

Full wwPDB X-ray Structure Validation Report (i)

May 13, 2020 – 08:34 am BST

PDB ID : 3OKA

Title: Crystal structure of Corynebacterium glutamicum PimB' in complex with

GDP-Man (triclinic crystal form)

Authors: Batt, S.M.; Jabeen, T.; Besra, G.S.; Futterer, K.

Deposited on : 2010-08-24

Resolution : 2.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.11

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0158

CCP4: 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

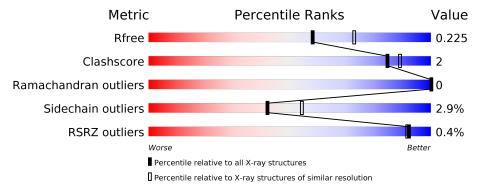
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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

Mol	Chain	Length	Quality of chain						
1	A	381		94%					
1	В	381		94%		5% •			
2	С	21	43%	10%	48%				
2	D	21	14%	10% 1	.0% 33%				



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6231 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.

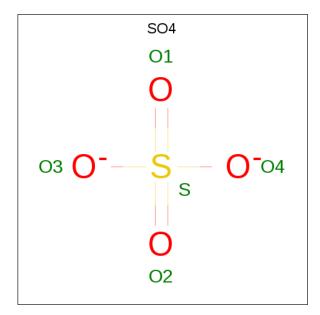
• Molecule 1 is a protein called GDP-mannose-dependent alpha-(1-6)-phosphatidylinositol monomannoside mannosyltransferase.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace
1	A	378	Total 2809	C 1779	± '	O 527	S 11	0	0	0
1	В	378	Total 2811	C 1777	N 494	O 529	S 11	0	0	0

• Molecule 2 is a protein called N-terminal His-affinity tag.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	С	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	0	0	0				
			91	53	25	13		0	
2	D	14	Total	С	N	О	0	0	0
	D	14	114	68	30	16	0		

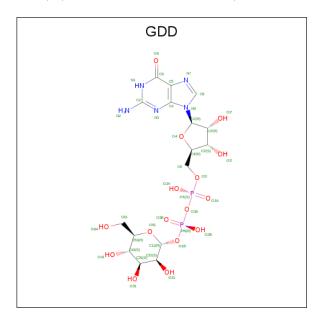
• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
3	A	1	Total O S	0	0	
		_	5 4 1		Ü	
3	A	1	Total O S	0	0	
		-	5 4 1	Ü	Ü	
3	A	1	Total O S	0	0	
	11	1	5 4 1	Ů	U	
3	В	1	Total O S	0	0	
	D	1	5 4 1	U	U	
3	В	1	Total O S	0	0	
)	Ъ	1	$\begin{array}{cccccccccccccccccccccccccccccccccccc$		O	
3	В	1	Total O S	0	0	
3	D	1	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	U		
3	В	1	Total O S	0	0	
3	D	1	5 4 1	0	0	
3	С	1	Total O S	0	0	
3		1	5 4 1	U	U	
3	D	1	Total O S	0	0	
3	D	1	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	0	0	
3	D	1	Total O S	0		
)	ש	1	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	0	0	

• Molecule 4 is GUANOSINE-5'-DIPHOSPHATE-ALPHA-D-MANNOSE (three-letter code: GDD) (formula: $C_{16}H_{25}N_5O_{16}P_2$).



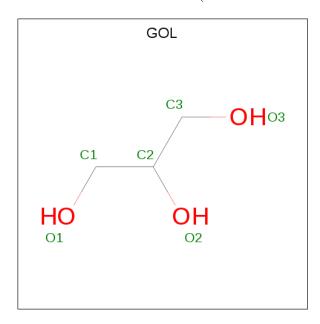
Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf	
4	A	1	Total	C	N	0	P	0	0
•		_	28	10	5	11	2		



Continued from previous page...

Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf	
4	D	1	Total	С	N	О	Р	0	0
4	D	В 1	28	10	5	11	2	U	

• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



\mathbf{Mol}	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0

• Molecule 6 is water.

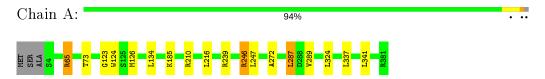
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	155	Total O 155 155	0	0
6	В	133	Total O 133 133	0	0
6	С	4	Total O 4 4	0	0
6	D	2	Total O 2 2	0	0



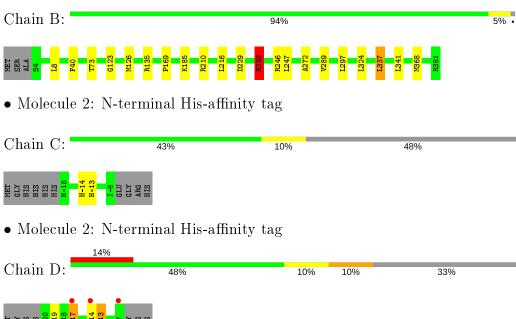
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

 $\bullet \ \, \text{Molecule 1: GDP-mannose-dependent alpha-(1-6)-phosphatidy linositol\ monomannoside mannosyltransferase}$



• Molecule 1: GDP-mannose-dependent alpha-(1-6)-phosphatidylinositol monomannoside mannosyltransferase







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	44.07Å 50.02Å 85.30Å	Depositor
a, b, c, α , β , γ	92.05° 92.68° 89.94°	Depositor
Resolution (Å)	43.80 - 2.20	Depositor
resolution (A)	43.80 - 2.20	EDS
% Data completeness	94.8 (43.80-2.20)	Depositor
(in resolution range)	94.8 (43.80-2.20)	EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) > 1$	4.98 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.189 , 0.221	Depositor
It, It free	0.192 , 0.225	DCC
R_{free} test set	1747 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	14.1	Xtriage
Anisotropy	0.395	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	$0.37 \; , 39.4$	EDS
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.099 for -h,k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6231	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.20% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: GOL, GDD, SO4

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		
MIOI		RMSZ	# Z >5	RMSZ	# Z > 5	
1	A	0.39	0/2866	0.61	4/3906 (0.1%)	
1	В	0.40	0/2868	0.61	4/3910 (0.1%)	
2	С	0.31	0/97	0.37	0/130	
2	D	0.31	0/121	0.44	0/163	
All	All	0.39	0/5952	0.60	8/8109 (0.1%)	

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	В	239	ARG	NE-CZ-NH2	-8.50	116.05	120.30
1	В	239	ARG	NE-CZ-NH1	8.32	124.46	120.30
1	A	246	ARG	NE-CZ-NH2	-8.15	116.22	120.30
1	A	246	ARG	NE-CZ-NH1	7.66	124.13	120.30
1	В	246	ARG	NE-CZ-NH1	-7.40	116.60	120.30
1	A	239	ARG	NE-CZ-NH1	-7.36	116.62	120.30
1	A	239	ARG	NE-CZ-NH2	7.24	123.92	120.30
1	В	246	ARG	NE-CZ-NH2	6.80	123.70	120.30

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	$\mathbf{H}(\mathbf{model})$	H(added)	Clashes	Symm-Clashes
1	Α	2809	0	2783	11	0
1	В	2811	0	2779	12	0
2	С	91	0	66	1	0
2	D	114	0	86	4	0
3	A	15	0	0	0	0
3	В	20	0	0	1	0
3	С	5	0	0	0	0
3	D	10	0	0	0	0
4	A	28	0	12	0	0
4	В	28	0	12	0	0
5	A	6	0	8	0	0
6	A	155	0	0	1	0
6	В	133	0	0	1	0
6	С	4	0	0	0	0
6	D	2	0	0	0	0
All	All	6231	0	5746	27	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 (27) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
		$\operatorname{distance}\left(\mathrm{\AA}\right)$	overlap (Å)
1:A:65:ARG:HH21	1:A:65:ARG:HG2	1.40	0.85
1:A:65:ARG:HH21	1:A:65:ARG:CG	1.94	0.80
1:B:324:LEU:HD11	1:B:341:LEU:HD21	1.70	0.73
1:A:123:GLY:O	1:A:126:MET:HG3	1.91	0.70
1:B:123:GLY:O	1:B:126:MET:HG3	1.92	0.69
1:A:324:LEU:HD11	1:A:341:LEU:HD21	1.73	0.69
1:A:65:ARG:HG2	1:A:65:ARG:NH2	2.10	0.62
1:A:210:ARG:HB2	6:A:387:HOH:O	2.00	0.62
2:D:-19:HIS:HB3	2:D:-17:HIS:CE1	2.37	0.60
1:B:210:ARG:HB2	6:B:389:HOH:O	2.06	0.55
1:A:124:TRP:CZ2	1:A:287:LEU:HD22	2.43	0.53
2:D:-14:HIS:HD2	2:D:-13:HIS:N	2.07	0.51
1:B:169:PRO:HD2	1:B:368:MET:HE1	1.95	0.48
2:C:-14:HIS:HD2	2:C:-13:HIS:N	2.12	0.47
1:A:65:ARG:CG	1:A:65:ARG:NH2	2.64	0.47
1:B:185:LYS:HG3	1:B:272:ALA:HA	1.96	0.46
1:B:135:ARG:HA	1:B:135:ARG:HD3	1.77	0.45
1:A:124:TRP:CE2	1:A:287:LEU:HD22	2.52	0.45
1:A:246:ARG:HG3	1:B:229:ASP:HA	1.98	0.45



$\alpha \cdots$	· ·	•	
Continued	trom	nromanne	naae
-	110111	picolous	payc

Atom-1	Atom-2	$egin{aligned} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{aligned}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:B:8:LEU:HD11	1:B:40:PHE:HB2	2.00	0.44
2:D:-14:HIS:C	2:D:-13:HIS:ND1	2.72	0.43
1:B:324:LEU:HD11	1:B:341:LEU:CD2	2.44	0.43
2:D:-14:HIS:CD2	2:D:-13:HIS:N	2.87	0.42
1:B:324:LEU:HD13	1:B:337:LEU:HG	2.02	0.42
1:B:239:ARG:NH2	3:B:601:SO4:O1	2.53	0.41
1:B:210:ARG:HH11	1:B:210:ARG:HG2	1.86	0.41
1:A:185:LYS:HG3	1:A:272:ALA:HA	2.03	0.41

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	Perce	${ m ntiles}$
1	A	376/381 (99%)	371 (99%)	5 (1%)	0	100	100
1	В	$376/381 \ (99\%)$	373 (99%)	3 (1%)	0	100	100
2	С	9/21 (43%)	9 (100%)	0	0	100	100
2	D	12/21~(57%)	12 (100%)	0	0	100	100
All	All	773/804 (96%)	765 (99%)	8 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	Perce	ntiles
1	A	286/308~(93%)	278 (97%)	8 (3%)	43	56
1	В	287/308 (93%)	280 (98%)	7 (2%)	49	62
2	С	9/18 (50%)	9 (100%)	0	100	100
2	D	11/18 (61%)	9 (82%)	2 (18%)	1	1
All	All	593/652 (91%)	576 (97%)	17 (3%)	42	54

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Α	65	ARG
1	A	73	THR
1	A	134	LEU
1	A	216	LEU
1	A	247	LEU
1	A	287	LEU
1	A	289	VAL
1	Α	337	LEU
1	В	73	THR
1	В	216	LEU
1	В	239	ARG
1	В	247	LEU
1	В	289	VAL
1	В	297	LEU
1	В	337	LEU
2	D	-17	HIS
2	D	-13	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	${f Res}$	Type
1	A	358	HIS
1	В	358	HIS
2	С	-14	HIS
2	С	-9	HIS
2	D	-14	HIS
2	D	-9	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.



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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

13 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).

Mal	Т	Chain	Dag	Link	Во	ond leng	ths	В	ond ang	gles
Mol	Type	Chain	m Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	В	603	=	4,4,4	0.13	0	6,6,6	0.10	0
3	SO4	A	603	-	4,4,4	0.14	0	6,6,6	0.21	0
3	SO4	D	702	-	4,4,4	0.17	0	6,6,6	0.15	0
3	SO4	В	602	-	4,4,4	0.12	0	6,6,6	0.18	0
3	SO4	D	701	-	4,4,4	0.15	0	6,6,6	0.14	0
3	SO4	С	700	-	4,4,4	0.16	0	6,6,6	0.20	0
3	SO4	A	601	-	4,4,4	0.16	0	6,6,6	0.14	0
3	SO4	В	601	-	4,4,4	0.16	0	6,6,6	0.15	0
3	SO4	В	604	-	4,4,4	0.12	0	6,6,6	0.11	0
4	GDD	A	701	-	24,30,42	3.18	6 (25%)	31,47,65	1.73	4 (12%)
4	GDD	В	701	_	24,30,42	3.17	6 (25%)	31,47,65	1.76	6 (19%)
5	GOL	A	801	-	5,5,5	0.40	0	5,5,5	0.26	0
3	SO4	A	602	_	4,4,4	0.15	0	6,6,6	0.09	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	\mathbf{Res}	Link	Chirals	Torsions	Rings
4	GDD	В	701	_	-	5/12/32/59	0/3/3/4



$Continued\ from\ previous\ page...$

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GDD	A	701	-	-	5/12/32/59	0/3/3/4
5	GOL	A	801	-	-	4/4/4/4	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(ext{\AA})$
4	A	701	GDD	PB-O3B	-7.81	1.25	1.50
4	В	701	GDD	PB-O3B	-7.79	1.25	1.50
4	A	701	GDD	PB-O2B	-7.64	1.25	1.54
4	В	701	GDD	PB-O2B	-7.62	1.25	1.54
4	В	701	GDD	PA-O1A	-7.19	1.25	1.50
4	A	701	GDD	PA-O1A	-7.14	1.25	1.50
4	A	701	GDD	PA-O2A	-6.43	1.25	1.55
4	В	701	GDD	PA-O2A	-6.37	1.25	1.55
4	В	701	GDD	PA-O5'	-3.57	1.44	1.59
4	A	701	GDD	PA-O5'	-3.51	1.45	1.59
4	A	701	GDD	PB-O1B	-2.65	1.44	1.54
4	В	701	GDD	PB-O1B	-2.61	1.44	1.54

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
4	A	701	GDD	N3-C2-N1	-4.99	120.57	127.22
4	В	701	GDD	N3-C2-N1	-4.97	120.60	127.22
4	A	701	GDD	C2-N3-C4	4.44	120.43	115.36
4	В	701	GDD	C2-N3-C4	4.36	120.33	115.36
4	В	701	GDD	C6-N1-C2	3.08	120.83	115.93
4	A	701	GDD	C6-N1-C2	2.98	120.67	115.93
4	В	701	GDD	C5-C6-N1	-2.83	119.57	123.43
4	A	701	GDD	C5-C6-N1	-2.78	119.63	123.43
4	В	701	GDD	C3'-C2'-C1'	2.31	104.45	100.98
4	В	701	GDD	C6-C5-C4	-2.07	118.82	120.80

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	701	GDD	C3'-C4'-C5'-O5'
4	A	701	GDD	O4'-C4'-C5'-O5'
4	A	701	GDD	C5'-O5'-PA-O1A
4	A	701	GDD	C5'-O5'-PA-O2A



Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	A	701	GDD	C5'-O5'-PA-O3A
4	В	701	GDD	C3'-C4'-C5'-O5'
4	В	701	GDD	O4'-C4'-C5'-O5'
4	В	701	GDD	C5'-O5'-PA-O2A
4	В	701	GDD	C5'-O5'-PA-O3A
5	A	801	GOL	C1-C2-C3-O3
5	A	801	GOL	O1-C1-C2-C3
5	A	801	GOL	O1-C1-C2-O2
5	A	801	GOL	O2-C2-C3-O3
4	В	701	GDD	C5'-O5'-PA-O1A

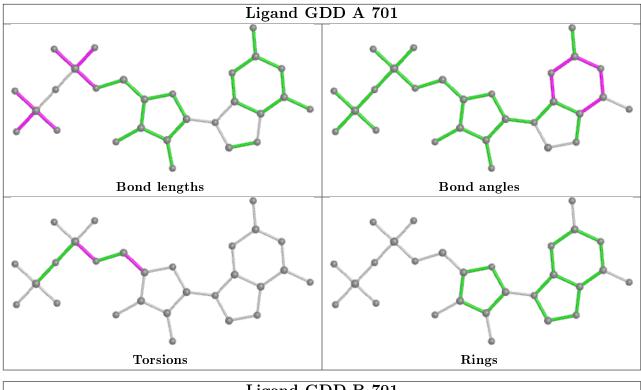
There are no ring outliers.

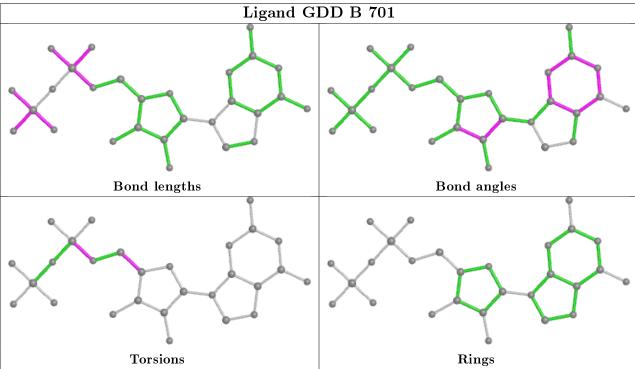
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	601	SO4	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$		$OWAB(\AA^2)$	Q < 0.9
1	A	378/381 (99%)	-0.46	0 10	0 100	5, 12, 19, 25	0
1	В	378/381 (99%)	-0.50	0 10	0 100	5, 12, 19, 26	0
2	С	11/21 (52%)	0.44	0 10	100	19, 21, 26, 28	0
2	D	14/21 (66%)	0.93	3 (21%	(a) 0 0	19, 23, 30, 31	0
All	All	781/804 (97%)	-0.44	3 (0%)	92 91	5, 12, 20, 31	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	-7	GLU	2.7
2	D	-14	HIS	2.4
2	D	-17	HIS	2.2

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

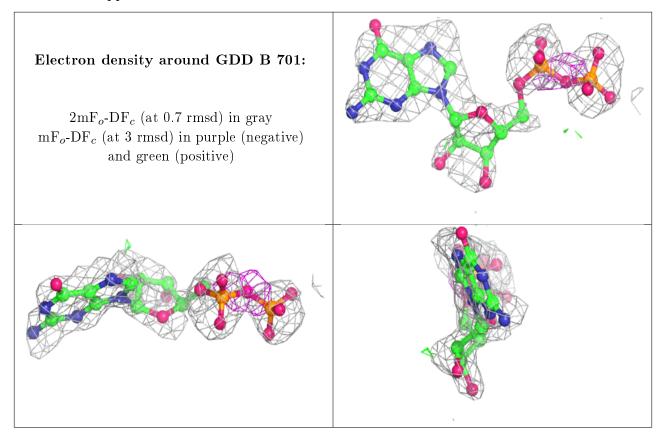
6.4 Ligands (i)

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

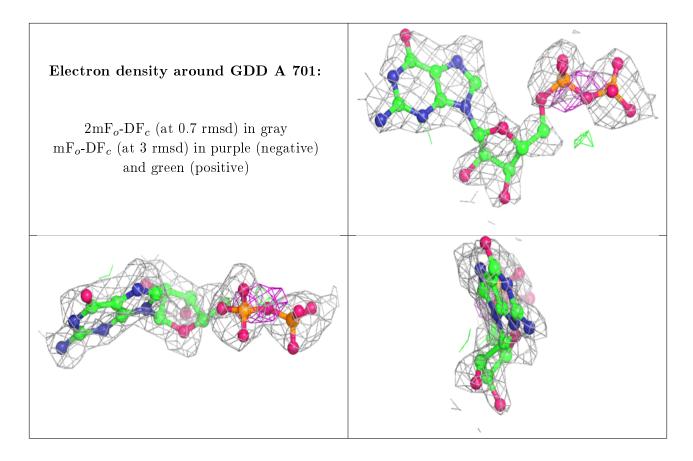


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
4	GDD	В	701	28/39	0.80	0.26	30,35,36,36	28
4	GDD	A	701	28/39	0.82	0.22	28,31,32,32	28
5	GOL	A	801	6/6	0.84	0.14	32,33,33,34	0
3	SO4	В	604	5/5	0.85	0.20	88,88,88,88	0
3	SO4	В	601	5/5	0.88	0.18	39,39,40,40	0
3	SO4	D	702	5/5	0.92	0.21	82,82,82,82	0
3	SO4	A	601	5/5	0.94	0.15	43,43,43,43	0
3	SO4	В	602	5/5	0.97	0.12	35,36,36,36	0
3	SO4	В	603	5/5	0.98	0.09	25,26,26,26	0
3	SO4	A	602	5/5	0.98	0.08	33,33,34,34	0
3	SO4	A	603	5/5	0.98	0.10	25,25,25,26	0
3	SO4	D	701	5/5	0.98	0.09	31,31,31,32	0
3	SO4	С	700	5/5	0.99	0.10	24,25,25,26	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.







6.5 Other polymers (i)

There are no such residues in this entry.

