

Full wwPDB X-ray Structure Validation Report (i)

Jul 26, 2023 – 02:08 AM EDT

:	1A47
:	CGTASE FROM THERMOANAEROBACTERIUM THERMOSULFURI-
	GENES EM1 IN COMPLEX WITH A MALTOHEXAOSE INHIBITOR
:	Uitdehaag, J.C.M.; Kalk, K.H.; Rozeboom, H.J.; Dijkstra, B.W.
:	1998-02-11
:	2.56 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 https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.34

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.56 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.



Motria	Whole archive	Similar resolution
wietric	$(\# { m Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
Clashscore	141614	1327 (2.58-2.54)
Ramachandran outliers	138981	1312(2.58-2.54)
Sidechain outliers	138945	1312(2.58-2.54)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain				
1	А	683	64%	30%	6%		
2	В	3	100%				
3	С	3	33%	67%			
4	D	2	50%	50%			



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5620 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		A	toms			ZeroOcc	AltConf	Trace
1	А	683	Total 5333	C 3377	N 885	O 1056	S 15	0	0	0

• Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	At	\mathbf{oms}		ZeroOcc	AltConf	Trace
2	В	3	Total 34	C 18	O 16	0	0	0

• Molecule 3 is an oligosaccharide called alpha-D-quinovopyranose-(1-4)-alpha-D-glucopyrano se-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	At	\mathbf{oms}		ZeroOcc	AltConf	Trace
3	С	3	Total 32	C 18	O 14	0	0	0

• Molecule 4 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.





Mol	Chain	Residues	At	oms		ZeroOcc	AltConf	Trace
4	D	2	Total 23	C 12	O 11	0	0	0

• Molecule 5 is 1-AMINO-2,3-DIHYDROXY-5-HYDROXYMETHYL CYCLOHEX-5-ENE (three-letter code: ADH) (formula: C₇H₁₃NO₃).



Mol	Chain	Residues	A	tor	ns		ZeroOcc	AltConf
5	А	1	Total 11	С 7	N 1	O 3	0	0

• Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	2	Total Ca 2 2	0	0

• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	185	Total O 185 185	0	0



3 Residue-property plots (i)

• Molecule 1: CYCLODEXTRIN GLYCOSYLTRANSFERASE

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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. 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. 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 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranos е

Chain B:

100%

GLC1 GLC2 GLC3

• Molecule 3: alpha-D-quinovopyranose-(1-4)-alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranos е

Chain C: 33%

67%



GLC1 GLC2 G6D3

• Molecule 4: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain D: 50% 50%

GLC1 GLC2



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	74.00Å 97.79Å 116.26Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 - 2.56	Depositor
% Data completeness	84.0 (8.00-2.56)	Depositor
(in resolution range)	01.0 (0.00 2.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
Refinement program	TNT 5D	Depositor
R, R_{free}	0.186 , 0.250	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5620	wwPDB-VP
Average B, all atoms $(Å^2)$	18.0	wwPDB-VP



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: ADH, G6D, GLC, CA $\,$

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	Bo	nd lengths	Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.61	13/5470~(0.2%)	0.93	85/7466 (1.1%)	

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	422	GLU	CD-OE2	5.44	1.31	1.25
1	А	486	GLU	CD-OE2	5.36	1.31	1.25
1	А	363	GLU	CD-OE2	5.33	1.31	1.25
1	А	147	GLU	CD-OE2	5.31	1.31	1.25
1	А	276	GLU	CD-OE2	5.29	1.31	1.25
1	А	154	GLU	CD-OE2	5.29	1.31	1.25
1	А	188	GLU	CD-OE2	5.25	1.31	1.25
1	А	599	GLU	CD-OE2	5.25	1.31	1.25
1	А	81	GLU	CD-OE2	5.18	1.31	1.25
1	А	545	GLU	CD-OE2	5.16	1.31	1.25
1	А	265	GLU	CD-OE2	5.06	1.31	1.25
1	А	609	GLU	CD-OE2	5.04	1.31	1.25
1	А	660	GLU	CD-OE2	5.03	1.31	1.25

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	417	ASP	CB-CG-OD1	7.16	124.74	118.30
1	А	197	ASP	CB-CG-OD2	-6.95	112.04	118.30
1	А	417	ASP	CB-CG-OD2	-6.84	112.15	118.30
1	А	89	ASP	CB-CG-OD1	-6.55	112.41	118.30
1	А	371	ASP	CB-CG-OD2	-6.39	112.55	118.30
1	А	53	ASP	CB-CG-OD2	-6.34	112.59	118.30
1	А	296	ASP	CB-CG-OD2	-6.32	112.61	118.30
1	А	225	ASP	CB-CG-OD2	-6.30	112.63	118.30



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	$Ideal(^{o})$
1	А	171	ASP	CB-CG-OD2	-6.23	112.69	118.30
1	А	329	ASP	CB-CG-OD2	-6.23	112.69	118.30
1	А	63	ASP	CB-CG-OD2	-6.20	112.72	118.30
1	А	105	ASP	CB-CG-OD2	-6.18	112.74	118.30
1	А	283	ASP	CB-CG-OD2	-6.14	112.77	118.30
1	А	37	ASP	CB-CG-OD2	-6.13	112.78	118.30
1	А	15	ASP	CB-CG-OD2	-6.13	112.78	118.30
1	А	305	ASP	CB-CG-OD2	-6.13	112.78	118.30
1	А	189	ASP	CB-CG-OD1	-6.11	112.80	118.30
1	А	331	ASP	CB-CG-OD2	-6.08	112.83	118.30
1	А	27	ASP	CB-CG-OD2	-6.07	112.83	118.30
1	А	474	ASP	CB-CG-OD2	-6.05	112.86	118.30
1	А	149	ASP	CB-CG-OD2	-6.02	112.88	118.30
1	А	458	ASP	CB-CG-OD2	-6.02	112.88	118.30
1	А	314	ASP	CB-CG-OD2	-6.01	112.89	118.30
1	А	221	ASP	CB-CG-OD2	-5.99	112.91	118.30
1	А	267	ASP	CB-CG-OD2	-5.99	112.91	118.30
1	А	209	ASP	CB-CG-OD2	-5.99	112.91	118.30
1	А	542	ASP	CB-CG-OD2	-5.98	112.92	118.30
1	А	326	ASP	CB-CG-OD2	-5.98	112.92	118.30
1	А	118	ASP	CB-CG-OD2	-5.97	112.93	118.30
1	А	245	ASP	CB-CG-OD2	-5.96	112.93	118.30
1	А	3	ASP	CB-CG-OD2	-5.96	112.94	118.30
1	А	518	ASP	CB-CG-OD2	-5.92	112.97	118.30
1	А	614	ASP	CB-CG-OD2	-5.89	113.00	118.30
1	А	183	ASP	CB-CG-OD2	-5.88	113.01	118.30
1	А	200	ASP	CB-CG-OD2	-5.87	113.02	118.30
1	А	160	ASP	CB-CG-OD2	-5.86	113.03	118.30
1	А	329	ASP	CB-CG-OD1	5.86	123.57	118.30
1	А	23	ASP	CB-CG-OD2	-5.85	113.03	118.30
1	А	299	ASP	CB-CG-OD2	-5.85	113.03	118.30
1	А	40	ASP	CB-CG-OD2	-5.84	113.04	118.30
1	А	89	ASP	CB-CG-OD2	5.84	123.56	118.30
1	А	543	ASP	CB-CG-OD2	-5.82	113.06	118.30
1	А	15	ASP	CB-CG-OD1	5.79	123.51	118.30
1	A	636	ASP	$CB-CG-\overline{OD2}$	-5.79	113.09	118.30
1	А	320	ASP	CB-CG-OD2	-5.78	113.10	118.30
1	А	371	ASP	CB-CG-OD1	5.78	123.50	118.30
1	A	27	ASP	CB-CG-OD1	5.78	123.50	118.30
1	А	305	ASP	CB-CG-OD1	5.74	123.46	118.30
1	А	105	ASP	CB-CG-OD1	5.74	123.46	118.30
1	A	299	ASP	CB-CG-OD1	5.72	123.45	118.30



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	53	ASP	CB-CG-OD1	5.71	123.44	118.30
1	А	225	ASP	CB-CG-OD1	5.71	123.44	118.30
1	А	37	ASP	CB-CG-OD1	5.64	123.37	118.30
1	А	171	ASP	CB-CG-OD1	5.63	123.37	118.30
1	А	331	ASP	CB-CG-OD1	5.63	123.36	118.30
1	А	3	ASP	CB-CG-OD1	5.63	123.36	118.30
1	А	63	ASP	CB-CG-OD1	5.62	123.36	118.30
1	А	230	ASP	CB-CG-OD2	-5.62	113.25	118.30
1	А	136	ASP	CB-CG-OD1	-5.61	113.26	118.30
1	А	189	ASP	CB-CG-OD2	5.59	123.33	118.30
1	А	296	ASP	CB-CG-OD1	5.58	123.32	118.30
1	А	326	ASP	CB-CG-OD1	5.58	123.32	118.30
1	А	197	ASP	CB-CG-OD1	5.49	123.24	118.30
1	А	40	ASP	CB-CG-OD1	5.48	123.23	118.30
1	А	314	ASP	CB-CG-OD1	5.46	123.22	118.30
1	А	149	ASP	CB-CG-OD1	5.45	123.21	118.30
1	А	636	ASP	CB-CG-OD1	5.45	123.21	118.30
1	А	518	ASP	CB-CG-OD1	5.43	123.19	118.30
1	А	542	ASP	CB-CG-OD1	5.43	123.19	118.30
1	А	458	ASP	CB-CG-OD1	5.43	123.19	118.30
1	А	474	ASP	CB-CG-OD1	5.43	123.19	118.30
1	А	283	ASP	CB-CG-OD1	5.42	123.17	118.30
1	А	267	ASP	CB-CG-OD1	5.40	123.16	118.30
1	А	200	ASP	CB-CG-OD1	5.39	123.15	118.30
1	А	209	ASP	CB-CG-OD1	5.38	123.14	118.30
1	А	543	ASP	CB-CG-OD1	5.35	123.12	118.30
1	А	160	ASP	CB-CG-OD1	5.33	123.10	118.30
1	А	118	ASP	CB-CG-OD1	5.32	123.09	118.30
1	А	221	ASP	CB-CG-OD1	5.31	123.08	118.30
1	А	245	ASP	CB-CG-OD1	5.27	123.05	118.30
1	А	614	ASP	CB-CG-OD1	5.27	123.05	118.30
1	А	23	ASP	CB-CG-OD1	5.24	123.02	118.30
1	А	136	ASP	CB-CG-OD2	5.17	122.95	118.30
1	А	320	ASP	CB-CG-OD1	5.16	122.94	118.30
1	А	183	ASP	CB-CG-OD1	5.14	122.93	118.30

Continued from previous page...

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	А	5333	0	5056	150	0
2	В	34	0	30	0	0
3	С	32	0	21	1	0
4	D	23	0	20	0	0
5	А	11	0	10	3	0
6	А	2	0	0	0	0
7	А	185	0	0	4	0
All	All	5620	0	5137	153	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 14.

All (153) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:311:THR:HG21	1:A:353:ARG:HH21	1.21	1.00
5:A:694:ADH:N1	5:A:694:ADH:C1	2.30	0.93
1:A:75:TRP:CZ2	1:A:228:ARG:HD3	2.06	0.91
1:A:301:MET:CG	1:A:419:TYR:HB2	2.02	0.88
1:A:311:THR:HG21	1:A:353:ARG:NH2	1.89	0.88
1:A:3:ASP:HA	1:A:8:ASN:HD22	1.41	0.84
1:A:648:LYS:HD2	1:A:660:GLU:HB3	1.60	0.83
1:A:3:ASP:HB3	1:A:518:ASP:CG	2.02	0.80
1:A:652:LYS:HG2	1:A:657:ILE:HD13	1.64	0.79
1:A:445:THR:HG22	1:A:479:PRO:HB3	1.63	0.79
1:A:301:MET:HG2	1:A:419:TYR:HB2	1.64	0.78
1:A:444:ILE:HD13	1:A:482:LEU:HB2	1.63	0.78
1:A:301:MET:HG3	1:A:419:TYR:HB2	1.66	0.77
1:A:386:THR:O	1:A:390:VAL:HG23	1.86	0.75
1:A:9:VAL:HG13	1:A:225:ASP:O	1.88	0.73
1:A:206:SER:OG	1:A:673:SER:HB2	1.89	0.73
1:A:417:ASP:HA	1:A:436:ARG:HD2	1.70	0.73
1:A:287:SER:O	1:A:291:ARG:HG3	1.89	0.72
1:A:9:VAL:HG22	1:A:225:ASP:HB3	1.72	0.72
1:A:307:MET:O	1:A:311:THR:HB	1.90	0.72



	lo uo pugom	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:498:SER:HB2	1:A:499:PRO:HD2	1.71	0.70	
1:A:209:ASP:O	1:A:213:LYS:HG3	1.91	0.70	
1:A:379:THR:HA	7:A:868:HOH:O	1.93	0.69	
1:A:558:TYR:CD1	1:A:578:ILE:HD12	2.29	0.68	
1:A:499:PRO:HB2	1:A:570:SER:HB3	1.76	0.68	
1:A:397:LEU:HD11	1:A:459:VAL:HG11	1.76	0.68	
1:A:432:VAL:HG13	1:A:489:VAL:HG22	1.75	0.68	
1:A:584:ILE:CG1	1:A:641:ALA:HB2	2.25	0.67	
1:A:9:VAL:HG11	1:A:253:VAL:HG12	1.77	0.66	
1:A:660:GLU:HG2	1:A:682:GLN:HB2	1.76	0.66	
1:A:444:ILE:CD1	1:A:482:LEU:HB2	2.26	0.64	
1:A:652:LYS:HD2	1:A:657:ILE:HD11	1.79	0.64	
1:A:595:THR:HB	1:A:599:GLU:HB3	1.82	0.62	
1:A:632:THR:HG22	7:A:864:HOH:O	1.99	0.61	
1:A:417:ASP:O	1:A:436:ARG:HG3	2.00	0.61	
1:A:584:ILE:HG13	1:A:641:ALA:HB2	1.82	0.61	
1:A:189:ASP:OD1	1:A:193:ARG:HD2	2.01	0.61	
1:A:3:ASP:HA	1:A:8:ASN:ND2	2.13	0.60	
1:A:274:ALA:HB2	1:A:281:LEU:HD12	1.81	0.60	
1:A:456:TYR:O	1:A:468:SER:HB2	2.01	0.60	
1:A:630:TYR:CG	1:A:631:PRO:HA	2.37	0.60	
1:A:187:TYR:O	1:A:191:ILE:HG13	2.02	0.60	
1:A:614:ASP:OD2	1:A:617:LYS:HD3	2.02	0.60	
1:A:89:ASP:O	1:A:93:GLY:HA2	2.02	0.59	
1:A:648:LYS:CD	1:A:660:GLU:HB3	2.32	0.59	
1:A:231:ALA:HB1	1:A:234:HIS:HD2	1.68	0.58	
1:A:38:LEU:HD23	1:A:86:VAL:HG22	1.84	0.58	
1:A:228:ARG:HG3	1:A:256:PHE:CE2	2.38	0.58	
1:A:595:THR:HG22	1:A:651:LYS:HE2	1.86	0.58	
1:A:47:LYS:HG2	1:A:372:PRO:HG3	1.85	0.57	
1:A:9:VAL:HG12	1:A:253:VAL:HA	1.87	0.57	
1:A:584:ILE:HG12	1:A:641:ALA:HB2	1.87	0.57	
1:A:395:ALA:HB3	1:A:396:PRO:HD3	1.87	0.56	
1:A:139:PRO:HB3	1:A:212:LEU:HD22	1.88	0.56	
5:A:694:ADH:N1	5:A:694:ADH:C7	2.69	0.55	
1:A:3:ASP:HB3	1:A:518:ASP:OD1	2.07	0.55	
1:A:424:LYS:HE3	1:A:426:GLY:O	2.07	0.54	
1:A:574:ASN:ND2	1:A:574:ASN:H	2.06	0.54	
1:A:499:PRO:HB2	1:A:570:SER:CB	2.38	0.53	
1:A:515:ILE:HD11	1:A:531:PHE:CZ	2.43	0.53	
1:A:342:VAL:HG22	7:A:715:HOH:O	2.09	0.53	



	lo uo pugom	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:509:THR:HG22	1:A:513:GLN:OE1	2.09	0.53
1:A:230:ASP:OD1	5:A:694:ADH:H1	2.09	0.53
1:A:340:ARG:N	1:A:341:PRO:HD2	2.24	0.52
1:A:652:LYS:CG	1:A:657:ILE:HD13	2.37	0.51
1:A:102:TRP:HB3	1:A:143:SER:HB3	1.92	0.51
1:A:292:GLN:HG2	1:A:298:THR:OG1	2.10	0.51
1:A:149:ASP:OD2	1:A:151:THR:HG22	2.12	0.49
1:A:192:TYR:HB2	1:A:626:VAL:HG11	1.94	0.49
1:A:261:LEU:HB2	1:A:284:PHE:HB3	1.93	0.49
1:A:339:THR:O	1:A:342:VAL:HG23	2.12	0.49
1:A:282:LEU:HD23	1:A:322:VAL:HB	1.95	0.49
1:A:652:LYS:HD2	1:A:657:ILE:CD1	2.43	0.49
1:A:588:PHE:O	1:A:634:TYR:HA	2.14	0.48
1:A:383:THR:HG22	1:A:388:TYR:CE2	2.49	0.47
1:A:35:THR:HG22	1:A:36:GLY:N	2.28	0.47
1:A:188:GLU:HB2	1:A:623:PHE:CD1	2.49	0.47
1:A:24:ARG:HG3	1:A:375:ARG:O	2.15	0.47
1:A:80:VAL:HA	1:A:108:ARG:O	2.15	0.47
1:A:408:THR:O	1:A:423:ARG:HA	2.15	0.47
1:A:87:LEU:HB2	1:A:95:SER:HB3	1.97	0.47
1:A:325:ILE:HB	1:A:333:PHE:CD2	2.51	0.46
1:A:471:VAL:HG22	1:A:477:VAL:HG22	1.98	0.46
1:A:580:THR:HB	1:A:640:PRO:HG3	1.98	0.46
1:A:311:THR:HG22	1:A:312:ALA:N	2.30	0.45
1:A:143:SER:HB2	1:A:144:PRO:HD2	1.97	0.45
1:A:429:VAL:HG12	1:A:430:ALA:N	2.31	0.45
3:C:2:GLC:H62	3:C:3:G6D:O5	2.16	0.45
1:A:35:THR:CG2	1:A:36:GLY:N	2.80	0.45
1:A:195:LEU:HD22	1:A:196:PHE:CD2	2.52	0.45
1:A:213:LYS:O	1:A:216:ILE:HG22	2.17	0.45
1:A:332:ARG:HG3	1:A:368:GLY:O	2.17	0.45
1:A:606:ASN:HB2	1:A:646:GLN:H	1.80	0.45
1:A:78:GLN:HG2	1:A:80:VAL:HG22	1.97	0.45
1:A:218:VAL:O	1:A:222:MET:HG2	2.17	0.45
1:A:302:TYR:HA	1:A:414:ILE:HD11	1.99	0.44
1:A:498:SER:HB2	1:A:499:PRO:CD	2.42	0.44
1:A:510:LYS:HE2	1:A:513:GLN:NE2	2.32	0.44
1:A:340:ARG:N	1:A:341:PRO:CD	2.80	0.44
1:A:305:ASP:O	1:A:309:GLN:HG2	2.17	0.44
1:A:340:ARG:HB3	1:A:341:PRO:HD3	2.00	0.44
1:A:108:ARG:HD3	1:A:161:ASN:ND2	2.32	0.44



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:140:ASN:HB3	7:A:700:HOH:O	2.17	0.44	
1:A:232:VAL:HG11	1:A:257:GLY:HA3	1.99	0.44	
1:A:395:ALA:N	1:A:396:PRO:HD2	2.33	0.44	
1:A:559:ASN:OD1	1:A:574:ASN:HB3	2.18	0.44	
1:A:604:THR:HG22	1:A:648:LYS:O	2.18	0.43	
1:A:24:ARG:NH2	1:A:98:TYR:CD2	2.86	0.43	
1:A:383:THR:HG22	1:A:388:TYR:CZ	2.52	0.43	
1:A:287:SER:HB2	1:A:324:PHE:O	2.17	0.43	
1:A:633:TRP:CD1	1:A:633:TRP:N	2.86	0.43	
1:A:231:ALA:HB1	1:A:234:HIS:CD2	2.51	0.43	
1:A:560:ILE:O	1:A:572:THR:HA	2.18	0.43	
1:A:9:VAL:CG1	1:A:253:VAL:HG12	2.47	0.43	
1:A:423:ARG:HB2	1:A:430:ALA:HB3	1.99	0.43	
1:A:47:LYS:HE3	1:A:92:PHE:CD1	2.53	0.43	
1:A:42:THR:O	1:A:43:HIS:HB2	2.19	0.43	
1:A:591:ASN:HB2	1:A:680:ASN:OD1	2.18	0.43	
1:A:37:ASP:O	1:A:48:LYS:HE3	2.19	0.42	
1:A:120:GLN:HG3	1:A:222:MET:CE	2.49	0.42	
1:A:233:LYS:O	1:A:233:LYS:HG2	2.18	0.42	
1:A:68:GLY:O	1:A:392:LYS:HG3	2.20	0.42	
1:A:411:GLN:HE21	1:A:413:TRP:N	2.18	0.42	
1:A:652:LYS:CD	1:A:657:ILE:CD1	2.98	0.42	
1:A:203:GLN:HE21	1:A:203:GLN:HB3	1.68	0.42	
1:A:639:VAL:HB	1:A:640:PRO:HD2	2.01	0.42	
1:A:195:LEU:O	1:A:196:PHE:HB2	2.20	0.42	
1:A:38:LEU:HD23	1:A:38:LEU:HA	1.75	0.42	
1:A:147:GLU:O	1:A:169:THR:HG23	2.20	0.42	
1:A:610:LEU:HA	1:A:610:LEU:HD12	1.78	0.42	
1:A:89:ASP:HB3	1:A:94:GLY:H	1.84	0.42	
1:A:143:SER:CB	1:A:144:PRO:HD2	2.50	0.42	
1:A:584:ILE:HG13	1:A:641:ALA:CB	2.49	0.42	
1:A:4:THR:HB	1:A:399:LYS:HD3	2.01	0.41	
1:A:92:PHE:CZ	1:A:372:PRO:HD2	2.55	0.41	
1:A:630:TYR:CD2	1:A:631:PRO:HA	2.55	0.41	
1:A:600:ASN:HB3	1:A:621:PRO:HB3	2.01	0.41	
1:A:648:LYS:HE2	1:A:664:ASN:OD1	2.20	0.41	
1:A:281:LEU:HD23	1:A:281:LEU:HA	1.94	0.41	
1:A:108:ARG:HD3	1:A:161:ASN:HD22	1.86	0.41	
1:A:531:PHE:CD1	1:A:531:PHE:N	2.88	0.41	
1:A:421:TYR:O	1:A:431:LEU:HD12	2.21	0.41	
1:A:518:ASP:OD1	1:A:545:GLU:HG3	2.20	0.41	



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:TYR:HB2	1:A:71:VAL:HG21	2.03	0.41
1:A:69:MET:O	1:A:392:LYS:HA	2.21	0.41
1:A:341:PRO:HD3	1:A:438:LEU:HD11	2.01	0.41
1:A:576:ILE:HD12	1:A:576:ILE:HA	1.74	0.41
1:A:500:LEU:O	1:A:519:GLY:HA3	2.21	0.40
1:A:513:GLN:O	1:A:549:LYS:HA	2.22	0.40
1:A:149:ASP:OD1	1:A:151:THR:HB	2.22	0.40
1:A:12:TYR:CE2	1:A:134:ILE:HD11	2.57	0.40
1:A:104:ARG:HG2	1:A:104:ARG:HH11	1.86	$0.\overline{40}$
1:A:205:ASN:HB3	1:A:208:ILE:HG12	2.03	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	А	681/683~(100%)	633~(93%)	44 (6%)	4 (1%)	25 33

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	22	THR
1	А	626	VAL
1	А	196	PHE
1	А	379	THR

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	А	583/583~(100%)	538~(92%)	45 (8%)	13	16

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ASP
1	А	10	VAL
1	А	45	SER
1	А	48	LYS
1	А	60	LYS
1	А	67	THR
1	А	75	TRP
1	А	80	VAL
1	А	117	THR
1	А	136	ASP
1	А	143	SER
1	А	151	THR
1	А	161	ASN
1	А	163	THR
1	А	195	LEU
1	А	203	GLN
1	А	228	ARG
1	А	229	LEU
1	А	242	ASN
1	А	270	ASN
1	А	301	MET
1	А	311	THR
1	А	318	ILE
1	А	342	VAL
1	А	353	ARG
1	А	413	TRP
1	А	436	ARG
1	А	473	SER
1	А	509	THR
1	А	524	THR
1	А	533	SER
1	А	540	SER
1	А	542	ASP
1	А	574	ASN
1	А	576	ILE



Mol	Chain	Res	Type
1	А	610	LEU
1	А	632	THR
1	А	639	VAL
1	А	645	ILE
1	А	648	LYS
1	А	650	ILE
1	А	653	ASN
1	А	656	THR
1	А	671	SER
1	А	677	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	8	ASN
1	А	43	HIS
1	А	62	ASN
1	А	120	GLN
1	А	161	ASN
1	А	270	ASN
1	А	297	ASN
1	А	382	ASN
1	А	410	GLN
1	А	411	GLN
1	А	574	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)

8 monosaccharides 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).

Mal	Turne	Chain	Dec	Tink	Bo	ond leng	ths	В	ond ang	les
INIOI	туре	Unain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLC	В	1	2	12,12,12	0.39	0	$17,\!17,\!17$	1.03	2 (11%)
2	GLC	В	2	2	11,11,12	0.47	0	$15,\!15,\!17$	1.14	1 (6%)
2	GLC	В	3	2	11,11,12	0.38	0	$15,\!15,\!17$	1.27	1 (6%)
3	GLC	С	1	3	12,12,12	0.35	0	$17,\!17,\!17$	0.95	1 (5%)
3	GLC	С	2	3	11,11,12	0.45	0	$15,\!15,\!17$	1.49	3 (20%)
3	G6D	С	3	5,3	9,9,11	0.37	0	10,12,16	1.46	2 (20%)
4	GLC	D	1	5,4	12,12,12	0.41	0	17,17,17	0.63	0
4	GLC	D	2	4	11,11,12	0.47	0	$15,\!15,\!17$	1.76	3 (20%)

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	В	1	2	-	2/2/22/22	0/1/1/1
2	GLC	В	2	2	-	0/2/19/22	0/1/1/1
2	GLC	В	3	2	-	2/2/19/22	0/1/1/1
3	GLC	С	1	3	-	0/2/22/22	0/1/1/1
3	GLC	С	2	3	-	0/2/19/22	0/1/1/1
3	G6D	С	3	5,3	-	-	0/1/1/1
4	GLC	D	1	5,4	-	0/2/22/22	0/1/1/1
4	GLC	D	2	4	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
4	D	2	GLC	C1-O5-C5	4.91	118.84	112.19
2	В	3	GLC	C1-O5-C5	3.71	117.22	112.19
3	С	2	GLC	O5-C1-C2	3.39	116.00	110.77
2	В	2	GLC	C1-O5-C5	3.29	116.65	112.19
3	С	2	GLC	C1-O5-C5	3.24	116.58	112.19
3	С	3	G6D	O5-C1-C2	2.87	115.20	110.77



Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
4	D	2	GLC	C3-C4-C5	2.64	114.95	110.24
3	С	3	G6D	O5-C5-C4	-2.54	106.79	109.34
2	В	1	GLC	C4-C3-C2	2.48	115.15	110.82
4	D	2	GLC	O5-C5-C4	2.32	116.47	110.83
3	С	1	GLC	C3-C4-C5	2.16	114.08	110.24
3	С	2	GLC	C1-C2-C3	2.09	112.23	109.67
2	В	1	GLC	C1-C2-C3	2.04	114.55	110.31

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	1	GLC	C4-C5-C6-O6
2	В	3	GLC	O5-C5-C6-O6
2	В	1	GLC	O5-C5-C6-O6
2	В	3	GLC	C4-C5-C6-O6
4	D	2	GLC	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	С	3	G6D	1	0
3	С	2	GLC	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.









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
5	ADH	A	694	4,3	11,11,11	8.26	5 (45%)	10,15,15	4.02	2 (20%)

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	ADH	А	694	4,3	-	1/2/18/18	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	А	694	ADH	C1-N1	26.53	2.30	1.47
5	А	694	ADH	C4-C5	-4.93	1.40	1.50
5	А	694	ADH	C1-C7	-2.86	1.43	1.50
5	А	694	ADH	C7-C5	2.75	1.42	1.33
5	А	694	ADH	C3-C2	-2.02	1.49	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
5	А	694	ADH	C7-C1-N1	-12.15	88.81	110.71
5	А	694	ADH	C2-C1-N1	3.46	118.44	111.40

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	А	694	ADH	C7-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	А	694	ADH	3	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)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

