



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 10:27 PM GMT

PDB ID : 5CPY
Title : Crystal structure of murine polyomavirus PTA strain VP1 in complex with the GD1a glycan
Authors : Liaci, A.M.; Buch, M.H.C.; Neu, U.; Stehle, T.
Deposited on : 2015-07-21
Resolution : 1.93 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

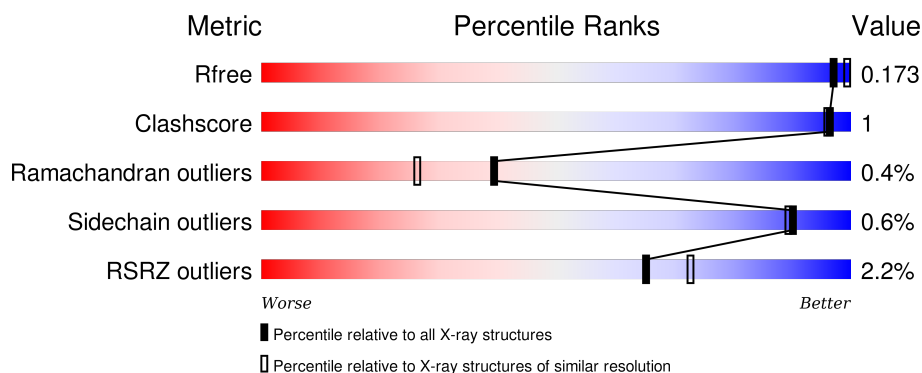
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.93 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	2910 (1.96-1.92)
Clashscore	102246	3095 (1.96-1.92)
Ramachandran outliers	100387	3062 (1.96-1.92)
Sidechain outliers	100360	3062 (1.96-1.92)
RSRZ outliers	91569	2915 (1.96-1.92)

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 $\leq 5\%$. 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	284	<div> <div>2%</div> <div>95%</div> <div>••</div> </div>
1	B	284	<div> <div>4%</div> <div>93%</div> <div>5% •</div> </div>
1	C	284	<div> <div>3%</div> <div>94%</div> <div>••</div> </div>
1	D	284	<div> <div>%</div> <div>96%</div> <div>•</div> </div>
1	E	284	<div> <div>%</div> <div>93%</div> <div>••</div> </div>

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
2	GOL	A	401	-	-	-	X
2	GOL	A	406	-	-	-	X
2	GOL	B	406	-	-	-	X
2	GOL	C	405	-	-	-	X
2	GOL	D	401	-	-	-	X
2	GOL	D	406	-	-	-	X
2	GOL	D	407	-	-	-	X
2	GOL	E	405	-	-	-	X
4	GAL	B	403	-	-	-	X
4	GAL	C	402	-	-	-	X

2 Entry composition [i](#)

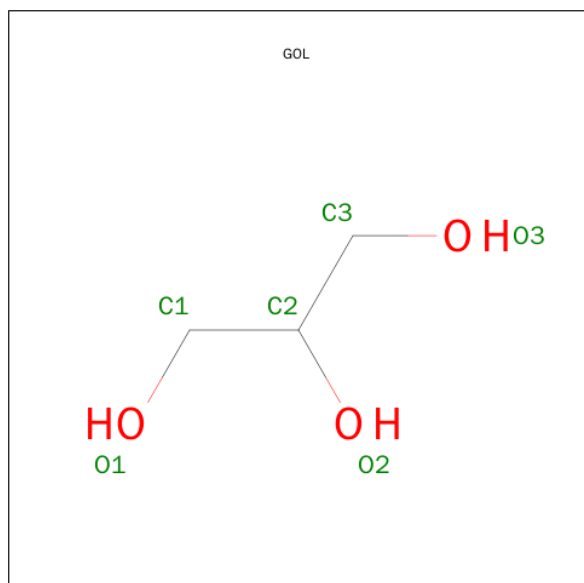
There are 6 unique types of molecules in this entry. The entry contains 13319 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	278	Total	C	N	O	S	0	11	0
			2229	1422	373	425	9			
1	B	278	Total	C	N	O	S	0	8	0
			2227	1415	374	430	8			
1	C	278	Total	C	N	O	S	0	7	0
			2215	1414	369	424	8			
1	D	283	Total	C	N	O	S	0	7	0
			2255	1431	375	436	13			
1	E	278	Total	C	N	O	S	0	9	0
			2224	1416	375	425	8			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



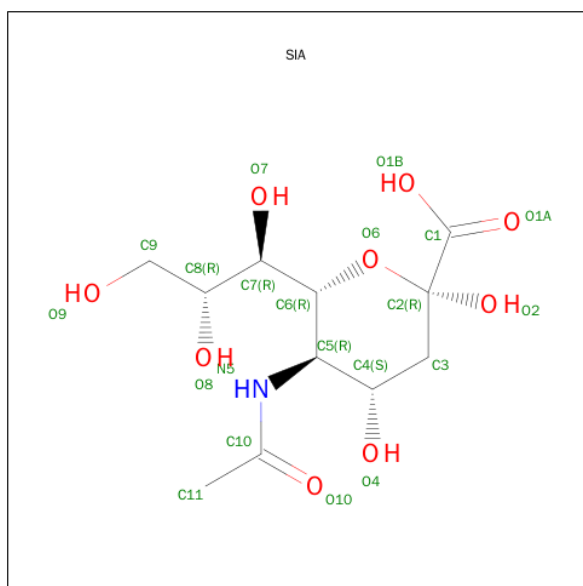
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		
2	E	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is O-SIALIC ACID (three-letter code: SIA) (formula: C₁₁H₁₉NO₉).



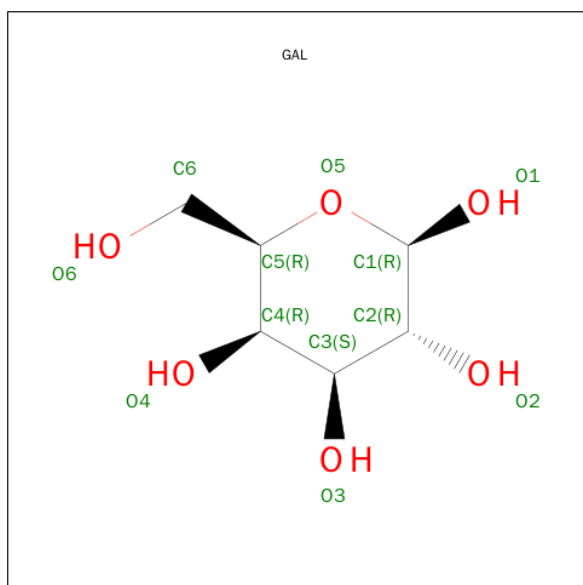
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			20	11	1	8		
3	B	1	Total	C	N	O	0	0
			20	11	1	8		
3	C	1	Total	C	N	O	0	0
			20	11	1	8		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			20	11	1	8		
3	E	1	Total	C	N	O	0	0
			20	11	1	8		

- Molecule 4 is BETA-D-GALACTOSE (three-letter code: GAL) (formula: C₆H₁₂O₆).



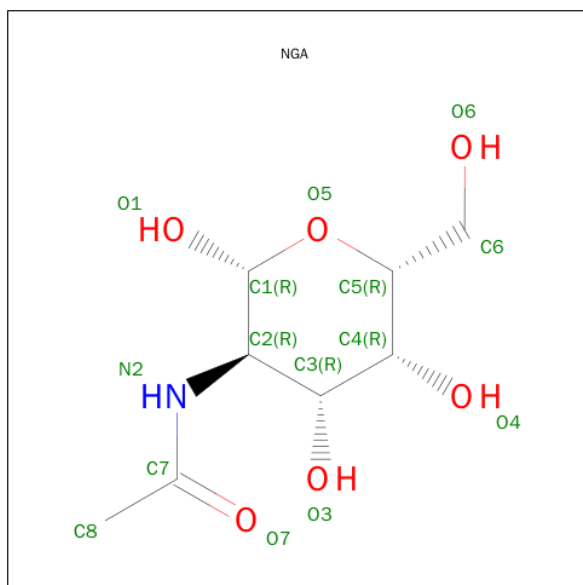
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			12	6	6		
4	B	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			12	6	6		
4	C	1	Total	C	O	0	0
			11	6	5		
4	C	1	Total	C	O	0	0
			12	6	6		
4	D	1	Total	C	O	0	0
			11	6	5		
4	D	1	Total	C	O	0	0
			12	6	6		
4	E	1	Total	C	O	0	0
			11	6	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	C	O	0	0
			12	6	6		

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



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	368	Total	O	0	0
			368	368		
6	B	331	Total	O	0	0
			331	331		
6	C	362	Total	O	0	0
			362	362		

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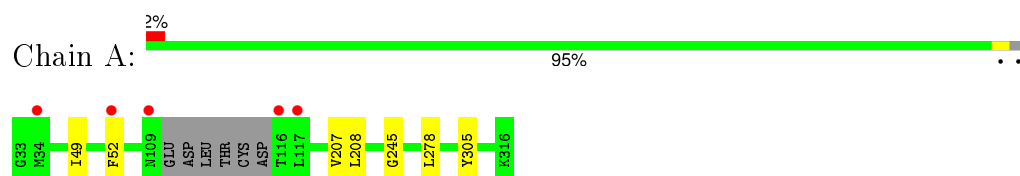
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	398	Total 398	O 398	0	0
6	E	387	Total 387	O 387	0	0

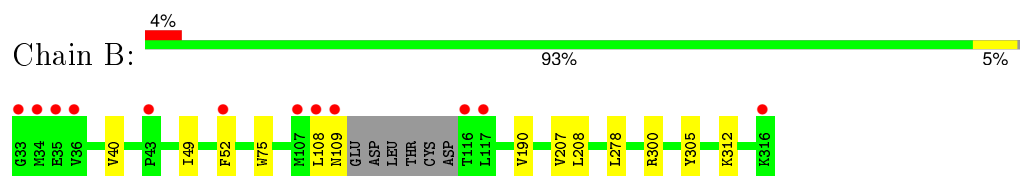
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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.

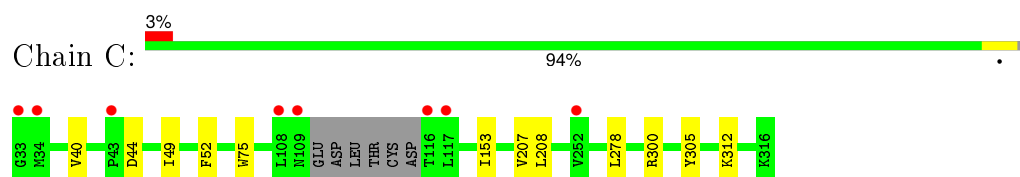
- Molecule 1: VP1



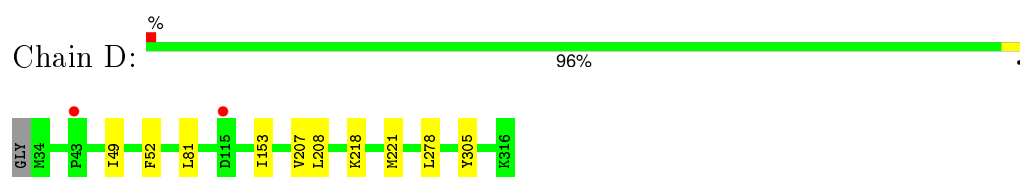
- Molecule 1: VP1



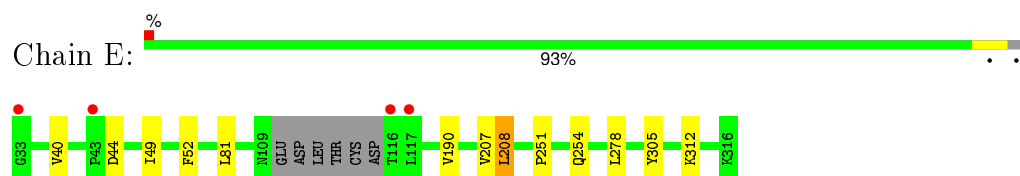
- Molecule 1: VP1



- Molecule 1: VP1



- Molecule 1: VP1



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	220.45Å 220.45Å 99.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.77 – 1.93 47.73 – 1.93	Depositor EDS
% Data completeness (in resolution range)	95.4 (47.77-1.93) 95.4 (47.73-1.93)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 1.92Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.153 , 0.174 0.152 , 0.173	Depositor DCC
R_{free} test set	5954 reflections (3.10%)	DCC
Wilson B-factor (Å ²)	19.1	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.3	EDS
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 198281 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13319	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% 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, 0.375 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, SIA, GAL, NGA

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	0/2310	0.53	0/3146
1	B	0.33	0/2295	0.52	0/3124
1	C	0.33	0/2295	0.52	0/3129
1	D	0.35	0/2330	0.53	0/3173
1	E	0.36	0/2299	0.53	0/3132
All	All	0.34	0/11529	0.52	0/15704

There are no bond length outliers.

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	2229	0	2218	4	0
1	B	2227	0	2200	6	0
1	C	2215	0	2207	9	0
1	D	2255	0	2234	8	0
1	E	2224	0	2207	10	0
2	A	8	0	7	0	0
2	B	8	0	8	0	0
2	C	4	0	3	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	14	0	15	0	0
2	E	4	0	4	0	0
3	A	20	0	17	0	0
3	B	20	0	17	0	0
3	C	20	0	17	0	0
3	D	20	0	17	0	0
3	E	20	0	17	0	0
4	A	23	0	20	0	0
4	B	23	0	20	0	0
4	C	23	0	20	0	0
4	D	23	0	20	0	0
4	E	23	0	20	0	0
5	A	14	0	12	0	0
5	B	14	0	12	0	0
5	C	14	0	12	0	0
5	D	14	0	12	0	0
5	E	14	0	12	0	0
6	A	368	0	0	0	0
6	B	331	0	0	0	0
6	C	362	0	0	2	0
6	D	398	0	0	0	0
6	E	387	0	0	1	0
All	All	13319	0	11348	32	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 1.

The worst 5 of 32 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:C:52[B]:PHE:CE2	6:C:706:HOH:O	2.14	1.01
1:E:49:ILE:HD11	1:E:278:LEU:HD23	1.73	0.71
1:C:52[B]:PHE:CD2	6:C:706:HOH:O	2.38	0.70
1:A:49:ILE:HD11	1:A:278:LEU:HD23	1.74	0.70
1:B:49:ILE:HD11	1:B:278:LEU:HD23	1.78	0.66

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	284/284 (100%)	276 (97%)	7 (2%)	1 (0%)	39	26
1	B	281/284 (99%)	274 (98%)	6 (2%)	1 (0%)	39	26
1	C	283/284 (100%)	275 (97%)	7 (2%)	1 (0%)	39	26
1	D	288/284 (101%)	278 (96%)	9 (3%)	1 (0%)	46	35
1	E	282/284 (99%)	274 (97%)	7 (2%)	1 (0%)	39	26
All	All	1418/1420 (100%)	1377 (97%)	36 (2%)	5 (0%)	39	26

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	207	VAL
1	A	207	VAL
1	B	207	VAL
1	C	207	VAL
1	E	207	VAL

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	251/250 (100%)	250 (100%)	1 (0%)	93	93
1	B	250/250 (100%)	248 (99%)	2 (1%)	86	85
1	C	250/250 (100%)	249 (100%)	1 (0%)	93	93
1	D	256/250 (102%)	255 (100%)	1 (0%)	93	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	250/250 (100%)	248 (99%)	2 (1%)	86	85
All	All	1257/1250 (101%)	1250 (99%)	7 (1%)	90	89

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	208	LEU
1	E	208	LEU
1	D	208	LEU
1	B	190	VAL
1	E	190	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	293	ASN

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](#)

29 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	GOL	A	401	-	3,3,5	0.49	0	2,2,5	0.29	0
3	SIA	A	402	4	17,20,21	0.36	0	18,28,31	0.72	0
4	GAL	A	403	3,5	11,11,12	0.45	0	15,15,17	0.70	0
5	NGA	A	404	4	14,14,15	0.35	0	15,19,21	0.61	0
4	GAL	A	405	5	12,12,12	0.46	0	17,17,17	0.83	1 (5%)
2	GOL	A	406	-	3,3,5	0.42	0	2,2,5	0.44	0
2	GOL	B	401	-	3,3,5	0.46	0	2,2,5	0.37	0
3	SIA	B	402	4	17,20,21	0.34	0	18,28,31	0.63	0
4	GAL	B	403	3,5	11,11,12	0.54	0	15,15,17	0.70	0
5	NGA	B	404	4	14,14,15	0.36	0	15,19,21	0.52	0
4	GAL	B	405	5	12,12,12	0.49	0	17,17,17	0.72	1 (5%)
2	GOL	B	406	-	3,3,5	0.43	0	2,2,5	0.46	0
3	SIA	C	401	4	17,20,21	0.43	0	18,28,31	0.63	0
4	GAL	C	402	3,5	11,11,12	0.62	0	15,15,17	0.57	0
5	NGA	C	403	4	14,14,15	0.41	0	15,19,21	0.59	0
4	GAL	C	404	5	12,12,12	0.49	0	17,17,17	0.52	0
2	GOL	C	405	-	3,3,5	0.43	0	2,2,5	0.42	0
2	GOL	D	401	-	5,5,5	0.28	0	5,5,5	0.22	0
3	SIA	D	402	4	17,20,21	0.33	0	18,28,31	0.69	0
4	GAL	D	403	3,5	11,11,12	0.47	0	15,15,17	0.61	0
5	NGA	D	404	4	14,14,15	0.35	0	15,19,21	0.58	0
4	GAL	D	405	5	12,12,12	0.47	0	17,17,17	0.84	1 (5%)
2	GOL	D	406	-	3,3,5	0.39	0	2,2,5	0.47	0
2	GOL	D	407	-	3,3,5	0.47	0	2,2,5	0.30	0
3	SIA	E	401	4	17,20,21	0.33	0	18,28,31	0.81	1 (5%)
4	GAL	E	402	3,5	11,11,12	0.57	0	15,15,17	0.66	0
5	NGA	E	403	4	14,14,15	0.35	0	15,19,21	0.60	0
4	GAL	E	404	5	12,12,12	0.47	0	17,17,17	0.74	0
2	GOL	E	405	-	3,3,5	0.41	0	2,2,5	0.49	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
2	GOL	A	401	-	-	0/1/1/4	0/0/0/0
3	SIA	A	402	4	-	0/14/34/38	0/1/1/1
4	GAL	A	403	3,5	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NGA	A	404	4	-	0/6/23/26	0/1/1/1
4	GAL	A	405	5	-	0/2/22/22	0/1/1/1
2	GOL	A	406	-	-	0/1/1/4	0/0/0/0
2	GOL	B	401	-	-	0/1/1/4	0/0/0/0
3	SIA	B	402	4	-	0/14/34/38	0/1/1/1
4	GAL	B	403	3,5	-	0/2/19/22	0/1/1/1
5	NGA	B	404	4	-	0/6/23/26	0/1/1/1
4	GAL	B	405	5	-	0/2/22/22	0/1/1/1
2	GOL	B	406	-	-	0/1/1/4	0/0/0/0
3	SIA	C	401	4	-	0/14/34/38	0/1/1/1
4	GAL	C	402	3,5	-	0/2/19/22	0/1/1/1
5	NGA	C	403	4	-	0/6/23/26	0/1/1/1
4	GAL	C	404	5	-	0/2/22/22	0/1/1/1
2	GOL	C	405	-	-	0/1/1/4	0/0/0/0
2	GOL	D	401	-	-	0/4/4/4	0/0/0/0
3	SIA	D	402	4	-	0/14/34/38	0/1/1/1
4	GAL	D	403	3,5	-	0/2/19/22	0/1/1/1
5	NGA	D	404	4	-	0/6/23/26	0/1/1/1
4	GAL	D	405	5	-	0/2/22/22	0/1/1/1
2	GOL	D	406	-	-	0/1/1/4	0/0/0/0
2	GOL	D	407	-	-	0/1/1/4	0/0/0/0
3	SIA	E	401	4	-	0/14/34/38	0/1/1/1
4	GAL	E	402	3,5	-	0/2/19/22	0/1/1/1
5	NGA	E	403	4	-	0/6/23/26	0/1/1/1
4	GAL	E	404	5	-	0/2/22/22	0/1/1/1
2	GOL	E	405	-	-	0/1/1/4	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	405	GAL	C3-C4-C5	-2.20	106.30	110.23
4	D	405	GAL	C3-C4-C5	-2.09	106.50	110.23
3	E	401	SIA	O9-C9-C8	-2.05	106.53	111.07
4	B	405	GAL	O5-C5-C6	2.11	111.85	106.38

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 [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	278/284 (97%)	-0.48	5 (1%) 71 78	11, 17, 39, 66	0
1	B	278/284 (97%)	-0.32	12 (4%) 39 48	14, 20, 40, 66	0
1	C	278/284 (97%)	-0.29	8 (2%) 55 63	13, 20, 44, 69	0
1	D	283/284 (99%)	-0.51	2 (0%) 89 92	12, 17, 33, 62	0
1	E	278/284 (97%)	-0.48	4 (1%) 78 83	11, 17, 40, 68	0
All	All	1395/1420 (98%)	-0.42	31 (2%) 65 73	11, 18, 40, 69	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	34	MET	5.2
1	A	34	MET	4.0
1	C	116	THR	4.0
1	E	116	THR	4.0
1	C	117	LEU	3.9

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. 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
2	GOL	A	401	4/6	0.82	0.16	10.17	38,41,41,51	0
2	GOL	D	407	4/6	0.76	0.33	7.75	39,43,47,55	0
2	GOL	D	401	6/6	0.83	0.20	5.96	40,46,57,59	0
4	GAL	C	402	11/12	0.95	0.14	4.70	19,22,30,30	0
2	GOL	C	405	4/6	0.90	0.25	4.57	43,44,49,67	0
2	GOL	B	406	4/6	0.90	0.22	4.41	42,49,58,61	0
2	GOL	D	406	4/6	0.93	0.24	4.09	33,39,43,44	0
2	GOL	E	405	4/6	0.90	0.25	3.32	43,47,49,49	0
2	GOL	A	406	4/6	0.90	0.16	2.68	42,51,52,58	0
4	GAL	B	403	11/12	0.97	0.10	2.44	19,24,30,30	0
2	GOL	B	401	4/6	0.95	0.30	1.76	32,37,56,58	0
3	SIA	C	401	20/21	0.96	0.12	1.62	17,23,33,55	0
4	GAL	E	402	11/12	0.98	0.08	1.52	16,20,22,24	0
3	SIA	A	402	20/21	0.97	0.10	0.81	15,18,29,37	0
4	GAL	D	403	11/12	0.98	0.07	0.51	17,19,21,23	0
3	SIA	B	402	20/21	0.97	0.10	0.11	20,24,37,52	0
3	SIA	D	402	20/21	0.97	0.07	-0.35	16,20,34,55	0
3	SIA	E	401	20/21	0.97	0.07	-0.56	14,19,25,44	0
4	GAL	A	403	11/12	0.98	0.06	-2.45	16,21,21,25	0
4	GAL	A	405	12/12	0.85	0.18	-	45,57,68,75	0
5	NGA	D	404	14/15	0.95	0.14	-	23,38,47,47	0
5	NGA	C	403	14/15	0.94	0.27	-	30,44,54,56	0
4	GAL	B	405	12/12	0.83	0.29	-	56,63,69,72	0
4	GAL	D	405	12/12	0.85	0.21	-	49,61,68,71	0
5	NGA	E	403	14/15	0.95	0.15	-	25,37,41,45	0
4	GAL	E	404	12/12	0.89	0.18	-	43,48,53,66	0
4	GAL	C	404	12/12	0.82	0.30	-	51,64,69,77	0
5	NGA	A	404	14/15	0.96	0.12	-	27,38,47,87	0
5	NGA	B	404	14/15	0.93	0.26	-	30,42,50,53	0

6.5 Other polymers ⓘ

There are no such residues in this entry.