



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 07:33 PM UTC

PDB ID : 5H42 / pdb_00005h42
Title : Crystal Structure of 1,2-beta-oligoglucan phosphorylase from Lachnoclostridium phytofermentans in complex with alpha-d-glucose-1-phosphate
Authors : Nakajima, M.; Tanaka, N.; Furukawa, N.; Nihira, T.; Kodutsumi, Y.; Takahashi, Y.; Sugimoto, N.; Miyanaga, A.; Fushinobu, S.; Taguchi, H.; Nakai, H.
Deposited on : 2016-10-28
Resolution : 2.10 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](#) ①) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtrriage (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

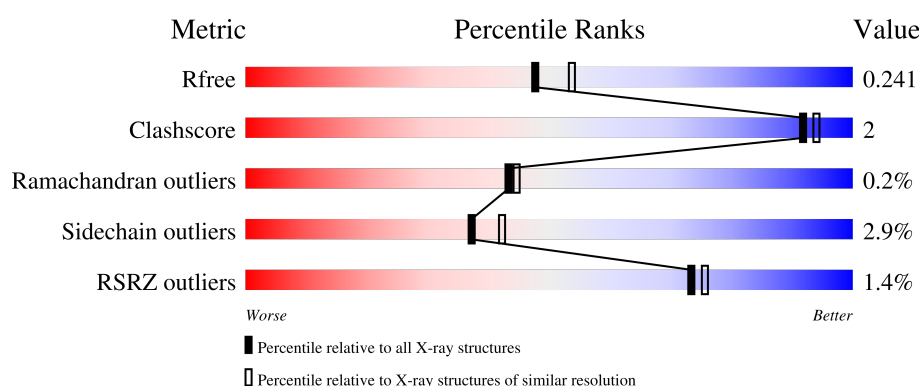
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	1122	92% 7% 92% 7%
1	B	1122	92% 7% 92% 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18512 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.

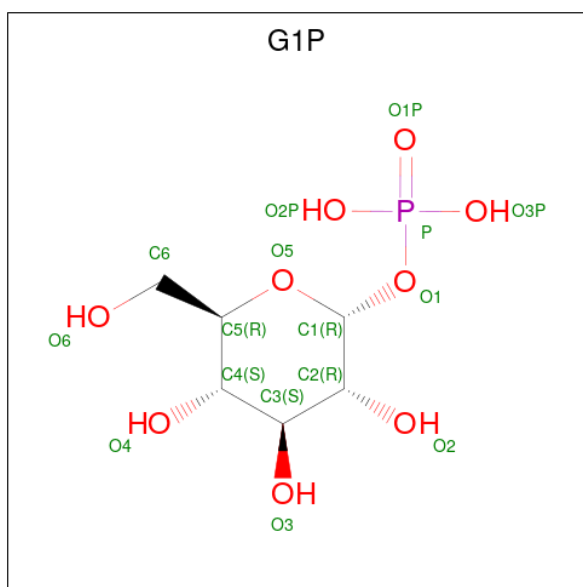
- Molecule 1 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1108	Total	C	N	O	S	0	0	0
			8882	5689	1478	1683	32			
1	B	1113	Total	C	N	O	S	0	0	0
			8918	5712	1483	1691	32			

There are 20 discrepancies between the modelled and reference sequences:

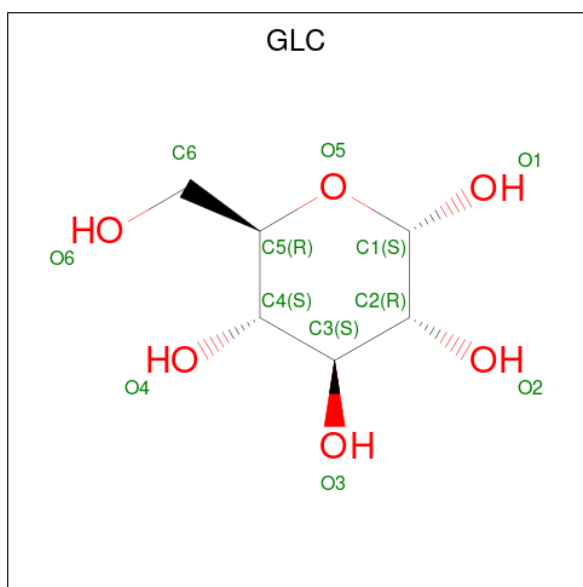
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP A9KJS6
A	1	GLY	-	expression tag	UNP A9KJS6
A	1114	LEU	-	expression tag	UNP A9KJS6
A	1115	GLU	-	expression tag	UNP A9KJS6
A	1116	HIS	-	expression tag	UNP A9KJS6
A	1117	HIS	-	expression tag	UNP A9KJS6
A	1118	HIS	-	expression tag	UNP A9KJS6
A	1119	HIS	-	expression tag	UNP A9KJS6
A	1120	HIS	-	expression tag	UNP A9KJS6
A	1121	HIS	-	expression tag	UNP A9KJS6
B	0	MET	-	expression tag	UNP A9KJS6
B	1	GLY	-	expression tag	UNP A9KJS6
B	1114	LEU	-	expression tag	UNP A9KJS6
B	1115	GLU	-	expression tag	UNP A9KJS6
B	1116	HIS	-	expression tag	UNP A9KJS6
B	1117	HIS	-	expression tag	UNP A9KJS6
B	1118	HIS	-	expression tag	UNP A9KJS6
B	1119	HIS	-	expression tag	UNP A9KJS6
B	1120	HIS	-	expression tag	UNP A9KJS6
B	1121	HIS	-	expression tag	UNP A9KJS6

- Molecule 2 is 1-O-phosphono-alpha-D-glucopyranose (CCD ID: G1P) (formula: C₆H₁₃O₉P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			16	6	9	1		
2	B	1	Total	C	O	P	0	0
			16	6	9	1		
2	B	1	Total	C	O	P	0	0
			16	6	9	1		

- Molecule 3 is alpha-D-glucopyranose (CCD ID: GLC) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			12	6	6		

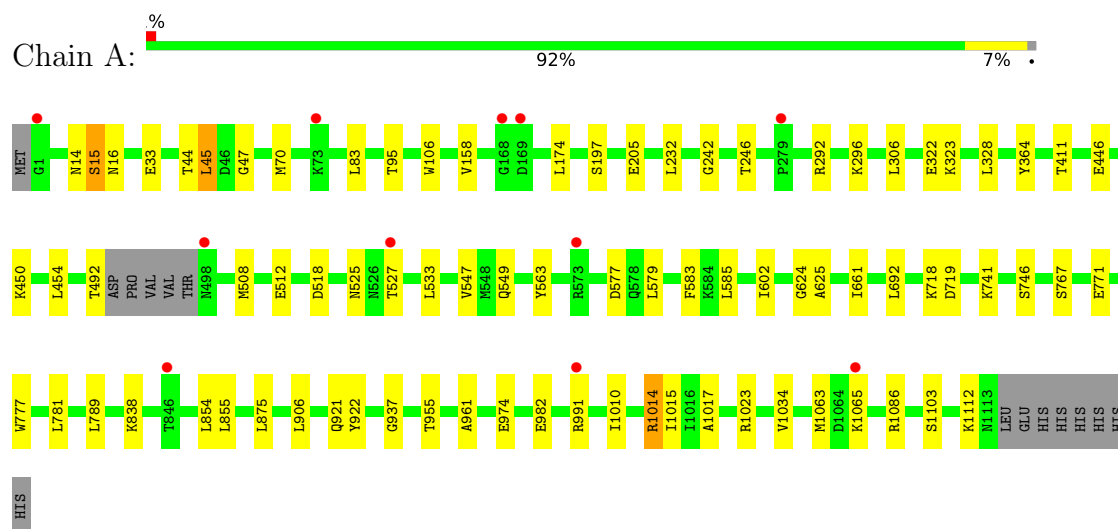
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	338	Total 338	O 338	0	0
4	B	314	Total 314	O 314	0	0

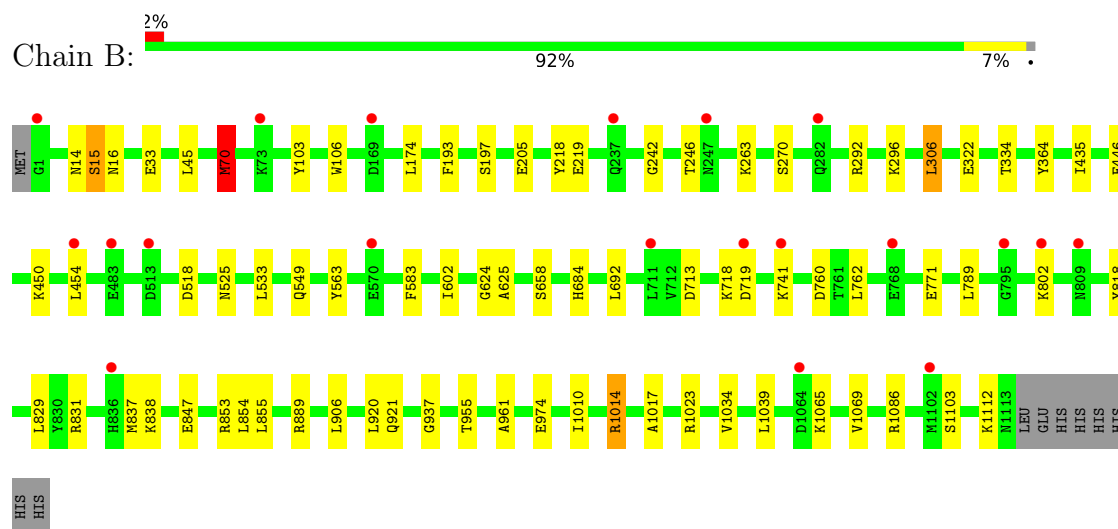
3 Residue-property plots [i](#)

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: Uncharacterized protein



- Molecule 1: Uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.47Å 94.78Å 156.85Å 90.00° 93.96° 90.00°	Depositor
Resolution (Å)	48.25 – 2.10 48.25 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.7 (48.25-2.10) 95.8 (48.25-2.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.195 , 0.236 0.201 , 0.241	Depositor DCC
R_{free} test set	6950 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	23.8	Xtriage
Anisotropy	0.083	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18512	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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: G1P, GLC

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	1.03	3/9105 (0.0%)	1.00	7/12364 (0.1%)
1	B	1.03	2/9143 (0.0%)	1.00	7/12420 (0.1%)
All	All	1.03	5/18248 (0.0%)	1.00	14/24784 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	411	THR	CA-C	8.43	1.56	1.52
1	A	1034	VAL	CA-C	-6.67	1.47	1.53
1	A	585	LEU	C-O	-5.52	1.17	1.23
1	B	193	PHE	N-CA	-5.23	1.40	1.46
1	B	1034	VAL	CA-C	-5.11	1.48	1.53

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1112	LYS	CB-CA-C	-8.60	95.56	109.75
1	A	512	GLU	N-CA-C	7.73	120.60	111.71
1	B	270	SER	N-CA-C	-6.28	100.07	110.17
1	A	1063	MET	CG-SD-CE	6.21	114.56	100.90
1	A	512	GLU	CA-C-N	-6.16	112.83	123.25
1	A	512	GLU	C-N-CA	-6.16	112.83	123.25
1	A	719	ASP	CB-CA-C	-5.71	99.96	109.55
1	B	525	ASN	N-CA-C	5.64	119.64	112.87
1	B	70	MET	CG-SD-CE	-5.37	89.09	100.90
1	B	70	MET	N-CA-CB	-5.17	102.25	110.22
1	A	854	LEU	N-CA-C	5.10	116.52	111.07
1	A	1015	ILE	CB-CA-C	-5.09	105.45	111.97
1	B	719	ASP	CB-CA-C	-5.07	101.03	109.55
1	B	854	LEU	N-CA-C	5.04	116.58	111.14

There are no chirality outliers.

There are no planarity outliers.

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	8882	0	8638	27	0
1	B	8918	0	8675	28	0
2	A	16	0	11	2	0
2	B	32	0	22	1	0
3	B	12	0	12	2	0
4	A	338	0	0	4	0
4	B	314	0	0	1	0
All	All	18512	0	17358	57	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 2.

All (57) 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:829:LEU:HD21	1:B:837:MET:HE2	1.41	0.99
1:B:829:LEU:HD21	1:B:837:MET:CE	1.95	0.95
1:A:525:ASN:CG	1:A:527:THR:OG1	2.28	0.77
1:A:525:ASN:ND2	1:A:527:THR:OG1	2.19	0.76
1:B:831:ARG:HD2	1:B:837:MET:HE3	1.76	0.67
1:B:45:LEU:O	1:B:70:MET:HE1	2.03	0.58
1:B:33:GLU:HB2	1:B:246:THR:HG21	1.89	0.55
1:B:518:ASP:HA	1:B:533:LEU:O	2.08	0.54
1:B:14:ASN:O	1:B:15:SER:C	2.53	0.52
1:A:518:ASP:HA	1:A:533:LEU:O	2.09	0.52
1:B:103:TYR:CE1	1:B:263:LYS:HE3	2.44	0.52
1:A:33:GLU:HB2	1:A:246:THR:HG21	1.90	0.52
1:B:831:ARG:CD	1:B:837:MET:HE3	2.40	0.51
1:A:44:THR:O	1:A:70:MET:HE1	2.10	0.51
1:B:306:LEU:CD2	3:B:1203:GLC:H62	2.42	0.49
1:A:955:THR:HG22	1:A:961:ALA:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1201:G1P:P	4:A:1302:HOH:O	2.69	0.49
1:B:955:THR:HG22	1:B:961:ALA:O	2.12	0.49
1:A:44:THR:C	1:A:70:MET:HE1	2.37	0.49
1:A:14:ASN:O	1:A:15:SER:C	2.56	0.48
1:B:197:SER:OG	1:B:205:GLU:OE1	2.29	0.48
1:A:937:GLY:HA3	1:A:1086:ARG:HD3	1.96	0.47
1:A:982:GLU:HG2	4:A:1542:HOH:O	2.14	0.47
1:A:16:ASN:HB3	1:A:33:GLU:HG3	1.98	0.46
1:A:47:GLY:N	1:A:70:MET:HE3	2.30	0.46
1:B:937:GLY:HA3	1:B:1086:ARG:HD3	1.98	0.46
1:A:450:LYS:NZ	1:A:563:TYR:O	2.32	0.46
1:B:450:LYS:NZ	1:B:563:TYR:O	2.30	0.46
1:A:45:LEU:C	1:A:70:MET:HE1	2.41	0.46
1:A:624:GLY:O	1:A:625:ALA:HB3	2.16	0.45
1:B:624:GLY:O	1:B:625:ALA:HB3	2.16	0.45
1:A:922:TYR:OH	2:A:1201:G1P:O1P	2.32	0.44
1:B:684:HIS:HE1	1:B:760:ASP:HA	1.83	0.44
1:A:492:THR:C	4:A:1326:HOH:O	2.61	0.44
1:A:583:PHE:CG	1:A:602:ILE:HD13	2.53	0.44
1:A:1017:ALA:HB1	1:A:1023:ARG:HG2	2.00	0.44
1:A:991:ARG:HD2	4:A:1566:HOH:O	2.17	0.44
2:B:1202:G1P:O3	3:B:1203:GLC:H1	2.17	0.44
1:A:1010:ILE:O	1:A:1014:ARG:HD2	2.18	0.44
1:B:1010:ILE:O	1:B:1014:ARG:HD2	2.18	0.44
1:B:435:ILE:HD11	1:B:454:LEU:HD22	2.00	0.44
1:A:197:SER:OG	1:A:205:GLU:OE1	2.29	0.43
1:A:777:TRP:CH2	1:A:781:LEU:HD22	2.54	0.43
1:B:818:TYR:CD1	1:B:837:MET:HE1	2.53	0.43
1:A:106:TRP:CZ2	1:A:242:GLY:HA3	2.53	0.42
1:B:658:SER:HA	1:B:713:ASP:O	2.20	0.42
1:A:508:MET:HA	1:A:547:VAL:O	2.20	0.42
1:B:853:ARG:NH1	4:B:1321:HOH:O	2.53	0.42
1:A:446:GLU:HG2	1:A:549:GLN:HG2	2.02	0.41
1:B:16:ASN:HB3	1:B:33:GLU:HG3	2.02	0.41
1:B:1017:ALA:HB1	1:B:1023:ARG:HG2	2.01	0.41
1:A:323:LYS:NZ	1:A:577:ASP:OD1	2.53	0.41
1:B:889:ARG:HA	1:B:920:LEU:O	2.19	0.41
1:B:106:TRP:CZ2	1:B:242:GLY:HA3	2.56	0.41
1:B:446:GLU:HG2	1:B:549:GLN:HG2	2.02	0.41
1:B:583:PHE:CG	1:B:602:ILE:HD13	2.56	0.41
1:B:218:TYR:CG	1:B:219:GLU:N	2.89	0.40

There are no symmetry-related clashes.

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	1104/1122 (98%)	1062 (96%)	40 (4%)	2 (0%)	43	44
1	B	1111/1122 (99%)	1065 (96%)	44 (4%)	2 (0%)	43	44
All	All	2215/2244 (99%)	2127 (96%)	84 (4%)	4 (0%)	43	44

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	906	LEU
1	B	15	SER
1	B	906	LEU
1	A	15	SER

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	970/984 (99%)	939 (97%)	31 (3%)	34	38
1	B	975/984 (99%)	950 (97%)	25 (3%)	40	46
All	All	1945/1968 (99%)	1889 (97%)	56 (3%)	37	42

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	LEU
1	A	83	LEU
1	A	95	THR
1	A	158	VAL
1	A	174	LEU
1	A	232	LEU
1	A	292	ARG
1	A	296	LYS
1	A	306	LEU
1	A	322	GLU
1	A	328	LEU
1	A	364	TYR
1	A	454	LEU
1	A	579	LEU
1	A	661	ILE
1	A	692	LEU
1	A	718	LYS
1	A	741	LYS
1	A	746	SER
1	A	767	SER
1	A	771	GLU
1	A	789	LEU
1	A	838	LYS
1	A	855	LEU
1	A	875	LEU
1	A	921	GLN
1	A	974	GLU
1	A	1014	ARG
1	A	1065	LYS
1	A	1103	SER
1	A	1112	LYS
1	B	70	MET
1	B	174	LEU
1	B	292	ARG
1	B	296	LYS
1	B	306	LEU
1	B	322	GLU
1	B	334	THR
1	B	364	TYR
1	B	692	LEU
1	B	718	LYS
1	B	741	LYS
1	B	762	LEU

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Mol	Chain	Res	Type
1	B	771	GLU
1	B	789	LEU
1	B	802	LYS
1	B	838	LYS
1	B	847	GLU
1	B	855	LEU
1	B	921	GLN
1	B	974	GLU
1	B	1014	ARG
1	B	1039	LEU
1	B	1065	LYS
1	B	1069	VAL
1	B	1103	SER

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	215	ASN
1	A	836	HIS
1	A	913	ASN
1	A	996	ASN
1	A	1027	ASN
1	A	1073	ASN
1	A	1080	ASN
1	B	136	ASN
1	B	175	GLN
1	B	215	ASN
1	B	392	GLN
1	B	472	ASN
1	B	488	GLN
1	B	675	HIS
1	B	725	GLN
1	B	809	ASN
1	B	913	ASN
1	B	1073	ASN
1	B	1080	ASN
1	B	1106	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	G1P	B	1201	-	15,16,16	0.81	0	24,24,24	0.82	0
2	G1P	B	1202	-	15,16,16	1.16	1 (6%)	24,24,24	2.15	7 (29%)
3	GLC	B	1203	-	12,12,12	1.16	1 (8%)	17,17,17	2.36	8 (47%)
2	G1P	A	1201	-	15,16,16	0.82	1 (6%)	24,24,24	1.19	2 (8%)

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	G1P	B	1201	-	-	3/7/27/27	0/1/1/1
2	G1P	B	1202	-	-	4/7/27/27	0/1/1/1
3	GLC	B	1203	-	-	0/2/22/22	0/1/1/1
2	G1P	A	1201	-	-	3/7/27/27	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1202	G1P	P-O1	3.80	1.66	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1203	GLC	C1-C2	2.78	1.58	1.52
2	A	1201	G1P	P-O1	2.18	1.63	1.59

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1202	G1P	C1-O5-C5	5.71	124.87	113.72
3	B	1203	GLC	O5-C1-C2	5.39	119.77	110.30
2	B	1202	G1P	O1-C1-C2	4.19	116.06	108.38
3	B	1203	GLC	C1-O5-C5	3.85	121.09	113.65
2	B	1202	G1P	O5-C1-O1	-3.60	106.66	111.36
3	B	1203	GLC	O2-C2-C1	3.49	117.29	109.25
2	A	1201	G1P	O3P-P-O2P	3.25	120.00	107.80
3	B	1203	GLC	O5-C5-C6	3.23	114.45	106.44
2	B	1202	G1P	O3-C3-C4	-3.19	102.87	110.38
3	B	1203	GLC	O3-C3-C4	-2.57	104.32	110.38
3	B	1203	GLC	C6-C5-C4	-2.48	106.92	113.02
2	A	1201	G1P	O2-C2-C1	-2.37	104.42	110.08
3	B	1203	GLC	C3-C4-C5	2.25	114.31	110.23
2	B	1202	G1P	O5-C5-C4	2.16	113.59	109.70
3	B	1203	GLC	O4-C4-C5	-2.11	104.14	109.32
2	B	1202	G1P	C1-C2-C3	2.10	114.43	110.01
2	B	1202	G1P	O5-C1-C2	2.05	114.58	110.37

There are no chirality outliers.

All (10) torsion outliers are listed below:

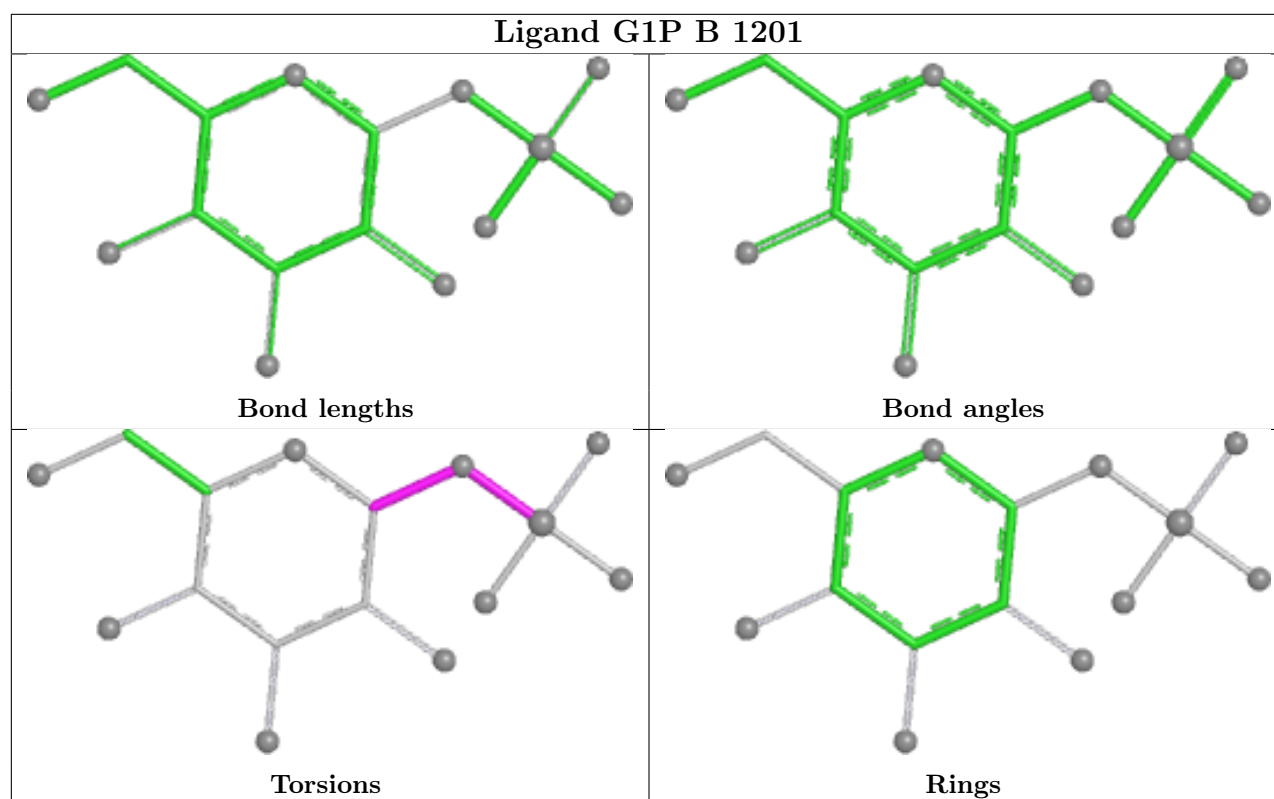
Mol	Chain	Res	Type	Atoms
2	A	1201	G1P	O5-C1-O1-P
2	B	1201	G1P	O5-C1-O1-P
2	B	1202	G1P	O5-C1-O1-P
2	B	1202	G1P	C2-C1-O1-P
2	B	1202	G1P	C4-C5-C6-O6
2	B	1202	G1P	O5-C5-C6-O6
2	A	1201	G1P	C1-O1-P-O3P
2	B	1201	G1P	C1-O1-P-O2P
2	A	1201	G1P	C1-O1-P-O1P
2	B	1201	G1P	C1-O1-P-O1P

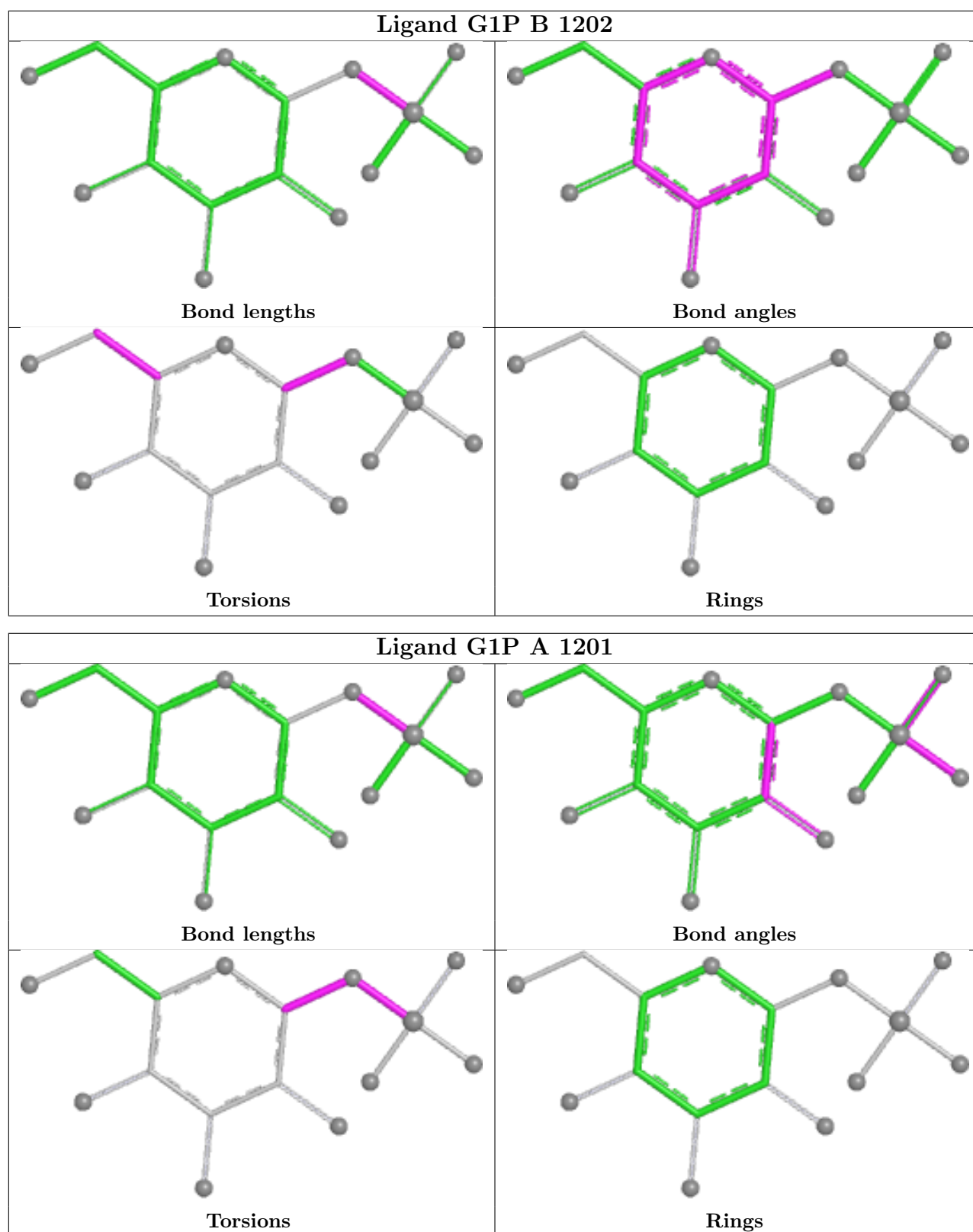
There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1202	G1P	1	0
3	B	1203	GLC	2	0
2	A	1201	G1P	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 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	1108/1122 (98%)	-0.01	11 (0%) 79 81	14, 23, 40, 63	0
1	B	1113/1122 (99%)	0.05	20 (1%) 67 70	15, 24, 42, 61	0
All	All	2221/2244 (98%)	0.02	31 (1%) 73 75	14, 24, 41, 63	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	73	LYS	4.0
1	A	498	ASN	3.5
1	B	836	HIS	3.3
1	B	247	ASN	3.1
1	B	1	GLY	3.0
1	B	1064	ASP	3.0
1	B	513	ASP	2.8
1	A	1	GLY	2.8
1	B	795	GLY	2.8
1	A	1065	LYS	2.8
1	B	768	GLU	2.7
1	B	809	ASN	2.6
1	A	527	THR	2.6
1	B	483	GLU	2.6
1	A	169	ASP	2.6
1	B	169	ASP	2.4
1	A	168	GLY	2.3
1	A	846	THR	2.3
1	B	802	LYS	2.3
1	B	282	GLN	2.2
1	B	73	LYS	2.2
1	B	237	GLN	2.2
1	B	719	ASP	2.2
1	B	570	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	711	LEU	2.1
1	A	279	PRO	2.1
1	A	991	ARG	2.1
1	B	741	LYS	2.1
1	B	1102	MET	2.0
1	B	454	LEU	2.0
1	A	573	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

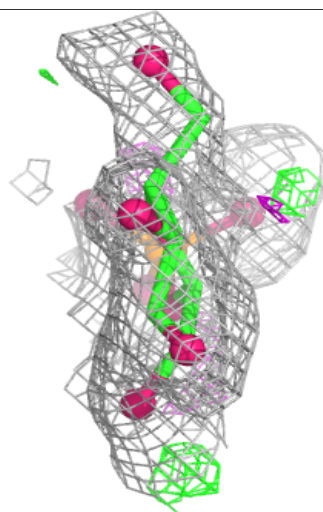
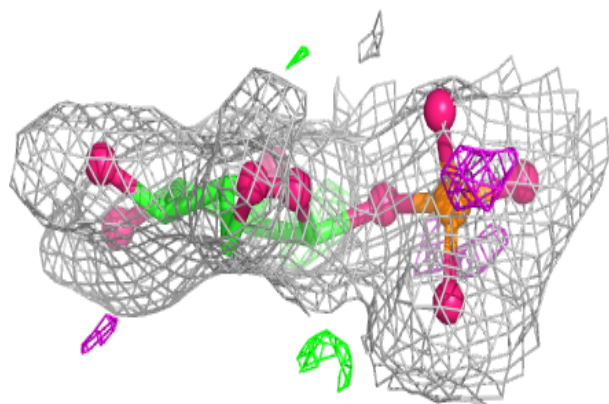
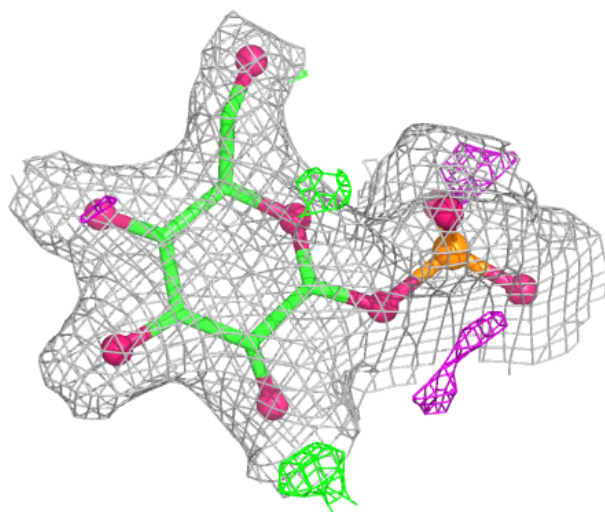
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	G1P	B	1202	16/16	0.76	0.14	36,46,74,77	0
3	GLC	B	1203	12/12	0.78	0.11	41,43,44,47	0
2	G1P	A	1201	16/16	0.96	0.06	21,23,34,36	0
2	G1P	B	1201	16/16	0.96	0.06	18,21,30,30	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.

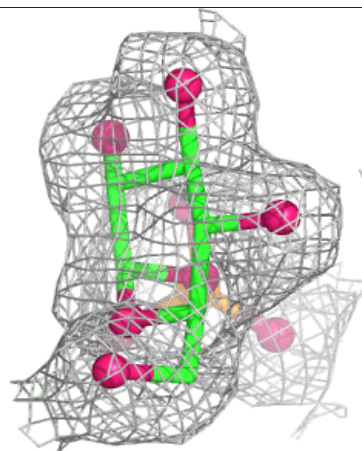
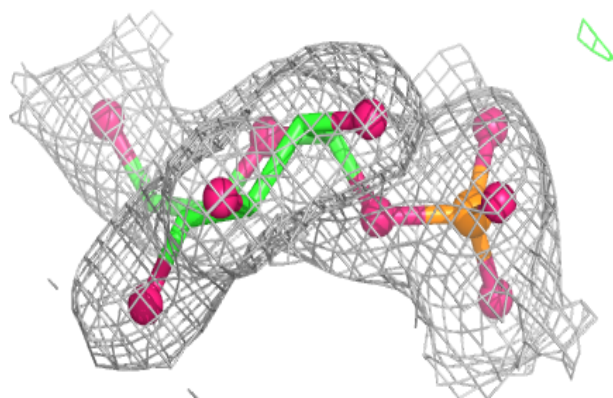
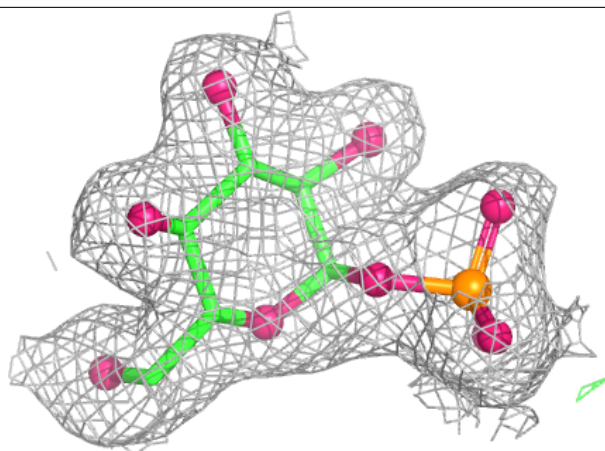
Electron density around G1P B 1202:

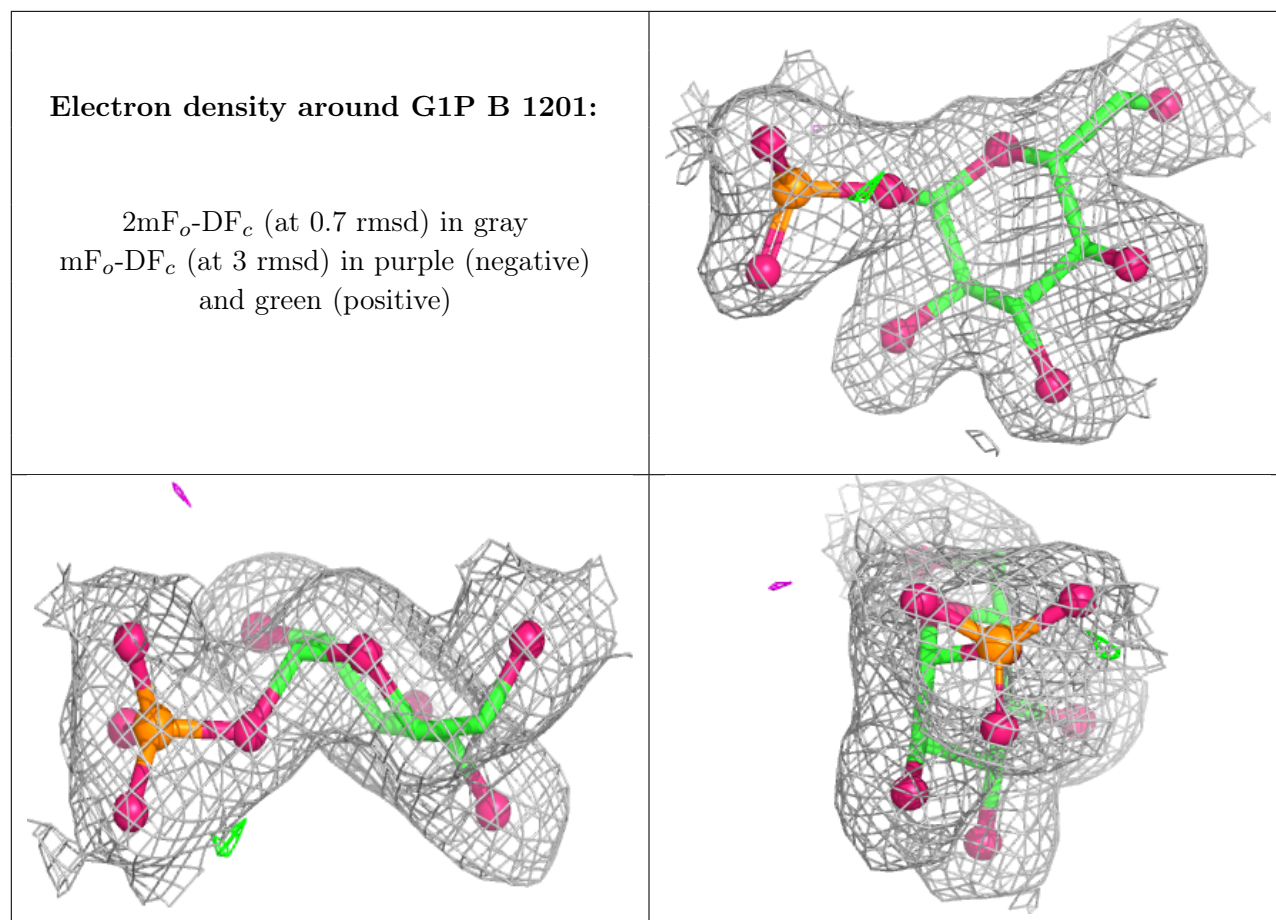
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around G1P A 1201:

$2mF_o-DF_c$ (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.