wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 11:56 AM GMT

PDB ID	:	3QI9
Title	:	Crystal structure of mouse CD1d-alpha-phosphotidylinositol with mouse Valpha14-Vbeta6 2A3-D NKT TCR
Authors	:	Clarke, A.J.; Rossjohn, J.
Deposited on	:	2011-01-26
Resolution	:	2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

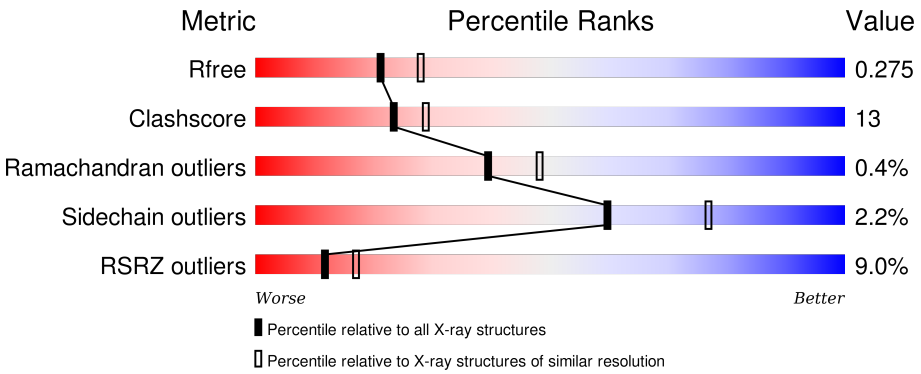
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	302	% 80% 15% • •
2	B	99	3% 88% 12%
3	C	207	19% 80% 13% • 5%
4	D	243	12% 83% 14% • •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	PII	A	405	-	-	-	X
9	GOL	D	300	-	-	-	X

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 6863 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 Antigen-presenting glycoprotein CD1d1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	290	2333	1486	406	427	14	6	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	HIS	ASP	SEE REMARK 999	UNP P11609
A	280	GLY	-	EXPRESSION TAG	UNP P11609
A	281	SER	-	EXPRESSION TAG	UNP P11609
A	282	LEU	-	EXPRESSION TAG	UNP P11609
A	283	HIS	-	EXPRESSION TAG	UNP P11609
A	284	HIS	-	EXPRESSION TAG	UNP P11609
A	285	ILE	-	EXPRESSION TAG	UNP P11609
A	286	LEU	-	EXPRESSION TAG	UNP P11609
A	287	ASP	-	EXPRESSION TAG	UNP P11609
A	288	ALA	-	EXPRESSION TAG	UNP P11609
A	289	GLN	-	EXPRESSION TAG	UNP P11609
A	290	LYS	-	EXPRESSION TAG	UNP P11609
A	291	MET	-	EXPRESSION TAG	UNP P11609
A	292	VAL	-	EXPRESSION TAG	UNP P11609
A	293	TRP	-	EXPRESSION TAG	UNP P11609
A	294	ASN	-	EXPRESSION TAG	UNP P11609
A	295	HIS	-	EXPRESSION TAG	UNP P11609
A	296	ARG	-	EXPRESSION TAG	UNP P11609
A	297	HIS	-	EXPRESSION TAG	UNP P11609
A	298	HIS	-	EXPRESSION TAG	UNP P11609
A	299	HIS	-	EXPRESSION TAG	UNP P11609
A	300	HIS	-	EXPRESSION TAG	UNP P11609
A	301	HIS	-	EXPRESSION TAG	UNP P11609
A	302	HIS	-	EXPRESSION TAG	UNP P11609

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	99	814	520	138	149	7	1	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	85	ALA	ASP	SEE REMARK 999	UNP P01887

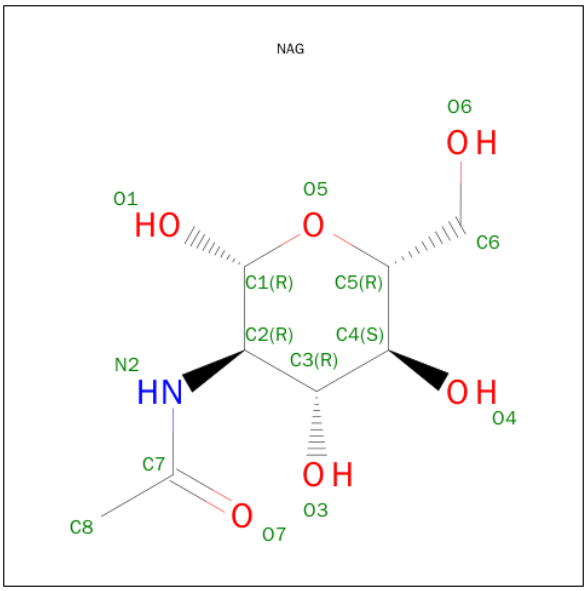
- Molecule 3 is a protein called NKT TCR V alpha 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	196	1514	938	260	309	7	3	0	0

- Molecule 4 is a protein called NKT TCR V beta 6 2A3-D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	239	1897	1201	326	363	7	5	0	0

- Molecule 5 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	14	8	1	5	0	0

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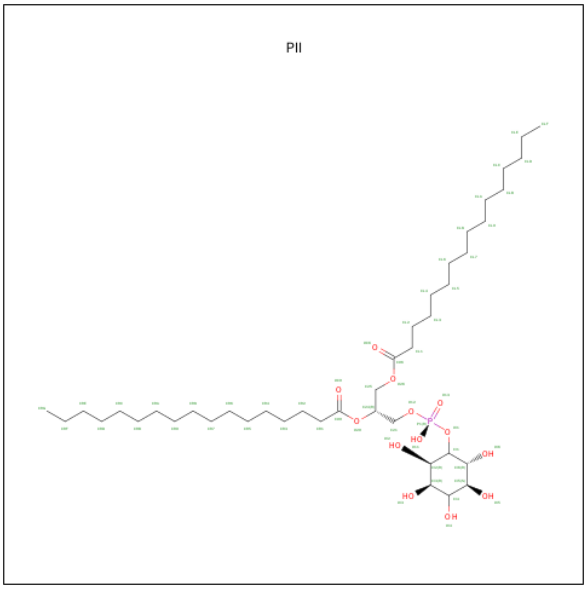
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	14	8	1	5	0	0

- Molecule 6 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
6	A	2	28	16	2	10	0	0

- Molecule 7 is 2-[(HYDROXY{[(2R,3R,5S,6R)-2,3,4,5,6-PENTAHYDROXYCYCLOHEXYL]OXY}PHOSPHORYL)OXY]-1-[(PALMITOYLOXY)METHYL]ETHYL HEPTADECANOATE (three-letter code: PII) (formula: $C_{42}H_{81}O_{13}P$).

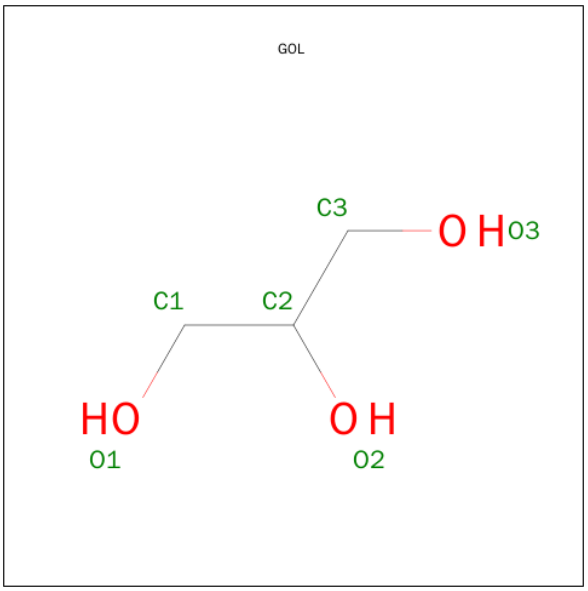


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
7	A	1	56	42	13	1	0	0

- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 9 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 10 is water.

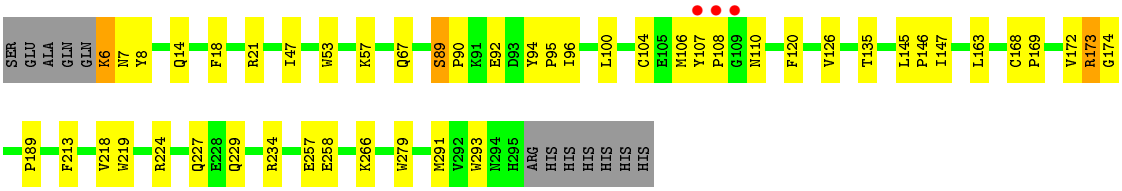
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
10	A	68	68	68	0	0
			Total	O		
10	B	26	26	26	0	0
			Total	O		
10	C	38	38	38	0	0
			Total	O		
10	D	48	48	48	0	0

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 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.

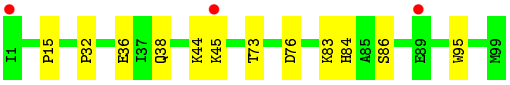
- Molecule 1: Antigen-presenting glycoprotein CD1d1

Chain A:



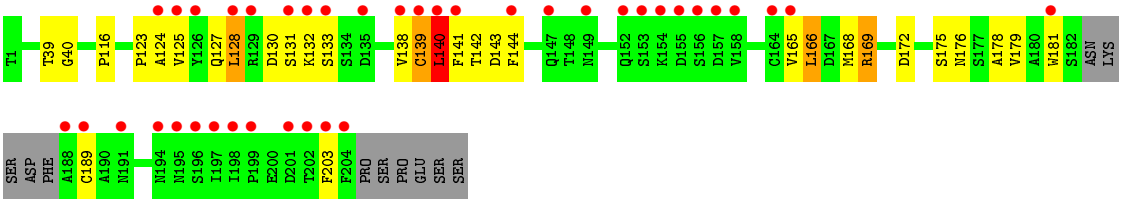
- Molecule 2: Beta-2-microglobulin

Chain B:



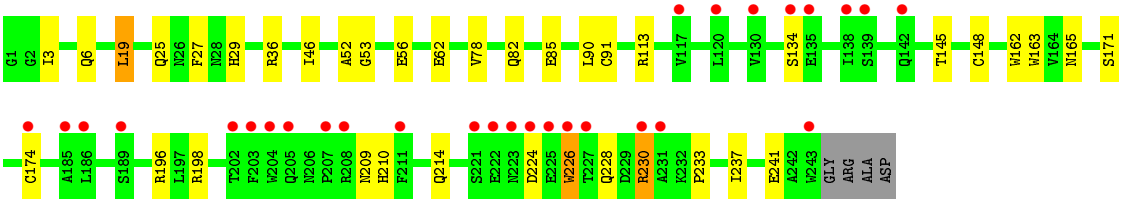
- Molecule 3: NKT TCR V alpha 14

Chain C:



- Molecule 4: NKT TCR V beta 6 2A3-D

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	95.70Å 95.70Å 289.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.31 – 2.30 39.30 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.31-2.30) 100.0 (39.30-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.10 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.247 , 0.275 0.249 , 0.275	Depositor DCC
R_{free} test set	3082 reflections (5.34%)	DCC
Wilson B-factor (Å^2)	47.6	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 30.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Outliers	0 of 60849 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6863	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.44% 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 (i)

5.1 Standard geometry (i)

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

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	0.66	2/2403 (0.1%)	0.53	0/3266
2	B	0.50	1/840 (0.1%)	0.50	0/1140
3	C	0.44	0/1539	0.49	0/2089
4	D	0.49	1/1944 (0.1%)	0.51	0/2636
All	All	0.55	4/6726 (0.1%)	0.51	0/9131

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	293	TRP	CD2-CE2	5.18	1.47	1.41
1	A	53	TRP	CD2-CE2	5.16	1.47	1.41
4	D	163	TRP	CD2-CE2	5.08	1.47	1.41
2	B	95	TRP	CD2-CE2	5.04	1.47	1.41

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	2333	0	2232	39	0
2	B	814	0	788	13	1
3	C	1514	0	1466	99	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1897	0	1830	45	0
5	A	28	0	26	0	0
6	A	28	0	25	0	0
7	A	56	0	80	2	0
8	A	1	0	0	0	0
9	B	6	0	8	0	0
9	D	6	0	8	0	0
10	A	68	0	0	1	0
10	B	26	0	0	0	0
10	C	38	0	0	0	0
10	D	48	0	0	0	0
All	All	6863	0	6463	174	1

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 13.

The worst 5 of 174 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)
3:C:141:PHE:CZ	3:C:144:PHE:HB3	1.40	1.56
3:C:168:MET:CE	4:D:198:ARG:HG2	1.31	1.54
3:C:40:GLY:CA	4:D:113:ARG:NH2	1.68	1.52
3:C:141:PHE:CE2	3:C:144:PHE:CD1	2.15	1.32
3:C:168:MET:HE1	4:D:198:ARG:CG	1.59	1.32

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:44:LYS:NZ	3:C:133:SER:OG[6_534]	1.89	0.31

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	288/302 (95%)	282 (98%)	5 (2%)	1 (0%)	46	57
2	B	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
3	C	192/207 (93%)	181 (94%)	9 (5%)	2 (1%)	19	21
4	D	237/243 (98%)	229 (97%)	8 (3%)	0	100	100
All	All	814/851 (96%)	787 (97%)	24 (3%)	3 (0%)	39	48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	89	SER
3	C	140	LEU
3	C	130	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	253/264 (96%)	251 (99%)	2 (1%)	86	94
2	B	92/93 (99%)	92 (100%)	0	100	100
3	C	175/186 (94%)	169 (97%)	6 (3%)	44	59
4	D	206/208 (99%)	198 (96%)	8 (4%)	39	53
All	All	726/751 (97%)	710 (98%)	16 (2%)	60	77

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	169	ARG
4	D	3	ILE
4	D	226	TRP
3	C	166	LEU
4	D	228	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	38	GLN
2	B	84	HIS
4	D	165	ASN
2	B	29	GLN
4	D	178	GLN

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)

2 carbohydrates 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	$\#\|Z\| > 2$
6	NAG	A	403	1,6	14,14,15	0.52	0	15,19,21	1.09	2 (13%)
6	NAG	A	404	6	14,14,15	0.61	0	15,19,21	1.09	1 (6%)

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
6	NAG	A	403	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	404	6	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	403	NAG	O4-C4-C3	-2.68	104.30	110.34
6	A	403	NAG	C4-C3-C2	2.32	114.83	111.23
6	A	404	NAG	C4-C3-C2	2.45	115.03	111.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	$\#\|Z\| > 2$
5	NAG	A	401	1	14,14,15	0.42	0	15,19,21	1.59	1 (6%)
5	NAG	A	402	1	14,14,15	0.43	0	15,19,21	1.21	1 (6%)
7	PII	A	405	-	56,56,56	2.07	3 (5%)	64,68,68	2.29	9 (14%)
9	GOL	B	100	-	5,5,5	0.22	0	5,5,5	0.31	0
9	GOL	D	300	-	5,5,5	0.24	0	5,5,5	0.19	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	Res	Link	Chirals	Torsions	Rings
5	NAG	A	401	1	-	0/6/23/26	0/1/1/1
5	NAG	A	402	1	-	0/6/23/26	0/1/1/1
7	PII	A	405	-	-	0/51/75/75	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	GOL	B	100	-	-	0/4/4/4	0/0/0/0
9	GOL	D	300	-	-	0/4/4/4	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	405	PII	C21-C24	-6.54	1.32	1.50
7	A	405	PII	C25-C24	3.13	1.59	1.50
7	A	405	PII	OC9-CO9	12.84	1.61	1.22

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	A	405	PII	O29-CO9-OC9	-10.34	95.91	123.67
7	A	405	PII	C25-C24-C21	-8.96	91.11	112.07
7	A	405	PII	OC9-CO9-CR1	-3.12	111.25	123.72
7	A	405	PII	O29-C24-C25	2.32	116.55	108.36
7	A	405	PII	O26-CO6-CL1	2.35	119.06	111.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	405	PII	2	0

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	290/302 (96%)	0.32	3 (1%)	84	88	33, 45, 59, 82	5 (1%)
2	B	99/99 (100%)	0.36	3 (3%)	54	63	34, 46, 61, 73	1 (1%)
3	C	196/207 (94%)	0.99	39 (19%)	1	2	29, 49, 113, 124	2 (1%)
4	D	239/243 (98%)	0.89	29 (12%)	6	9	31, 63, 94, 103	3 (1%)
All	All	824/851 (96%)	0.65	74 (8%)	12	17	29, 48, 96, 124	11 (1%)

The worst 5 of 74 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	141	PHE	9.8
3	C	140	LEU	7.1
3	C	133	SER	6.2
3	C	132	LYS	5.9
4	D	211	PHE	5.5

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)

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, 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	LLDF	B-factors(Å^2)	Q<0.9
6	NAG	A	404	14/15	0.78	0.19	-	71,74,79,81	0
6	NAG	A	403	14/15	0.91	0.15	-	56,58,62,67	0

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. 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, 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	LLDF	B-factors(Å^2)	Q<0.9
9	GOL	D	300	6/6	0.74	0.33	5.23	70,76,77,77	0
7	PII	A	405	56/56	0.85	0.25	3.26	45,57,64,66	11
9	GOL	B	100	6/6	0.68	0.22	1.84	66,67,69,70	0
5	NAG	A	402	14/15	0.91	0.15	0.21	51,53,55,55	0
5	NAG	A	401	14/15	0.71	0.39	-	52,54,55,55	0
8	MG	A	406	1/1	0.89	0.26	-	62,62,62,62	0

6.5 Other polymers (i)

There are no such residues in this entry.