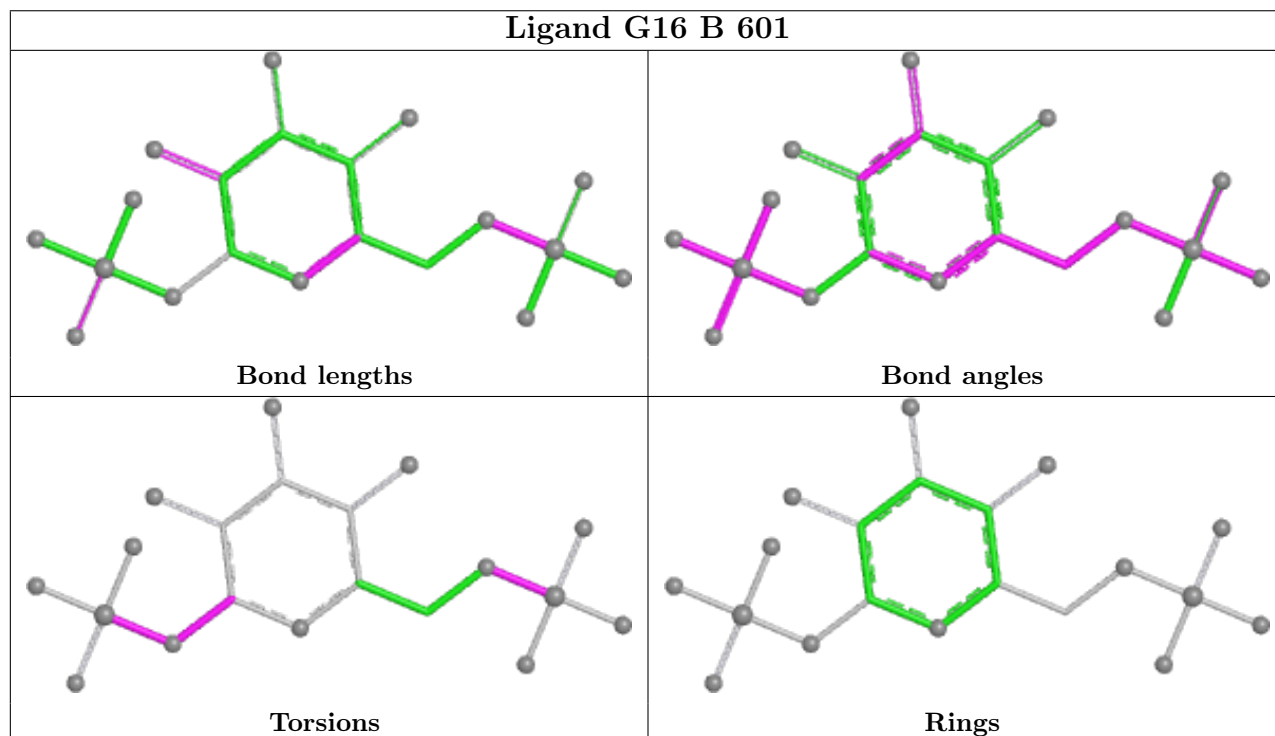
Mol	Chain	Res	Type	Atoms
2	A	601	G16	C4-C5-C6-O6
2	A	601	G16	O5-C5-C6-O6
2	B	601	G16	C6-O6-P-O3P
2	B	601	G16	C1-O1-P'-O3X
2	A	601	G16	O5-C1-O1-P'
2	B	601	G16	O5-C1-O1-P'

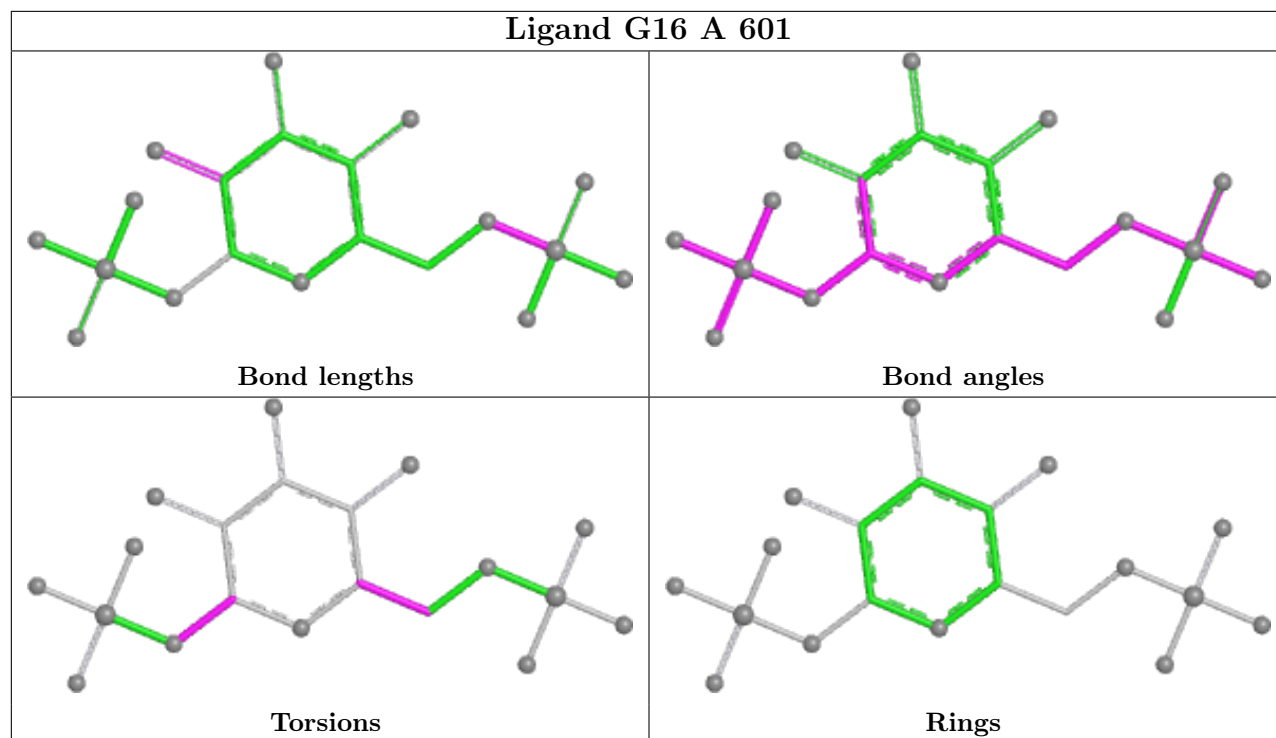
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	G16	2	0
2	A	601	G16	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 [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	556/560 (99%)	0.30	10 (1%) 68 70	20, 35, 60, 83	0
1	B	558/560 (99%)	0.46	22 (3%) 39 41	23, 40, 72, 100	0
All	All	1114/1120 (99%)	0.38	32 (2%) 51 54	20, 37, 67, 100	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	398	GLN	4.7
1	B	396	ALA	4.5
1	A	473	LEU	4.3
1	B	209	PHE	3.9
1	A	474	ASP	3.8
1	A	475	GLY	3.6
1	B	201	GLU	3.3
1	B	233	GLY	3.3
1	B	391	ILE	2.8
1	B	208	ASP	2.7
1	A	-2	LEU	2.7
1	B	264	VAL	2.6
1	B	289	GLY	2.5
1	A	524	ASN	2.4
1	B	265	GLU	2.4
1	B	404	PRO	2.3
1	A	403	THR	2.3
1	B	476	SER	2.3
1	A	196	PHE	2.3
1	A	207	LYS	2.2
1	B	393	ALA	2.2
1	A	342	SER	2.2
1	B	198[A]	LEU	2.1
1	B	268	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	471	THR	2.1
1	B	225	VAL	2.1
1	B	261	HIS	2.1
1	B	388	TRP	2.1
1	B	334	VAL	2.0
1	B	401	ASN	2.0
1	B	395	VAL	2.0
1	B	335	ALA	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](#)

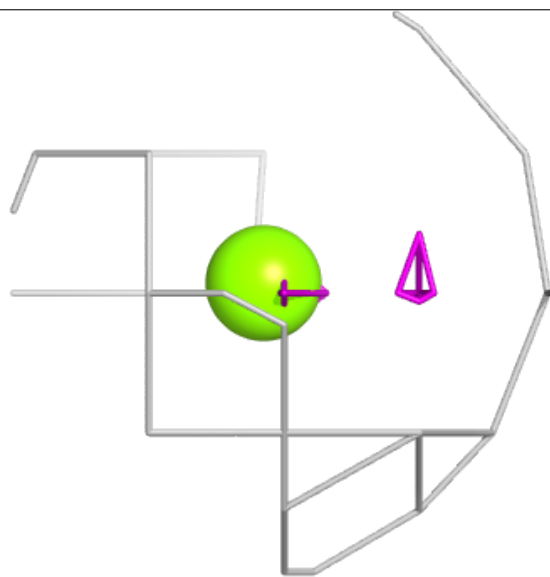
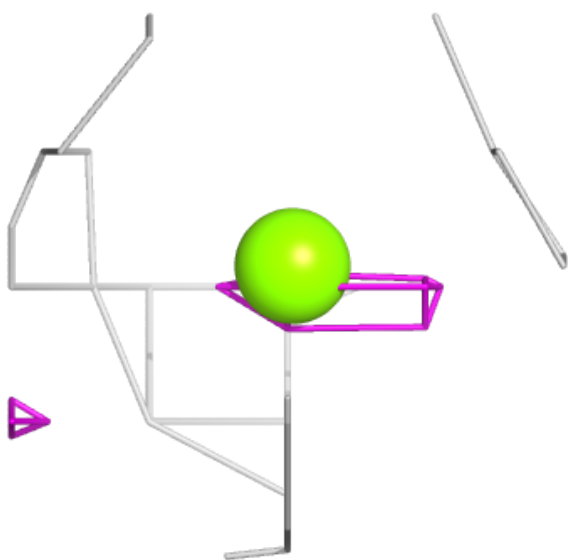
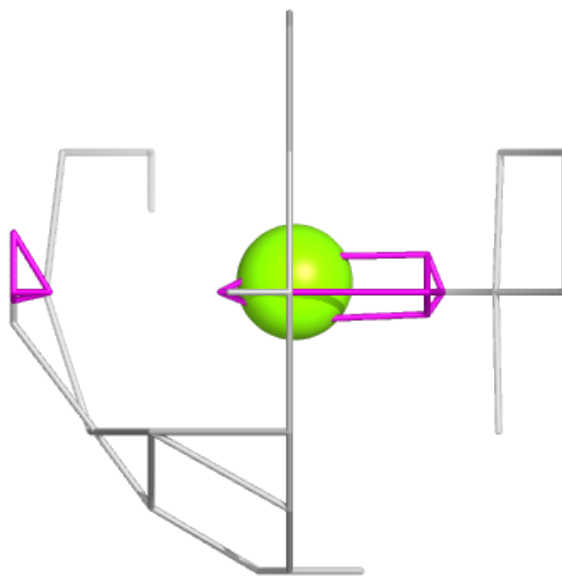
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	B	602	1/1	0.89	0.07	20,20,20,20	0
3	MG	A	602	1/1	0.91	0.08	14,14,14,14	0
2	G16	B	601	20/20	0.93	0.17	24,33,44,45	0
2	G16	A	601	20/20	0.96	0.17	26,30,34,36	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.

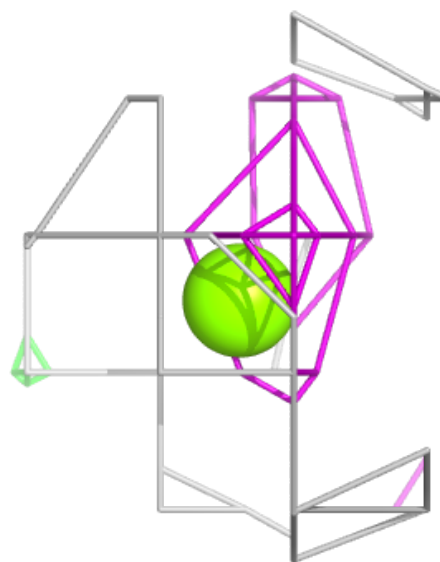
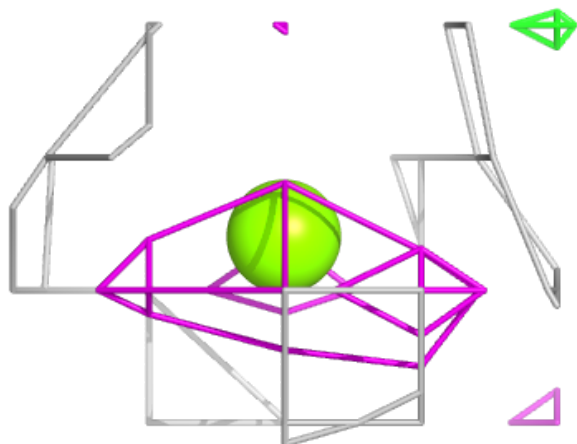
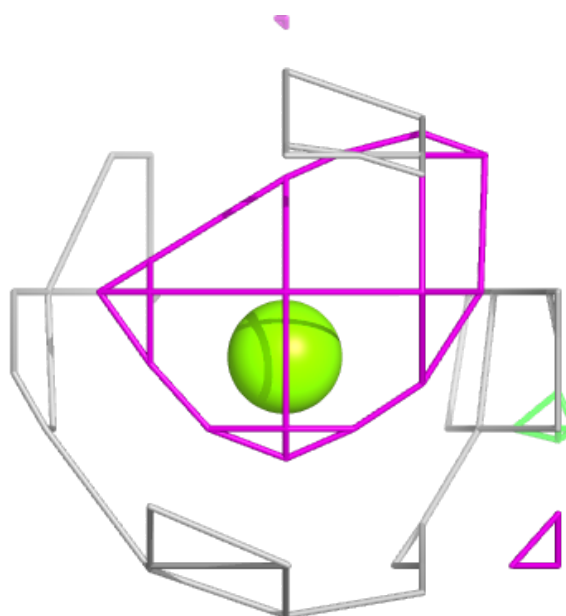
Electron density around MG B 602:

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



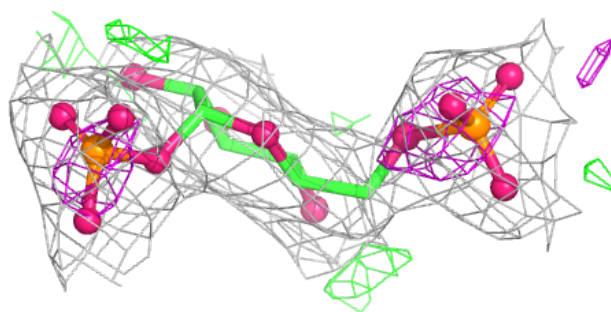
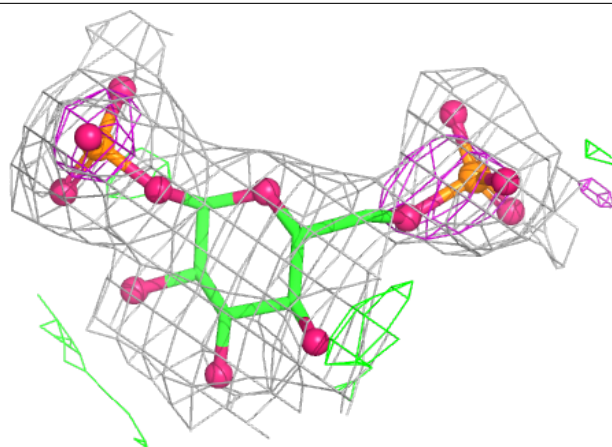
Electron density around MG A 602:

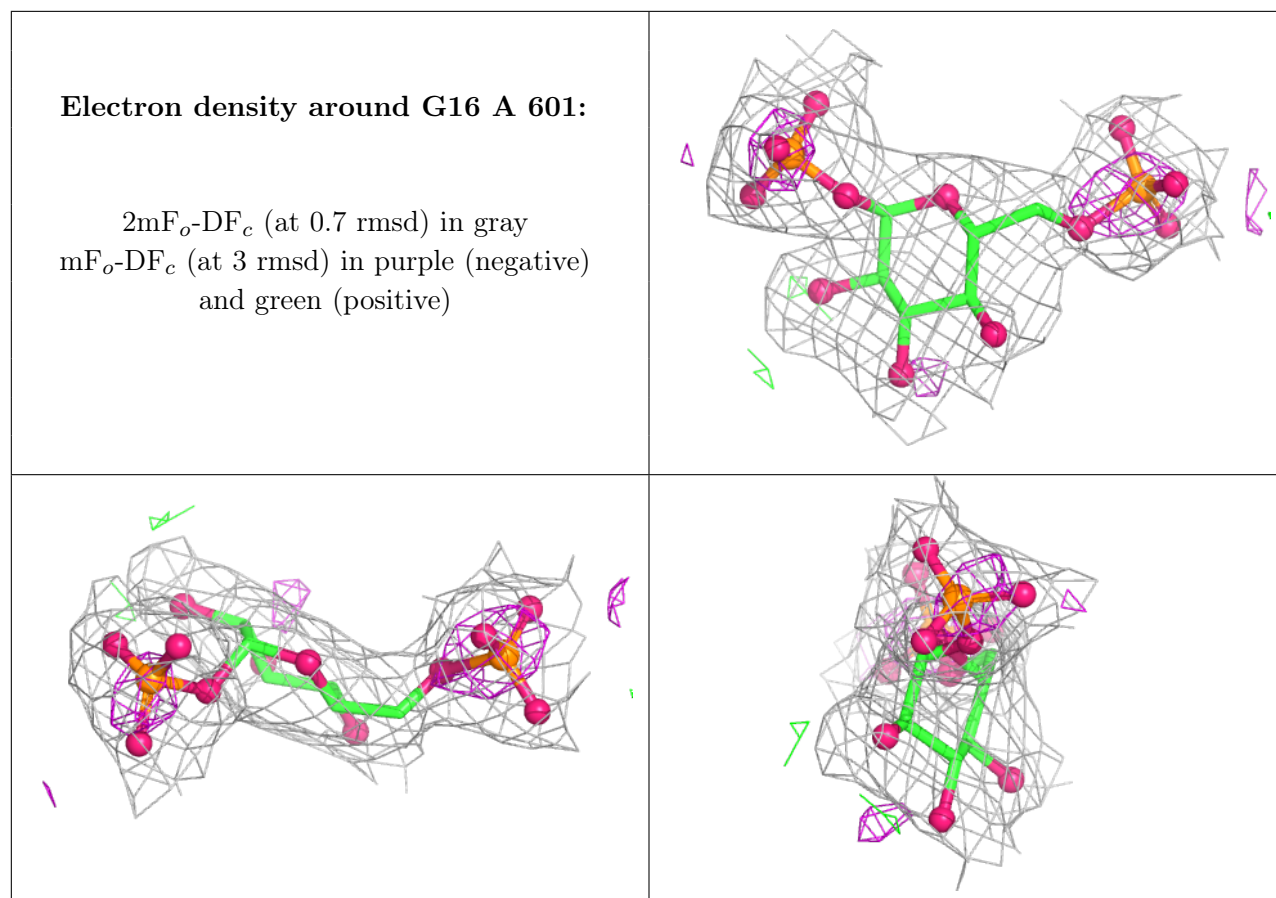
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around G16 B 601:

$2mF_o-DF_c$ (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.