Full wwPDB X-ray Structure Validation Report (i)

Dec 16, 2023 – 11:03 am GMT

PDB ID	:	2X5Z
Title	:	Crystal structure of T. maritima GDP-mannose pyrophosphorylase in complex with GDP-mannose.
Authors	:	Pelissier, M.C.; Lesley, S.; Kuhn, P.; Bourne, Y.
Deposited on	:	2010-02-12
Resolution	:	2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

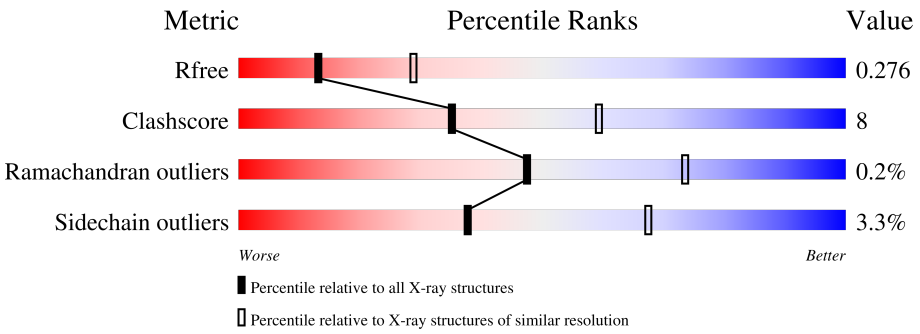
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	336	80% 18% ••
1	B	336	76% 21% ••

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5513 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.

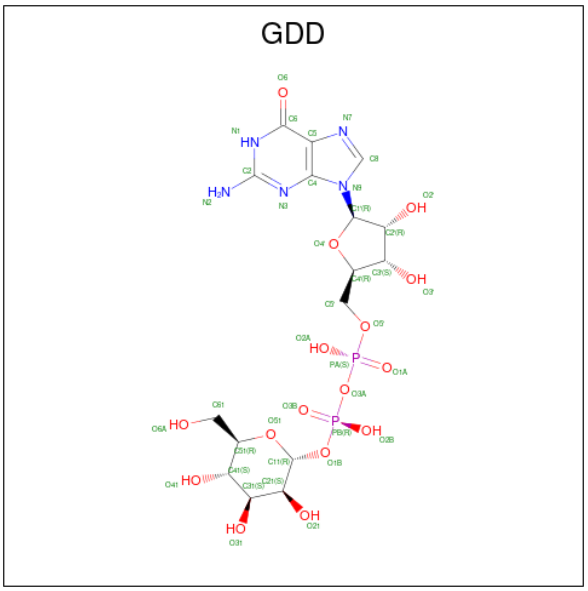
- Molecule 1 is a protein called MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	333	2698	1743	439	507	9	0	0	0
1	B	333	2698	1743	439	507	9	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	VAL	MET	engineered mutation	UNP Q9X0C3
A	261	LEU	VAL	engineered mutation	UNP Q9X0C3
B	1	VAL	MET	engineered mutation	UNP Q9X0C3
B	261	LEU	VAL	engineered mutation	UNP Q9X0C3

- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE-ALPHA-D-MANNOSE (three-letter code: GDD) (formula: $C_{16}H_{25}N_5O_{16}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	39	16	5	16	2	0	0
			Total	C	N	O	P		
2	B	1	39	16	5	16	2	0	0

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

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

- Molecule 4 is water.

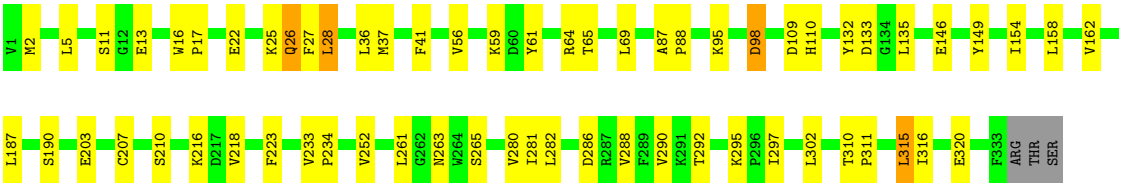
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	23	23	23	0	0
			Total	O		
4	B	15	15	15	0	0

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. 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. 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.

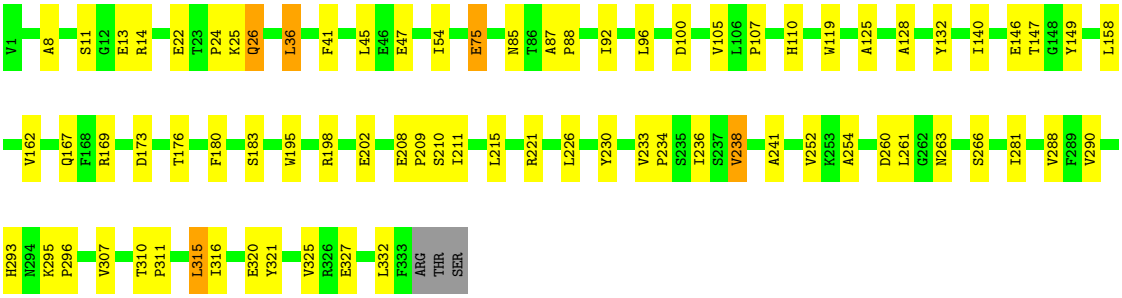
• Molecule 1: MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE

Chain A:



• Molecule 1: MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	84.23Å 96.03Å 217.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 46.88 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.70) 99.8 (46.88-2.70)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.66 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.191 , 0.244 0.242 , 0.276	Depositor DCC
R_{free} test set	1257 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	56.3	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 53.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	5513	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GDD, MG

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	0.70	1/2760 (0.0%)	0.73	0/3731
1	B	0.66	1/2760 (0.0%)	0.69	0/3731
All	All	0.68	2/5520 (0.0%)	0.71	0/7462

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	207	CYS	CB-SG	-7.49	1.69	1.82
1	B	14	ARG	C-O	5.19	1.33	1.23

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2698	0	2723	40	0
1	B	2698	0	2723	53	0
2	A	39	0	23	0	0
2	B	39	0	23	2	0
3	A	1	0	0	0	0
4	A	23	0	0	0	0
4	B	15	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5513	0	5492	90	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 8.

All (90) 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:11:SER:HB2	1:A:13:GLU:OE1	1.56	1.03
1:A:281:ILE:HD11	1:B:332:LEU:HD13	1.44	0.97
1:B:92:ILE:HD11	1:B:226:LEU:HD11	1.49	0.91
1:B:87:ALA:HA	1:B:238:VAL:HG23	1.70	0.73
1:B:87:ALA:HB3	1:B:88:PRO:HD3	1.70	0.73
1:B:22:GLU:O	1:B:24:PRO:HD3	1.88	0.72
1:B:11:SER:HB3	1:B:13:GLU:OE1	1.89	0.72
1:B:85:ASN:N	2:B:601:GDD:O6	2.29	0.66
1:B:36:LEU:HD11	1:B:261:LEU:HD13	1.79	0.64
1:B:75:GLU:O	1:B:221:ARG:NH1	2.31	0.64
1:A:5:LEU:HD11	1:A:56:VAL:CG2	2.29	0.63
1:B:25:LYS:NZ	1:B:261:LEU:O	2.32	0.62
1:A:292:THR:HG22	1:A:297:ILE:HD13	1.82	0.61
1:A:162:VAL:HG22	1:A:252:VAL:HG22	1.83	0.59
1:A:98:ASP:OD1	1:A:98:ASP:N	2.36	0.59
1:A:288:VAL:HG12	1:A:290:VAL:HG23	1.84	0.58
1:B:92:ILE:CD1	1:B:226:LEU:HD11	2.28	0.58
1:A:110:HIS:CE1	1:A:190:SER:O	2.56	0.58
2:B:601:GDD:O2A	2:B:601:GDD:O3B	2.21	0.58
1:A:37:MET:HE1	1:A:65:THR:HG23	1.86	0.58
1:B:281:ILE:HD12	1:B:281:ILE:N	2.19	0.57
1:B:173:ASP:OD1	1:B:173:ASP:C	2.43	0.56
1:A:280:VAL:HG12	1:A:282:LEU:HD11	1.88	0.56
1:B:236:ILE:HG12	1:B:241:ALA:HB2	1.87	0.56
1:A:146:GLU:HG2	1:A:149:TYR:CE2	2.40	0.56
1:A:87:ALA:HB3	1:A:88:PRO:HD3	1.88	0.56
1:A:25:LYS:HA	1:A:28:LEU:HD22	1.88	0.55
1:A:59:LYS:HD2	1:A:223:PHE:CZ	2.41	0.54
1:B:149:TYR:OH	1:B:260:ASP:HB3	2.08	0.53
1:A:25:LYS:NZ	1:A:261:LEU:O	2.41	0.53
1:A:5:LEU:HD11	1:A:56:VAL:HG23	1.89	0.53
1:A:95:LYS:NZ	1:A:216:LYS:O	2.40	0.53
1:B:263:ASN:O	1:B:266:SER:HB2	2.10	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295:LYS:HE2	1:B:311:PRO:HA	1.91	0.52
1:A:263:ASN:OD1	1:A:265:SER:HB3	2.09	0.52
1:A:280:VAL:HG12	1:A:282:LEU:CD1	2.39	0.52
1:A:5:LEU:HD11	1:A:56:VAL:HG21	1.93	0.50
1:A:37:MET:CE	1:A:65:THR:HG23	2.41	0.50
1:A:61:TYR:O	1:A:65:THR:OG1	2.26	0.49
1:B:211:ILE:HG23	1:B:215:LEU:HD12	1.95	0.48
1:B:233:VAL:HG13	1:B:234:PRO:HD2	1.94	0.48
1:A:302:LEU:HD12	1:B:316:ILE:HG22	1.96	0.48
1:B:96:LEU:HD13	1:B:221:ARG:NH2	2.29	0.48
1:A:36:LEU:HD23	1:A:109:ASP:HA	1.96	0.48
1:A:281:ILE:CD1	1:B:332:LEU:HD13	2.32	0.47
1:A:315:LEU:HD22	1:A:316:ILE:N	2.29	0.47
1:A:288:VAL:HG12	1:A:290:VAL:CG2	2.45	0.47
1:B:288:VAL:HG12	1:B:290:VAL:HG23	1.97	0.46
1:A:135:LEU:HD11	1:A:203:GLU:HG2	1.96	0.46
1:B:125:ALA:O	1:B:128:ALA:HB3	2.16	0.46
1:A:27:PHE:CE2	1:A:64:ARG:HG2	2.51	0.46
1:B:54:ILE:HD13	1:B:96:LEU:HD12	1.97	0.45
1:B:209:PRO:O	1:B:210:SER:C	2.54	0.45
1:B:41:PHE:CE2	1:B:45:LEU:HD11	2.51	0.45
1:A:95:LYS:HE2	1:A:218:VAL:O	2.17	0.45
1:A:154:ILE:HD11	1:A:187:LEU:HG	1.97	0.45
1:B:105:VAL:HG21	1:B:195:TRP:CZ2	2.52	0.45
1:A:310:THR:HB	1:A:311:PRO:CD	2.48	0.44
1:B:47:GLU:HG3	1:B:119:TRP:CG	2.52	0.44
1:A:146:GLU:HG2	1:A:149:TYR:CD2	2.53	0.44
1:B:140:ILE:HD13	1:B:254:ALA:HB3	1.99	0.44
1:B:47:GLU:HG3	1:B:119:TRP:CD2	2.52	0.44
1:B:8:ALA:HB1	1:B:26:GLN:NE2	2.33	0.44
1:B:132:TYR:CG	1:B:158:LEU:HD23	2.53	0.44
1:B:162:VAL:HG22	1:B:252:VAL:HG22	2.00	0.44
1:B:295:LYS:HB2	1:B:296:PRO:CD	2.48	0.43
1:B:320:GLU:HG2	1:B:321:TYR:CD1	2.53	0.43
1:A:132:TYR:CZ	1:A:158:LEU:HB3	2.54	0.43
1:B:146:GLU:HG2	1:B:149:TYR:CD2	2.53	0.43
1:B:325:VAL:HG12	1:B:325:VAL:O	2.18	0.43
1:B:96:LEU:HD22	1:B:221:ARG:HH21	1.84	0.43
1:B:92:ILE:HD11	1:B:226:LEU:CD1	2.34	0.43
1:B:107:PRO:HG2	1:B:110:HIS:CE1	2.54	0.43
1:B:167:GLN:OE1	1:B:169:ARG:NH2	2.48	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:307:VAL:HA	1:B:315:LEU:O	2.20	0.42
1:A:233:VAL:HA	1:A:234:PRO:HD3	1.90	0.42
1:B:295:LYS:HB2	1:B:296:PRO:HD2	2.01	0.41
1:A:26:GLN:H	1:A:26:GLN:HG3	1.52	0.41
1:B:96:LEU:HD23	1:B:96:LEU:HA	1.89	0.41
1:B:176:THR:HG22	1:B:180:PHE:CZ	2.55	0.41
1:A:41:PHE:CD2	1:A:69:LEU:HD22	2.55	0.41
1:B:147:THR:O	1:B:147:THR:CG2	2.69	0.41
1:B:169:ARG:HB2	1:B:169:ARG:HH21	1.86	0.41
1:B:260:ASP:OD1	1:B:260:ASP:C	2.58	0.41
1:B:169:ARG:HH21	1:B:169:ARG:CB	2.34	0.41
1:B:310:THR:HB	1:B:311:PRO:CD	2.51	0.41
1:A:16:TRP:CG	1:A:17:PRO:HA	2.55	0.40
1:B:310:THR:HB	1:B:311:PRO:HD2	2.03	0.40
1:A:5:LEU:CD1	1:A:56:VAL:HG23	2.50	0.40
1:B:198:ARG:O	1:B:202:GLU:HG2	2.22	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	331/336 (98%)	320 (97%)	10 (3%)	1 (0%)	41 66
1	B	331/336 (98%)	321 (97%)	10 (3%)	0	100 100
All	All	662/672 (98%)	641 (97%)	20 (3%)	1 (0%)	47 73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	133	ASP

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	299/302 (99%)	290 (97%)	9 (3%)	41	70
1	B	299/302 (99%)	288 (96%)	11 (4%)	34	63
All	All	598/604 (99%)	578 (97%)	20 (3%)	38	67

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	MET
1	A	22	GLU
1	A	26	GLN
1	A	28	LEU
1	A	98	ASP
1	A	210	SER
1	A	286	ASP
1	A	315	LEU
1	A	320	GLU
1	B	26	GLN
1	B	36	LEU
1	B	75	GLU
1	B	100	ASP
1	B	183	SER
1	B	208	GLU
1	B	230	TYR
1	B	238	VAL
1	B	293	HIS
1	B	315	LEU
1	B	327	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 3 ligands modelled in this entry, 1 is 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	GDD	A	601	3	35,42,42	1.56	2 (5%)	46,65,65	1.54	10 (21%)
2	GDD	B	601	-	35,42,42	1.41	2 (5%)	46,65,65	1.72	11 (23%)

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	GDD	A	601	3	-	4/19/59/59	0/4/4/4
2	GDD	B	601	-	-	3/19/59/59	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	GDD	O6-C6	6.80	1.37	1.23
2	B	601	GDD	O6-C6	6.54	1.36	1.23
2	A	601	GDD	C5-C6	-4.77	1.37	1.47
2	B	601	GDD	C5-C6	-3.05	1.41	1.47

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	601	GDD	PB-O3A-PA	-5.74	113.14	132.83
2	A	601	GDD	PB-O3A-PA	-3.96	119.24	132.83
2	B	601	GDD	O3A-PB-O1B	3.86	110.26	102.48
2	A	601	GDD	C8-N7-C5	3.54	109.73	102.99
2	B	601	GDD	C5-C6-N1	3.38	119.92	113.95
2	B	601	GDD	C2-N1-C6	-3.01	119.55	125.10
2	A	601	GDD	O5'-PA-O1A	-3.00	97.35	109.07
2	A	601	GDD	O2A-PA-O1A	2.71	125.66	112.24
2	A	601	GDD	C5-C6-N1	2.63	118.60	113.95
2	A	601	GDD	O51-C51-C61	2.55	112.77	106.44
2	A	601	GDD	O2B-PB-O3B	2.52	124.71	112.24
2	B	601	GDD	O2B-PB-O3B	2.49	124.56	112.24
2	B	601	GDD	O2B-PB-O1B	-2.45	97.12	106.78
2	B	601	GDD	O2A-PA-O1A	2.37	123.94	112.24
2	B	601	GDD	C8-N7-C5	2.28	107.34	102.99
2	A	601	GDD	C2-N1-C6	-2.23	120.98	125.10
2	A	601	GDD	O3'-C3'-C2'	-2.14	104.90	111.82
2	A	601	GDD	O2A-PA-O5'	2.11	117.55	107.75
2	B	601	GDD	N2-C2-N1	2.10	121.19	116.71
2	B	601	GDD	O51-C11-C21	-2.09	105.93	110.35
2	B	601	GDD	O51-C51-C61	2.02	111.46	106.44

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	GDD	O51-C51-C61-O6A
2	A	601	GDD	C41-C51-C61-O6A
2	B	601	GDD	O51-C51-C61-O6A
2	A	601	GDD	C21-C11-O1B-PB
2	B	601	GDD	C21-C11-O1B-PB
2	A	601	GDD	C11-O1B-PB-O3A
2	B	601	GDD	C41-C51-C61-O6A

There are no ring outliers.

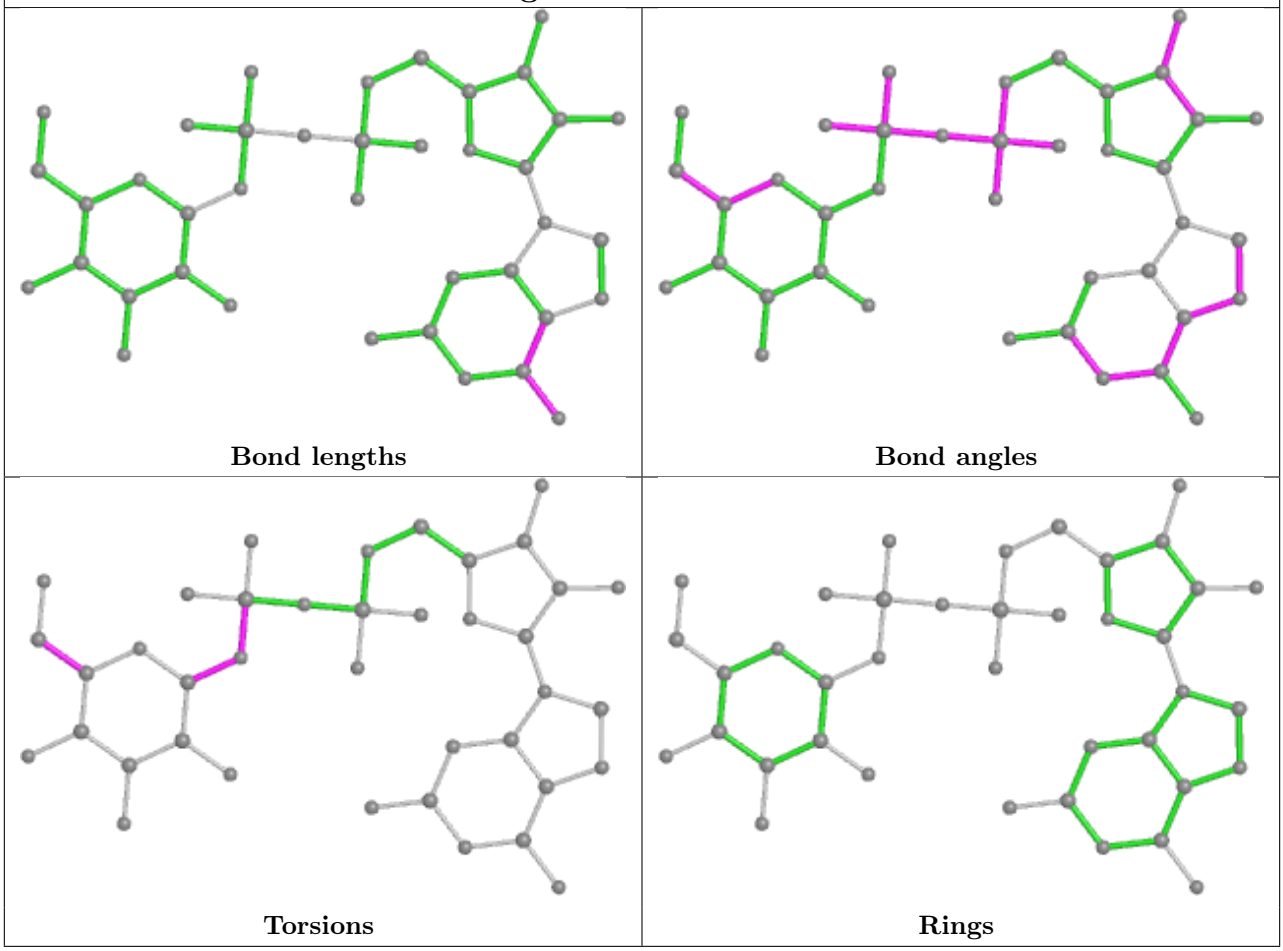
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	GDD	2	0

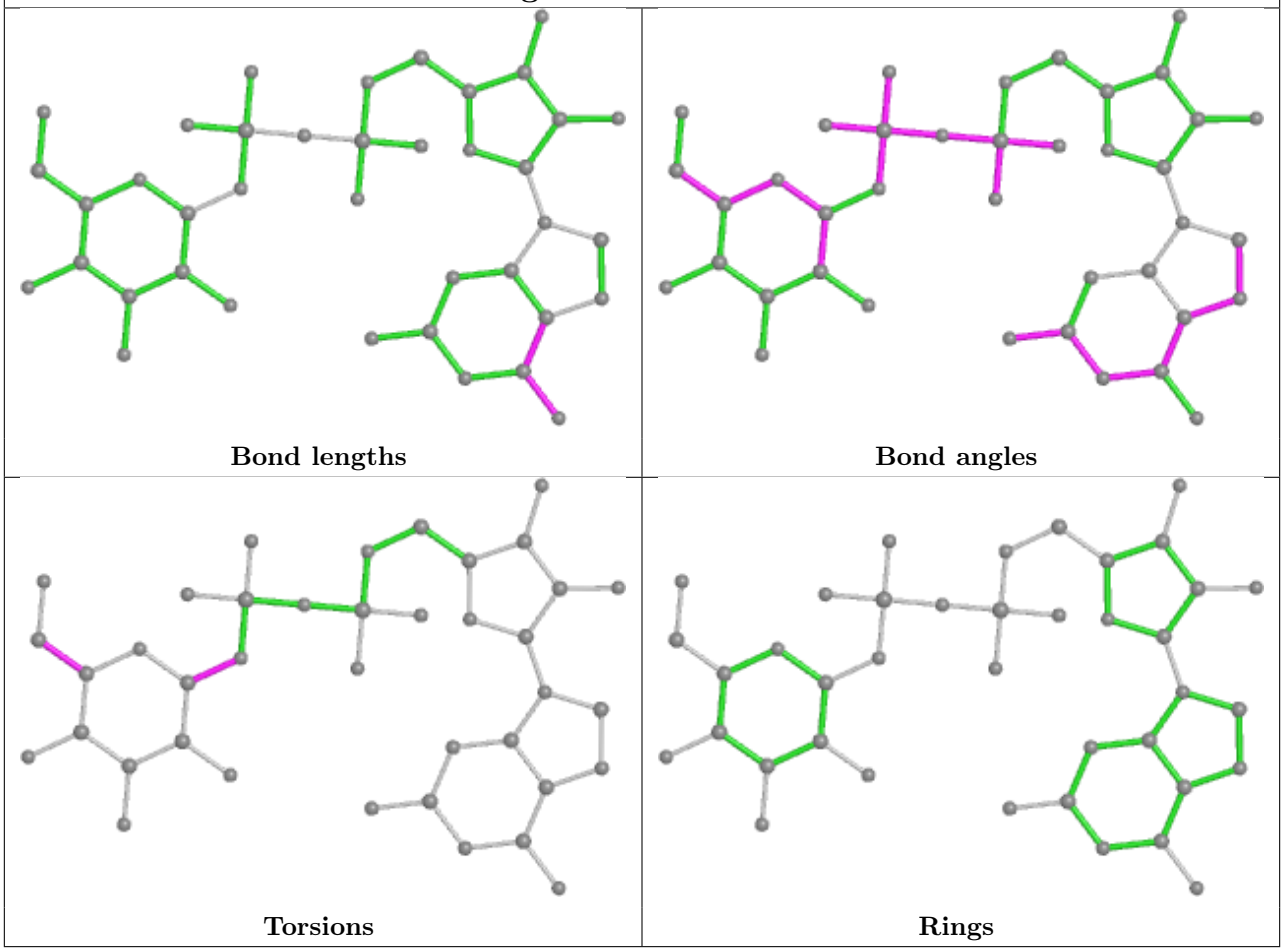
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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 GDD A 601



Ligand GDD B 601



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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

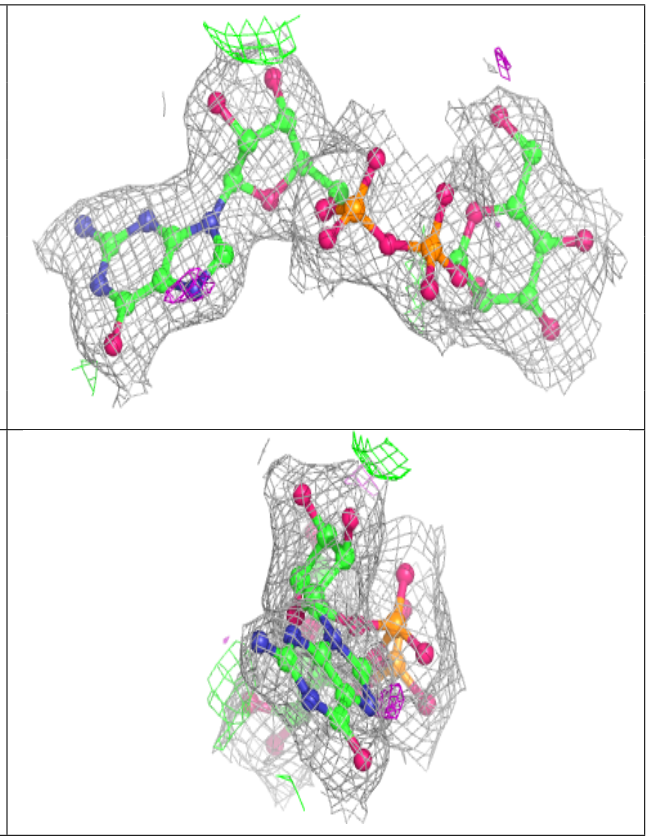
6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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.

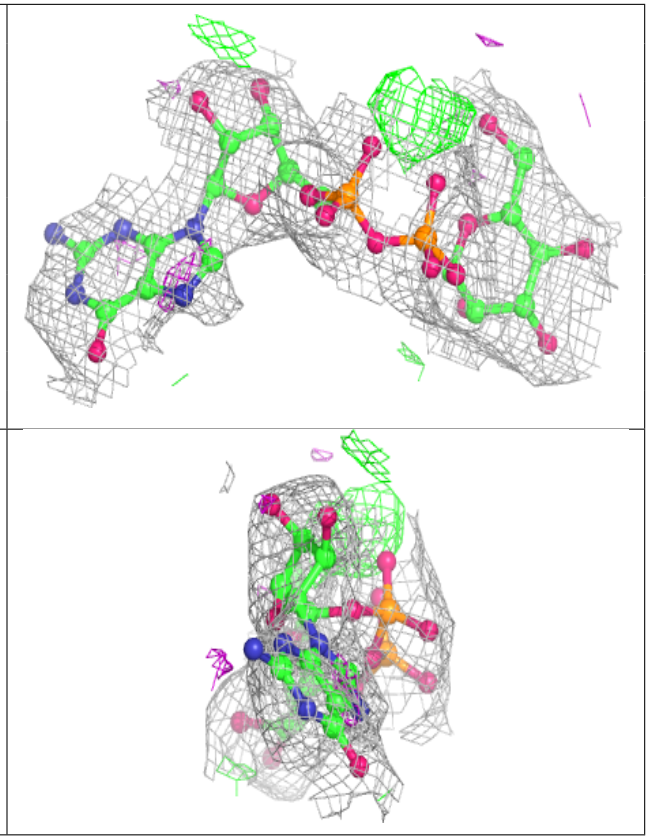
Electron density around GDD A 601:

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



Electron density around GDD 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)

Unable to reproduce the depositors R factor - this section is therefore empty.