Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:33 AM GMT

PDB ID	:	2DIJ
Title	:	COMPLEX OF A Y195F MUTANT CGTASE FROM B. CIRCULANS STRAIN 251 COMPLEXED WITH A MALTONONAOSE INHIBITOR AT PH 9.8 OBTAINED AFTER SOAKING THE CRYSTAL WITH ACARBOSE AND MALTOHEXAOSE
Authors	:	Strokopytov, B.V.; Knegtel, R.M.A.; Uitdehaag, J.C.M.; Dijkstra, B.W.
Deposited on	:	1998-05-27
Resolution	:	2.60 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:

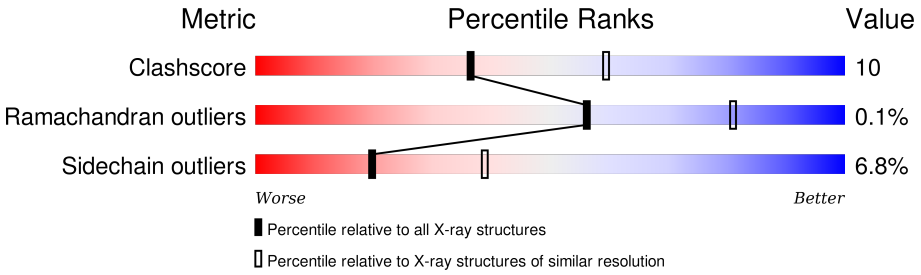
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 2.60 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))
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	686	71% 25% ·

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 5603 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 CYCLODEXTRIN GLYCOSYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	686	Total	C	N	O	S	0	0	0
			5263	3321	900	1026	16			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	195	PHE	TYR	ENGINEERED	UNP P43379

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

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

- Molecule 3 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	3	Total	C	O	0	0
			34	18	16		

- Molecule 4 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	5	Total	C	O	0	0
			56	30	26		

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	2	Total	C	O	0	0
			21	12	9		

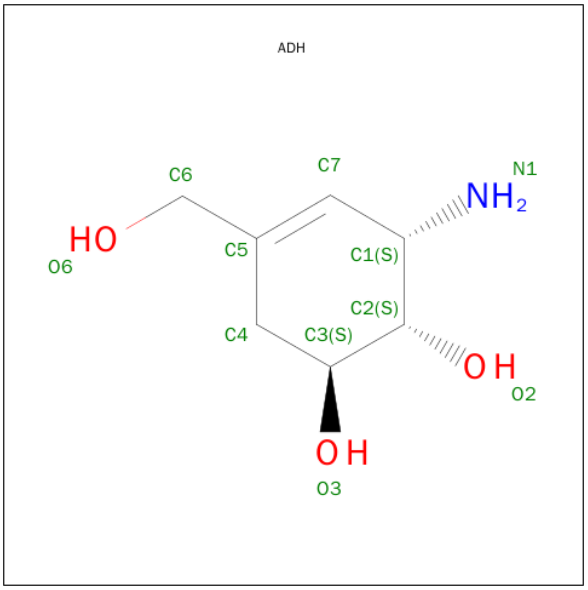
- Molecule 6 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	6	Total C O 67 36 31	0	0

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	2	Total Ca 2 2	0	0

- Molecule 8 is 1-AMINO-2,3-DIHYDROXY-5-HYDROXYMETHYL CYCLOHEX-5-ENE (three-letter code: ADH) (formula: $C_7H_{13}NO_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C N O 11 7 1 3	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	126	Total O 126 126	0	0

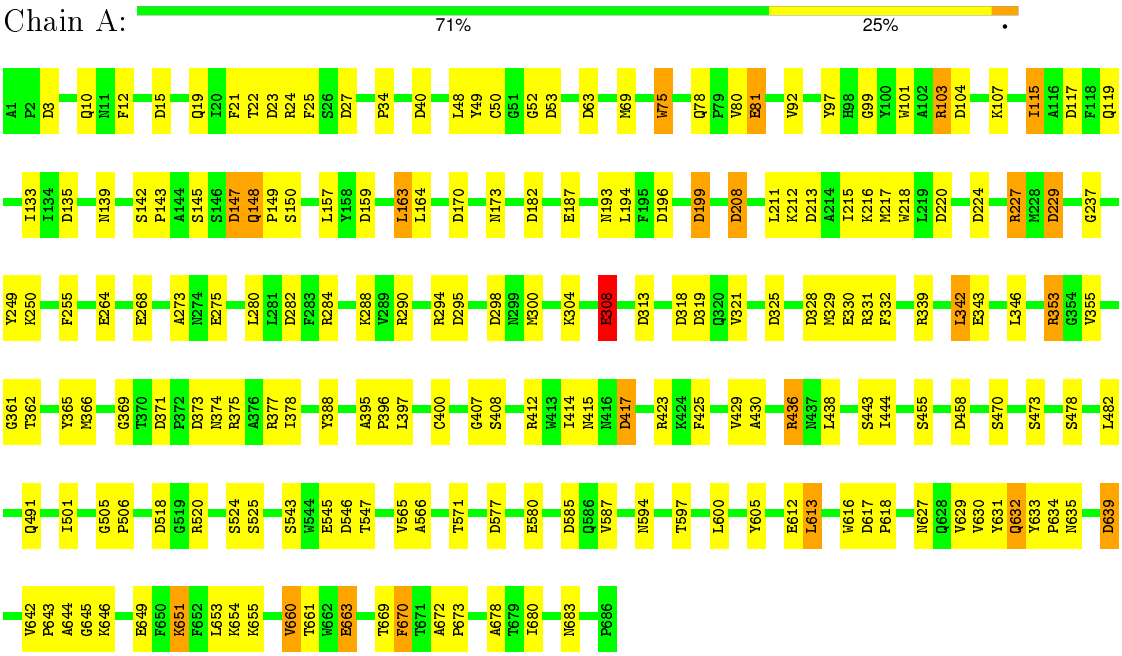
3 Residue-property plots (i)

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.

Note EDS was not executed.

- Molecule 1: CYCLODEXTRIN GLYCOSYLTRANSFERASE

Chain A:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	119.96Å 111.28Å 67.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.60	Depositor
% Data completeness (in resolution range)	94.1 (8.00-2.60)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
Refinement program	TNT V. 5-D	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5603	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, GLC, ADH, G6D

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	13/5393 (0.2%)	0.96	74/7350 (1.0%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	545	GLU	CD-OE2	5.69	1.31	1.25
1	A	580	GLU	CD-OE2	5.54	1.31	1.25
1	A	268	GLU	CD-OE2	5.39	1.31	1.25
1	A	264	GLU	CD-OE2	5.38	1.31	1.25
1	A	275	GLU	CD-OE2	5.34	1.31	1.25
1	A	308	GLU	CD-OE2	5.26	1.31	1.25
1	A	343	GLU	CD-OE2	5.25	1.31	1.25
1	A	330	GLU	CD-OE2	5.24	1.31	1.25
1	A	663	GLU	CD-OE2	5.23	1.31	1.25
1	A	187	GLU	CD-OE2	5.22	1.31	1.25
1	A	612	GLU	CD-OE2	5.20	1.31	1.25
1	A	649	GLU	CD-OE2	5.13	1.31	1.25
1	A	81	GLU	CD-OE2	5.10	1.31	1.25

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	371	ASP	CB-CG-OD2	-7.65	111.42	118.30
1	A	196	ASP	CB-CG-OD1	6.95	124.55	118.30
1	A	328	ASP	CB-CG-OD2	-6.93	112.06	118.30
1	A	63	ASP	CB-CG-OD2	-6.66	112.31	118.30
1	A	325	ASP	CB-CG-OD2	-6.53	112.42	118.30
1	A	371	ASP	CB-CG-OD1	6.53	124.18	118.30
1	A	224	ASP	CB-CG-OD2	-6.50	112.45	118.30
1	A	318	ASP	CB-CG-OD2	-6.47	112.47	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	135	ASP	CB-CG-OD2	-6.47	112.48	118.30
1	A	170	ASP	CB-CG-OD2	-6.43	112.51	118.30
1	A	196	ASP	CB-CG-OD2	-6.38	112.56	118.30
1	A	104	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	A	373	ASP	CB-CG-OD2	-6.26	112.67	118.30
1	A	213	ASP	CB-CG-OD2	-6.25	112.67	118.30
1	A	617	ASP	CB-CG-OD2	-6.25	112.67	118.30
1	A	27	ASP	CB-CG-OD2	-6.21	112.71	118.30
1	A	182	ASP	CB-CG-OD2	-6.19	112.73	118.30
1	A	117	ASP	CB-CG-OD2	-6.18	112.74	118.30
1	A	63	ASP	CB-CG-OD1	6.18	123.86	118.30
1	A	319	ASP	CB-CG-OD2	-6.16	112.76	118.30
1	A	147	ASP	CB-CG-OD2	-6.15	112.77	118.30
1	A	135	ASP	CB-CG-OD1	6.13	123.82	118.30
1	A	3	ASP	CB-CG-OD2	-6.13	112.78	118.30
1	A	585	ASP	CB-CG-OD2	-6.12	112.79	118.30
1	A	417	ASP	CB-CG-OD2	-6.10	112.81	118.30
1	A	208	ASP	CB-CG-OD2	-6.10	112.81	118.30
1	A	199	ASP	CB-CG-OD2	-6.09	112.81	118.30
1	A	328	ASP	CB-CG-OD1	6.08	123.78	118.30
1	A	313	ASP	CB-CG-OD2	-6.05	112.85	118.30
1	A	518	ASP	CB-CG-OD2	-6.02	112.89	118.30
1	A	282	ASP	CB-CG-OD2	-5.97	112.93	118.30
1	A	229	ASP	CB-CG-OD2	-5.97	112.93	118.30
1	A	617	ASP	CB-CG-OD1	5.95	123.66	118.30
1	A	458	ASP	CB-CG-OD2	-5.93	112.96	118.30
1	A	23	ASP	CB-CG-OD2	-5.93	112.97	118.30
1	A	325	ASP	CB-CG-OD1	5.92	123.63	118.30
1	A	170	ASP	CB-CG-OD1	5.86	123.57	118.30
1	A	298	ASP	CB-CG-OD1	5.84	123.56	118.30
1	A	104	ASP	CB-CG-OD1	5.82	123.54	118.30
1	A	53	ASP	CB-CG-OD2	-5.82	113.06	118.30
1	A	3	ASP	CB-CG-OD1	5.79	123.51	118.30
1	A	15	ASP	CB-CG-OD2	-5.77	113.11	118.30
1	A	577	ASP	CB-CG-OD2	-5.73	113.14	118.30
1	A	298	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	A	224	ASP	CB-CG-OD1	5.70	123.43	118.30
1	A	318	ASP	CB-CG-OD1	5.67	123.40	118.30
1	A	229	ASP	CB-CG-OD1	5.64	123.37	118.30
1	A	159	ASP	CB-CG-OD2	-5.63	113.23	118.30
1	A	458	ASP	CB-CG-OD1	5.60	123.34	118.30
1	A	40	ASP	CB-CG-OD2	-5.57	113.29	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	199	ASP	CB-CG-OD1	5.55	123.30	118.30
1	A	295	ASP	CB-CG-OD2	-5.53	113.32	118.30
1	A	585	ASP	CB-CG-OD1	5.51	123.26	118.30
1	A	40	ASP	CB-CG-OD1	5.50	123.25	118.30
1	A	577	ASP	CB-CG-OD1	5.49	123.24	118.30
1	A	53	ASP	CB-CG-OD1	5.49	123.24	118.30
1	A	27	ASP	CB-CG-OD1	5.48	123.23	118.30
1	A	546	ASP	CB-CG-OD2	-5.46	113.38	118.30
1	A	208	ASP	CB-CG-OD1	5.44	123.19	118.30
1	A	220	ASP	CB-CG-OD2	-5.33	113.50	118.30
1	A	282	ASP	CB-CG-OD1	5.32	123.08	118.30
1	A	373	ASP	CB-CG-OD1	5.32	123.08	118.30
1	A	147	ASP	CB-CG-OD1	5.29	123.06	118.30
1	A	417	ASP	CB-CG-OD1	5.28	123.05	118.30
1	A	182	ASP	CB-CG-OD1	5.28	123.05	118.30
1	A	117	ASP	CB-CG-OD1	5.25	123.03	118.30
1	A	23	ASP	CB-CG-OD1	5.23	123.01	118.30
1	A	213	ASP	CB-CG-OD1	5.16	122.94	118.30
1	A	331	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	A	159	ASP	CB-CG-OD1	5.13	122.92	118.30
1	A	518	ASP	CB-CG-OD1	5.12	122.91	118.30
1	A	639	ASP	CB-CG-OD2	-5.10	113.71	118.30
1	A	313	ASP	CB-CG-OD1	5.04	122.83	118.30
1	A	319	ASP	CB-CG-OD1	5.01	122.81	118.30

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	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5263	0	5025	100	0
2	A	23	0	21	0	0
3	A	34	0	30	1	0
4	A	56	0	48	1	0
5	A	21	0	19	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	67	0	56	4	0
7	A	2	0	0	0	0
8	A	11	0	11	2	0
9	A	126	0	0	3	0
All	All	5603	0	5210	102	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 10.

All (102) 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:69:MET:HG3	1:A:388:TYR:CE2	2.12	0.84
1:A:670:PHE:CE2	1:A:680:ILE:HD11	2.13	0.84
1:A:75:TRP:CZ2	1:A:227:ARG:HD3	2.18	0.78
1:A:423:ARG:HG3	1:A:423:ARG:HH11	1.49	0.78
1:A:227:ARG:HH21	1:A:229:ASP:HB2	1.51	0.76
1:A:19:GLN:HG3	1:A:75:TRP:CD2	2.20	0.75
1:A:142:SER:HB2	1:A:143:PRO:HD2	1.72	0.71
1:A:101:TRP:HE1	6:A:706:GLC:H61	1.56	0.69
1:A:25:PHE:HB3	9:A:749:HOH:O	1.93	0.68
1:A:115:ILE:O	1:A:119:GLN:HG3	1.94	0.68
1:A:249:TYR:CE2	1:A:250:LYS:HD2	2.32	0.65
1:A:304:LYS:O	1:A:308:GLU:HG2	1.99	0.63
1:A:19:GLN:HG3	1:A:75:TRP:CE3	2.35	0.62
1:A:145:SER:HA	6:A:711:GLC:O2	1.98	0.62
1:A:444:ILE:HD13	1:A:482:LEU:HB2	1.81	0.61
1:A:414:ILE:HG12	1:A:415:ASN:N	2.15	0.61
1:A:597:THR:O	1:A:654:LYS:HE2	2.01	0.60
1:A:395:ALA:HB3	1:A:396:PRO:HD3	1.83	0.60
1:A:651:LYS:HE2	3:A:693:GLC:O3	2.03	0.59
1:A:12:PHE:CE2	1:A:133:ILE:HD11	2.38	0.59
1:A:566:ALA:HA	1:A:571:THR:O	2.05	0.57
1:A:147:ASP:O	1:A:149:PRO:HD3	2.04	0.56
1:A:444:ILE:CD1	1:A:482:LEU:HB2	2.35	0.56
1:A:642:VAL:HB	1:A:643:PRO:HD2	1.87	0.55
1:A:633:TYR:CG	1:A:634:PRO:HA	2.41	0.55
1:A:423:ARG:HG3	1:A:423:ARG:NH1	2.13	0.55
1:A:157:LEU:O	1:A:164:LEU:HB2	2.07	0.54
1:A:520:ARG:HD3	1:A:547:THR:HG22	1.90	0.53
1:A:501:ILE:HD11	1:A:565:VAL:HG13	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:645:GLY:HA2	1:A:672:ALA:O	2.09	0.53
1:A:227:ARG:NH2	1:A:229:ASP:HB2	2.23	0.53
1:A:505:GLY:HA2	1:A:506:PRO:C	2.28	0.52
1:A:142:SER:HB2	1:A:143:PRO:CD	2.39	0.52
1:A:227:ARG:HG3	1:A:255:PHE:CE2	2.44	0.51
1:A:81:GLU:CD	1:A:103:ARG:HD3	2.31	0.51
1:A:227:ARG:HH21	1:A:229:ASP:CB	2.23	0.51
1:A:163:LEU:HD22	1:A:164:LEU:N	2.26	0.51
1:A:651:LYS:HE3	1:A:663:GLU:O	2.11	0.51
1:A:81:GLU:OE1	1:A:103:ARG:HD3	2.12	0.50
1:A:408:SER:O	1:A:423:ARG:HA	2.12	0.49
1:A:80:VAL:HA	1:A:107:LYS:O	2.11	0.49
1:A:594:ASN:HB2	1:A:683:ASN:OD1	2.12	0.49
1:A:208:ASP:O	1:A:212:LYS:HG3	2.11	0.49
1:A:670:PHE:CD2	1:A:680:ILE:HD11	2.47	0.48
1:A:294:ARG:HB2	1:A:332:PHE:CZ	2.48	0.48
1:A:673:PRO:HG3	1:A:678:ALA:HB2	1.95	0.48
1:A:600:LEU:CD1	4:A:697:GLC:H3	2.42	0.48
1:A:342:LEU:HD11	1:A:362:THR:HG23	1.96	0.48
1:A:669:THR:O	1:A:670:PHE:HB3	2.13	0.48
1:A:339:ARG:HG2	1:A:365:TYR:CD1	2.49	0.48
1:A:633:TYR:CD2	1:A:634:PRO:HA	2.50	0.47
6:A:709:GLC:H62	6:A:710:GLC:H5	1.97	0.47
1:A:417:ASP:O	1:A:436:ARG:HG3	2.15	0.46
1:A:34:PRO:HG2	1:A:49:TYR:CG	2.50	0.46
1:A:75:TRP:CE2	1:A:227:ARG:HD3	2.49	0.46
1:A:78:GLN:HB3	1:A:99:GLY:O	2.16	0.46
1:A:395:ALA:N	1:A:396:PRO:HD2	2.30	0.45
1:A:643:PRO:HB2	1:A:646:LYS:HG3	1.98	0.45
1:A:147:ASP:HB2	6:A:711:GLC:O3	2.16	0.45
1:A:669:THR:HG22	1:A:670:PHE:N	2.32	0.45
1:A:227:ARG:NH2	1:A:229:ASP:CB	2.80	0.45
1:A:24:ARG:NH2	1:A:97:TYR:CD1	2.85	0.45
1:A:273:ALA:HB2	1:A:280:LEU:HD12	1.97	0.45
1:A:164:LEU:HA	1:A:164:LEU:HD23	1.73	0.45
1:A:361:GLY:HA3	1:A:366:MET:SD	2.56	0.45
1:A:627:ASN:O	1:A:632:GLN:HA	2.17	0.44
1:A:237:GLY:HA3	1:A:639:ASP:O	2.17	0.44
1:A:397:LEU:HA	1:A:400:CYS:SG	2.58	0.44
5:A:704:G6D:HC63	8:A:705:ADH:H3	1.99	0.44
1:A:300:MET:HB2	1:A:415:ASN:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:660:VAL:CG2	1:A:661:THR:N	2.81	0.44
1:A:605:TYR:CE1	1:A:655:LYS:HB2	2.53	0.43
1:A:10:GLN:HG3	9:A:816:HOH:O	2.19	0.43
1:A:669:THR:HG22	1:A:670:PHE:H	1.83	0.42
1:A:163:LEU:HD23	1:A:163:LEU:HA	1.76	0.42
1:A:211:LEU:HD23	1:A:211:LEU:HA	1.88	0.42
1:A:395:ALA:N	1:A:396:PRO:CD	2.83	0.42
1:A:80:VAL:HG12	1:A:218:TRP:CZ2	2.55	0.42
1:A:369:GLY:O	1:A:374:ASN:HB3	2.20	0.42
1:A:215:ILE:HA	1:A:215:ILE:HD12	1.83	0.42
1:A:346:LEU:HA	1:A:346:LEU:HD23	1.87	0.42
1:A:429:VAL:HG12	1:A:430:ALA:N	2.33	0.41
1:A:353:ARG:O	1:A:353:ARG:HD3	2.20	0.41
1:A:288:LYS:HB2	1:A:288:LYS:HE2	1.80	0.41
1:A:22:THR:O	1:A:52:GLY:HA3	2.19	0.41
1:A:630:VAL:HG12	1:A:631:TYR:CE1	2.56	0.41
1:A:651:LYS:HG2	1:A:663:GLU:HB3	2.01	0.41
1:A:148:GLN:NE2	1:A:148:GLN:HA	2.35	0.41
1:A:193:ASN:OD1	1:A:199:ASP:HB2	2.21	0.41
1:A:670:PHE:CZ	1:A:680:ILE:HD11	2.55	0.41
1:A:616:TRP:O	1:A:618:PRO:HD3	2.21	0.41
1:A:139:ASN:HB3	9:A:755:HOH:O	2.21	0.41
1:A:321:VAL:HG22	1:A:355:VAL:HB	2.03	0.41
1:A:50:CYS:HB3	1:A:377:ARG:HH21	1.85	0.41
1:A:587:VAL:HG13	1:A:644:ALA:HB2	2.02	0.41
1:A:613:LEU:HD12	1:A:613:LEU:HA	1.87	0.41
1:A:407:GLY:HA2	1:A:425:PHE:HB2	2.03	0.40
1:A:229:ASP:OD1	8:A:705:ADH:H1	2.20	0.40
1:A:633:TYR:HA	1:A:635:ASN:N	2.36	0.40
1:A:374:ASN:OD1	1:A:375:ARG:HG3	2.21	0.40
1:A:378:ILE:HG23	1:A:378:ILE:O	2.21	0.40
1:A:273:ALA:HB2	1:A:280:LEU:CD1	2.51	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	684/686 (100%)	656 (96%)	27 (4%)	1 (0%)	56 81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	629	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	556/556 (100%)	518 (93%)	38 (7%)	20 39

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

Mol	Chain	Res	Type
1	A	21	PHE
1	A	48	LEU
1	A	75	TRP
1	A	92	VAL
1	A	103	ARG
1	A	115	ILE
1	A	148	GLN
1	A	150	SER
1	A	163	LEU
1	A	173	ASN
1	A	194	LEU
1	A	216	LYS
1	A	217	MET
1	A	227	ARG
1	A	284	ARG
1	A	290	ARG

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Mol	Chain	Res	Type
1	A	308	GLU
1	A	329	MET
1	A	342	LEU
1	A	353	ARG
1	A	412	ARG
1	A	436	ARG
1	A	438	LEU
1	A	443	SER
1	A	455	SER
1	A	470	SER
1	A	473	SER
1	A	478	SER
1	A	491	GLN
1	A	524	SER
1	A	525	SER
1	A	543	SER
1	A	613	LEU
1	A	632	GLN
1	A	651	LYS
1	A	653	LEU
1	A	660	VAL
1	A	670	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	62	ASN
1	A	120	ASN
1	A	410	GLN
1	A	416	ASN
1	A	453	GLN
1	A	479	ASN
1	A	632	GLN

5.3.3 RNA

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)

18 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	$\#\|Z\| > 2$
2	GLC	A	690	2	11,11,12	0.49	0	15,15,17	0.79	0
2	GLC	A	691	2	12,12,12	0.38	0	17,17,17	0.76	0
3	GLC	A	693	3	11,11,12	0.42	0	15,15,17	0.57	0
3	GLC	A	694	3	11,11,12	0.45	0	15,15,17	0.77	0
3	GLC	A	695	3	12,12,12	0.39	0	17,17,17	0.93	1 (5%)
4	GLC	A	697	4	11,11,12	0.39	0	15,15,17	0.54	0
4	GLC	A	698	4	11,11,12	0.45	0	15,15,17	1.35	3 (20%)
4	GLC	A	699	4	11,11,12	0.42	0	15,15,17	0.62	0
4	GLC	A	700	4	11,11,12	0.40	0	15,15,17	0.81	0
4	GLC	A	701	4	12,12,12	0.37	0	17,17,17	0.87	0
5	GLC	A	703	5	11,11,12	0.37	0	15,15,17	0.82	0
5	G6D	A	704	8,5	10,10,11	0.48	0	13,14,16	1.24	1 (7%)
6	GLC	A	706	8,6	11,11,12	0.49	0	15,15,17	1.41	3 (20%)
6	GLC	A	707	6	11,11,12	0.41	0	15,15,17	0.98	1 (6%)
6	GLC	A	708	6	11,11,12	0.47	0	15,15,17	0.89	1 (6%)
6	GLC	A	709	6	11,11,12	0.44	0	15,15,17	0.71	0
6	GLC	A	710	6	11,11,12	0.45	0	15,15,17	1.06	1 (6%)
6	GLC	A	711	6	12,12,12	0.35	0	17,17,17	1.21	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	GLC	A	690	2	-	0/2/18/22	0/1/1/1
2	GLC	A	691	2	-	0/2/22/22	0/1/1/1
3	GLC	A	693	3	-	0/2/18/22	0/1/1/1
3	GLC	A	694	3	-	0/2/18/22	0/1/1/1
3	GLC	A	695	3	-	0/2/22/22	0/1/1/1
4	GLC	A	697	4	-	0/2/18/22	0/1/1/1
4	GLC	A	698	4	-	0/2/18/22	0/1/1/1
4	GLC	A	699	4	-	0/2/18/22	0/1/1/1
4	GLC	A	700	4	-	0/2/18/22	0/1/1/1
4	GLC	A	701	4	-	0/2/22/22	0/1/1/1
5	GLC	A	703	5	-	0/2/18/22	0/1/1/1
5	G6D	A	704	8,5	-	0/0/16/20	0/1/1/1
6	GLC	A	706	8,6	-	0/2/18/22	0/1/1/1
6	GLC	A	707	6	-	0/2/18/22	0/1/1/1
6	GLC	A	708	6	-	0/2/18/22	0/1/1/1
6	GLC	A	709	6	-	0/2/18/22	0/1/1/1
6	GLC	A	710	6	-	0/2/18/22	0/1/1/1
6	GLC	A	711	6	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	706	GLC	C4-C5-C6	-2.52	107.73	112.38
4	A	698	GLC	C4-C5-C6	-2.16	108.39	112.38
6	A	710	GLC	C4-C3-C2	-2.08	107.72	110.56
3	A	695	GLC	C1-O5-C5	2.03	117.23	113.47
6	A	706	GLC	O5-C5-C4	2.17	114.02	109.97
6	A	707	GLC	O5-C1-C2	2.19	113.28	109.80
4	A	698	GLC	O5-C5-C4	2.22	114.10	109.97
6	A	708	GLC	O5-C1-C2	2.29	113.45	109.80
4	A	698	GLC	C1-O5-C5	3.12	119.21	113.47
6	A	706	GLC	C1-O5-C5	3.25	119.46	113.47
5	A	704	G6D	O5-C1-C2	3.30	115.05	109.80

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	693	GLC	1	0
4	A	697	GLC	1	0
5	A	704	G6D	1	0
6	A	706	GLC	1	0
6	A	709	GLC	1	0
6	A	710	GLC	1	0
6	A	711	GLC	2	0

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	$\#\|Z\| > 2$
8	ADH	A	705	5,6	10,11,11	2.02	3 (30%)	8,15,15	0.99	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
8	ADH	A	705	5,6	-	0/1/18/18	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	705	ADH	C4-C5	-4.87	1.41	1.50
8	A	705	ADH	C1-C7	-3.01	1.42	1.49
8	A	705	ADH	C7-C5	2.39	1.42	1.33

There are no bond angle outliers.

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
8	A	705	ADH	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.