



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 11:46 AM UTC

PDB ID : 7P5O / pdb_00007p5o
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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

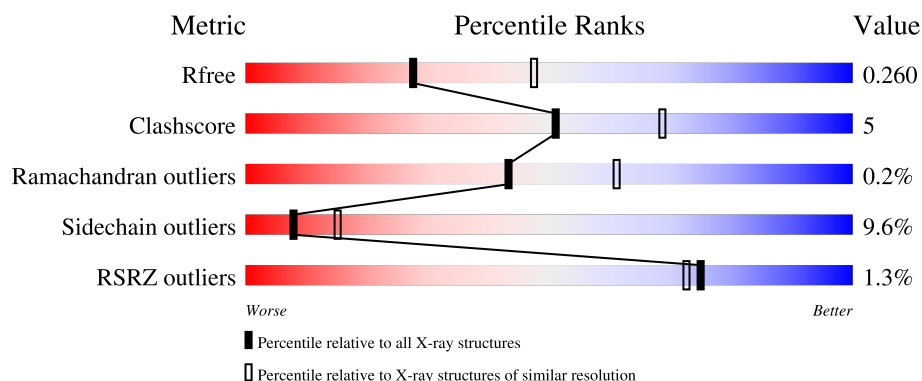
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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}	180053	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (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	% 81% 15% ..
1	B	560	2% 84% 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.

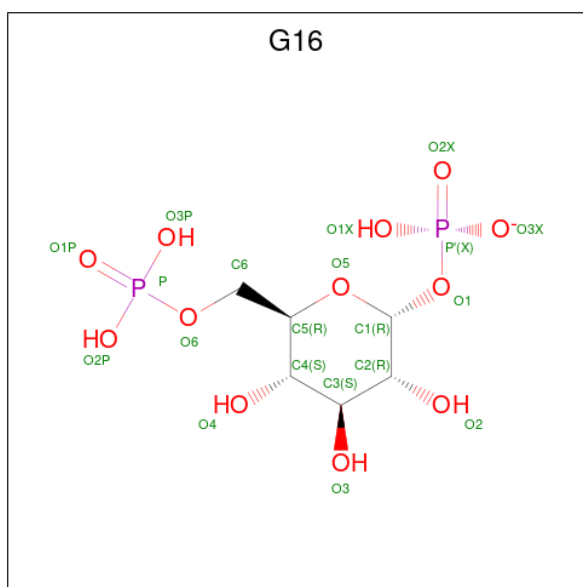
- Molecule 1 is a protein called Phosphoglucomutase.

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

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 (CCD ID: G16) (formula: C₆H₁₃O₁₂P₂) (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 (CCD ID: 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		

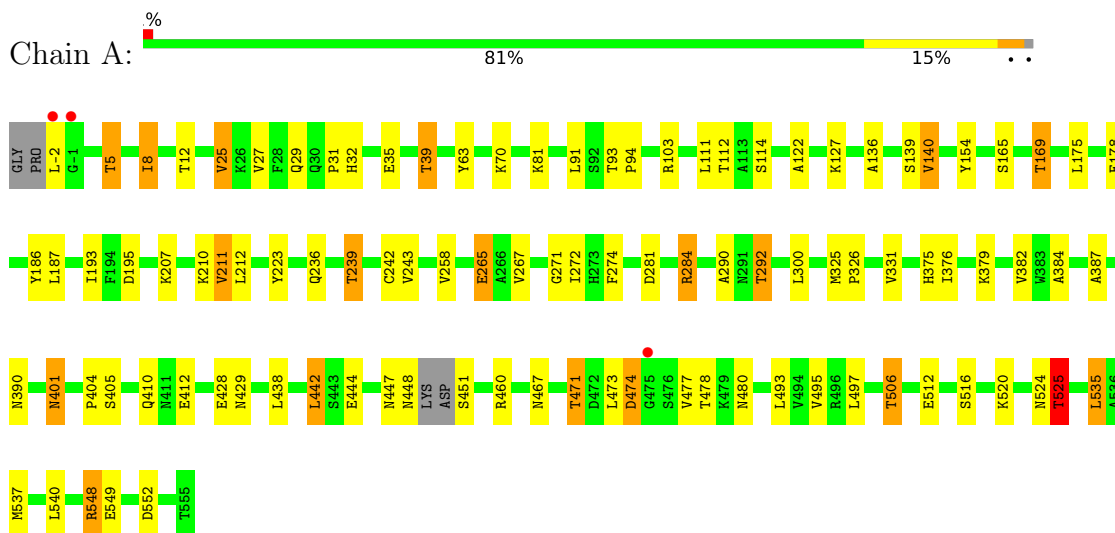
- Molecule 4 is water.

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

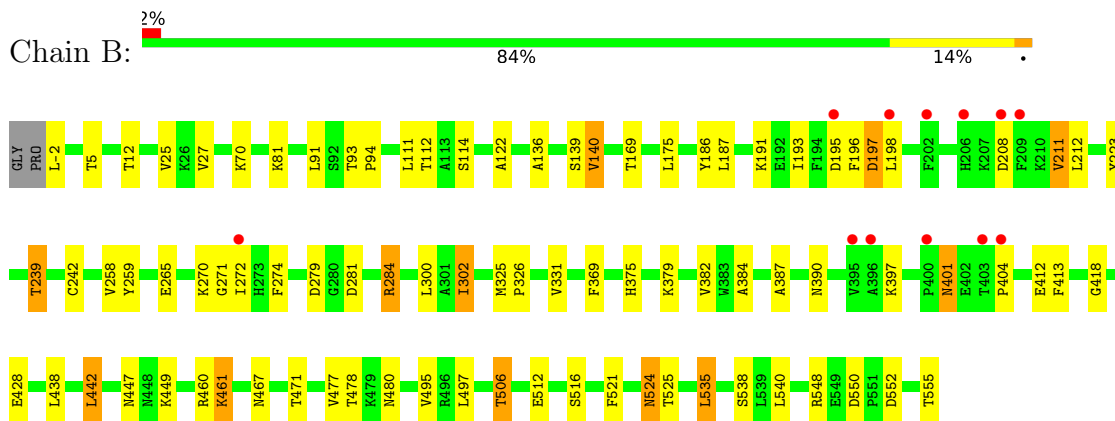
3 Residue-property plots

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: Phosphoglucumutase



• Molecule 1: Phosphoglucumutase



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)	Xtriage
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 (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	40.4	Xtriage
Anisotropy	0.542	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
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

Xtriage'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

5.1 Standard geometry

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	1.07	1/4371 (0.0%)	1.45	10/5916 (0.2%)
1	B	1.08	0/4385	1.44	6/5937 (0.1%)
All	All	1.08	1/8756 (0.0%)	1.45	16/11853 (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
1	B	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	243	VAL	N-CA	5.54	1.50	1.46

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	292	THR	CB-CA-C	6.15	119.75	111.70
1	A	223	TYR	CA-C-N	5.90	126.49	119.94
1	A	223	TYR	C-N-CA	5.90	126.49	119.94
1	B	223	TYR	CA-C-N	5.71	126.27	119.94
1	B	223	TYR	C-N-CA	5.71	126.27	119.94
1	B	524	ASN	CB-CA-C	5.62	118.27	109.84
1	A	265	GLU	N-CA-CB	5.42	118.18	110.06
1	A	429	ASN	CA-C-N	5.38	128.64	120.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	429	ASN	C-N-CA	5.38	128.64	120.95
1	B	279	ASP	CA-C-N	5.33	126.01	119.99
1	B	279	ASP	C-N-CA	5.33	126.01	119.99
1	A	525	THR	CB-CA-C	5.21	119.70	110.85
1	B	461	LYS	CB-CA-C	5.16	118.84	110.22
1	A	169	THR	CB-CA-C	5.14	119.19	109.37
1	A	524	ASN	CB-CA-C	5.09	116.79	109.71
1	A	474	ASP	CA-CB-CG	5.02	117.62	112.60

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

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	44	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	89	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 (89) 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
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:B:438:LEU:HD23	1:B:438:LEU:C	2.36	0.50
1:A:5:THR:HG22	4:A:749:HOH:O	2.11	0.50
1:A:535:LEU:C	1:A:535:LEU:HD13	2.37	0.49
1:B:369:PHE:CZ	1:B:555:THR:HG21	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:506:THR:HG23	4:A:869:HOH:O	2.11	0.49
1:B:535:LEU:C	1:B:535:LEU:HD13	2.38	0.49
1:B:535:LEU:C	1:B:535:LEU:CD1	2.86	0.49
1:A:535:LEU:C	1:A:535:LEU:CD1	2.86	0.48
1:A:438:LEU:C	1:A:438:LEU:HD23	2.39	0.47
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: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:473:LEU:N	1:A:473:LEU:HD23	2.31	0.44
1:B:239:THR:HG23	1:B:242:CYS:HB3	2.00	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:493:LEU:C	1:A:493:LEU:HD12	2.47	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%)	43	61
1	B	558/560 (100%)	542 (97%)	15 (3%)	1 (0%)	43	61
All	All	1111/1120 (99%)	1077 (97%)	32 (3%)	2 (0%)	43	61

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%)	416 (90%)	47 (10%)	7	13
1	B	463/465 (100%)	421 (91%)	42 (9%)	9	17
All	All	926/930 (100%)	837 (90%)	89 (10%)	8	15

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-2	LEU
1	A	5	THR
1	A	8	ILE
1	A	12	THR
1	A	25	VAL
1	A	27	VAL
1	A	31	PRO
1	A	39	THR
1	A	70	LYS
1	A	81	LYS
1	A	91	LEU
1	A	111	LEU
1	A	139	SER
1	A	140	VAL
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	211	VAL
1	A	212	LEU
1	A	236	GLN
1	A	239	THR
1	A	258	VAL
1	A	265	GLU
1	A	284	ARG
1	A	300	LEU
1	A	331	VAL
1	A	379	LYS
1	A	401	ASN
1	A	412	GLU
1	A	442	LEU
1	A	444	GLU
1	A	460	ARG

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Mol	Chain	Res	Type
1	A	471	THR
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	520	LYS
1	A	525	THR
1	A	535	LEU
1	A	548	ARG
1	B	5	THR
1	B	12	THR
1	B	27	VAL
1	B	70	LYS
1	B	81	LYS
1	B	91	LEU
1	B	111	LEU
1	B	139	SER
1	B	140	VAL
1	B	169	THR
1	B	175	LEU
1	B	187	LEU
1	B	208	ASP
1	B	211	VAL
1	B	212	LEU
1	B	239	THR
1	B	258	VAL
1	B	265	GLU
1	B	284	ARG
1	B	300	LEU
1	B	302	ILE
1	B	331	VAL
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	449	LYS
1	B	460	ARG

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Mol	Chain	Res	Type
1	B	461	LYS
1	B	478	THR
1	B	495	VAL
1	B	497	LEU
1	B	506	THR
1	B	512	GLU
1	B	516	SER
1	B	524	ASN
1	B	525	THR
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 (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	ASN
1	A	249	ASN
1	A	273	HIS
1	A	305	HIS
1	A	306	HIS
1	A	358	ASN
1	A	401	ASN
1	A	410	GLN
1	A	411	ASN
1	A	429	ASN
1	A	448	ASN
1	A	480	ASN
1	A	532	ASN
1	B	9	GLN
1	B	98	ASN
1	B	305	HIS
1	B	306	HIS
1	B	341	GLN
1	B	401	ASN
1	B	410	GLN
1	B	411	ASN
1	B	415	GLN
1	B	429	ASN
1	B	480	ASN
1	B	532	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	A	601	3	19,20,20	1.43	2 (10%)	30,31,31	1.79	9 (30%)
2	G16	B	601	3	19,20,20	1.75	5 (26%)	30,31,31	1.86	8 (26%)

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	A	601	3	-	3/11/31/31	0/1/1/1
2	G16	B	601	3	-	4/11/31/31	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	G16	P-O6	3.62	1.71	1.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	G16	O5-C5	3.20	1.52	1.44
2	A	601	G16	P-O6	3.18	1.70	1.60
2	A	601	G16	O2-C2	3.00	1.50	1.43
2	B	601	G16	O2-C2	2.37	1.48	1.43
2	B	601	G16	P'-O3X	-2.19	1.46	1.54
2	B	601	G16	C6-C5	2.03	1.57	1.51

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	G16	O1-P'-O2X	-4.61	92.91	109.33
2	B	601	G16	C1-O5-C5	3.91	121.35	113.72
2	A	601	G16	O3X-P'-O1	-3.67	91.54	105.85
2	B	601	G16	O3X-P'-O1	-3.38	92.69	105.85
2	A	601	G16	O3X-P'-O1X	3.19	119.75	107.80
2	A	601	G16	O5-C1-O1	-2.99	107.46	111.36
2	B	601	G16	O3X-P'-O1X	2.98	118.98	107.80
2	A	601	G16	O1-C1-C2	2.97	113.82	108.38
2	A	601	G16	O3P-P-O6	-2.90	99.11	106.67
2	A	601	G16	O1-P'-O2X	-2.88	99.05	109.33
2	B	601	G16	O5-C5-C6	2.86	112.37	106.69
2	B	601	G16	O3X-P'-O2X	2.44	120.35	110.83
2	B	601	G16	O3-C3-C2	-2.39	104.73	110.38
2	A	601	G16	O6-C6-C5	2.32	116.90	108.99
2	A	601	G16	O3P-P-O2P	2.27	116.32	107.80
2	A	601	G16	C1-O5-C5	2.24	118.10	113.72
2	B	601	G16	O3P-P-O2P	2.07	115.58	107.80

There are no chirality outliers.

All (7) torsion outliers are listed below:

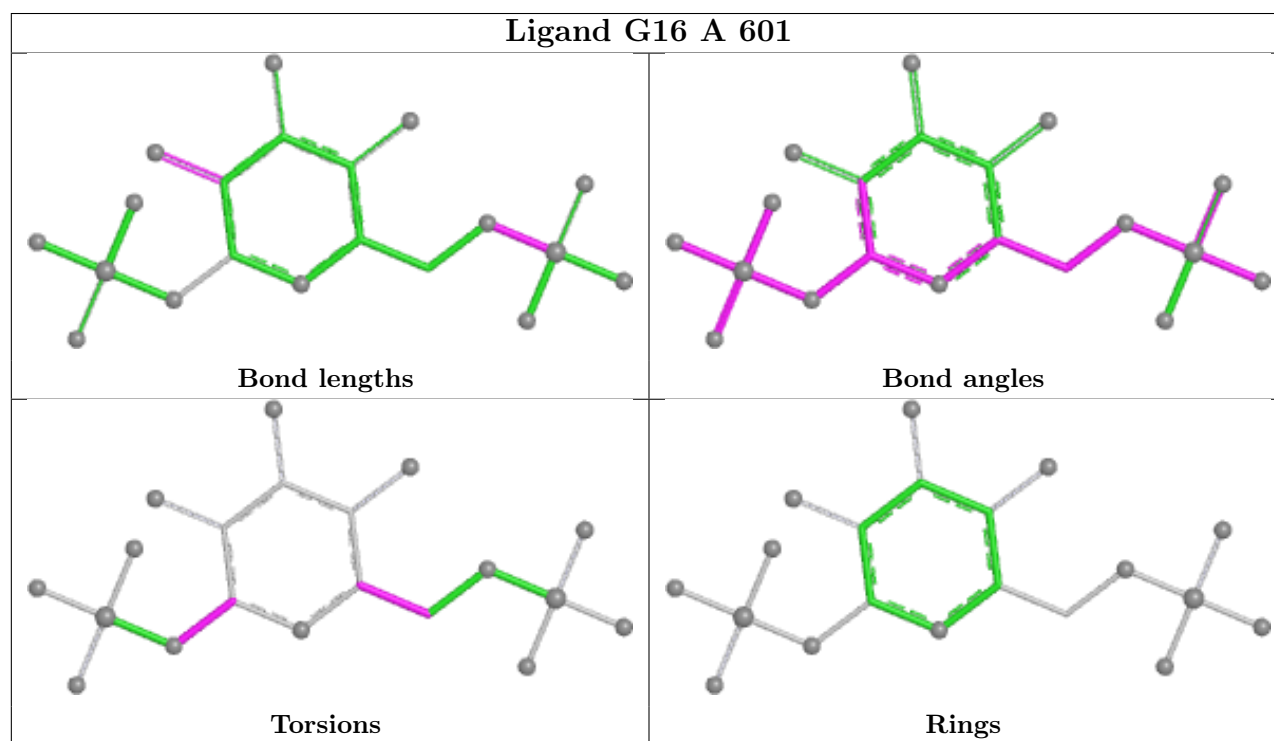
Mol	Chain	Res	Type	Atoms
2	A	601	G16	C4-C5-C6-O6
2	A	601	G16	O5-C5-C6-O6
2	B	601	G16	C6-O6-P-O3P
2	B	601	G16	C1-O1-P'-O2X
2	A	601	G16	O5-C1-O1-P'
2	B	601	G16	O5-C1-O1-P'
2	B	601	G16	C1-O1-P'-O3X

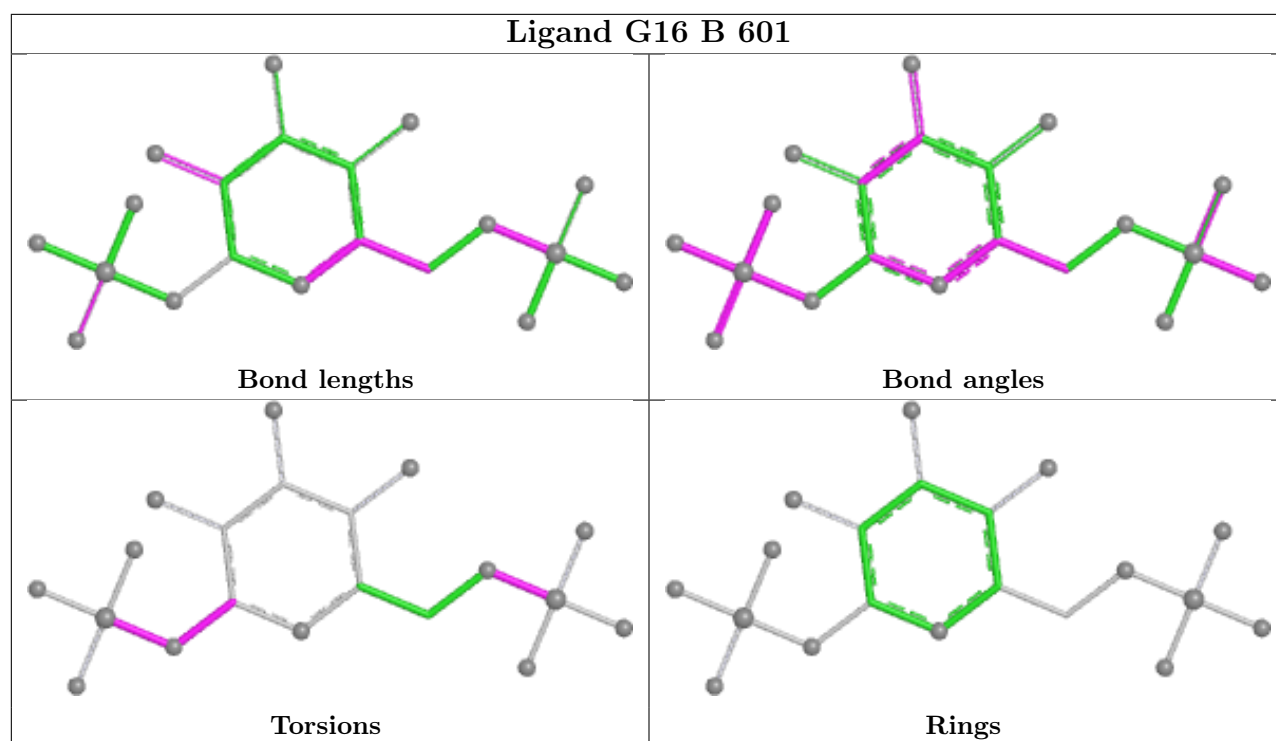
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	G16	2	0
2	B	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%)	-0.25	3 (0%) 87 85	18, 35, 60, 83	1 (0%)
1	B	558/560 (99%)	-0.02	12 (2%) 62 59	23, 40, 72, 100	2 (0%)
All	All	1114/1120 (99%)	-0.13	15 (1%) 75 72	18, 37, 67, 100	3 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	-2	LEU	4.0
1	A	475	GLY	3.0
1	B	396	ALA	2.6
1	B	208	ASP	2.4
1	B	198[A]	LEU	2.4
1	B	195	ASP	2.4
1	B	400	PRO	2.2
1	B	403	THR	2.2
1	B	404	PRO	2.1
1	B	272	ILE	2.1
1	B	395	VAL	2.1
1	A	-1	GLY	2.1
1	B	202	PHE	2.0
1	B	209	PHE	2.0
1	B	206	HIS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

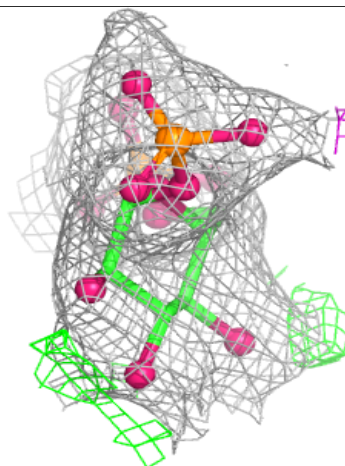
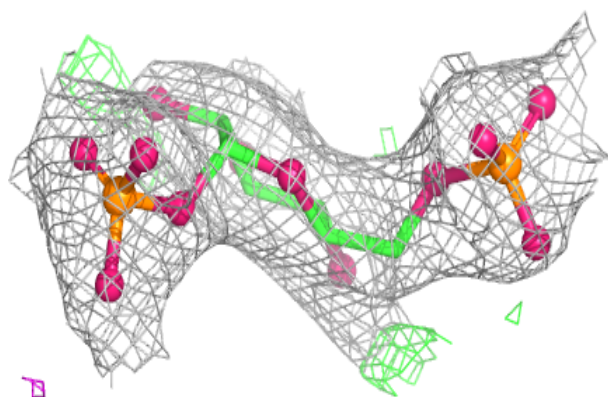
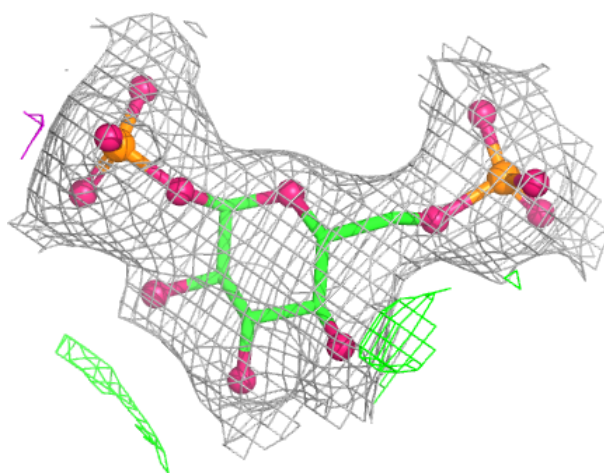
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	G16	B	601	20/20	0.97	0.06	24,33,44,45	0
2	G16	A	601	20/20	0.98	0.05	26,30,34,36	0
3	MG	A	602	1/1	0.99	0.04	14,14,14,14	0
3	MG	B	602	1/1	1.00	0.02	20,20,20,20	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.

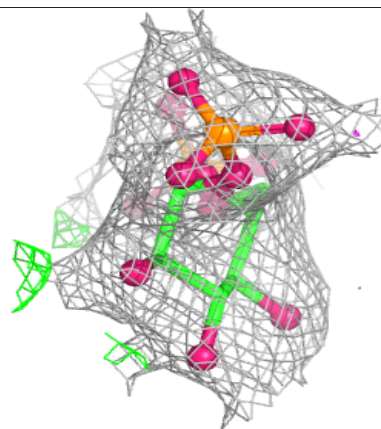
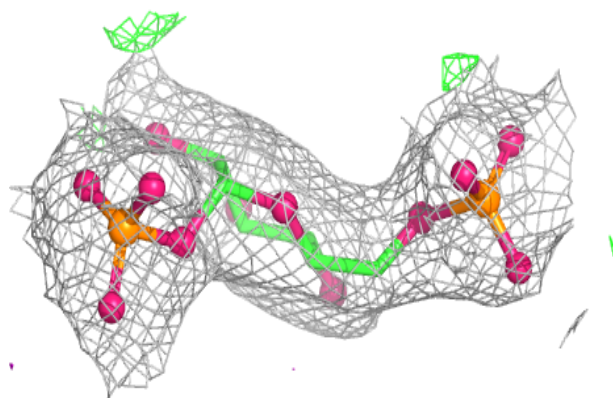
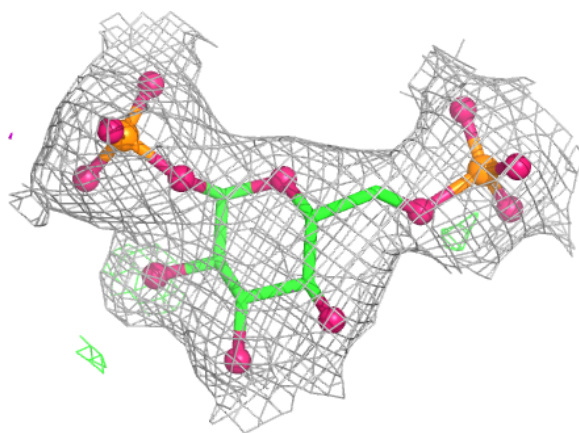
Electron density around G16 B 601:

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



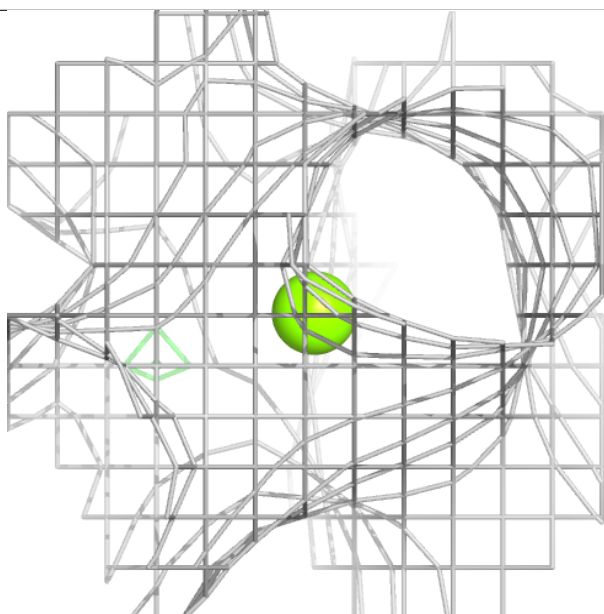
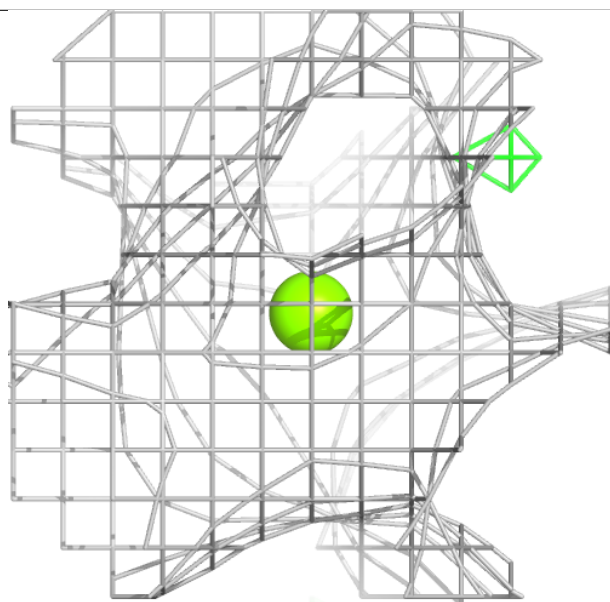
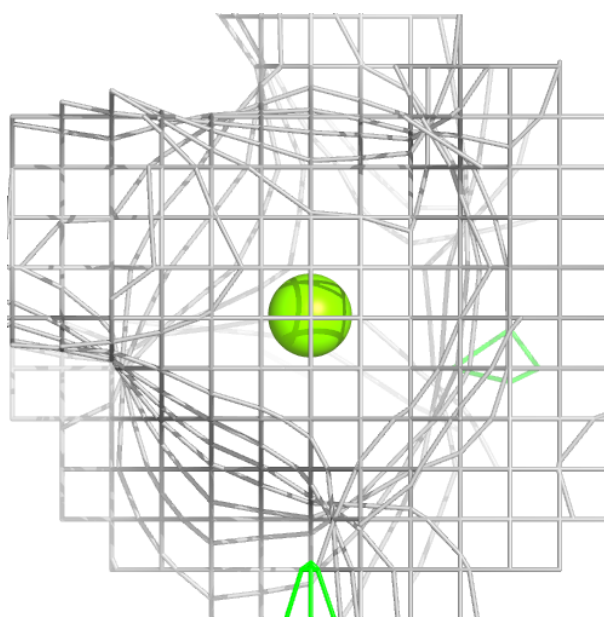
Electron density around G16 A 601:

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



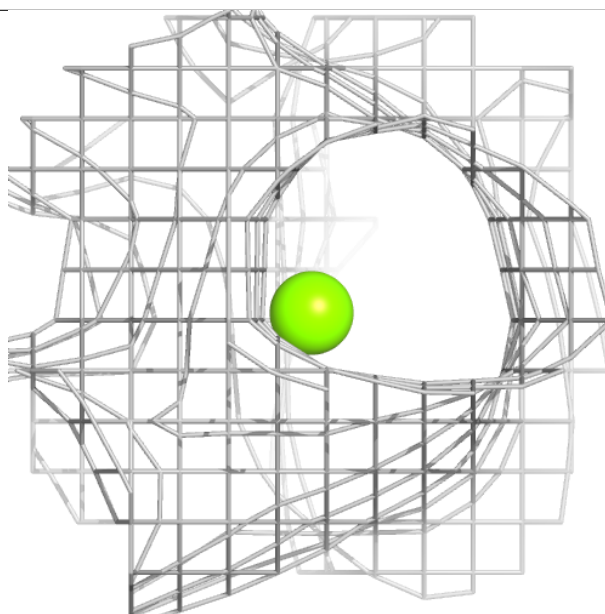
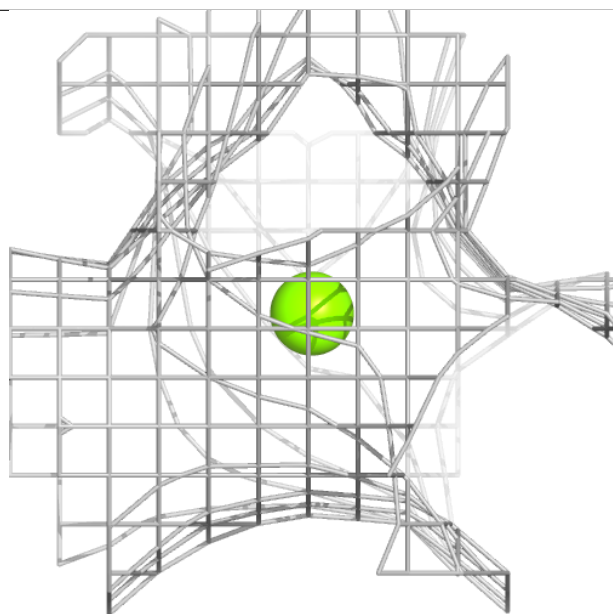
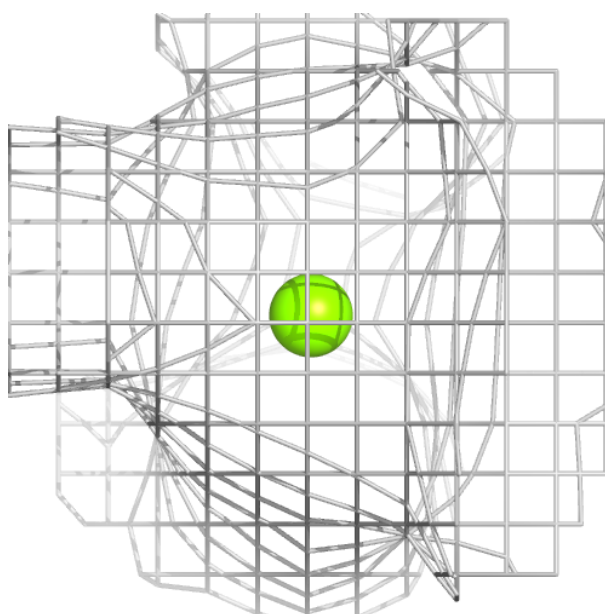
Electron density around MG A 602:

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



Electron density around 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.