



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 12:41 pm GMT

PDB ID : 2Z4T
Title : Crystal Structure of Vibrionaceae Photobacterium sp. JT-ISH-224 2,6-sialyltransferase in a Ternary Complex with Donor Product CMP and Acceptor Substrate Lactose
Authors : Kakuta, Y.; Okino, N.; Kajiwara, H.; Ichikawa, M.; Takakura, Y.; Ito, M.; Yamamoto, T.
Deposited on : 2007-06-25
Resolution : 2.50 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

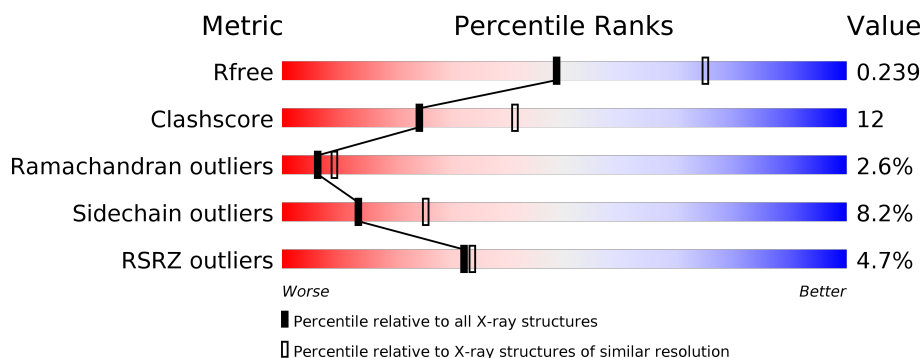
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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	514	<div> <div>4%</div> <div>71%</div> <div>18%</div> <div>6%</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
6	GOL	A	3000	-	-	-	X
6	GOL	A	3002	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	GOL	A	3003	-	-	-	X

2 Entry composition [i](#)

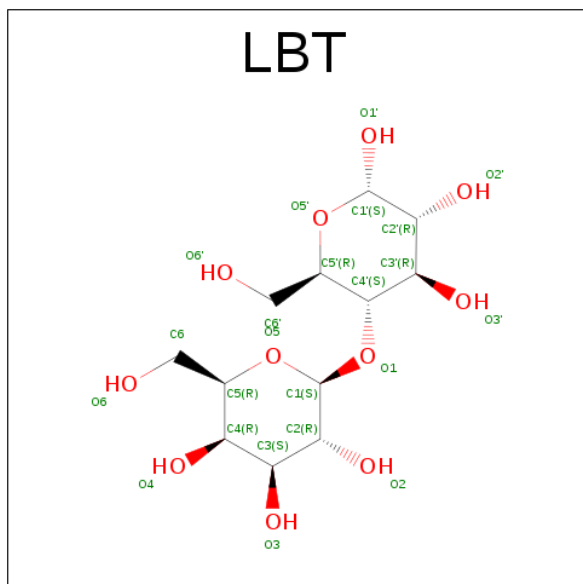
There are 7 unique types of molecules in this entry. The entry contains 4393 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Beta-galactoside alpha-2,6-sialyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	493	Total	C	N	O	S	2	10	0
			4025	2564	664	784	13			

- Molecule 2 is SUGAR (LACTOSE) (three-letter code: LBT) (formula: C₁₂H₂₂O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			23	12	11		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).

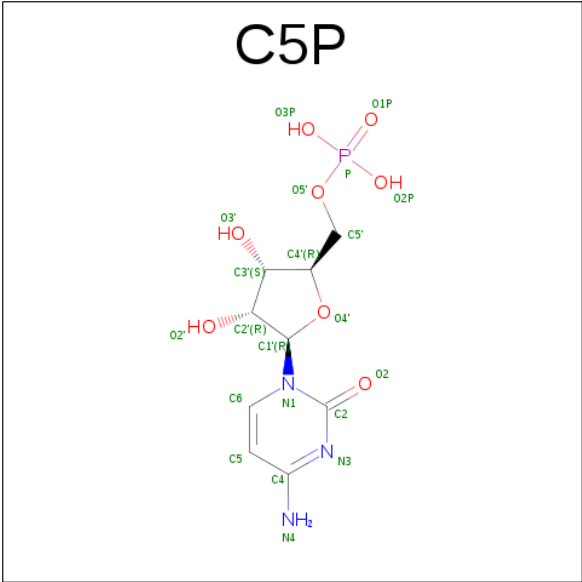


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

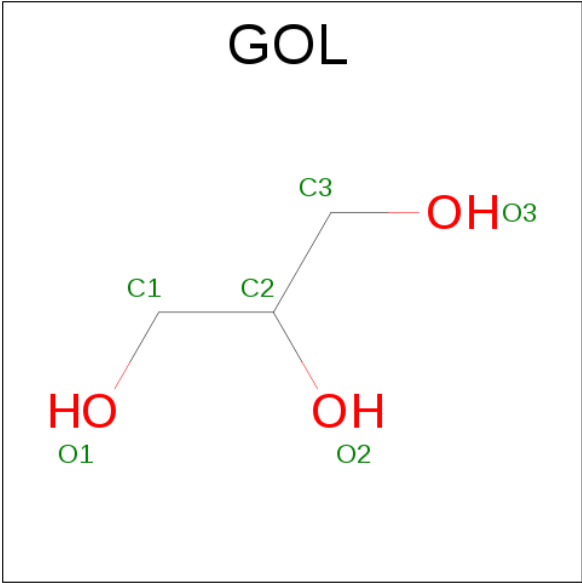
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Mg	0	0
			3	3		

- Molecule 5 is CYTIDINE-5'-MONOPHOSPHATE (three-letter code: C5P) (formula: C₉H₁₄N₃O₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			21	9	3	8	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		

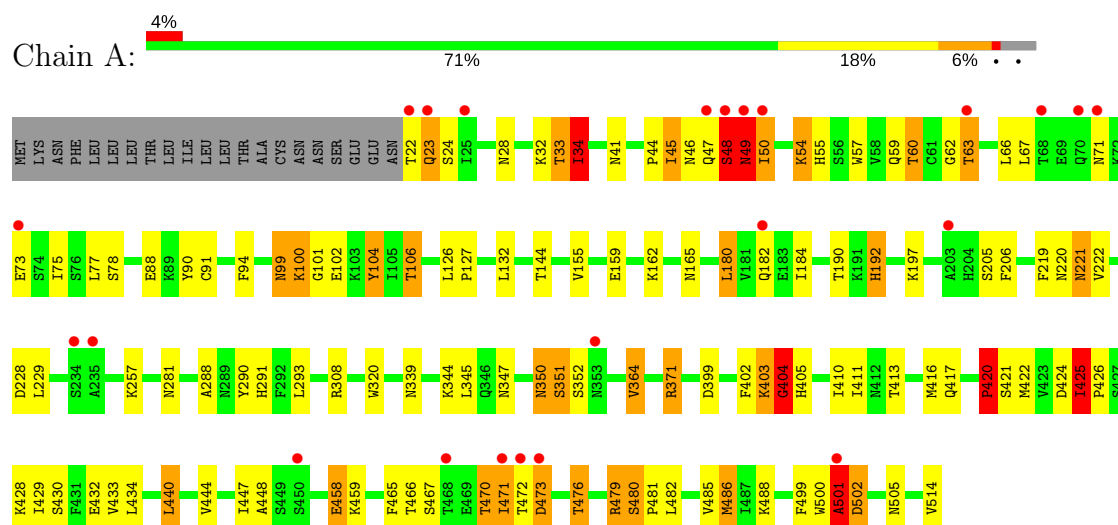
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	281	Total	O	0	0
			281	281		

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.

- Molecule 1: Beta-galactoside alpha-2,6-sialyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	90.29Å 90.29Å 204.33Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.31 – 2.50 41.29 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (41.31-2.50) 99.8 (41.29-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.32 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.192 , 0.243 0.190 , 0.239	Depositor DCC
R_{free} test set	1727 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	37.9	Xtriage
Anisotropy	0.326	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 35.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4393	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: PO4, GOL, MG, LBT, C5P

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	0.73	3/4136 (0.1%)	1.04	23/5622 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	11

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	104	TYR	CD1-CE1	-18.32	1.11	1.39
1	A	192[A]	HIS	CG-CD2	-12.60	1.14	1.35
1	A	192[B]	HIS	CG-CD2	-12.60	1.14	1.35

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	104	TYR	CG-CD1-CE1	30.67	145.84	121.30
1	A	104	TYR	CB-CG-CD1	24.38	135.63	121.00
1	A	104	TYR	CD1-CE1-CZ	-12.97	108.13	119.80
1	A	104	TYR	CD1-CG-CD2	-12.40	104.26	117.90
1	A	206	PHE	N-CA-C	-8.49	88.06	111.00
1	A	486	MET	N-CA-C	-7.84	89.83	111.00
1	A	350	ASN	N-CA-C	7.83	132.13	111.00
1	A	33	THR	C-N-CA	6.88	138.91	121.70
1	A	501[A]	ALA	N-CA-C	6.88	129.58	111.00
1	A	501[B]	ALA	N-CA-C	6.88	129.58	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	350	ASN	C-N-CA	6.39	137.67	121.70
1	A	192[A]	HIS	CG-CD2-NE2	6.38	121.32	109.20
1	A	192[B]	HIS	CG-CD2-NE2	6.38	121.32	109.20
1	A	404	GLY	N-CA-C	-6.12	97.80	113.10
1	A	49	ASN	N-CA-C	6.04	127.29	111.00
1	A	54	LYS	N-CA-C	-5.82	95.30	111.00
1	A	420	PRO	C-N-CA	5.72	136.00	121.70
1	A	34	ILE	N-CA-CB	5.62	123.73	110.80
1	A	425	ILE	N-CA-C	5.60	126.11	111.00
1	A	501[A]	ALA	C-N-CA	5.27	134.87	121.70
1	A	501[B]	ALA	C-N-CA	5.27	134.87	121.70
1	A	55	HIS	N-CA-CB	-5.25	101.15	110.60
1	A	364	VAL	CB-CA-C	-5.06	101.78	111.40

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	100	LYS	Peptide
1	A	205	SER	Peptide
1	A	33	THR	Peptide
1	A	403	LYS	Peptide
1	A	404	GLY	Peptide
1	A	420	PRO	Peptide
1	A	424	ASP	Peptide
1	A	48	SER	Peptide
1	A	485	VAL	Peptide
1	A	501[A]	ALA	Peptide
1	A	54	LYS	Peptide

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	4025	0	3958	101	0
2	A	23	0	22	0	0
3	A	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	3	0	0	0	0
5	A	21	0	12	1	0
6	A	30	0	40	4	0
7	A	281	0	0	20	0
All	All	4393	0	4032	101	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 12.

All (101) 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:499:PHE:O	1:A:502[A]:ASP:HB3	1.48	1.12
1:A:339:ASN:HD22	1:A:428:LYS:HE2	1.33	0.93
1:A:49:ASN:HA	1:A:50:ILE:HG22	1.53	0.90
1:A:482:LEU:HG	1:A:486:MET:HE3	1.56	0.85
1:A:48:SER:HB2	1:A:49:ASN:O	1.77	0.84
1:A:22:THR:N	1:A:23:GLN:HA	1.93	0.83
1:A:99:ASN:HD22	1:A:99:ASN:H	1.26	0.82
1:A:221:ASN:HD22	1:A:221:ASN:H	1.27	0.81
1:A:32[A]:LYS:HE3	7:A:5161:HOH:O	1.80	0.80
1:A:59:GLN:HE22	1:A:66:LEU:H	1.26	0.80
1:A:465:PHE:CE1	1:A:486:MET:HE1	2.18	0.79
1:A:28:ASN:HB3	1:A:106:THR:HB	1.66	0.77
1:A:339:ASN:HD22	1:A:428:LYS:CE	1.98	0.76
1:A:471:ILE:HG22	1:A:473:ASP:N	2.00	0.76
1:A:482:LEU:HG	1:A:486:MET:CE	2.19	0.72
1:A:502[B]:ASP:OD2	7:A:5227:HOH:O	2.09	0.70
1:A:339:ASN:ND2	1:A:428:LYS:HE2	2.06	0.69
1:A:514:VAL:HG12	7:A:5204:HOH:O	1.92	0.69
1:A:63:THR:CG2	1:A:88:GLU:OE1	2.43	0.67
1:A:24:SER:HA	7:A:5267:HOH:O	1.95	0.67
1:A:403:LYS:CE	1:A:429:ILE:O	2.43	0.66
1:A:63:THR:HG23	1:A:88:GLU:OE1	1.95	0.66
1:A:126:LEU:HD21	1:A:293:LEU:HD13	1.77	0.66
1:A:403:LYS:HE2	1:A:429:ILE:O	1.95	0.65
1:A:44:PRO:O	1:A:106:THR:HG21	1.97	0.65
1:A:49:ASN:HA	1:A:50:ILE:CG2	2.24	0.64
1:A:71:ASN:HA	7:A:5186:HOH:O	1.97	0.64
1:A:403:LYS:NZ	1:A:404:GLY:O	2.26	0.63
1:A:220:ASN:HB3	7:A:5248:HOH:O	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:320:TRP:CH2	1:A:432:GLU:HG3	2.36	0.61
1:A:59:GLN:NE2	1:A:66:LEU:H	1.97	0.60
1:A:159[B]:GLU:HG2	7:A:5230:HOH:O	2.01	0.59
1:A:182[B]:GLN:HG2	7:A:5128:HOH:O	2.00	0.59
1:A:371[B]:ARG:NH1	7:A:5241:HOH:O	2.34	0.59
1:A:48:SER:CB	1:A:49:ASN:O	2.51	0.59
1:A:448:ALA:HB1	1:A:486:MET:HE1	1.85	0.58
1:A:192[B]:HIS:HE1	7:A:5112:HOH:O	1.88	0.57
1:A:45:ILE:HD11	1:A:104:TYR:HB3	1.88	0.56
1:A:347:ASN:O	1:A:351:SER:HB2	2.06	0.56
1:A:47:GLN:O	1:A:48:SER:HB2	2.06	0.55
1:A:291[A]:HIS:HD2	7:A:5010:HOH:O	1.89	0.55
1:A:45:ILE:HG23	1:A:47:GLN:H	1.71	0.55
1:A:471:ILE:HB	1:A:472:THR:HA	1.89	0.55
1:A:99:ASN:HD22	1:A:99:ASN:N	2.00	0.55
1:A:458:GLU:O	7:A:5240:HOH:O	2.18	0.54
1:A:440:LEU:HB3	1:A:459:LYS:HE3	1.90	0.54
1:A:99:ASN:ND2	1:A:99:ASN:H	2.03	0.53
1:A:47:GLN:O	1:A:48:SER:CB	2.57	0.52
1:A:448:ALA:HB1	1:A:486:MET:CE	2.39	0.52
1:A:221:ASN:N	1:A:221:ASN:HD22	2.03	0.52
1:A:288:ALA:O	6:A:3002:GOL:H11	2.09	0.52
1:A:471:ILE:HG13	7:A:5070:HOH:O	2.09	0.52
1:A:34:ILE:H	1:A:144:THR:HG21	1.76	0.51
1:A:126:LEU:HB3	1:A:127:PRO:HD3	1.92	0.51
1:A:470:THR:CG2	1:A:471:ILE:N	2.75	0.50
1:A:447:ILE:HD12	1:A:500[A]:TRP:HE1	1.77	0.50
1:A:221:ASN:ND2	1:A:221:ASN:H	2.03	0.49
1:A:352:SER:HB3	1:A:399:ASP:OD2	2.13	0.49
1:A:465:PHE:CE1	1:A:486:MET:CE	2.93	0.49
1:A:502[B]:ASP:H	1:A:514:VAL:HG11	1.78	0.49
1:A:63:THR:HG22	1:A:88:GLU:OE1	2.12	0.48
1:A:402:PHE:HB2	1:A:422:MET:SD	2.53	0.48
1:A:60:THR:HG22	1:A:91:CYS:HB2	1.94	0.48
1:A:197:LYS:HE3	7:A:5283:HOH:O	2.13	0.47
1:A:41:ASN:HA	1:A:77:LEU:O	2.15	0.47
1:A:467:SER:HB2	1:A:500[B]:TRP:CD1	2.49	0.47
1:A:505:ASN:HB2	6:A:3003:GOL:H12	1.98	0.46
1:A:180:LEU:HD22	1:A:184:ILE:HD11	1.97	0.46
1:A:458:GLU:HG2	7:A:5096:HOH:O	2.16	0.45
1:A:417:GLN:HG3	7:A:5132:HOH:O	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:PHE:HB3	1:A:222:VAL:HG13	1.98	0.45
1:A:470:THR:O	1:A:471:ILE:C	2.54	0.45
1:A:344:LYS:HE3	6:A:3000:GOL:H32	1.98	0.45
1:A:476:THR:O	1:A:479:ARG:HB2	2.16	0.44
1:A:465:PHE:HE1	1:A:486:MET:CE	2.30	0.44
1:A:22:THR:N	1:A:23:GLN:CA	2.73	0.44
1:A:416:MET:SD	1:A:422:MET:CE	3.05	0.44
1:A:59:GLN:HE22	1:A:66:LEU:N	2.05	0.44
1:A:62:GLY:HA3	1:A:90:TYR:CD2	2.53	0.43
1:A:57:TRP:CH2	1:A:94:PHE:HB2	2.54	0.43
1:A:229:LEU:HD13	1:A:290:TYR:CZ	2.54	0.43
1:A:73:GLU:OE1	1:A:73:GLU:HA	2.19	0.43
1:A:471:ILE:HB	1:A:472:THR:CA	2.49	0.43
1:A:416:MET:SD	1:A:422:MET:HE3	2.60	0.42
1:A:46:ASN:HB2	7:A:5166:HOH:O	2.19	0.42
1:A:440:LEU:HB2	7:A:5012:HOH:O	2.20	0.42
1:A:499:PHE:O	1:A:501[A]:ALA:N	2.52	0.41
1:A:257:LYS:HB2	1:A:281:ASN:ND2	2.35	0.41
1:A:480:SER:HA	1:A:481:PRO:HD3	1.95	0.41
1:A:482:LEU:HD21	1:A:486:MET:HE2	2.02	0.41
1:A:67:LEU:HB2	7:A:5060:HOH:O	2.20	0.41
1:A:100:LYS:N	1:A:101:GLY:HA2	2.35	0.41
1:A:471:ILE:HG23	7:A:5120:HOH:O	2.19	0.41
1:A:403:LYS:HZ2	5:A:1427:C5P:C2	2.34	0.41
1:A:228:ASP:OD1	1:A:291[A]:HIS:HE1	2.03	0.40
1:A:371[A]:ARG:HB2	1:A:411:ILE:CG1	2.51	0.40
1:A:67:LEU:HA	1:A:67:LEU:HD12	1.89	0.40
1:A:32[A]:LYS:HE2	1:A:34:ILE:CG2	2.51	0.40
1:A:229:LEU:HD13	1:A:290:TYR:CE1	2.57	0.40
1:A:426:PRO:HD3	6:A:3000:GOL:H31	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	501/514 (98%)	472 (94%)	14 (3%)	15 (3%)	5 7

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	ILE
1	A	48	SER
1	A	351	SER
1	A	421	SER
1	A	471	ILE
1	A	502[A]	ASP
1	A	502[B]	ASP
1	A	501[A]	ALA
1	A	501[B]	ALA
1	A	425	ILE
1	A	473	ASP
1	A	50	ILE
1	A	404	GLY
1	A	405	HIS
1	A	420	PRO

5.3.2 Protein sidechains ⓘ

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	460/472 (98%)	422 (92%)	38 (8%)	13 25

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	34	ILE
1	A	45	ILE
1	A	49	ASN

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Mol	Chain	Res	Type
1	A	60	THR
1	A	63	THR
1	A	75	ILE
1	A	78	SER
1	A	99	ASN
1	A	102	GLU
1	A	106	THR
1	A	132	LEU
1	A	155	VAL
1	A	162	LYS
1	A	165	ASN
1	A	180	LEU
1	A	221	ASN
1	A	308	ARG
1	A	345	LEU
1	A	350	ASN
1	A	364	VAL
1	A	371[A]	ARG
1	A	371[B]	ARG
1	A	410	ILE
1	A	413	THR
1	A	425	ILE
1	A	430	SER
1	A	433	VAL
1	A	434	LEU
1	A	440	LEU
1	A	444	VAL
1	A	458	GLU
1	A	466	THR
1	A	470	THR
1	A	476	THR
1	A	479	ARG
1	A	480	SER
1	A	488	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	99	ASN
1	A	130	GLN
1	A	146	GLN

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Mol	Chain	Res	Type
1	A	165	ASN
1	A	187	GLN
1	A	189	GLN
1	A	221	ASN
1	A	252	ASN
1	A	281	ASN
1	A	319	GLN
1	A	331	GLN
1	A	339	ASN
1	A	350	ASN
1	A	353	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](#)

Of 12 ligands modelled in this entry, 3 are monoatomic - leaving 9 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	C5P	A	1427	-	19,22,22	0.97	1 (5%)	23,33,33	1.21	3 (13%)
2	LBT	A	2000	-	24,24,24	0.62	0	35,35,35	0.86	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	GOL	A	3000	-	5,5,5	0.58	0	5,5,5	0.96	0
6	GOL	A	3001	-	5,5,5	0.31	0	5,5,5	0.23	0
6	GOL	A	3002	-	5,5,5	0.51	0	5,5,5	0.69	0
6	GOL	A	3003	-	5,5,5	0.28	0	5,5,5	0.53	0
6	GOL	A	3004	-	5,5,5	0.41	0	5,5,5	0.24	0
3	PO4	A	4000	-	4,4,4	0.67	0	6,6,6	0.72	0
3	PO4	A	4001	-	4,4,4	0.63	0	6,6,6	0.59	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	C5P	A	1427	-	-	0/6/26/26	0/2/2/2
2	LBT	A	2000	-	-	0/8/48/48	0/2/2/2
6	GOL	A	3000	-	-	0/4/4/4	0/0/0/0
6	GOL	A	3001	-	-	0/4/4/4	0/0/0/0
6	GOL	A	3002	-	-	0/4/4/4	0/0/0/0
6	GOL	A	3003	-	-	0/4/4/4	0/0/0/0
6	GOL	A	3004	-	-	0/4/4/4	0/0/0/0
3	PO4	A	4000	-	-	0/0/0/0	0/0/0/0
3	PO4	A	4001	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1427	C5P	C2'-C1'	-2.36	1.49	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1427	C5P	O2'-C2'-C1'	-2.72	103.11	111.61
5	A	1427	C5P	O2P-P-O1P	2.15	118.93	110.50
5	A	1427	C5P	O4'-C1'-N1	2.29	112.67	108.08
2	A	2000	LBT	C6'-C5'-C4'	2.57	120.25	113.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1427	C5P	1	0
6	A	3000	GOL	2	0
6	A	3002	GOL	1	0
6	A	3003	GOL	1	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 ⓘ

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, 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	493/514 (95%)	0.36	23 (4%) 32 34	32, 43, 61, 78	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	472	THR	5.1
1	A	70	GLN	5.0
1	A	49	ASN	5.0
1	A	22	THR	3.8
1	A	471	ILE	3.6
1	A	353	ASN	3.2
1	A	48	SER	3.2
1	A	47	GLN	3.0
1	A	68	THR	3.0
1	A	50	ILE	3.0
1	A	73	GLU	3.0
1	A	23	GLN	2.8
1	A	235	ALA	2.8
1	A	63	THR	2.3
1	A	182[A]	GLN	2.3
1	A	468	THR	2.3
1	A	25	ILE	2.2
1	A	234	SER	2.2
1	A	203	ALA	2.1
1	A	450	SER	2.1
1	A	71	ASN	2.1
1	A	473	ASP	2.0
1	A	501[A]	ALA	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 [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(\AA^2)	Q<0.9
6	GOL	A	3000	6/6	0.81	0.60	19.22	57,59,60,60	0
6	GOL	A	3002	6/6	0.63	0.37	5.22	63,68,68,69	0
6	GOL	A	3003	6/6	0.81	0.35	3.32	61,62,64,64	0
6	GOL	A	3001	6/6	0.88	0.23	-0.15	66,66,67,67	0
4	MG	A	5000	1/1	0.92	0.21	-0.15	39,39,39,39	0
4	MG	A	5001	1/1	0.98	0.17	-0.83	35,35,35,35	0
2	LBT	A	2000	23/23	0.94	0.13	-2.09	32,42,50,51	0
5	C5P	A	1427	21/21	0.99	0.08	-3.56	22,23,26,28	0
6	GOL	A	3004	6/6	0.99	0.10	-4.39	27,27,28,28	0
4	MG	A	5002	1/1	0.80	0.25	-	54,54,54,54	0
3	PO4	A	4001	5/5	0.87	0.27	-	89,89,89,90	0
3	PO4	A	4000	5/5	0.92	0.40	-	67,67,68,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.