



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 02:54 pm GMT

PDB ID : 3CK9
Title : B. thetaiotaomicron SusD with maltoheptaose
Authors : Koropatkin, N.M.; Martens, E.C.; Gordon, J.I.; Smith, T.J.
Deposited on : 2008-03-14
Resolution : 2.20 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

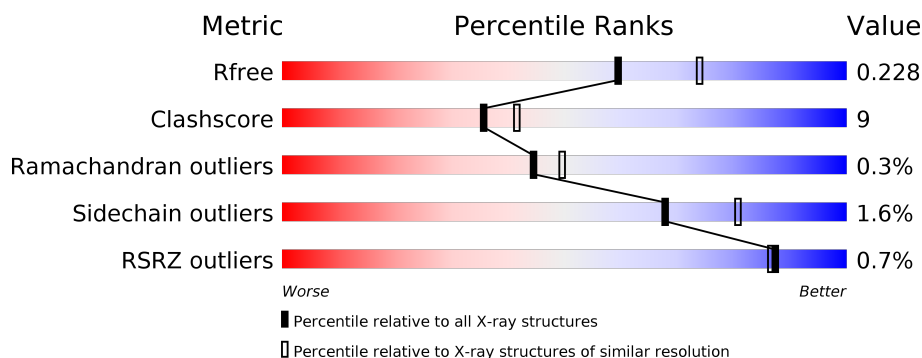
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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	527	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 16%, green 80%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 80% 16% • • </div> </div>
1	B	527	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 76%, yellow 20%, orange 3%, grey 1%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 76% 20% • • </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	GLC	A	801	-	-	-	X
2	GLC	A	807	X	-	-	X
5	EDO	A	731	-	-	-	X
5	EDO	A	737	-	-	-	X
5	EDO	A	747	-	-	-	X
5	EDO	B	734	-	-	-	X
5	EDO	B	741	-	-	X	X
5	EDO	B	748	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9125 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 SusD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	508	Total	C	N	O	S	0	0	0
			4075	2562	701	793	19			
1	B	515	Total	C	N	O	S	0	0	0
			4121	2590	709	803	19			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	GLY	-	EXPRESSION TAG	UNP Q8A1G2
A	100	LYS	GLU	SEE REMARK 999	UNP Q8A1G2
B	25	GLY	-	EXPRESSION TAG	UNP Q8A1G2
B	100	LYS	GLU	SEE REMARK 999	UNP Q8A1G2

- Molecule 2 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	7	Total	C	O	0	0
			78	42	36		

- Molecule 3 is a polymer of unknown type called SUGAR (6-MER).

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

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Ca	0	0
			2	2		
4	A	2	Total	Ca	0	0
			2	2		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

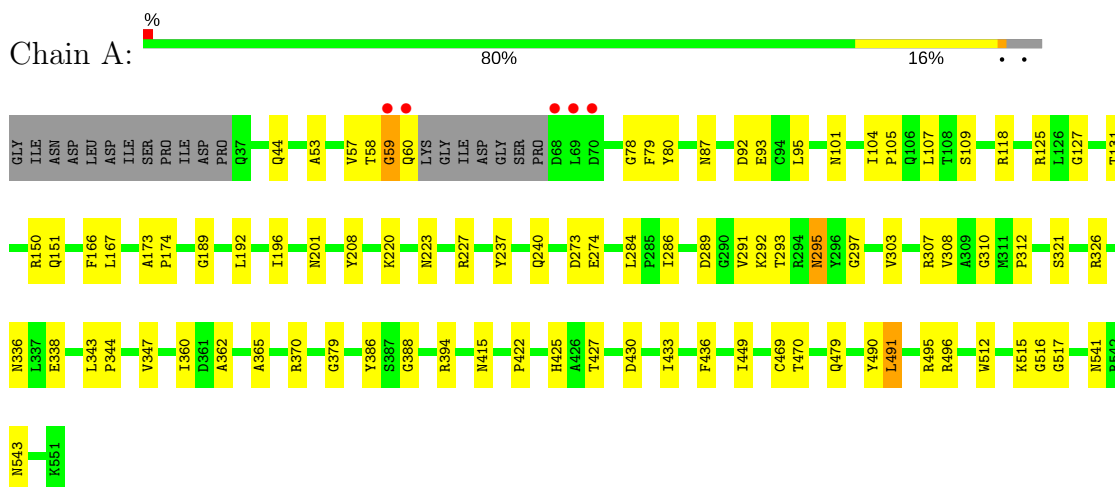
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	407	Total 407	O 407	0	0
6	B	321	Total 321	O 321	0	0

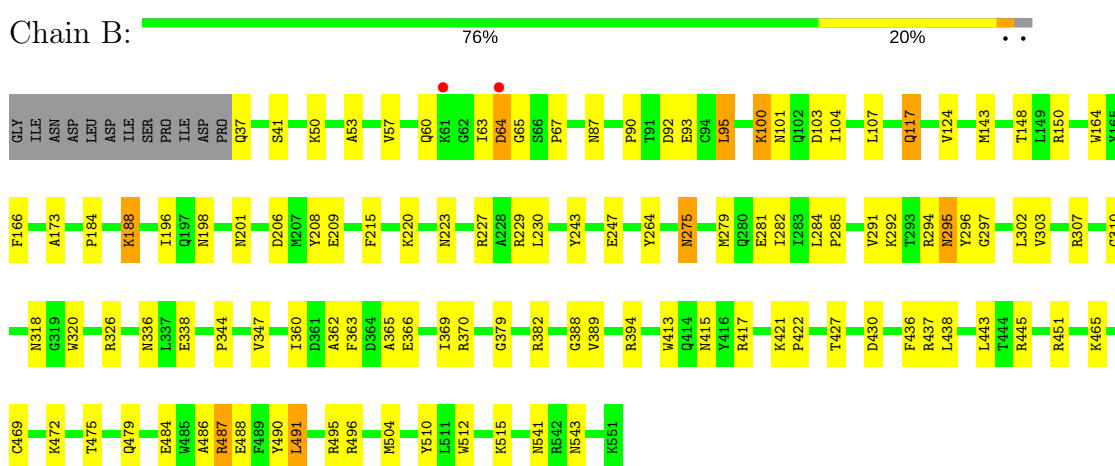
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: SusD



• Molecule 1: SusD



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	59.61Å 73.22Å 83.38Å 65.06° 72.19° 69.73°	Depositor
Resolution (Å)	60.20 – 2.20 60.26 – 2.18	Depositor EDS
% Data completeness (in resolution range)	94.6 (60.20-2.20) 82.1 (60.26-2.18)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.90 (at 2.18Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.185 , 0.222 0.192 , 0.228	Depositor DCC
R_{free} test set	5665 reflections (10.15%)	DCC
Wilson B-factor (Å ²)	13.0	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9125	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.04% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.34	0/4167	0.56	0/5638
1	B	0.34	0/4215	0.59	1/5704 (0.0%)
All	All	0.34	0/8382	0.58	1/11342 (0.0%)

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
2	A	1	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	65	GLY	N-CA-C	-6.74	96.25	113.10

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	807	GLC	C1

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	4075	0	3879	62	0
1	B	4121	0	3926	87	0
2	A	78	0	66	2	0
3	B	67	0	57	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	20	0	29	2	0
5	B	32	0	48	7	0
6	A	407	0	0	7	0
6	B	321	0	0	7	0
All	All	9125	0	8005	150	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 9.

All (150) 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)
2:A:801:GLC:O3	2:A:807:GLC:H1	1.57	1.05
1:A:44:GLN:HE21	1:A:151:GLN:HE22	1.18	0.90
1:B:484:GLU:HA	1:B:487:ARG:HH12	1.39	0.86
1:B:201:ASN:HD22	1:B:227:ARG:HH12	1.22	0.85
1:B:484:GLU:HA	1:B:487:ARG:NH1	1.93	0.84
1:B:275:ASN:N	1:B:279:MET:HE2	1.96	0.80
1:A:174:PRO:O	5:A:737:EDO:H22	1.84	0.78
1:A:93:GLU:HG3	1:A:495:ARG:HG2	1.66	0.77
1:A:166:PHE:HB3	1:A:173:ALA:HB2	1.66	0.77
1:A:44:GLN:HE21	1:A:151:GLN:NE2	1.83	0.77
1:B:100:LYS:HA	1:B:100:LYS:HE3	1.68	0.76
1:A:201:ASN:HD22	1:A:227:ARG:HH12	1.37	0.71
1:B:90:PRO:HB3	1:B:107:LEU:O	1.90	0.71
1:B:284:LEU:HB3	1:B:436:PHE:HB2	1.71	0.71
1:B:487:ARG:HH11	1:B:487:ARG:HB2	1.56	0.71
1:B:166:PHE:HB3	1:B:173:ALA:HB2	1.73	0.69
1:A:291:VAL:HG23	1:A:292:LYS:HG3	1.75	0.69
1:A:101:ASN:HB2	1:A:104:ILE:HG13	1.73	0.68
1:B:201:ASN:HD22	1:B:227:ARG:NH1	1.91	0.68
1:B:295:ASN:ND2	1:B:297:GLY:H	1.92	0.67
1:A:470:THR:HG21	6:A:1151:HOH:O	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:LEU:HB3	1:A:436:PHE:HB2	1.76	0.66
1:B:93:GLU:HG3	1:B:495:ARG:HG2	1.78	0.66
1:A:87:ASN:HD22	1:A:496:ARG:HB3	1.62	0.64
1:A:295:ASN:ND2	1:A:297:GLY:H	1.96	0.63
1:B:504:MET:HB3	1:B:510:TYR:HB3	1.79	0.63
1:B:291:VAL:HG23	1:B:292:LYS:HG3	1.81	0.62
1:B:188:LYS:H	1:B:188:LYS:HD3	1.65	0.61
1:B:150:ARG:HD3	1:B:208:TYR:CE1	2.37	0.60
1:B:303:VAL:O	1:B:307:ARG:HG2	2.02	0.60
1:A:87:ASN:ND2	1:A:496:ARG:HB3	2.17	0.59
1:B:184:PRO:HB2	6:B:1245:HOH:O	2.02	0.59
1:B:275:ASN:H	1:B:279:MET:HE2	1.68	0.58
1:A:344:PRO:HB2	1:A:347:VAL:HG23	1.86	0.58
1:B:150:ARG:HG3	1:B:150:ARG:HH11	1.69	0.58
1:A:479:GLN:NE2	6:A:1211:HOH:O	2.36	0.57
1:B:67:PRO:HG2	1:B:124:VAL:CG1	2.34	0.57
1:A:422:PRO:HG3	1:B:362:ALA:HB1	1.87	0.57
1:B:365:ALA:HB2	1:B:370:ARG:HD3	1.86	0.56
1:B:320:TRP:HE1	5:B:741:EDO:H11	1.70	0.56
1:B:363:PHE:CE1	1:B:389:VAL:HG11	2.41	0.55
1:B:344:PRO:HB2	1:B:347:VAL:HG23	1.87	0.55
1:B:427:THR:HG21	5:B:741:EDO:H21	1.87	0.55
1:B:95:LEU:HD13	1:B:326:ARG:NE	2.22	0.54
1:B:101:ASN:HB2	1:B:104:ILE:HG13	1.89	0.54
1:B:53:ALA:O	1:B:57:VAL:HG22	2.07	0.54
1:B:209:GLU:OE2	1:B:220:LYS:HE3	2.08	0.54
1:B:201:ASN:ND2	1:B:227:ARG:HH12	2.00	0.54
1:A:59:GLY:C	1:A:60:GLN:HG3	2.28	0.53
1:A:273:ASP:OD1	1:A:274:GLU:HG3	2.09	0.53
1:A:150:ARG:HD3	1:A:208:TYR:CE1	2.44	0.53
1:B:164:TRP:CZ2	1:B:229:ARG:HD3	2.44	0.53
1:B:484:GLU:CD	1:B:487:ARG:HH12	2.12	0.53
1:A:365:ALA:HB2	1:A:370:ARG:HD3	1.92	0.52
1:A:289:ASP:OD1	1:A:291:VAL:HG22	2.08	0.52
1:B:37:GLN:N	1:B:41:SER:HG	2.08	0.52
1:B:487:ARG:HH11	1:B:487:ARG:CB	2.23	0.52
1:B:541:ASN:ND2	6:B:1245:HOH:O	2.43	0.52
1:B:60:GLN:HB2	1:B:63:ILE:HB	1.92	0.51
1:B:541:ASN:OD1	1:B:543:ASN:HB2	2.11	0.51
1:A:53:ALA:O	1:A:57:VAL:HG22	2.11	0.51
1:A:394:ARG:HG2	1:A:394:ARG:HH11	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:TYR:CZ	1:B:451:ARG:HD2	2.46	0.50
1:A:344:PRO:HB3	6:A:1193:HOH:O	2.11	0.50
1:B:366:GLU:HG3	6:B:1191:HOH:O	2.12	0.50
1:B:318:ASN:HD22	5:B:741:EDO:C1	2.25	0.50
1:A:78:GLY:HA3	6:A:808:HOH:O	2.11	0.50
1:B:296:TYR:CE1	5:B:742:EDO:H21	2.48	0.49
1:A:104:ILE:HB	1:A:105:PRO:HD3	1.94	0.49
1:A:95:LEU:HG	1:A:326:ARG:HG2	1.95	0.49
1:B:310:GLY:O	1:B:360:ILE:HD13	2.12	0.49
1:A:127:GLY:O	1:A:131:THR:HG23	2.12	0.49
1:B:150:ARG:HG3	1:B:150:ARG:NH1	2.27	0.49
1:B:50:LYS:HG3	6:B:1062:HOH:O	2.12	0.49
1:B:281:GLU:HG3	1:B:438:LEU:HB3	1.96	0.48
1:A:166:PHE:CB	1:A:173:ALA:HB2	2.41	0.47
1:B:208:TYR:O	1:B:220:LYS:HG3	2.15	0.47
1:A:201:ASN:HD22	1:A:227:ARG:NH1	2.09	0.47
1:B:486:ALA:O	1:B:490:TYR:HB3	2.15	0.47
1:A:80:TYR:CE2	1:A:433:ILE:HG21	2.50	0.47
1:B:188:LYS:HD3	1:B:188:LYS:N	2.29	0.47
1:A:310:GLY:O	1:A:360:ILE:HD13	2.15	0.46
1:B:394:ARG:HG3	1:B:394:ARG:HH11	1.79	0.46
1:B:143:MET:HB2	1:B:148:THR:HG21	1.97	0.46
1:B:87:ASN:HD22	1:B:496:ARG:HD3	1.80	0.46
1:A:201:ASN:ND2	1:A:227:ARG:HH12	2.11	0.46
1:B:379:GLY:O	1:B:469:CYS:HA	2.15	0.46
1:A:92:ASP:HB3	1:A:512:TRP:CD2	2.51	0.46
1:B:282:ILE:HG21	1:B:285:PRO:HB3	1.98	0.46
1:B:294:ARG:HB2	5:B:742:EDO:H12	1.97	0.46
1:B:427:THR:CG2	5:B:741:EDO:H21	2.45	0.46
1:A:308:VAL:HB	1:A:321:SER:HB3	1.97	0.46
1:B:487:ARG:NH1	1:B:487:ARG:HB2	2.29	0.46
1:A:336:ASN:OD1	1:A:338:GLU:HB2	2.16	0.46
1:A:312:PRO:HD3	1:A:360:ILE:HG21	1.98	0.46
1:B:223:ASN:O	1:B:227:ARG:HG3	2.16	0.45
1:B:302:LEU:HD13	1:B:413:TRP:CE2	2.51	0.45
1:A:220:LYS:O	1:A:223:ASN:HB3	2.16	0.45
2:A:801:GLC:C3	2:A:807:GLC:H1	2.43	0.45
1:B:150:ARG:HD2	6:B:1034:HOH:O	2.16	0.45
1:B:92:ASP:HB3	1:B:512:TRP:CD2	2.52	0.45
1:B:417:ARG:HD3	1:B:421:LYS:O	2.16	0.44
1:A:512:TRP:CE2	1:A:515:LYS:HB2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:LEU:HD22	1:A:118:ARG:HD2	2.00	0.44
1:B:264:TYR:CE1	1:B:382:ARG:HG2	2.53	0.44
1:A:286:ILE:HB	1:A:433:ILE:HB	2.00	0.44
1:B:87:ASN:HA	1:B:496:ARG:HB3	2.00	0.43
1:B:247:GLU:HG3	1:B:445:ARG:HG3	1.99	0.43
1:B:103:ASP:HB2	1:B:117:GLN:HG2	1.99	0.43
1:A:415:ASN:HD21	1:A:430:ASP:H	1.64	0.43
1:A:303:VAL:O	1:A:307:ARG:HG2	2.19	0.43
1:A:425:HIS:CE1	1:A:427:THR:HB	2.54	0.43
1:B:92:ASP:HB3	1:B:512:TRP:CG	2.53	0.43
1:A:192:LEU:O	1:A:196:ILE:HG13	2.19	0.43
1:A:490:TYR:O	1:A:491:LEU:HB2	2.19	0.43
1:B:150:ARG:NH1	1:B:206:ASP:O	2.51	0.43
1:B:484:GLU:CD	1:B:487:ARG:NH1	2.72	0.42
1:B:295:ASN:HD22	1:B:295:ASN:C	2.23	0.42
1:A:379:GLY:O	1:A:469:CYS:HA	2.19	0.42
1:B:415:ASN:HD21	1:B:430:ASP:H	1.68	0.42
1:A:362:ALA:HB1	1:B:422:PRO:HG3	2.01	0.42
1:A:87:ASN:HD22	1:A:496:ARG:HD3	1.84	0.42
1:B:437:ARG:NH2	1:B:488:GLU:OE2	2.42	0.42
1:A:109:SER:HB2	1:A:517:GLY:N	2.34	0.42
1:B:369:ILE:HD12	1:B:388:GLY:HA2	2.02	0.42
5:A:731:EDO:H21	6:A:1135:HOH:O	2.19	0.42
1:B:336:ASN:OD1	1:B:338:GLU:HB2	2.20	0.41
1:B:284:LEU:CB	1:B:436:PHE:HB2	2.46	0.41
1:A:109:SER:O	1:A:516:GLY:HA2	2.20	0.41
1:B:490:TYR:O	1:B:491:LEU:HB2	2.19	0.41
1:B:87:ASN:HA	1:B:87:ASN:HD22	1.69	0.41
1:B:196:ILE:HG22	1:B:230:LEU:HD11	2.03	0.41
1:B:515:LYS:HA	6:B:1097:HOH:O	2.21	0.41
1:B:215:PHE:CZ	1:B:285:PRO:HG3	2.56	0.41
1:B:479:GLN:HB2	6:B:1071:HOH:O	2.19	0.41
1:A:295:ASN:C	1:A:295:ASN:HD22	2.23	0.41
1:A:541:ASN:OD1	1:A:543:ASN:HB2	2.21	0.41
1:B:475:THR:HG23	1:B:475:THR:O	2.20	0.41
1:A:386:TYR:CZ	1:A:388:GLY:HA3	2.56	0.41
1:A:167:LEU:HD11	1:A:237:TYR:HB3	2.02	0.40
1:A:79:PHE:HA	1:A:125:ARG:HG2	2.03	0.40
1:A:92:ASP:HB3	1:A:512:TRP:CG	2.56	0.40
1:A:449:ILE:HG23	6:A:1044:HOH:O	2.20	0.40
1:A:59:GLY:N	6:A:879:HOH:O	2.16	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:486:ALA:HB2	1:B:495:ARG:CZ	2.51	0.40
1:A:289:ASP:HB3	1:A:293:THR:H	1.85	0.40
1:A:58:THR:O	1:A:59:GLY:O	2.39	0.40
1:B:294:ARG:CB	5:B:742:EDO:H12	2.51	0.40
1:B:465:LYS:HG3	1:B:472:LYS:HE3	2.03	0.40
1:A:343:LEU:HD12	1:A:344:PRO:HD2	2.02	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	504/527 (96%)	482 (96%)	20 (4%)	2 (0%)	38	41
1	B	513/527 (97%)	489 (95%)	23 (4%)	1 (0%)	51	58
All	All	1017/1054 (96%)	971 (96%)	43 (4%)	3 (0%)	44	49

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	59	GLY
1	B	64	ASP
1	A	189	GLY

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	425/441 (96%)	422 (99%)	3 (1%)	87	93
1	B	430/441 (98%)	419 (97%)	11 (3%)	51	64
All	All	855/882 (97%)	841 (98%)	14 (2%)	68	81

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	240	GLN
1	A	295	ASN
1	A	491	LEU
1	B	64	ASP
1	B	95	LEU
1	B	100	LYS
1	B	117	GLN
1	B	188	LYS
1	B	198	ASN
1	B	275	ASN
1	B	295	ASN
1	B	443	LEU
1	B	487	ARG
1	B	491	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	87	ASN
1	A	151	GLN
1	A	201	ASN
1	A	240	GLN
1	A	295	ASN
1	A	331	GLN
1	A	415	ASN
1	A	452	GLN
1	A	479	GLN
1	A	540	ASN
1	A	543	ASN
1	B	44	GLN
1	B	87	ASN
1	B	151	GLN
1	B	201	ASN

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Mol	Chain	Res	Type
1	B	275	ASN
1	B	295	ASN
1	B	318	ASN
1	B	331	GLN
1	B	415	ASN
1	B	479	GLN
1	B	540	ASN
1	B	543	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](#)

13 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	801	2	11,11,12	0.67	0	13,15,17	0.70	0
2	GLC	A	802	2	11,11,12	1.29	1 (9%)	13,15,17	1.02	0
2	GLC	A	803	2	11,11,12	1.36	1 (9%)	13,15,17	1.20	1 (7%)
2	GLC	A	804	2	11,11,12	1.30	1 (9%)	13,15,17	1.15	1 (7%)
2	GLC	A	805	2	11,11,12	1.11	0	13,15,17	0.85	0
2	GLC	A	806	2	11,11,12	0.94	0	13,15,17	1.01	0
2	GLC	A	807	2	12,12,12	0.88	0	17,17,17	0.78	0
3	GLC	B	901	3	12,12,12	1.07	0	17,17,17	0.73	0
3	GLC	B	902	3	11,11,12	1.18	0	13,15,17	0.83	0
3	GLC	B	903	3	11,11,12	1.11	0	13,15,17	0.68	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GLC	B	904	3	11,11,12	1.15	0	13,15,17	0.76	0
3	GLC	B	905	3	11,11,12	1.31	1 (9%)	13,15,17	0.86	0
3	GLC	B	906	3	11,11,12	1.29	2 (18%)	13,15,17	0.70	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	801	2	-	0/2/19/22	0/1/1/1
2	GLC	A	802	2	-	0/2/19/22	0/1/1/1
2	GLC	A	803	2	-	0/2/19/22	0/1/1/1
2	GLC	A	804	2	-	0/2/19/22	0/1/1/1
2	GLC	A	805	2	-	0/2/19/22	0/1/1/1
2	GLC	A	806	2	-	0/2/19/22	0/1/1/1
2	GLC	A	807	2	1/1/5/5	0/2/22/22	0/1/1/1
3	GLC	B	901	3	-	0/2/22/22	0/1/1/1
3	GLC	B	902	3	-	0/2/19/22	0/1/1/1
3	GLC	B	903	3	-	0/2/19/22	0/1/1/1
3	GLC	B	904	3	-	0/2/19/22	0/1/1/1
3	GLC	B	905	3	-	0/2/19/22	0/1/1/1
3	GLC	B	906	3	-	0/2/19/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	802	GLC	O5-C1	2.08	1.47	1.43
3	B	906	GLC	O5-C1	2.27	1.47	1.43
3	B	905	GLC	O5-C1	2.32	1.47	1.43
3	B	906	GLC	C2-C3	2.34	1.55	1.52
2	A	804	GLC	C4-C5	2.58	1.58	1.53
2	A	803	GLC	O5-C1	2.78	1.48	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	804	GLC	O4-C4-C3	-2.46	105.00	110.36
2	A	803	GLC	C1-C2-C3	-2.46	106.53	109.65

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	807	GLC	C1

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	GLC	2	0
2	A	807	GLC	2	0

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 4 are monoatomic - leaving 13 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	EDO	A	730	-	3,3,3	0.64	0	2,2,2	0.29	0
5	EDO	A	731	4	3,3,3	0.62	0	2,2,2	0.28	0
5	EDO	A	736	-	3,3,3	0.62	0	2,2,2	0.33	0
5	EDO	A	737	-	3,3,3	0.54	0	2,2,2	0.45	0
5	EDO	A	747	-	3,3,3	0.68	0	2,2,2	0.33	0
5	EDO	B	732	-	3,3,3	0.65	0	2,2,2	0.32	0
5	EDO	B	733	-	3,3,3	0.69	0	2,2,2	0.33	0
5	EDO	B	734	-	3,3,3	0.67	0	2,2,2	0.33	0
5	EDO	B	741	-	3,3,3	0.61	0	2,2,2	0.35	0
5	EDO	B	742	-	3,3,3	0.65	0	2,2,2	0.32	0
5	EDO	B	744	-	3,3,3	0.63	0	2,2,2	0.35	0
5	EDO	B	748	-	3,3,3	0.66	0	2,2,2	0.34	0
5	EDO	B	749	-	3,3,3	0.61	0	2,2,2	0.40	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	EDO	A	730	-	-	0/1/1/1	0/0/0/0
5	EDO	A	731	4	-	0/1/1/1	0/0/0/0
5	EDO	A	736	-	-	0/1/1/1	0/0/0/0
5	EDO	A	737	-	-	0/1/1/1	0/0/0/0
5	EDO	A	747	-	-	0/1/1/1	0/0/0/0
5	EDO	B	732	-	-	0/1/1/1	0/0/0/0
5	EDO	B	733	-	-	0/1/1/1	0/0/0/0
5	EDO	B	734	-	-	0/1/1/1	0/0/0/0
5	EDO	B	741	-	-	0/1/1/1	0/0/0/0
5	EDO	B	742	-	-	0/1/1/1	0/0/0/0
5	EDO	B	744	-	-	0/1/1/1	0/0/0/0
5	EDO	B	748	-	-	0/1/1/1	0/0/0/0
5	EDO	B	749	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	731	EDO	1	0
5	A	737	EDO	1	0
5	B	741	EDO	4	0
5	B	742	EDO	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](#)

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	508/527 (96%)	-0.40	5 (0%)	82 81	5, 14, 29, 49	0
1	B	515/527 (97%)	-0.35	2 (0%)	92 91	7, 15, 30, 45	0
All	All	1023/1054 (97%)	-0.37	7 (0%)	87 86	5, 15, 29, 49	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	60	GLN	4.9
1	A	59	GLY	4.1
1	A	70	ASP	3.4
1	B	61	LYS	3.2
1	B	64	ASP	2.9
1	A	69	LEU	2.4
1	A	68	ASP	2.2

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	GLC	A	807	12/12	0.74	0.27	4.69	24,29,30,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	GLC	A	801	11/12	0.77	0.21	2.96	28,34,36,36	0
3	GLC	B	902	11/12	0.93	0.13	1.74	16,17,18,18	0
3	GLC	B	903	11/12	0.92	0.14	0.99	11,15,17,20	0
3	GLC	B	901	12/12	0.88	0.13	0.68	22,24,26,30	0
2	GLC	A	806	11/12	0.94	0.11	-0.78	20,21,22,23	0
2	GLC	A	805	11/12	0.95	0.09	-1.12	17,19,20,22	0
3	GLC	B	904	11/12	0.88	0.17	-	22,25,28,34	0
2	GLC	A	802	11/12	0.83	0.15	-	28,30,31,33	0
3	GLC	B	906	11/12	0.53	0.51	-	50,51,52,54	0
2	GLC	A	803	11/12	0.92	0.12	-	27,28,31,33	0
2	GLC	A	804	11/12	0.90	0.12	-	24,25,27,28	0
3	GLC	B	905	11/12	0.81	0.24	-	36,40,45,46	0

6.4 Ligands ⓘ

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
5	EDO	A	747	4/4	0.95	0.19	5.27	20,21,23,24	0
5	EDO	B	748	4/4	0.96	0.17	4.47	15,19,20,21	0
5	EDO	A	731	4/4	0.97	0.15	4.23	21,22,23,26	0
5	EDO	B	734	4/4	0.85	0.22	2.84	33,34,34,35	0
5	EDO	B	741	4/4	0.89	0.16	2.26	34,35,35,36	0
5	EDO	A	737	4/4	0.81	0.16	2.21	28,30,30,34	0
5	EDO	A	736	4/4	0.85	0.13	1.91	27,28,29,29	0
5	EDO	B	744	4/4	0.90	0.17	1.37	30,32,33,34	0
5	EDO	B	749	4/4	0.92	0.13	0.92	24,25,25,28	0
5	EDO	A	730	4/4	0.93	0.11	0.16	27,27,28,28	0
4	CA	A	600	1/1	0.99	0.09	-1.79	15,15,15,15	0
4	CA	A	710	1/1	0.99	0.09	-1.90	20,20,20,20	0
4	CA	B	700	1/1	0.99	0.07	-7.38	15,15,15,15	0
4	CA	B	720	1/1	0.98	0.06	-	20,20,20,20	0
5	EDO	B	732	4/4	0.91	0.20	-	36,37,37,37	0
5	EDO	B	733	4/4	0.78	0.28	-	40,40,41,41	0
5	EDO	B	742	4/4	0.85	0.23	-	39,40,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.