Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 11:25 AM GMT

PDB ID	:	3OY7
Title	:	Crystal structure of a virus encoded glycosyltransferase in complex with GDP-mannose
Authors	:	Xiang, Y.; Rossmann, M.G.
Deposited on	:	2010-09-23
Resolution	:	2.73 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
http://wwpdb.org/validation/2016/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:

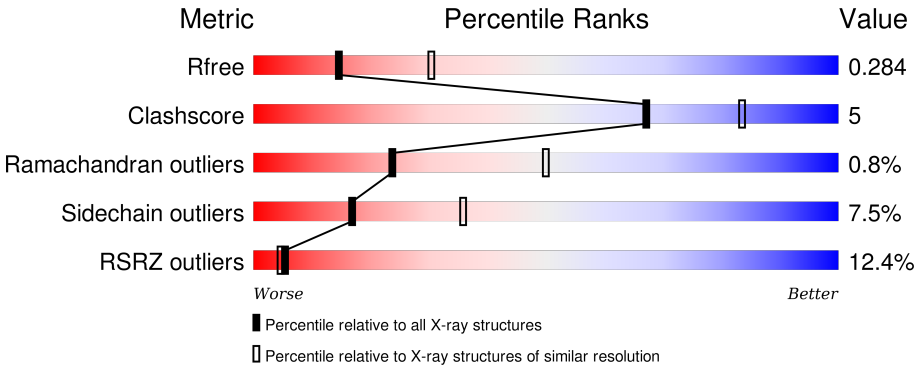
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.73 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}	91344	3050 (2.78-2.70)
Clashscore	102246	3424 (2.78-2.70)
Ramachandran outliers	100387	3367 (2.78-2.70)
Sidechain outliers	100360	3368 (2.78-2.70)
RSRZ outliers	91569	3055 (2.78-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	413	3% 77% 15% • 5%
1	B	413	20% 80% 13% • 5%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6289 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.

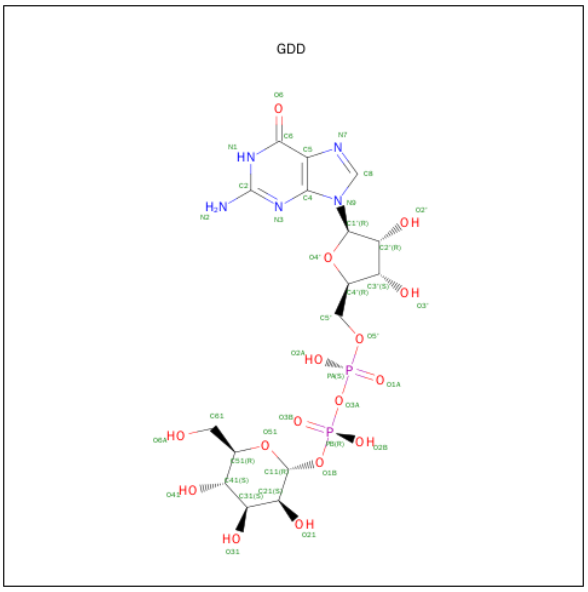
- Molecule 1 is a protein called Glycosyltransferase B736L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	0	0
			3101	1983	531	568	19			
1	B	392	Total	C	N	O	S	0	0	0
			3101	1983	531	568	19			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	406	LEU	-	EXPRESSION TAG	UNP A7IXR1
A	407	GLU	-	EXPRESSION TAG	UNP A7IXR1
A	408	HIS	-	EXPRESSION TAG	UNP A7IXR1
A	409	HIS	-	EXPRESSION TAG	UNP A7IXR1
A	410	HIS	-	EXPRESSION TAG	UNP A7IXR1
A	411	HIS	-	EXPRESSION TAG	UNP A7IXR1
A	412	HIS	-	EXPRESSION TAG	UNP A7IXR1
A	413	HIS	-	EXPRESSION TAG	UNP A7IXR1
B	406	LEU	-	EXPRESSION TAG	UNP A7IXR1
B	407	GLU	-	EXPRESSION TAG	UNP A7IXR1
B	408	HIS	-	EXPRESSION TAG	UNP A7IXR1
B	409	HIS	-	EXPRESSION TAG	UNP A7IXR1
B	410	HIS	-	EXPRESSION TAG	UNP A7IXR1
B	411	HIS	-	EXPRESSION TAG	UNP A7IXR1
B	412	HIS	-	EXPRESSION TAG	UNP A7IXR1
B	413	HIS	-	EXPRESSION TAG	UNP A7IXR1

- 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
2	A	1	Total	C	N	O	P	0	0
			39	16	5	16	2		
2	B	1	Total	C	N	O	P	0	0
			39	16	5	16	2		

- Molecule 3 is water.

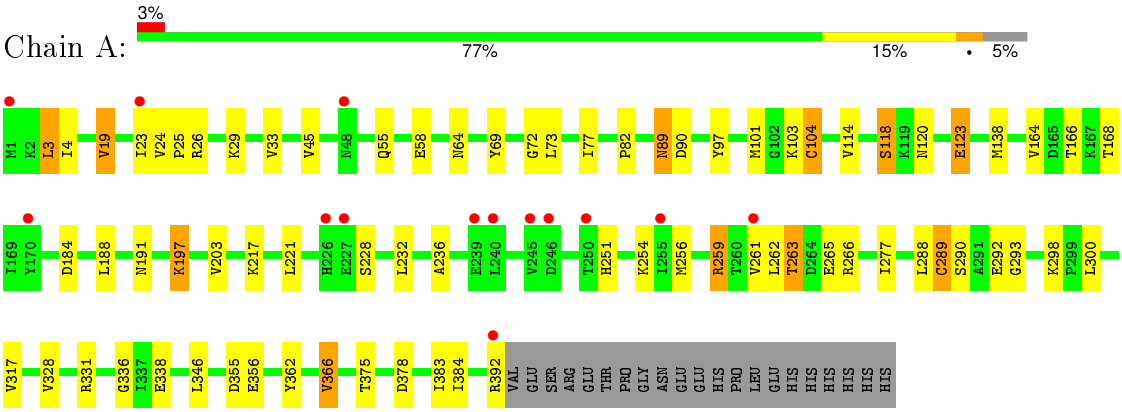
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	O	0	0
			5	5		
3	B	4	Total	O	0	0
			4	4		

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 errors 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.

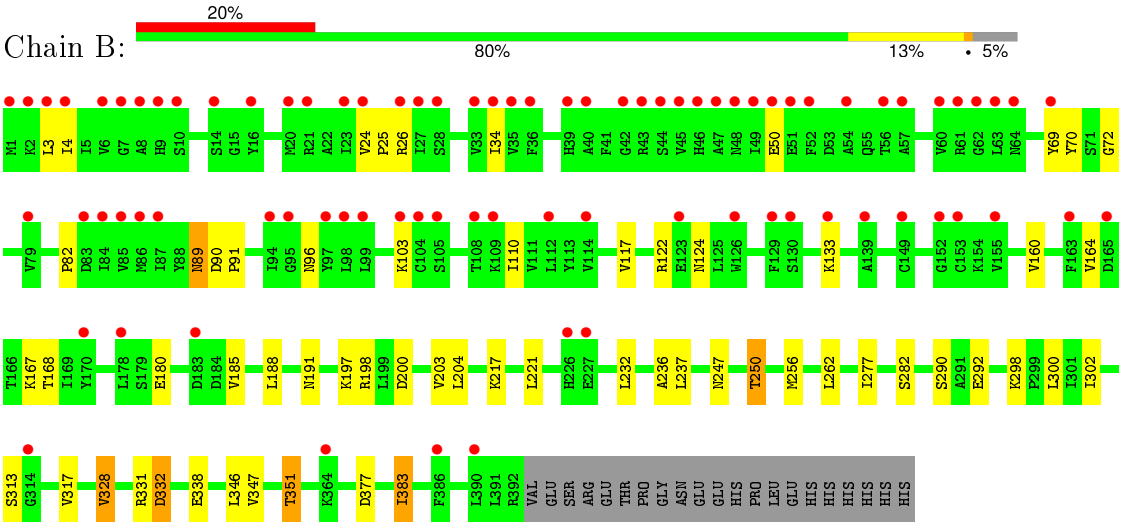
- Molecule 1: Glycosyltransferase B736L

Chain A:



- Molecule 1: Glycosyltransferase B736L

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	154.25Å 243.19Å 67.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	130.19 – 2.73 43.42 – 2.73	Depositor EDS
% Data completeness (in resolution range)	98.7 (130.19-2.73) 98.7 (43.42-2.73)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	3.12 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.257 , 0.290 0.254 , 0.284	Depositor DCC
R_{free} test set	1701 reflections (5.32%)	DCC
Wilson B-factor (Å^2)	63.4	Xtriage
Anisotropy	0.559	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 63.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 33700 reflections	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	6289	wwPDB-VP
Average B, all atoms (Å^2)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GDD

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	0.35	0/3168	0.53	1/4284 (0.0%)
1	B	0.34	0/3168	0.51	0/4284
All	All	0.35	0/6336	0.52	1/8568 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	3	LEU	CA-CB-CG	5.55	128.07	115.30

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	3101	0	3089	35	0
1	B	3101	0	3089	26	0
2	A	39	0	23	0	0
2	B	39	0	23	0	0
3	A	5	0	0	0	0
3	B	4	0	0	0	0
All	All	6289	0	6224	60	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 (60) 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:191:ASN:HB3	1:A:197:LYS:HG2	1.42	1.01
1:A:259:ARG:HG3	1:A:259:ARG:HH11	1.41	0.84
1:B:200:ASP:O	1:B:204:LEU:HB2	1.92	0.70
1:A:259:ARG:CG	1:A:259:ARG:HH11	2.04	0.69
1:A:77:ILE:HD13	1:A:101:MET:HE3	1.76	0.67
1:A:191:ASN:HB3	1:A:197:LYS:CG	2.23	0.64
1:A:288:LEU:O	1:A:289:CYS:HB2	1.99	0.63
1:A:123:GLU:HG2	1:B:237:LEU:HD22	1.80	0.61
1:B:277:ILE:HB	1:B:300:LEU:HD23	1.83	0.60
1:B:89:ASN:HD22	1:B:90:ASP:H	1.48	0.60
1:B:160:VAL:HG13	1:B:383:ILE:HD11	1.85	0.58
1:A:138:MET:HE1	1:A:383:ILE:HG23	1.85	0.58
1:A:164:VAL:CG2	1:A:292:GLU:HG2	2.35	0.56
1:B:221:LEU:HD22	1:B:256:MET:HB2	1.87	0.56
1:A:4:ILE:HD12	1:A:82:PRO:HG3	1.87	0.56
1:B:203:VAL:HG13	1:B:236:ALA:HB2	1.87	0.55
1:B:26:ARG:HD3	1:B:377:ASP:OD1	2.06	0.54
1:A:89:ASN:HD22	1:A:90:ASP:H	1.54	0.54
1:B:191:ASN:HB3	1:B:197:LYS:HD3	1.90	0.54
1:B:347:VAL:O	1:B:351:THR:HG23	2.08	0.53
1:A:101:MET:O	1:A:104:CYS:HB2	2.10	0.52
1:B:282:SER:HB2	1:B:338:GLU:HB3	1.91	0.52
1:B:203:VAL:HG21	1:B:232:LEU:HB3	1.90	0.52
1:B:4:ILE:HG13	1:B:82:PRO:HB3	1.91	0.52
1:B:69:TYR:CE2	1:B:72:GLY:HA3	2.46	0.50
1:A:19:VAL:HG23	1:A:23:ILE:HD12	1.94	0.50
1:A:263:THR:HG23	1:A:266:ARG:HG3	1.93	0.49
1:A:55:GLN:O	1:A:58:GLU:HB3	2.12	0.49
1:B:34:ILE:HG22	1:B:50:GLU:HB3	1.95	0.49
1:A:26:ARG:HA	1:A:29:LYS:HE2	1.95	0.48
1:A:277:ILE:HG13	1:A:293:GLY:HA3	1.95	0.48
1:B:4:ILE:HG12	1:B:34:ILE:HD11	1.96	0.46
1:B:328:VAL:O	1:B:328:VAL:CG1	2.63	0.46
1:A:375:THR:HG23	1:A:378:ASP:H	1.80	0.46
1:B:164:VAL:HG21	1:B:292:GLU:HG2	1.98	0.45
1:A:203:VAL:HG21	1:A:232:LEU:HB3	1.98	0.45
1:A:164:VAL:HG21	1:A:292:GLU:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:160:VAL:CG1	1:B:383:ILE:HD11	2.46	0.45
1:A:164:VAL:HG21	1:A:292:GLU:HG2	1.98	0.45
1:B:4:ILE:HD12	1:B:82:PRO:HG3	1.99	0.45
1:A:259:ARG:CG	1:A:259:ARG:NH1	2.70	0.44
1:A:290:SER:HB2	1:A:300:LEU:HD13	1.99	0.44
1:B:302:ILE:HG12	1:B:317:VAL:HG11	2.00	0.44
1:A:24:VAL:HB	1:A:25:PRO:HD3	2.00	0.44
1:A:73:LEU:HD22	1:A:97:TYR:CD2	2.53	0.43
1:A:288:LEU:O	1:A:289:CYS:CB	2.65	0.43
1:A:118:SER:HB3	1:A:338:GLU:HG2	2.00	0.43
1:A:392:ARG:HE	1:A:392:ARG:HA	1.83	0.43
1:A:203:VAL:HG13	1:A:236:ALA:HB2	2.01	0.43
1:B:122:ARG:NH2	1:B:332:ASP:O	2.51	0.43
1:B:110:ILE:HD12	1:B:133:LYS:HB2	2.01	0.43
1:B:70:TYR:CE2	1:B:96:ASN:HB2	2.54	0.42
1:A:120:ASN:O	1:A:336:GLY:HA2	2.20	0.42
1:A:362:TYR:O	1:A:366:VAL:HG22	2.20	0.41
1:A:123:GLU:CD	1:A:123:GLU:H	2.23	0.41
1:B:247:ASN:HB3	1:B:250:THR:HG23	2.02	0.41
1:A:221:LEU:HD22	1:A:256:MET:HB2	2.02	0.41
1:A:251:HIS:HA	1:A:254:LYS:HE3	2.02	0.41
1:B:24:VAL:N	1:B:25:PRO:HD2	2.35	0.41
1:A:69:TYR:CE2	1:A:72:GLY:HA3	2.56	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	390/413 (94%)	374 (96%)	14 (4%)	2 (0%)	34 62
1	B	390/413 (94%)	368 (94%)	18 (5%)	4 (1%)	19 43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	780/826 (94%)	742 (95%)	32 (4%)	6 (1%)	24 50

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	228	SER
1	B	290	SER
1	B	313	SER
1	A	289	CYS
1	B	124	ASN
1	B	91	PRO

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	341/361 (94%)	310 (91%)	31 (9%)	12 25
1	B	341/361 (94%)	321 (94%)	20 (6%)	24 49
All	All	682/722 (94%)	631 (92%)	51 (8%)	17 36

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	19	VAL
1	A	33	VAL
1	A	45	VAL
1	A	64	ASN
1	A	89	ASN
1	A	103	LYS
1	A	104	CYS
1	A	114	VAL
1	A	118	SER
1	A	123	GLU
1	A	166	THR

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Mol	Chain	Res	Type
1	A	168	THR
1	A	184	ASP
1	A	188	LEU
1	A	197	LYS
1	A	217	LYS
1	A	259	ARG
1	A	261	VAL
1	A	262	LEU
1	A	263	THR
1	A	265	GLU
1	A	298	LYS
1	A	317	VAL
1	A	328	VAL
1	A	331	ARG
1	A	346	LEU
1	A	355	ASP
1	A	356	GLU
1	A	366	VAL
1	A	384	ILE
1	B	3	LEU
1	B	89	ASN
1	B	103	LYS
1	B	117	VAL
1	B	167	LYS
1	B	168	THR
1	B	180	GLU
1	B	185	VAL
1	B	188	LEU
1	B	198	ARG
1	B	217	LYS
1	B	250	THR
1	B	262	LEU
1	B	298	LYS
1	B	328	VAL
1	B	331	ARG
1	B	332	ASP
1	B	346	LEU
1	B	351	THR
1	B	383	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	ASN
1	A	191	ASN
1	A	226	HIS
1	B	39	HIS
1	B	55	GLN
1	B	89	ASN
1	B	251	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)

2 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	GDD	A	414	-	34,42,42	1.30	4 (11%)	47,65,65	2.00	11 (23%)
2	GDD	B	414	-	34,42,42	1.28	4 (11%)	47,65,65	1.71	9 (19%)

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	414	-	-	0/19/59/59	0/4/4/4
2	GDD	B	414	-	-	0/19/59/59	0/4/4/4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	414	GDD	O51-C11	2.14	1.47	1.41
2	A	414	GDD	O51-C11	2.46	1.48	1.41
2	B	414	GDD	O4'-C1'	2.51	1.44	1.41
2	A	414	GDD	O4'-C1'	2.70	1.44	1.41
2	B	414	GDD	C2-N1	3.12	1.40	1.35
2	A	414	GDD	C2-N1	3.14	1.41	1.35
2	B	414	GDD	C6-N1	4.02	1.40	1.33
2	A	414	GDD	C6-N1	4.06	1.40	1.33

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	414	GDD	C4'-O4'-C1'	-6.12	102.99	109.72
2	B	414	GDD	N3-C2-N1	-4.58	120.47	127.44
2	A	414	GDD	N3-C2-N1	-4.57	120.48	127.44
2	B	414	GDD	PB-O3A-PA	-4.16	121.04	132.73
2	A	414	GDD	C5-C6-N1	-3.65	118.60	123.59
2	B	414	GDD	C5-C6-N1	-3.57	118.71	123.59
2	B	414	GDD	C4'-O4'-C1'	-3.21	106.20	109.72
2	A	414	GDD	PB-O3A-PA	-3.08	124.08	132.73
2	B	414	GDD	C4-C5-N7	-2.70	107.00	109.48
2	A	414	GDD	C4-C5-N7	-2.36	107.31	109.48
2	A	414	GDD	O4'-C1'-N9	2.21	112.72	108.10
2	B	414	GDD	C6-N1-C2	2.29	119.12	115.94
2	A	414	GDD	O3A-PA-O5'	2.36	109.21	102.94
2	A	414	GDD	C6-N1-C2	2.47	119.36	115.94
2	B	414	GDD	O51-C11-C21	2.70	115.82	110.28
2	B	414	GDD	C11-O51-C51	3.21	119.98	113.75
2	B	414	GDD	O51-C51-C41	3.86	116.92	109.68
2	A	414	GDD	C11-O51-C51	3.86	121.25	113.75
2	A	414	GDD	O51-C11-O1B	4.06	116.72	111.36
2	A	414	GDD	O51-C51-C41	5.04	119.15	109.68

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

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, 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	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	392/413 (94%)	0.12	14 (3%) 46 49	46, 68, 108, 136	0
1	B	392/413 (94%)	1.00	83 (21%) 1 1	47, 101, 214, 246	0
All	All	784/826 (94%)	0.56	97 (12%) 5 4	46, 79, 193, 246	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	86	MET	9.8
1	B	109	LYS	7.7
1	B	3	LEU	7.5
1	B	99	LEU	7.4
1	B	84	ILE	7.2
1	A	226	HIS	6.9
1	B	33	VAL	6.8
1	B	97	TYR	6.6
1	B	43	ARG	6.3
1	B	34	ILE	6.2
1	B	56	THR	5.7
1	B	35	VAL	5.5
1	B	36	PHE	5.5
1	B	83	ASP	5.4
1	B	61	ARG	5.3
1	B	44	SER	5.3
1	B	63	LEU	5.2
1	A	227	GLU	5.1
1	B	227	GLU	5.1
1	B	226	HIS	5.1
1	B	27	ILE	5.0
1	B	60	VAL	5.0
1	B	170	TYR	5.0
1	B	20	MET	5.0

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Mol	Chain	Res	Type	RSRZ
1	B	153	CYS	4.6
1	B	45	VAL	4.5
1	B	87	ILE	4.4
1	B	149	CYS	4.4
1	B	103	LYS	4.3
1	B	85	VAL	4.3
1	B	1	MET	4.2
1	B	8	ALA	4.0
1	A	170	TYR	4.0
1	B	51	GLU	3.8
1	B	126	TRP	3.8
1	B	64	ASN	3.7
1	B	104	CYS	3.7
1	B	40	ALA	3.7
1	B	386	PHE	3.5
1	B	46	HIS	3.5
1	B	95	GLY	3.4
1	B	98	LEU	3.4
1	B	133	LYS	3.2
1	B	130	SER	3.1
1	B	4	ILE	3.1
1	B	23	ILE	3.1
1	B	6	VAL	3.1
1	B	390	LEU	3.0
1	B	364	LYS	2.9
1	B	139	ALA	2.9
1	B	49	ILE	2.8
1	B	42	GLY	2.8
1	B	50	GLU	2.8
1	B	21	ARG	2.7
1	B	79	VAL	2.7
1	B	9	HIS	2.7
1	B	24	VAL	2.7
1	B	48	ASN	2.6
1	B	47	ALA	2.6
1	B	57	ALA	2.6
1	A	240	LEU	2.5
1	B	54	ALA	2.5
1	B	183	ASP	2.5
1	A	23	ILE	2.5
1	B	123	GLU	2.5
1	A	1	MET	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	69	TYR	2.5
1	A	245	VAL	2.4
1	B	14	SER	2.4
1	A	392	ARG	2.3
1	B	39	HIS	2.3
1	B	10	SER	2.3
1	B	7	GLY	2.3
1	B	165	ASP	2.3
1	B	152	GLY	2.3
1	B	163	PHE	2.3
1	B	114	VAL	2.3
1	B	2	LYS	2.2
1	B	105	SER	2.2
1	B	178	LEU	2.2
1	B	28	SER	2.2
1	B	52	PHE	2.2
1	B	16	TYR	2.2
1	B	129	PHE	2.1
1	A	261	VAL	2.1
1	B	155	VAL	2.1
1	B	26	ARG	2.1
1	A	255	ILE	2.1
1	B	62	GLY	2.1
1	A	48	ASN	2.1
1	B	314	GLY	2.1
1	B	94	ILE	2.0
1	A	239	GLU	2.0
1	A	246	ASP	2.0
1	B	112	LEU	2.0
1	A	250	THR	2.0
1	B	108	THR	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
2	GDD	A	414	39/39	0.88	0.25	1.36	86,88,90,90	0
2	GDD	B	414	39/39	0.90	0.16	-1.13	99,101,101,101	0

6.5 Other polymers

There are no such residues in this entry.