

Full wwPDB X-ray Structure Validation Report (i)

Aug 23, 2023 - 04:40 AM EDT

PDB ID	:	3C6E
Title	:	Crystal structure of the precursor membrane protein- envelope protein het-
		erodimer from the dengue 2 virus at neutral pH
Authors	:	Li, L.
Deposited on	:	2008-02-04
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 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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (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 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% 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	А	402	3% 59%			34%	• • •			
2	С	130	38%	21%	••	38%				
3	В	4		100%						

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
3	NAG	В	1	Х	-	Х	-
3	MAN	В	3	-	-	-	Х
3	MAN	В	4	Х	-	-	Х
4	NDG	С	1396	-	-	Х	-



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3811 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 Envelope protein E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	390	Total 3046	C 1926	N 524	O 569	S 27	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	-7	GLY	-	expression tag	UNP 009234
А	-6	GLU	-	expression tag	UNP 009234
А	-5	ASN	-	expression tag	UNP 009234
А	-4	LEU	-	expression tag	UNP 009234
А	-3	TYR	-	expression tag	UNP 009234
А	-2	PHE	-	expression tag	UNP 009234
А	-1	GLN	-	expression tag	UNP 009234
А	0	GLY	-	expression tag	UNP 009234

• Molecule 2 is a protein called prM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	С	81	Total 640	C 396	N 106	0 128	S 10	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	87	SER	ARG	engineered mutation	UNP 009234
С	88	THR	ARG	engineered mutation	UNP 009234
С	91	SER	ARG	engineered mutation	UNP 009234

• Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyran ose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-gl ucopyranose.





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	В	4	Total 50	C 28	N 2	O 20	0	0	0

• Molecule 4 is 2-acetamido-2-deoxy-alpha-D-glucopyranose (three-letter code: NDG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	С	1	Total 15	C 8	N 1	O 6	0	0

• Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	С	1	Total 15	C 8	N 1	O 6	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	38	Total O 38 38	0	0
6	С	7	Total O 7 7	0	0



3 Residue-property plots (i)

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 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: Envelope protein E

 $\bullet \ {\it Molecule 3: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose}$

Chain B:

100%





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	71.10Å 108.37Å 108.96Å	Deperitor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
$\mathbf{P}_{\text{assolution}}(\hat{\mathbf{A}})$	50.00 - 2.60	Depositor
Resolution (A)	43.24 - 2.59	EDS
% Data completeness	99.7 (50.00-2.60)	Depositor
(in resolution range)	99.5(43.24-2.59)	EDS
R _{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) > 1$	4.07 (at 2.61Å)	Xtriage
Refinement program	CNS	Depositor
P. P.	0.250 , 0.293	Depositor
n, n_{free}	0.250 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor $(Å^2)$	57.4	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.32 , 52.3	EDS
L-test for twinning ²	$< L > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.019 for -h,l,k	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3811	wwPDB-VP
Average B, all atoms $(Å^2)$	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.01% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: NDG, NAG, MAN

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).

Mal	Chain	Bo	nd lengths	Bond angles		
Moi Chain		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.54	2/3106~(0.1%)	0.78	7/4186~(0.2%)	
2	С	0.61	2/652~(0.3%)	0.69	1/883~(0.1%)	
All	All	0.55	4/3758~(0.1%)	0.77	8/5069~(0.2%)	

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	С	0	1

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
1	А	335	ILE	C-N	-15.23	1.05	1.34
1	А	334	LYS	C-N	-13.74	1.02	1.34
2	С	48	THR	C-N	-9.51	1.12	1.34
2	С	49	ILE	C-N	-7.05	1.17	1.34

All (4) bond length outliers are listed below:

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	334	LYS	O-C-N	-9.85	106.94	122.70
1	А	384	PRO	N-CA-C	-8.39	90.28	112.10
1	А	383	GLU	N-CA-C	8.19	133.10	111.00
1	А	332	PRO	N-CA-C	-8.06	91.14	112.10
1	А	334	LYS	C-N-CA	7.27	139.88	121.70
1	А	334	LYS	CA-C-N	6.80	132.16	117.20
1	А	329	ASP	N-CA-C	5.34	125.41	111.00



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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	С	48	THR	O-C-N	-5.29	114.23	122.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	С	49	ILE	Mainchain

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	3046	0	3045	151	0
2	С	640	0	609	30	0
3	В	50	0	39	12	0
4	С	15	0	12	10	0
5	С	15	0	15	6	0
6	А	38	0	0	4	0
6	С	7	0	0	0	0
All	All	3811	0	3720	188	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 25.

All (188) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 9	Interatomic	Clash
Atom-1	Atom-2	$distance ({ m \AA})$	overlap (Å)
1:A:188:ARG:HD3	1:A:284:LYS:HD2	1.24	1.11
2:C:2:HIS:NE2	3:B:4:MAN:O2	1.96	0.98
1:A:198:LEU:HD22	1:A:277:LEU:HD13	1.46	0.97
2:C:2:HIS:HE2	3:B:4:MAN:HO2	1.13	0.93
1:A:75:PRO:O	1:A:76:THR:HB	1.72	0.87
4:C:1396:NDG:O3	5:C:1397:NAG:H1	1.76	0.86
1:A:147:GLU:HB3	1:A:157:LYS:HE3	1.58	0.83
1:A:188:ARG:CD	1:A:284:LYS:HD2	2.08	0.83



	loue page	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:170:ILE:HG12	1:A:184:GLU:HB2	1.64	0.80
1:A:83:ASN:HD22	1:A:83:ASN:N	1.82	0.77
1:A:56:LEU:HD22	1:A:213:PHE:HE2	1.49	0.76
1:A:73:ARG:HG3	1:A:80:PRO:HB3	1.66	0.76
1:A:303:THR:HA	1:A:382:VAL:HG21	1.67	0.75
1:A:309:VAL:HG11	1:A:323:ARG:HH21	1.52	0.75
1:A:388:LYS:H	1:A:388:LYS:HD2	1.51	0.74
1:A:351:LEU:HB3	1:A:353:THR:O	1.88	0.74
1:A:347:VAL:HG23	6:A:1436:HOH:O	1.88	0.73
1:A:99:ARG:HE	1:A:103:ASN:ND2	1.86	0.73
1:A:148:GLU:OE2	1:A:364:PRO:HB2	1.90	0.72
1:A:41:LEU:HD21	1:A:292:LEU:HD11	1.71	0.71
1:A:83:ASN:ND2	1:A:83:ASN:H	1.89	0.70
1:A:166:PRO:HB3	1:A:187:PRO:HG2	1.75	0.69
1:A:149:HIS:O	1:A:150:ALA:CB	2.41	0.68
1:A:201:MET:HE2	1:A:257:GLU:HG3	1.75	0.68
1:A:67:ASN:OD1	3:B:1:NAG:O5	2.10	0.67
1:A:59:TYR:CD1	1:A:220:TRP:HB3	2.30	0.66
1:A:178:TYR:CE1	1:A:295:LYS:HB3	2.30	0.66
1:A:83:ASN:N	1:A:83:ASN:ND2	2.42	0.66
1:A:56:LEU:HD23	1:A:57:ARG:HB2	1.79	0.65
2:C:69:ASN:OD1	4:C:1396:NDG:O1	2.15	0.64
1:A:333:CYS:O	1:A:357:ILE:HG23	1.98	0.64
1:A:38:LYS:HE2	1:A:292:LEU:O	1.98	0.63
1:A:388:LYS:H	1:A:388:LYS:CD	2.12	0.63
1:A:165:THR:HG23	1:A:166:PRO:HD2	1.80	0.63
2:C:57:ARG:HH11	2:C:57:ARG:HG3	1.64	0.62
1:A:360:GLU:HB2	1:A:363:SER:HB3	1.82	0.62
1:A:148:GLU:CD	1:A:364:PRO:HB2	2.21	0.62
1:A:148:GLU:CD	1:A:364:PRO:O	2.39	0.61
1:A:123:LYS:HE3	1:A:202:GLU:OE1	2.01	0.61
1:A:188:ARG:HD3	1:A:284:LYS:CD	2.17	0.61
1:A:302:CYS:SG	1:A:334:LYS:O	2.58	0.60
4:C:1396:NDG:H4	5:C:1397:NAG:H5	1.81	0.60
1:A:182:THR:HG23	1:A:288:ARG:HB3	1.82	0.60
1:A:147:GLU:CB	1:A:157:LYS:HE3	2.30	0.60
2:C:2:HIS:CE1	3:B:4:MAN:HO2	2.20	0.60
1:A:334:LYS:HA	1:A:357:ILE:HG12	1.83	0.59
2:C:69:ASN:HD21	4:C:1396:NDG:C1	2.15	0.59
4:C:1396:NDG:C4	5:C:1397:NAG:H5	2.32	0.59
1:A:64:LYS:HB2	1:A:122:LYS:HE3	1.84	0.59



	,	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:56:LEU:HD23	1:A:56:LEU:C	2.23	0.59	
2:C:69:ASN:ND2	4:C:1396:NDG:C1	2.66	0.58	
1:A:309:VAL:HB	1:A:323:ARG:HB3	1.85	0.58	
1:A:131:GLN:HB2	6:A:1414:HOH:O	2.03	0.57	
1:A:131:GLN:O	1:A:133:GLU:O	2.23	0.57	
1:A:165:THR:CG2	1:A:166:PRO:HD2	2.35	0.57	
1:A:-3:TYR:CE1	1:A:1:MET:HE1	2.39	0.57	
1:A:303:THR:HG23	1:A:303:THR:O	2.05	0.57	
2:C:2:HIS:CE1	3:B:4:MAN:O2	2.58	0.57	
1:A:334:LYS:HE2	1:A:355:ASN:OD1	2.05	0.56	
1:A:166:PRO:HB3	1:A:187:PRO:CG	2.36	0.56	
2:C:4:THR:HG23	2:C:11:HIS:HB3	1.87	0.56	
2:C:52:LYS:HD3	2:C:72:SER:OG	2.06	0.56	
1:A:383:GLU:O	1:A:383:GLU:HG2	2.06	0.56	
1:A:-2:PHE:CE2	1:A:1:MET:HE2	2.41	0.55	
1:A:160:LYS:HE3	6:A:1418:HOH:O	2.06	0.55	
1:A:326:TYR:C	1:A:328:GLY:N	2.60	0.55	
1:A:201:MET:CE	1:A:257:GLU:HG3	2.37	0.55	
2:C:16:ARG:O	2:C:16:ARG:HD3	2.06	0.55	
1:A:13:GLU:HG3	1:A:34:MET:O	2.06	0.54	
1:A:56:LEU:HD22	1:A:213:PHE:CE2	2.37	0.54	
1:A:-2:PHE:CD2	1:A:1:MET:HE2	2.42	0.54	
1:A:218:LEU:HD11	1:A:260:MET:HE1	1.88	0.54	
1:A:7:SER:HB3	1:A:316:GLN:HE22	1.73	0.53	
1:A:167:GLN:O	1:A:167:GLN:HG2	2.07	0.53	
1:A:326:TYR:O	1:A:328:GLY:N	2.41	0.53	
1:A:37:ASN:O	1:A:38:LYS:HD2	2.09	0.53	
1:A:325:GLN:OE1	1:A:362:ASP:HA	2.08	0.53	
1:A:301:MET:O	1:A:302:CYS:C	2.47	0.52	
1:A:386:GLN:O	1:A:388:LYS:HD2	2.10	0.52	
1:A:147:GLU:OE1	1:A:157:LYS:NZ	2.42	0.52	
2:C:31:VAL:HG21	5:C:1397:NAG:O3	2.10	0.52	
2:C:60:GLU:HG3	2:C:61:PRO:HD2	1.92	0.52	
2:C:49:ILE:O	2:C:49:ILE:HG13	2.10	0.52	
4:C:1396:NDG:O4	5:C:1397:NAG:H5	2.10	0.52	
1:A:148:GLU:OE2	1:A:323:ARG:NH1	2.43	0.52	
1:A:323:ARG:HG3	1:A:366:ASN:OD1	2.10	0.52	
1:A:130:VAL:O	1:A:193:PHE:HB3	2.10	0.52	
2:C:31:VAL:O	4:C:1396:NDG:H3	2.10	0.51	
1:A:18:GLY:O	1:A:288:ARG:NH2	2.43	0.51	
1:A:382:VAL:O	1:A:384:PRO:HD2	2.11	0.51	



	ti a	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:357:ILE:HG22	1:A:358:VAL:N	2.26	0.51
2:C:34:CYS:HA	2:C:68:CYS:HA	1.92	0.51
3:B:1:NAG:O3	3:B:2:NDG:C1	2.59	0.51
1:A:201:MET:HE1	1:A:257:GLU:HA	1.92	0.51
2:C:49:ILE:HD11	2:C:77:TYR:CZ	2.46	0.51
1:A:-3:TYR:HE2	1:A:366:ASN:HD21	1.59	0.51
2:C:18:GLU:O	2:C:21:LYS:HG2	2.11	0.51
1:A:67:ASN:HD22	3:B:1:NAG:C7	2.24	0.51
1:A:186:SER:C	1:A:188:ARG:H	2.14	0.51
1:A:272:MET:HB2	1:A:276:ASN:O	2.10	0.50
3:B:1:NAG:H62	3:B:2:NDG:C7	2.41	0.50
1:A:340:MET:CE	1:A:379:ILE:HG13	2.41	0.50
1:A:2:ARG:HG3	1:A:2:ARG:HH11	1.76	0.50
1:A:237:LEU:O	1:A:252:VAL:HG23	2.13	0.49
1:A:172:GLU:OE2	1:A:182:THR:HB	2.13	0.49
1:A:26:GLU:OE2	1:A:282:HIS:CD2	2.66	0.48
2:C:57:ARG:HG3	2:C:57:ARG:NH1	2.26	0.48
1:A:149:HIS:O	1:A:150:ALA:HB2	2.13	0.48
1:A:382:VAL:O	1:A:384:PRO:CD	2.61	0.48
1:A:148:GLU:OE1	1:A:364:PRO:HB2	2.14	0.48
1:A:89:ARG:HG2	1:A:229:SER:HB3	1.94	0.48
1:A:15:VAL:HG22	1:A:15:VAL:O	2.14	0.48
1:A:357:ILE:CG2	1:A:358:VAL:N	2.76	0.48
1:A:20:TRP:NE1	1:A:288:ARG:NH1	2.62	0.48
1:A:41:LEU:CD2	1:A:292:LEU:HD11	2.43	0.48
1:A:324:VAL:HG11	1:A:380:ILE:HD13	1.95	0.47
1:A:2:ARG:O	1:A:6:MET:HG3	2.14	0.47
3:B:1:NAG:HO3	3:B:2:NDG:C1	2.27	0.47
1:A:67:ASN:ND2	3:B:1:NAG:C7	2.77	0.47
1:A:172:GLU:OE2	1:A:172:GLU:HA	2.14	0.47
1:A:210:ARG:C	1:A:212:TRP:H	2.18	0.47
2:C:24:LEU:HD23	2:C:33:MET:HA	1.97	0.47
1:A:165:THR:HG22	1:A:167:GLN:H	1.79	0.47
1:A:218:LEU:HD11	1:A:260:MET:CE	2.45	0.47
1:A:301:MET:HG3	1:A:336:PRO:HG3	1.96	0.47
1:A:75:PRO:O	1:A:76:THR:CB	2.52	0.46
1:A:133:GLU:HA	1:A:166:PRO:HG2	1.98	0.46
1:A:379:ILE:HG21	1:A:386:GLN:NE2	2.30	0.46
1:A:149:HIS:O	1:A:150:ALA:HB3	2.14	0.46
1:A:350:ARG:HD2	1:A:370:GLU:OE1	2.15	0.46
1:A:59:TYR:CE1	1:A:220:TRP:HB3	2.50	0.46



	le as pagem	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:232:ILE:O	1:A:233:GLN:HG2	2.16	0.46
1:A:-2:PHE:CD2	1:A:1:MET:CE	2.99	0.45
1:A:374:GLY:O	1:A:392:PHE:HA	2.16	0.45
1:A:67:ASN:HD22	3:B:1:NAG:C8	2.29	0.45
1:A:210:ARG:O	1:A:211:GLN:HB2	2.17	0.45
1:A:99:ARG:HE	1:A:103:ASN:HD22	1.62	0.44
1:A:259:ALA:O	1:A:263:ALA:HB2	2.17	0.44
5:C:1397:NAG:O1	5:C:1397:NAG:H83	2.17	0.44
1:A:261:HIS:C	1:A:263:ALA:H	2.19	0.44
1:A:-2:PHE:HZ	1:A:4:ILE:HD12	1.82	0.44
1:A:133:GLU:HB2	6:A:1416:HOH:O	2.17	0.44
1:A:133:GLU:HA	1:A:166:PRO:CG	2.48	0.44
1:A:359:THR:HG22	1:A:360:GLU:HG3	1.99	0.44
2:C:69:ASN:ND2	4:C:1396:NDG:O1	2.51	0.44
1:A:235:GLU:H	1:A:235:GLU:CD	2.19	0.44
2:C:29:ASP:OD1	2:C:29:ASP:N	2.51	0.44
1:A:232:ILE:O	1:A:233:GLN:CG	2.66	0.43
1:A:260:MET:O	1:A:263:ALA:HB3	2.18	0.43
1:A:187:PRO:O	1:A:188:ARG:C	2.56	0.43
1:A:363:SER:O	1:A:365:VAL:HG23	2.18	0.43
2:C:57:ARG:C	2:C:58:GLN:HG2	2.38	0.43
1:A:102:GLY:HA3	2:C:62:GLU:HB3	2.01	0.43
1:A:56:LEU:CD2	1:A:57:ARG:HB2	2.47	0.43
1:A:64:LYS:HG2	1:A:65:LEU:N	2.33	0.43
1:A:323:ARG:HD3	1:A:364:PRO:HB3	1.99	0.43
1:A:16:SER:HB3	1:A:19:SER:HB3	2.01	0.43
1:A:355:ASN:N	1:A:356:PRO:CD	2.82	0.43
1:A:303:THR:O	1:A:329:ASP:HB3	2.19	0.43
1:A:217:PRO:O	1:A:218:LEU:HD23	2.20	0.42
1:A:73:ARG:NE	1:A:80:PRO:HA	2.35	0.42
1:A:392:PHE:CE2	1:A:394:LYS:HB2	2.54	0.42
2:C:73:THR:HG22	2:C:74:TRP:O	2.18	0.42
1:A:162:ILE:O	1:A:162:ILE:HG13	2.18	0.42
1:A:322:ILE:HD11	1:A:378:ILE:HD13	2.02	0.42
1:A:16:SER:HB3	1:A:19:SER:CB	2.49	0.42
1:A:85:GLU:OE1	1:A:94:HIS:NE2	2.47	0.42
1:A:102:GLY:HA2	2:C:60:GLU:O	2.20	0.42
1:A:58:LYS:O	1:A:220:TRP:HA	2.19	0.42
1:A:221:LEU:HG	1:A:231:TRP:CE3	2.55	0.42
2:C:16:ARG:HG3	2:C:43:GLU:OE2	2.20	0.42
1:A:221:LEU:HD13	1:A:225:ASP:OD2	2.20	0.41



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:C:69:ASN:OD1	2:C:69:ASN:C	2.59	0.41
2:C:69:ASN:CG	4:C:1396:NDG:O1	2.59	0.41
3:B:2:NDG:C4	3:B:3:MAN:C1	2.86	0.41
1:A:136:GLU:OE2	1:A:163:LYS:HD3	2.20	0.41
1:A:137:TYR:N	1:A:137:TYR:CD1	2.87	0.41
1:A:135:LEU:HD23	1:A:135:LEU:HA	1.84	0.41
1:A:257:GLU:HG2	1:A:261:HIS:CD2	2.56	0.41
1:A:76:THR:O	1:A:76:THR:HG23	2.20	0.41
1:A:218:LEU:CD1	1:A:260:MET:HE1	2.50	0.41
1:A:233:GLN:HA	1:A:235:GLU:OE2	2.21	0.41
1:A:320:ILE:O	1:A:368:GLU:HA	2.20	0.41
1:A:83:ASN:HD22	1:A:83:ASN:H	1.49	0.40
1:A:361:LYS:O	1:A:362:ASP:HB2	2.21	0.40
2:C:49:ILE:HD11	2:C:77:TYR:OH	2.20	0.40
1:A:148:GLU:OE1	1:A:364:PRO:O	2.39	0.40
1:A:311:GLU:H	1:A:311:GLU:HG2	1.73	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	380/402~(94%)	345~(91%)	32~(8%)	3~(1%)	19 39
2	С	79/130~(61%)	70~(89%)	9 (11%)	0	100 100
All	All	459/532~(86%)	415 (90%)	41 (9%)	3 (1%)	22 43

All (3) Ramachandran outliers are listed below:

10101	Ullalli	Res	Type
1	А	329	ASP
1	А	383	GLU



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Mol	Chain	Res	Type
1	А	384	PRO

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	339/348~(97%)	316~(93%)	23~(7%)	16	32	
2	С	75/118~(64%)	65~(87%)	10 (13%)	4	7	
All	All	414/466~(89%)	381~(92%)	33~(8%)	12	24	

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	38	LYS
1	А	41	LEU
1	А	76	THR
1	А	83	ASN
1	А	84	GLU
1	А	103	ASN
1	А	120	ARG
1	А	172	GLU
1	А	182	THR
1	А	286	ARG
1	А	287	LEU
1	А	300	SER
1	А	323	ARG
1	А	326	TYR
1	А	329	ASP
1	А	331	SER
1	А	332	PRO
1	А	346	HIS
1	А	350	ARG
1	А	362	ASP
1	А	377	TYR
1	А	382	VAL



Mol	Chain	Res	Type
1	А	388	LYS
2	С	16	ARG
2	С	17	GLN
2	С	29	ASP
2	С	36	LEU
2	С	37	MET
2	С	41	LEU
2	С	48	THR
2	С	56	LEU
2	С	58	GLN
2	С	71	THR

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	-1	GLN
1	А	37	ASN
1	А	83	ASN
1	А	103	ASN
1	А	200	GLN
1	А	203	ASN
1	А	248	GLN
1	А	261	HIS
1	А	316	GLN
2	С	7	ASN
2	С	17	GLN

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)

4 monosaccharides are modelled in this entry.



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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			Tinle	Bond lengths			Bond angles			
IVIOI	Moi Type Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
3	NAG	В	1	1,3	14,14,15	0.52	0	17,19,21	4.72	2 (11%)
3	NDG	В	2	3	14,14,15	1.86	1 (7%)	17,19,21	1.69	4 (23%)
3	MAN	В	3	3	11,11,12	0.87	1 (9%)	15,15,17	0.89	1 (6%)
3	MAN	В	4	3	11,11,12	1.10	1 (9%)	15,15,17	2.91	4 (26%)

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
3	NAG	В	1	1,3	1/1/5/7	5/6/23/26	0/1/1/1
3	NDG	В	2	3	-	4/6/23/26	0/1/1/1
3	MAN	В	3	3	-	2/2/19/22	0/1/1/1
3	MAN	В	4	3	1/1/4/5	1/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$
3	В	2	NDG	C2-N2	-6.53	1.35	1.46
3	В	4	MAN	C6-C5	-2.49	1.43	1.51
3	В	3	MAN	O3-C3	2.28	1.48	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	В	1	NAG	O4-C4-C5	17.43	152.57	109.30
3	В	4	MAN	C6-C5-C4	8.46	132.82	113.00
3	В	1	NAG	O4-C4-C3	-8.31	91.13	110.35
3	В	4	MAN	O5-C5-C6	5.42	115.70	107.20
3	В	2	NDG	C2-N2-C7	4.64	129.51	122.90
3	В	4	MAN	O6-C6-C5	3.74	124.14	111.29
3	В	2	NDG	C1-C2-N2	3.38	116.27	110.49



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	В	4	MAN	C1-O5-C5	2.95	116.19	112.19
3	В	3	MAN	O3-C3-C4	2.79	116.79	110.35
3	В	2	NDG	O7-C7-N2	2.69	126.90	121.95
3	В	2	NDG	C8-C7-N2	-2.05	112.62	116.10

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	В	1	NAG	C1
3	В	4	MAN	C5

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	В	1	NAG	C8-C7-N2-C2
3	В	1	NAG	O7-C7-N2-C2
3	В	2	NDG	C8-C7-N2-C2
3	В	2	NDG	O7-C7-N2-C2
3	В	4	MAN	O5-C5-C6-O6
3	В	1	NAG	C1-C2-N2-C7
3	В	3	MAN	O5-C5-C6-O6
3	В	3	MAN	C4-C5-C6-O6
3	В	1	NAG	C4-C5-C6-O6
3	В	2	NDG	O5-C5-C6-O6
3	В	1	NAG	O5-C5-C6-O6
3	В	2	NDG	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	2	NDG	4	0
3	В	1	NAG	7	0
3	В	4	MAN	4	0
3	В	3	MAN	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)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mal Trme Chair		Chain	Dec	Deg Link	Bo	ond leng	ths	Bond angles		
MOI	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
4	NDG	С	1396	-	$15,\!15,\!15$	0.41	0	21,21,21	0.77	0
5	NAG	С	1397	-	15,15,15	0.46	0	21,21,21	0.63	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
4	NDG	С	1396	-	-	3/6/26/26	0/1/1/1
5	NAG	С	1397	-	-	5/6/26/26	0/1/1/1



There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	С	1396	NDG	C1-C2-N2-C7
5	С	1397	NAG	C1-C2-N2-C7
5	С	1397	NAG	C8-C7-N2-C2
5	С	1397	NAG	O7-C7-N2-C2
4	С	1396	NDG	C4-C5-C6-O6
4	С	1396	NDG	O5-C5-C6-O6
5	С	1397	NAG	C4-C5-C6-O6
5	С	1397	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	С	1396	NDG	10	0
5	С	1397	NAG	6	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	С	2
1	А	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	С	49:ILE	С	50:THR	N	1.17
1	С	48:THR	С	49:ILE	N	1.12
1	А	335:ILE	С	336:PRO	N	1.05
1	А	334:LYS	С	335:ILE	N	1.02



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, 95^{th} 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	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q<0.9
1	А	390/402~(97%)	0.21	13 (3%) 46 39	27, 62, 105, 141	0
2	С	81/130~(62%)	-0.02	0 100 100	23, 51, 79, 95	0
All	All	471/532 (88%)	0.17	13 (2%) 53 46	23, 59, 104, 141	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	362	ASP	4.0
1	А	329	ASP	3.7
1	А	149	HIS	2.8
1	А	203	ASN	2.8
1	А	56	LEU	2.5
1	А	191	LEU	2.5
1	А	184	GLU	2.4
1	А	360	GLU	2.4
1	А	383	GLU	2.4
1	А	150	ALA	2.3
1	А	366	ASN	2.2
1	А	-3	TYR	2.1
1	А	148	GLU	2.1

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. The B-factors column lists the minimum,



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	$\mathbf{Q}{<}0.9$
3	MAN	В	3	11/12	0.46	0.54	$169,\!184,\!191,\!193$	0
3	MAN	В	4	11/12	0.56	0.53	171,172,175,177	0
3	NAG	В	1	14/15	0.80	0.21	88,89,90,90	0
3	NDG	В	2	14/15	0.83	0.29	103,107,120,144	0

median, 95^{th} 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.

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



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. The B-factors column lists the minimum, median, 95^{th} 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
5	NAG	С	1397	15/15	0.73	0.24	88,90,92,93	0
4	NDG	С	1396	15/15	0.89	0.18	$58,\!63,\!65,\!67$	0



6.5 Other polymers (i)

There are no such residues in this entry.

