

Full wwPDB X-ray Structure Validation Report (i)

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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 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	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
$\operatorname{CCP4}$:	$7.0.044 \ (Gargrove)$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 2.80 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	$3140 \ (2.80-2.80)$
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 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	284	% 62%		32%	• •				
1	С	284	65%		30%					
1	Е	284	4% 55%	23%	• 2	20%				
2	В	102	% • 75%		19%	• •				
2	D	102	66%		29%	•••				
2	F	102	26% 53%	25%	• 2	20%				



Mol	Chain	Length	Quality of chain					
3	G	4		100%				
4	Н	3	33%	67%	•			
5	Ι	2	50%	50%	•			

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
4	NAG	Η	1	-	-	Х	-
4	FUC	Н	2	-	-	Х	-
8	SO4	А	307	_	-	Х	-



2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 8983 atoms, of which 12 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Λ	973	Total	С	Ν	Ο	S	26	0	Ο
	л	215	2198	1406	385	400	7	20	0	0
1	C	274	Total	С	Ν	Ο	S	57	0	0
		214	2208	1412	388	401	7	57	0	0
1	Б	220	Total	С	Ν	Ο	S	122	0	0
		220	1843	1187	314	337	5	155	0	0

• Molecule 1 is a protein called Antigen-presenting glycoprotein CD1d.

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	expression tag	UNP P15813
A	1	ASP	-	expression tag	UNP P15813
A	2	PRO	-	expression tag	UNP P15813
А	42	GLN	ASN	engineered mutation	UNP P15813
A	108	GLN	ASN	engineered mutation	UNP P15813
A	163	GLN	ASN	engineered mutation	UNP P15813
A	278	HIS	-	expression tag	UNP P15813
A	279	HIS	-	expression tag	UNP P15813
А	280	HIS	-	expression tag	UNP P15813
A	281	HIS	-	expression tag	UNP P15813
A	282	HIS	-	expression tag	UNP P15813
A	283	HIS	-	expression tag	UNP P15813
С	0	ALA	-	expression tag	UNP P15813
C	1	ASP	-	expression tag	UNP P15813
С	2	PRO	-	expression tag	UNP P15813
С	42	GLN	ASN	engineered mutation	UNP P15813
С	108	GLN	ASN	engineered mutation	UNP P15813
С	163	GLN	ASN	engineered mutation	UNP P15813
C	278	HIS	-	expression tag	UNP P15813
С	279	HIS	-	expression tag	UNP P15813
С	280	HIS	-	expression tag	UNP P15813
C	281	HIS	-	expression tag	UNP P15813
C	282	HIS	_	expression tag	UNP P15813

There are 36 discrepancies between the modelled and reference sequences:



Chain	Residue	Modelled	Actual	Comment	Reference
С	283	HIS	-	expression tag	UNP P15813
E	0	ALA	-	expression tag	UNP P15813
E	1	ASP	-	expression tag	UNP P15813
E	2	PRO	-	expression tag	UNP P15813
E	42	GLN	ASN	engineered mutation	UNP P15813
Е	108	GLN	ASN	engineered mutation	UNP P15813
Е	163	GLN	ASN	engineered mutation	UNP P15813
E	278	HIS	-	expression tag	UNP P15813
Е	279	HIS	-	expression tag	UNP P15813
E	280	HIS	-	expression tag	UNP P15813
E	281	HIS	-	expression tag	UNP P15813
Е	282	HIS	-	expression tag	UNP P15813
E	283	HIS	-	expression tag	UNP P15813

• Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
0	В	00	Total	С	Ν	Ο	S	0	0	
	D	99	828	528	140	157	3	9	0	0
0	р	100	Total	С	Ν	0	S	14	0	0
	D	100	835	533	141	158	3	14	0	0
0	Б	0.0	Total	С	Ν	0	S	19	0	0
	Ľ	02	636	410	108	116	2	12	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	-2	ALA	-	expression tag	UNP P61769
В	-1	ASP	-	expression tag	UNP P61769
В	0	PRO	-	expression tag	UNP P61769
D	-2	ALA	-	expression tag	UNP P61769
D	-1	ASP	-	expression tag	UNP P61769
D	0	PRO	-	expression tag	UNP P61769
F	-2	ALA	-	expression tag	UNP P61769
F	-1	ASP	-	expression tag	UNP P61769
F	0	PRO	-	expression tag	UNP P61769

• Molecule 3 is an oligosaccharide called alpha-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-be ta-D-glucopyranose-(1-4)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyr anose.





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	4	Total 48	C 28	N 2	O 18	0	0	0

• Molecule 4 is an oligosaccharide called alpha-L-fucopyranose-(1-3)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
4	Н	3	Total 34	C 20	N 1	O 13	0	0	0

• Molecule 5 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-bet a-D-glucopyranose.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
5	Ι	2	Total 24	С 14	N 1	O 9	0	0	0

• Molecule 6 is (4R,7R,18E)-4,7-dihydroxy-N,N,N-trimethyl-10-oxo-3,5,9-trioxa-4-phosphahe ptacos-18-en-1-aminium 4-oxide (three-letter code: LSC) (formula: C₂₆H₅₃NO₇P).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
6	Δ	1	Total	С	Ν	Ο	Р	0	0	
0	0 A	L	35	26	1	7	1	0		
6	C	1	Total	С	Ν	Ο	Р	0	0	
			35	26	1	7	1	0		

• Molecule 7 is HEXANE (three-letter code: HEX) (formula: C_6H_{14}).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	1	$\begin{array}{cc} {\rm Total} & {\rm C} \\ 6 & 6 \end{array}$	0	0

 $\bullet\,$ Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: ${\rm O_4S}).$





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
8	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
8	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
8	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
8	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
8	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
8	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
8	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
8	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
8	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
8	F	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 9 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
9	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
9	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
9	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
9	С	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
9	D	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
9	D	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0

 $\bullet\,$ Molecule 10 is UNDECANE (three-letter code: UND) (formula: $\mathrm{C}_{11}\mathrm{H}_{24}).$





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	А	1	Total C 11 11	0	0



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	Е	1	TotalC44	0	0

• Molecule 12 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	А	58	Total H O 68 10 58	0	0
12	В	20	TotalO2020	0	0
12	С	31	Total O 31 31	0	0
12	D	10	Total H O 12 2 10	0	0
12	Е	8	Total O 8 8	0	0
12	F	2	$\begin{array}{ccc} {\rm Total} & {\rm O} \\ 2 & 2 \end{array}$	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: Antigen-presenting glycoprotein CD1d



• Molecule 4: alpha-L-fucopyranose-(1-3)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:	33%	67%
NAG1 FUC2 FUC3		

• Molecule 5: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:

50%

50%







4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants	108.61\AA 127.19 Å 332.64\AA	Deperitor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
$\mathbf{B}_{\mathrm{ascolution}}(\mathbf{\hat{A}})$	46.03 - 2.80	Depositor
Resolution (A)	46.03 - 2.80	EDS
% Data completeness	97.2 (46.03-2.80)	Depositor
(in resolution range)	97.3(46.03-2.80)	EDS
R_{merge}	0.12	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.49 (at 2.81 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.7.3_928	Depositor
D D.	0.213 , 0.259	Depositor
Π, Π_{free}	0.208 , 0.252	DCC
R_{free} test set	2841 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	58.9	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33, 61.2	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8983	wwPDB-VP
Average B, all atoms $(Å^2)$	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.75% 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: GOL, NAG, HEX, NBU, UND, SO4, LSC, FUC

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	Bond	lengths	Bond angles		
		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.24	0/2264	0.41	0/3081	
1	С	0.23	0/2275	0.42	0/3096	
1	Е	0.21	0/1894	0.39	0/2571	
2	В	0.26	0/851	0.43	0/1152	
2	D	0.23	0/859	0.41	0/1163	
2	F	0.20	0/649	0.38	0/877	
All	All	0.23	0/8792	0.41	0/11940	

There are no bond length outliers.

There are no bond angle outliers.

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	2198	0	2131	102	0
1	С	2208	0	2139	95	0
1	Е	1843	0	1755	64	0
2	В	828	0	794	24	0
2	D	835	0	801	35	0
2	F	636	0	558	30	0
3	G	48	0	43	7	0



3U0P

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Н	34	0	31	8	0
5	Ι	24	0	22	3	0
6	А	35	0	52	20	0
6	С	35	0	52	3	0
7	А	6	0	14	0	0
8	А	15	0	0	2	0
8	С	20	0	0	1	0
8	D	15	0	0	1	0
8	F	5	0	0	1	0
9	А	12	0	16	4	0
9	В	12	0	16	6	0
9	С	6	0	8	1	0
9	D	12	0	16	2	0
10	А	11	0	24	0	0
11	Ε	4	0	10	1	0
12	А	58	10	0	6	0
12	В	20	0	0	2	0
12	С	31	0	0	2	0
12	D	10	2	0	1	0
12	Е	8	0	0	1	0
12	F	2	0	0	0	0
All	All	8971	12	8482	362	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 22.

All (362) 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)
6:A:305:LSC:H12	6:A:305:LSC:H17	1.26	1.16
6:A:305:LSC:H30A	6:A:305:LSC:C22	1.77	1.13
4:H:1:NAG:H4	4:H:2:FUC:H5	1.35	1.07
6:A:305:LSC:H22	6:A:305:LSC:H30A	1.08	1.05
6:A:305:LSC:H22	6:A:305:LSC:C30	1.91	1.00
1:C:187:PRO:HB3	1:C:211:PHE:HB3	1.49	0.94
1:A:108:GLN:HG2	1:A:109:ALA:H	1.33	0.93
1:A:200:GLY:O	12:A:426:HOH:O	1.87	0.91
1:A:108:GLN:HG2	1:A:109:ALA:N	1.86	0.89
1:A:29:LEU:HD12	1:A:29:LEU:N	1.89	0.87
1:E:204:LEU:O	1:E:205:VAL:HG22	1.75	0.87
1:A:47:VAL:H	1:A:67:GLN:NE2	1.74	0.85



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
6:A:305:LSC:C12	6:A:305:LSC:H17	2.07	0.85
1:A:187:PRO:HB3	1:A:211:PHE:HB3	1.57	0.85
1:C:130:SER:HB3	1:C:155:ARG:HH11	1.41	0.84
1:C:46:THR:HA	1:C:67:GLN:OE1	1.77	0.83
1:A:46:THR:HA	1:A:67:GLN:HE21	1.43	0.83
1:C:236:LEU:HD23	2:D:10:TYR:CE1	2.14	0.82
1:E:204:LEU:O	1:E:205:VAL:HG13	1.80	0.82
1:E:118:PHE:HB2	1:E:123:ILE:HD13	1.62	0.81
1:E:46:THR:HA	1:E:67:GLN:HE22	1.46	0.81
1:C:278:HIS:HB3	1:C:279:HIS:C	2.01	0.80
2:D:17:ASN:OD1	2:D:97:ARG:NH2	2.13	0.80
4:H:1:NAG:C4	4:H:2:FUC:H5	2.12	0.79
1:A:166:CYS:HB3	1:A:167:PRO:HD3	1.63	0.79
1:E:190:TRP:O	1:E:207:HIS:HB2	1.82	0.79
1:A:108:GLN:CG	1:A:109:ALA:H	1.95	0.78
4:H:1:NAG:H4	4:H:2:FUC:C5	2.12	0.78
1:E:265:HIS:CD2	1:E:267:SER:HB2	2.18	0.78
1:E:42:GLN:HA	1:E:74:ARG:NH1	1.99	0.77
1:A:251:VAL:HG22	1:A:255:GLU:HB2	1.66	0.77
2:B:1:ILE:HG12	2:B:85:VAL:CG2	2.14	0.76
2:F:29:GLY:HA2	2:F:61:SER:HB2	1.67	0.76
1:C:195:PRO:HD3	2:D:99:MET:HG3	1.68	0.74
1:C:166:CYS:HB3	1:C:167:PRO:HD3	1.69	0.74
1:A:195:PRO:CD	2:B:99:MET:HG2	2.17	0.74
1:C:65:THR:O	1:C:69:ILE:HG13	1.88	0.73
1:A:251:VAL:CG2	1:A:255:GLU:HB2	2.19	0.73
2:F:15:ALA:HB1	2:F:72:PRO:HG3	1.70	0.72
1:C:190:TRP:CD2	2:D:14:PRO:HG3	2.25	0.72
1:C:217:TRP:HA	8:C:306:SO4:O1	1.90	0.71
1:C:133:PRO:HD3	1:C:145:ILE:HG12	1.70	0.71
1:E:15:ILE:CD1	2:F:54:LEU:HD22	2.19	0.71
1:E:166:CYS:HB3	1:E:167:PRO:HD3	1.74	0.70
1:A:45:ASP:HB3	1:A:71:ARG:CZ	2.21	0.70
1:A:47:VAL:H	1:A:67:GLN:HE22	1.39	0.70
1:A:35:LEU:HD22	1:A:181:LEU:HD13	1.74	0.70
1:C:130:SER:HB3	1:C:155:ARG:NH1	2.07	0.70
2:B:57:SER:CB	9:B:3001:GOL:H32	2.22	0.70
1:C:190:TRP:CE3	2:D:14:PRO:HG3	2.26	0.69
1:E:177:GLY:O	1:E:181:LEU:HD23	1.92	0.69
2:B:1:ILE:HG12	2:B:85:VAL:HG21	1.74	0.69
6:A:305:LSC:C30	6:A:305:LSC:C22	2.60	0.68



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:C:163:GLN:HE22	1:E:155:ARG:HH21	1.41	0.68
1:A:217:TRP:CZ2	1:A:219:LYS:HD2	2.28	0.68
1:C:195:PRO:CD	2:D:99:MET:HG3	2.23	0.68
1:E:128:GLY:O	1:E:129:THR:OG1	2.05	0.68
1:E:64:GLU:HA	1:E:67:GLN:HB3	1.74	0.68
1:C:278:HIS:H	1:C:279:HIS:HA	1.59	0.68
1:A:130:SER:HA	1:A:155:ARG:HD3	1.75	0.68
1:A:45:ASP:HB3	1:A:71:ARG:NE	2.10	0.67
1:A:246:ARG:HB3	9:A:311:GOL:H31	1.77	0.66
6:A:305:LSC:H16	6:A:305:LSC:C20	2.26	0.66
3:G:1:NAG:H62	3:G:3:NAG:O3	1.94	0.66
1:E:40:TRP:CE3	1:E:47:VAL:HG22	2.30	0.66
1:A:46:THR:CA	1:A:67:GLN:HE21	2.07	0.66
6:A:305:LSC:H30A	6:A:305:LSC:C21	2.25	0.66
8:A:307:SO4:O3	12:A:405:HOH:O	2.13	0.66
1:E:46:THR:HA	1:E:67:GLN:NE2	2.09	0.66
1:C:94:LEU:HD22	1:C:118:PHE:CE1	2.31	0.66
1:E:265:HIS:HD2	1:E:267:SER:HB2	1.59	0.66
2:F:54:LEU:HD23	2:F:55:SER:N	2.11	0.66
5:I:1:NAG:H62	5:I:2:FUC:O2	1.95	0.65
1:A:128:GLY:HA2	12:A:448:HOH:O	1.96	0.65
1:A:217:TRP:HB3	1:A:264:LYS:HB2	1.78	0.65
1:A:195:PRO:HD2	2:B:99:MET:HG2	1.78	0.65
1:C:278:HIS:H	1:C:279:HIS:CA	2.09	0.64
1:A:90:LEU:CD1	6:A:305:LSC:H1	2.28	0.64
2:D:9:VAL:HG11	2:D:95:TRP:HB2	1.80	0.64
6:A:305:LSC:HO33	6:A:305:LSC:P24	2.21	0.63
1:A:216:VAL:HG22	1:A:217:TRP:N	2.13	0.63
1:E:204:LEU:O	1:E:205:VAL:CG2	2.47	0.63
1:C:216:VAL:HG22	1:C:217:TRP:N	2.14	0.63
2:F:54:LEU:HD21	2:F:62:PHE:CD1	2.34	0.63
2:B:1:ILE:HG12	2:B:85:VAL:HG22	1.81	0.63
6:A:305:LSC:H16	6:A:305:LSC:H20A	1.79	0.62
6:A:305:LSC:H20	12:A:440:HOH:O	1.99	0.62
1:C:279:HIS:ND1	1:C:279:HIS:N	2.47	0.62
2:F:35:ILE:O	2:F:35:ILE:HG23	1.98	0.62
1:A:30:ALA:HB3	1:A:38:HIS:HB2	1.81	0.62
1:E:59:SER:O	1:E:62:GLN:N	2.33	0.62
1:E:187:PRO:HB3	1:E:211:PHE:HB3	1.82	0.61
1:A:214:LYS:HE3	1:A:243:TRP:CH2	2.35	0.61
6:A:305:LSC:O33	6:A:305:LSC:O25	2.17	0.61



		Interatomic	Clash
Atom-1	Atom-2	distance $(Å)$	overlan (Å)
1:C:249:LEU:C	1:C:249:LEU:HD23	2 21	0.61
1:A:152:LYS:NZ	8:A:307:SO4:O3	2.27	0.61
2:F:57:SER:HB3	8:F:3000:SO4:O2	2.00	0.61
1:A:195:PRO:HD3	2:B:99:MET:HG2	1.80	0.61
1:A:204:LEU:HD22	1:A:277:TRP:CE3	2.36	0.61
1:C:278:HIS:CB	1:C:279:HIS:C	2.69	0.60
2:F:13:HIS:HB3	2:F:14:PRO:HD2	1.82	0.59
1:A:29:LEU:N	1:A:29:LEU:CD1	2.61	0.59
2:B:57:SER:HB2	9:B:3001:GOL:H32	1.83	0.59
3:G:1:NAG:H62	3:G:3:NAG:C2	2.32	0.59
1:C:216:VAL:HG22	1:C:217:TRP:H	1.68	0.59
1:E:122:ASP:OD1	12:E:401:HOH:O	2.16	0.59
1:C:168:GLN:HG2	1:E:160:TRP:HD1	1.68	0.59
1:E:216:VAL:HG23	1:E:265:HIS:HB2	1.83	0.59
5:I:1:NAG:C6	5:I:2:FUC:O2	2.49	0.59
1:C:96:LEU:HD21	6:C:304:LSC:H1A	1.84	0.58
1:E:276:TYR:O	1:E:277:TRP:CB	2.51	0.58
4:H:1:NAG:C4	4:H:2:FUC:C5	2.78	0.58
1:E:204:LEU:O	1:E:205:VAL:CG1	2.50	0.58
1:E:213:PRO:HB2	1:E:215:PRO:HD2	1.85	0.58
1:C:186:LYS:HG2	1:C:267:SER:HB3	1.86	0.58
1:C:246:ARG:HD2	12:C:406:HOH:O	2.04	0.58
1:A:7:LEU:HD13	1:A:103:GLU:OE1	2.02	0.58
1:C:94:LEU:HD22	1:C:118:PHE:HE1	1.68	0.57
1:C:60:ASP:O	1:C:63:TRP:HB3	2.03	0.57
2:D:57:SER:HB3	9:D:105:GOL:H2	1.85	0.57
2:B:21:ASN:HB3	2:B:70:PHE:CE1	2.40	0.57
1:C:268:LEU:HD13	1:C:273:ILE:HG13	1.87	0.57
1:A:245:LEU:HD12	1:A:246:ARG:H	1.69	0.57
1:E:15:ILE:HD13	2:F:54:LEU:HD22	1.85	0.57
1:E:213:PRO:O	1:E:265:HIS:HE1	1.89	0.56
1:A:219:LYS:HA	1:A:230:THR:HG21	1.87	0.56
4:H:1:NAG:O6	4:H:2:FUC:H5	2.04	0.56
2:B:29:GLY:HA2	2:B:61:SER:HB2	1.85	0.56
2:D:0:PRO:HG2	2:D:1:ILE:H	1.71	0.56
2:D:33:SER:HB3	2:D:62:PHE:CE2	2.41	0.56
2:F:33:SER:HB3	2:F:62:PHE:CE2	$2.\overline{40}$	0.56
1:A:122:ASP:HB3	1:A:134:THR:HG21	1.88	0.56
1:C:234:ASP:HB2	1:C:236:LEU:HD11	1.88	0.56
1:C:249:LEU:CD2	1:C:251:VAL:HB	2.35	0.56
1:A:263:VAL:HB	1:A:273:ILE:HB	1.87	0.56



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:C:262:ARG:HH22	9:C:308:GOL:H32	1.71	0.56
2:F:15:ALA:HB1	2:F:72:PRO:CG	2.33	0.56
1:E:191:LEU:HD23	1:E:206:CYS:HA	1.88	0.55
2:F:55:SER:HB3	2:F:63:TYR:CE1	2.42	0.55
1:A:47:VAL:N	1:A:67:GLN:NE2	2.51	0.55
2:D:45:ARG:HB2	8:D:104:SO4:O3	2.05	0.55
1:E:58:PHE:CZ	1:E:169:PHE:HB2	2.41	0.54
1:A:214:LYS:N	1:A:215:PRO:HD2	2.22	0.54
2:D:97:ARG:HG3	12:D:208:HOH:O	2.08	0.54
1:C:201:ARG:NE	12:C:407:HOH:O	2.40	0.54
3:G:1:NAG:H62	3:G:3:NAG:H2	1.89	0.54
1:A:19:ALA:HB1	3:G:4:FUC:O2	2.08	0.54
1:C:40:TRP:CH2	1:C:74:ARG:HB2	2.43	0.54
1:E:186:LYS:HA	1:E:267:SER:OG	2.07	0.54
2:F:21:ASN:HB3	2:F:70:PHE:CE1	2.44	0.53
1:A:214:LYS:HE3	1:A:243:TRP:CZ3	2.44	0.53
1:A:45:ASP:O	1:A:71:ARG:NH2	2.40	0.53
1:C:116:VAL:HG11	1:C:124:LEU:HD11	1.90	0.53
1:E:131:TRP:CD1	1:E:148:LEU:HB3	2.42	0.53
1:C:40:TRP:HH2	1:C:74:ARG:HB2	1.74	0.53
1:E:214:LYS:N	1:E:215:PRO:CD	2.72	0.53
1:A:35:LEU:HD22	1:A:181:LEU:CD1	2.39	0.53
1:A:49:SER:HB3	1:A:54:SER:HB2	1.89	0.53
2:B:1:ILE:O	12:B:3118:HOH:O	2.19	0.53
1:A:214:LYS:HG3	1:A:243:TRP:CE2	2.44	0.52
1:A:13:LEU:HG	2:B:56:PHE:CZ	2.43	0.52
2:F:15:ALA:CB	2:F:72:PRO:HG3	2.39	0.52
1:A:108:GLN:CG	1:A:109:ALA:N	2.54	0.52
2:D:13:HIS:HB3	2:D:14:PRO:HD2	1.91	0.52
1:E:204:LEU:C	1:E:205:VAL:HG13	2.29	0.52
1:C:13:LEU:HG	2:D:56:PHE:CZ	2.45	0.52
1:E:49:SER:HB3	1:E:54:SER:HB2	1.91	0.52
1:A:90:LEU:HD13	6:A:305:LSC:H1	1.91	0.52
2:D:54:LEU:HD21	2:D:62:PHE:HB3	1.91	0.52
1:A:251:VAL:CG2	1:A:255:GLU:CB	2.87	0.52
2:B:57:SER:HB3	9:B:3001:GOL:H32	1.91	0.52
1:C:53:TRP:HB2	1:C:176:SER:OG	2.09	0.52
2:D:9:VAL:CG1	2:D:95:TRP:HB2	2.39	0.52
1:A:29:LEU:HD12	1:A:29:LEU:H	1.71	0.52
1:C:214:LYS:N	1:C:215:PRO:HD2	2.25	0.52
1:A:46:THR:HA	1:A:67:GLN:NE2	2.19	0.51



		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:49:SER:HB3	1:A:54:SER:CB	2.39	0.51
1:C:119:GLN:HA	1:C:119:GLN:OE1	2.11	0.51
1:C:145:ILE:HG22	1:C:146:GLN:N	2.24	0.51
5:I:1:NAG:O3	5:I:1:NAG:O7	2.22	0.51
1:C:234:ASP:HB2	1:C:236:LEU:CD1	2.40	0.51
2:D:4:THR:OG1	2:D:5:PRO:HD2	2.10	0.51
1:E:94:LEU:HA	1:E:119:GLN:HE22	1.76	0.51
1:C:29:LEU:HD23	1:C:29:LEU:N	2.26	0.51
1:E:151:ASP:OD2	11:E:303:NBU:H12	2.10	0.51
1:A:119:GLN:HA	1:A:119:GLN:OE1	2.10	0.50
1:A:51:LYS:O	1:A:54:SER:HB2	2.11	0.50
2:B:70:PHE:HA	9:B:3000:GOL:H2	1.92	0.50
1:A:199:PRO:CB	1:A:200:GLY:HA2	2.41	0.50
1:C:49:SER:HB3	1:C:54:SER:HB2	1.93	0.50
2:F:11:SER:HB2	2:F:21:ASN:HD21	1.75	0.50
1:A:116:VAL:HG11	1:A:124:LEU:HD11	1.94	0.50
1:A:183:LYS:HE3	9:A:310:GOL:H31	1.94	0.50
1:C:73:TYR:HE1	6:C:304:LSC:H10	1.77	0.50
1:E:145:ILE:HG22	1:E:146:GLN:N	2.25	0.50
1:A:116:VAL:CG1	1:A:124:LEU:CD1	2.90	0.49
2:B:37:VAL:HB	2:B:66:TYR:CE1	2.47	0.49
2:F:5:PRO:HB3	2:F:30:PHE:HB3	1.94	0.49
1:E:19:ALA:O	1:E:92:TYR:HB3	2.12	0.49
1:A:90:LEU:HD12	6:A:305:LSC:H1	1.94	0.49
1:C:268:LEU:CD1	1:C:273:ILE:HG13	2.42	0.49
2:D:83:ASN:ND2	2:D:90:PRO:HG3	2.28	0.49
6:A:305:LSC:C17	6:A:305:LSC:C12	2.88	0.48
1:C:118:PHE:HB2	1:C:123:ILE:HD13	1.95	0.48
1:A:246:ARG:NH2	9:A:311:GOL:H11	2.28	0.48
2:B:9:VAL:CG1	2:B:23:LEU:HD11	2.42	0.48
1:E:204:LEU:O	1:E:205:VAL:CB	2.62	0.48
2:F:70:PHE:HZ	2:F:95:TRP:CH2	2.32	0.48
1:A:216:VAL:HG22	1:A:217:TRP:H	1.78	0.48
1:C:116:VAL:CG1	1:C:124:LEU:CD1	2.92	0.48
1:C:220:TRP:CB	1:C:249:LEU:HD12	2.43	0.48
1:A:79:ARG:HG3	1:A:80:ASP:N	2.29	0.48
3:G:1:NAG:O4	3:G:2:FUC:H2	2.12	0.48
1:E:119:GLN:OE1	1:E:119:GLN:HA	2.13	0.48
2:F:95:TRP:CD1	2:F:96:ASP:N	2.81	0.48
1:A:116:VAL:CG1	1:A:124:LEU:HD12	2.44	0.48
2:F:54:LEU:HD23	2:F:54:LEU:C	2.35	0.48



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
6:A:305:LSC:O33	6:A:305:LSC:P24	2.72	0.47
1:A:245:LEU:HD12	1:A:246:ARG:N	2.29	0.47
1:A:51:LYS:HE3	1:A:180:GLU:OE2	2.14	0.47
1:A:201:ARG:HA	12:A:426:HOH:O	2.15	0.47
1:A:268:LEU:HD13	1:A:273:ILE:HG13	1.97	0.47
2:B:59:ASP:O	2:B:60:TRP:HB2	2.14	0.47
1:E:14:GLN:HB3	1:E:98:VAL:HB	1.97	0.47
2:F:31:HIS:HA	2:F:32:PRO:C	2.35	0.47
1:C:103:GLU:O	1:C:103:GLU:HG3	2.14	0.47
2:D:55:SER:HB3	2:D:63:TYR:CE1	2.49	0.47
1:E:40:TRP:CE3	1:E:47:VAL:CG2	2.96	0.47
1:A:46:THR:CA	1:A:67:GLN:NE2	2.78	0.47
2:F:33:SER:HB3	2:F:62:PHE:CZ	2.49	0.47
1:C:163:GLN:HE22	1:E:155:ARG:NH2	2.11	0.47
1:E:42:GLN:HG2	1:E:42:GLN:O	2.15	0.47
1:A:18:PHE:CD1	1:A:18:PHE:N	2.82	0.47
1:A:60:ASP:OD1	1:A:60:ASP:N	2.48	0.47
1:C:278:HIS:H	1:C:279:HIS:C	2.17	0.47
4:H:1:NAG:C4	4:H:2:FUC:O5	2.62	0.47
1:A:19:ALA:HA	1:A:93:PRO:HB3	1.96	0.47
1:C:20:ASN:O	1:C:22:SER:N	2.48	0.47
1:C:278:HIS:N	1:C:279:HIS:C	2.68	0.47
2:D:33:SER:HB2	2:D:54:LEU:HD11	1.97	0.46
1:C:222:ARG:NH2	1:C:255:GLU:O	2.46	0.46
1:A:118:PHE:HB2	1:A:123:ILE:HD13	1.98	0.46
1:A:145:ILE:HG23	1:A:149:ASN:ND2	2.30	0.46
1:E:265:HIS:O	1:E:265:HIS:CG	2.68	0.46
1:A:129:THR:N	12:A:448:HOH:O	2.13	0.46
1:A:183:LYS:CE	9:A:310:GOL:H31	2.46	0.46
2:D:47:GLU:O	2:D:49:VAL:HG22	2.15	0.46
1:A:251:VAL:HG21	1:A:255:GLU:HB2	1.96	0.46
1:A:190:TRP:CZ3	2:B:14:PRO:HD3	2.51	0.46
2:B:48:LYS:HG3	12:B:3112:HOH:O	2.15	0.46
2:F:35:ILE:HD11	2:F:82:VAL:HG11	1.98	0.46
1:A:256:ALA:O	1:A:259:LEU:HB2	2.16	0.46
1:A:204:LEU:HD22	1:A:277:TRP:CD2	2.50	0.46
1:C:212:TYR:CD1	1:C:212:TYR:C	2.89	0.45
1:E:116:VAL:HG11	1:E:124:LEU:HD11	1.98	0.45
1:C:24:THR:HG23	1:C:24:THR:O	2.16	0.45
1:A:216:VAL:CG2	1:A:217:TRP:N	2.79	0.45
1:A:186:LYS:HA	1:A:267:SER:OG	2.17	0.45



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:204:LEU:HD22	1:A:277:TRP:CZ3	2.52	0.45
1:C:118:PHE:HB3	1:C:123:ILE:HG21	1.99	0.45
1:C:236:LEU:HB3	2:D:10:TYR:OH	2.16	0.45
2:F:35:ILE:HD11	2:F:82:VAL:CG1	2.46	0.45
1:A:166:CYS:HB3	1:A:167:PRO:CD	2.41	0.45
6:A:305:LSC:C33	6:A:305:LSC:O35	2.64	0.45
2:D:29:GLY:HA2	2:D:61:SER:HB2	1.98	0.45
1:A:189:ALA:HA	1:A:207:HIS:O	2.17	0.45
1:C:73:TYR:CE1	6:C:304:LSC:H10	2.52	0.45
1:A:35:LEU:CD2	1:A:181:LEU:HD13	2.46	0.44
1:A:251:VAL:HG22	1:A:255:GLU:CB	2.44	0.44
1:C:251:VAL:HG22	1:C:252:VAL:N	2.32	0.44
1:E:213:PRO:O	1:E:265:HIS:CE1	2.69	0.44
1:C:164:GLY:O	1:C:168:GLN:HG3	2.18	0.44
1:A:45:ASP:O	1:A:71:ARG:NE	2.51	0.44
2:D:54:LEU:HD22	2:D:55:SER:N	2.33	0.44
2:D:64:LEU:HD13	2:D:66:TYR:HE1	1.82	0.44
1:C:217:TRP:CZ2	1:C:219:LYS:HD3	2.52	0.44
1:C:92:TYR:HB3	1:C:93:PRO:HA	1.98	0.44
1:C:94:LEU:HD22	1:C:118:PHE:CZ	2.53	0.44
2:B:71:THR:N	9:B:3000:GOL:H12	2.33	0.43
2:D:12:ARG:CB	2:D:22:PHE:HB2	2.48	0.43
6:A:305:LSC:H21	6:A:305:LSC:H30A	1.99	0.43
1:A:13:LEU:HB2	1:A:29:LEU:HD13	2.00	0.43
1:C:193:ARG:CZ	1:C:202:LEU:CD2	2.96	0.43
1:C:214:LYS:HG3	1:C:243:TRP:CE2	2.54	0.43
1:C:42:GLN:HG2	1:C:74:ARG:NH1	2.34	0.43
1:A:234:ASP:O	1:A:236:LEU:HD13	2.18	0.43
1:C:64:GLU:HA	1:C:67:GLN:HB3	1.99	0.43
2:F:2:GLN:HA	2:F:2:GLN:OE1	2.17	0.43
1:C:249:LEU:HD23	1:C:250:ASP:N	2.33	0.43
1:E:29:LEU:HD12	1:E:31:TRP:NE1	2.34	0.43
1:C:217:TRP:HB3	1:C:264:LYS:HB2	2.00	0.43
1:A:10:LEU:O	1:A:101:GLY:HA3	2.19	0.43
1:A:105:HIS:O	1:A:107:GLY:HA2	2.18	0.43
1:C:199:PRO:HA	1:C:200:GLY:HA2	1.80	0.43
1:A:60:ASP:O	1:A:64:GLU:N	2.44	0.43
1:C:278:HIS:N	1:C:279:HIS:CA	2.76	0.43
2:B:71:THR:HB	9:B:3000:GOL:H12	2.01	0.43
1:C:265:HIS:ND1	1:C:267:SER:HB2	2.34	0.43
2:D:49:VAL:HG12	2:D:68:THR:HB	2.01	0.43



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:E:189:ALA:HB1	1:E:207:HIS:O	2.18	0.43
1:E:18:PHE:CD2	1:E:24:THR:HG22	2.54	0.43
1:E:212:TYR:HA	1:E:213:PRO:C	2.39	0.43
2:F:35:ILE:O	2:F:35:ILE:CG2	2.65	0.43
1:C:130:SER:HA	1:C:155:ARG:HD2	2.01	0.42
2:D:33:SER:HB3	2:D:62:PHE:CZ	2.54	0.42
1:E:129:THR:HG22	1:E:159:GLN:OE1	2.18	0.42
6:A:305:LSC:O33	6:A:305:LSC:H16	2.19	0.42
1:C:278:HIS:CA	1:C:279:HIS:C	2.87	0.42
2:D:23:LEU:HB2	2:D:70:PHE:CD1	2.54	0.42
1:E:151:ASP:OD1	1:E:151:ASP:C	2.58	0.42
4:H:1:NAG:O3	4:H:1:NAG:O7	2.36	0.42
1:C:216:VAL:CG2	1:C:217:TRP:H	2.32	0.42
1:C:236:LEU:HB3	2:D:10:TYR:CZ	2.55	0.42
1:A:147:VAL:O	1:A:150:GLN:HB2	2.18	0.42
1:A:264:LYS:HG2	1:A:272:ASP:OD2	2.18	0.42
1:C:59:SER:O	1:C:63:TRP:HB2	2.19	0.42
1:C:103:GLU:CG	1:C:103:GLU:O	2.68	0.42
1:E:207:HIS:CE1	1:E:246:ARG:HG3	2.55	0.42
2:F:85:VAL:HG22	2:F:85:VAL:O	2.19	0.42
1:C:7:LEU:HD13	1:C:103:GLU:OE2	2.20	0.42
1:E:170:VAL:O	1:E:174:LEU:HG	2.19	0.42
2:B:3:ARG:HH11	2:B:61:SER:HB3	1.85	0.42
4:H:1:NAG:O4	4:H:2:FUC:O5	2.37	0.42
1:A:251:VAL:HG21	1:A:255:GLU:CB	2.50	0.42
1:C:10:LEU:HB2	1:C:170:VAL:HG22	2.02	0.42
2:B:37:VAL:HB	2:B:66:TYR:CZ	2.55	0.41
2:D:17:ASN:HB2	9:D:103:GOL:O2	2.19	0.41
1:C:195:PRO:HD2	2:D:99:MET:HG3	2.01	0.41
1:E:118:PHE:CB	1:E:123:ILE:HD13	2.43	0.41
1:C:164:GLY:HA3	1:E:159:GLN:NE2	2.35	0.41
1:C:216:VAL:CG2	1:C:217:TRP:N	2.80	0.41
2:D:55:SER:HB3	2:D:63:TYR:CZ	2.55	0.41
1:E:266:SER:HA	1:E:269:GLU:HA	2.02	0.41
1:A:31:TRP:CZ3	1:A:36:GLN:HB2	2.56	0.41
3:G:2:FUC:O4	3:G:2:FUC:C1	2.65	0.41
1:E:129:THR:O	1:E:155:ARG:NE	2.54	0.41
1:C:15:ILE:HD13	2:D:54:LEU:HD13	2.02	0.41
1:E:145:ILE:HD12	1:E:145:ILE:HA	1.89	0.41
1:C:249:LEU:HD22	1:C:251:VAL:HB	2.02	0.41
1:C:252:VAL:O	1:C:253:ALA:C	2.58	0.41



		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:197:PRO:HG3	1:A:250:ASP:OD1	2.21	0.41
1:C:212:TYR:CG	1:C:213:PRO:HA	2.56	0.41
1:A:129:THR:O	1:A:155:ARG:HD2	2.21	0.41
2:B:64:LEU:HD13	2:B:66:TYR:HE1	1.86	0.41
1:C:193:ARG:CZ	1:C:202:LEU:HD21	2.51	0.41
1:A:198:GLY:HA3	1:A:199:PRO:HA	1.87	0.41
1:A:28:GLY:C	1:A:29:LEU:HD12	2.41	0.41
1:C:212:TYR:CD1	1:C:213:PRO:N	2.89	0.41
1:E:244:TYR:CG	1:E:245:LEU:N	2.89	0.41
1:A:106:PRO:HA	1:A:107:GLY:HA2	1.65	0.40
1:A:59:SER:OG	1:A:62:GLN:HB2	2.21	0.40
1:C:168:GLN:HG2	1:E:160:TRP:CD1	2.51	0.40
2:F:70:PHE:HE2	2:F:95:TRP:CZ3	2.39	0.40
1:E:57:THR:O	1:E:57:THR:HG22	2.21	0.40
2:F:54:LEU:HD21	2:F:62:PHE:HD1	1.85	0.40
3:G:1:NAG:H62	3:G:3:NAG:C1	2.52	0.40
1:C:15:ILE:HD13	2:D:62:PHE:CE1	2.56	0.40
1:E:25:ARG:HA	1:E:42:GLN:OE1	2.22	0.40
2:F:12:ARG:CB	2:F:22:PHE:HB2	2.52	0.40
1:A:51:LYS:HD2	1:A:53:TRP:CZ2	2.57	0.40
1:C:249:LEU:CD2	1:C:249:LEU:C	2.89	0.40
2:F:70:PHE:CE2	2:F:95:TRP:CZ3	3.09	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	271/284~(95%)	253~(93%)	18 (7%)	0	100 100
1	С	272/284~(96%)	252~(93%)	16~(6%)	4 (2%)	10 33
1	Ε	214/284~(75%)	201 (94%)	11 (5%)	2(1%)	17 46



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
2	В	97/102~(95%)	94~(97%)	3 (3%)	0	100	100
2	D	98/102~(96%)	94 (96%)	4 (4%)	0	100	100
2	F	65/102~(64%)	63~(97%)	2(3%)	0	100	100
All	All	1017/1158~(88%)	957 (94%)	54 (5%)	6 (1%)	25	56

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All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Ε	205	VAL
1	С	198	GLY
1	С	21	SER
1	С	179	SER
1	С	128	GLY
1	Е	128	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	Percer	ntiles
1	А	239/249~(96%)	228~(95%)	11 (5%)	27	60
1	С	240/249~(96%)	234~(98%)	6(2%)	47	80
1	Е	201/249~(81%)	197~(98%)	4 (2%)	55	84
2	В	94/96~(98%)	89~(95%)	5(5%)	22	54
2	D	95/96~(99%)	92~(97%)	3 (3%)	39	73
2	F	67/96~(70%)	64 (96%)	3 (4%)	27	60
All	All	936/1035~(90%)	904 (97%)	32 (3%)	37	71

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	29	LEU
1	А	54	SER



Mol	Chain	Res	Type
1	А	60	ASP
1	А	70	PHE
1	А	91	SER
1	А	114	PHE
1	А	116	VAL
1	А	181	LEU
1	А	236	LEU
1	А	249	LEU
1	А	259	LEU
2	В	4	THR
2	В	54	LEU
2	В	57	SER
2	В	70	PHE
2	В	99	MET
1	С	35	LEU
1	С	103	GLU
1	С	116	VAL
1	С	259	LEU
1	С	267	SER
1	С	279	HIS
2	D	12	ARG
2	D	49	VAL
2	D	54	LEU
1	Е	29	LEU
1	Е	116	VAL
1	E	145	ILE
1	E	206	CYS
2	F	4	THR
2	F	22	PHE
2	F	70	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	67	GLN
1	С	105	HIS
1	С	163	GLN
1	Е	265	HIS



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)

9 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	Mol Type Chain Res I		Tink	Bo	Bond lengths			Bond angles		
	туре	Type Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	G	1	1,3	14,14,15	0.68	0	17,19,21	1.89	4 (23%)
3	FUC	G	2	3	10, 10, 11	0.67	0	14,14,16	1.40	1 (7%)
3	NAG	G	3	3	14, 14, 15	0.48	0	17,19,21	1.65	2 (11%)
3	FUC	G	4	3	10, 10, 11	0.72	0	14,14,16	0.97	1 (7%)
4	NAG	Н	1	1,4	14,14,15	0.60	0	17,19,21	1.14	2 (11%)
4	FUC	Н	2	4	10, 10, 11	0.56	0	14,14,16	1.64	4 (28%)
4	FUC	Н	3	4	10, 10, 11	0.61	0	14,14,16	1.69	3 (21%)
5	NAG	I	1	1,5	14, 14, 15	0.54	0	17,19,21	0.76	0
5	FUC	I	2	5	10,10,11	0.75	0	14,14,16	0.88	1(7%)

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	G	1	1,3	-	2/6/23/26	0/1/1/1
3	FUC	G	2	3	-	-	0/1/1/1
3	NAG	G	3	3	-	3/6/23/26	0/1/1/1
3	FUC	G	4	3	-	_	0/1/1/1



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	Н	1	1,4	-	5/6/23/26	0/1/1/1
4	FUC	Н	2	4	-	-	0/1/1/1
4	FUC	Н	3	4	-	-	0/1/1/1
5	NAG	Ι	1	1,5	-	5/6/23/26	0/1/1/1
5	FUC	Ι	2	5	-	-	0/1/1/1

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	G	1	NAG	C1-O5-C5	4.96	118.92	112.19
3	G	3	NAG	C1-O5-C5	-4.69	105.84	112.19
4	Н	3	FUC	C1-C2-C3	4.35	115.01	109.67
3	G	2	FUC	C1-C2-C3	-3.68	105.14	109.67
3	G	1	NAG	O4-C4-C5	3.68	118.44	109.30
3	G	3	NAG	O5-C5-C6	3.67	112.96	107.20
4	Н	2	FUC	C1-C2-C3	3.30	113.72	109.67
4	Н	2	FUC	C1-O5-C5	3.22	120.09	112.78
4	Н	3	FUC	C1-O5-C5	2.57	118.61	112.78
4	Н	3	FUC	O5-C1-C2	2.48	114.60	110.77
4	Н	2	FUC	O5-C5-C4	2.45	113.92	109.52
3	G	1	NAG	O5-C5-C4	-2.38	105.04	110.83
3	G	1	NAG	O3-C3-C4	-2.31	105.01	110.35
4	Н	1	NAG	O3-C3-C4	2.29	115.64	110.35
3	G	4	FUC	C2-C3-C4	-2.24	107.02	110.89
5	Ι	2	FUC	O5-C1-C2	-2.18	107.41	110.77
4	Н	2	FUC	C6-C5-C4	-2.17	109.06	113.07
4	Н	1	NAG	C3-C4-C5	2.02	113.85	110.24

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms
4	Н	1	NAG	C3-C2-N2-C7
4	Н	1	NAG	C8-C7-N2-C2
4	Н	1	NAG	O7-C7-N2-C2
5	Ι	1	NAG	C3-C2-N2-C7
3	G	3	NAG	C8-C7-N2-C2
3	G	3	NAG	O7-C7-N2-C2
4	Н	1	NAG	C4-C5-C6-O6
5	Ι	1	NAG	O5-C5-C6-O6



Mol	Chain	Res	Type	Atoms
3	G	1	NAG	C8-C7-N2-C2
4	Н	1	NAG	O5-C5-C6-O6
3	G	1	NAG	O7-C7-N2-C2
5	Ι	1	NAG	C4-C5-C6-O6
3	G	3	NAG	O5-C5-C6-O6
5	Ι	1	NAG	C8-C7-N2-C2
5	Ι	1	NAG	O7-C7-N2-C2

There are no ring outliers.

8 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	Ι	2	FUC	2	0
4	Н	1	NAG	8	0
3	G	1	NAG	5	0
3	G	4	FUC	1	0
5	Ι	1	NAG	3	0
4	Н	2	FUC	7	0
3	G	3	NAG	4	0
3	G	2	FUC	2	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)

23 ligands are modelled in this entry.



3U0P

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	Tune	Chain	Dog	Tink	Bo	ond leng	ths	В	ond ang	gles
	Type	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	GOL	А	310	-	5, 5, 5	0.35	0	$5,\!5,\!5$	0.28	0
9	GOL	В	3001	-	5, 5, 5	0.40	0	$5,\!5,\!5$	0.32	0
9	GOL	D	103	-	5, 5, 5	0.36	0	$5,\!5,\!5$	0.27	0
10	UND	А	312	-	10, 10, 10	0.23	0	$9,\!9,\!9$	0.54	0
7	HEX	A	306	-	5, 5, 5	0.23	0	$4,\!4,\!4$	0.38	0
8	SO4	С	306	-	4,4,4	0.13	0	$6,\!6,\!6$	0.11	0
8	SO4	A	309	-	4,4,4	0.13	0	$6,\!6,\!6$	0.06	0
8	SO4	С	309	-	4,4,4	0.15	0	6,6,6	0.10	0
8	SO4	С	307	-	4,4,4	0.14	0	$6,\!6,\!6$	0.05	0
8	SO4	А	307	-	4,4,4	0.15	0	6,6,6	0.07	0
9	GOL	С	308	-	5, 5, 5	0.36	0	$5,\!5,\!5$	0.37	0
8	SO4	F	3000	-	4,4,4	0.13	0	6,6,6	0.08	0
8	SO4	D	104	-	4,4,4	0.15	0	6,6,6	0.04	0
8	SO4	С	305	-	4,4,4	0.13	0	6,6,6	0.08	0
6	LSC	С	304	-	34,34,34	0.87	1 (2%)	$39,\!41,\!41$	0.75	1 (2%)
8	SO4	А	308	-	4,4,4	0.15	0	$6,\!6,\!6$	0.08	0
9	GOL	А	311	-	5, 5, 5	0.36	0	$5,\!5,\!5$	0.27	0
6	LSC	A	305	-	34,34,34	0.87	1 (2%)	$39,\!41,\!41$	0.73	0
9	GOL	В	3000	-	5, 5, 5	0.36	0	$5,\!5,\!5$	0.31	0
9	GOL	D	105	-	5,5,5	0.34	0	5, 5, 5	0.30	0
8	SO4	D	102	-	4,4,4	0.14	0	6,6,6	0.08	0
8	SO4	D	101	-	4,4,4	0.13	0	6,6,6	0.07	0
11	NBU	Е	303	-	3,3,3	0.32	0	2,2,2	0.61	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	\mathbf{Res}	Link	Chirals	Torsions	Rings
9	GOL	А	311	-	-	0/4/4/4	-
11	NBU	Е	303	-	-	0/1/1/1	-
9	GOL	А	310	-	-	2/4/4/4	-
6	LSC	С	304	-	-	21/36/36/36	-



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	GOL	В	3001	-	-	2/4/4/4	-
9	GOL	D	103	-	-	2/4/4/4	-
10	UND	А	312	-	-	2/8/8/8	-
9	GOL	С	308	-	-	2/4/4/4	-
6	LSC	А	305	-	-	21/36/36/36	-
9	GOL	В	3000	-	-	4/4/4/4	-
7	HEX	А	306	-	-	0/3/3/3	-
9	GOL	D	105	-	-	2/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
6	С	304	LSC	O19-C18	4.19	1.45	1.33
6	А	305	LSC	O19-C18	4.16	1.45	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
6	С	304	LSC	C30-C31-N32	-2.03	108.99	115.78

There are no chirality outliers.

All (58) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	А	310	GOL	O1-C1-C2-C3
9	В	3001	GOL	O1-C1-C2-C3
9	D	103	GOL	O1-C1-C2-C3
9	С	308	GOL	O1-C1-C2-C3
6	С	304	LSC	C22-O23-P24-O25
6	С	304	LSC	C30-O35-P24-O25
6	А	305	LSC	C21-C22-O23-P24
6	А	305	LSC	C30-O35-P24-O23
6	А	305	LSC	C30-O35-P24-O25
6	А	305	LSC	C30-O35-P24-O34
6	А	305	LSC	O32-C18-O19-C20
6	А	305	LSC	C17-C18-O19-C20
6	А	305	LSC	C14-C15-C16-C17
6	А	305	LSC	O33-C21-C22-O23
6	С	304	LSC	C17-C18-O19-C20
9	В	3001	GOL	O1-C1-C2-O2



Mol	Chain	Res	Type	Atoms
6	С	304	LSC	O32-C18-O19-C20
6	С	304	LSC	C22-O23-P24-O35
6	С	304	LSC	C30-O35-P24-O23
6	А	305	LSC	C22-O23-P24-O35
6	А	305	LSC	C20-C21-C22-O23
6	С	304	LSC	C30-C31-N32-C34
6	С	304	LSC	C30-C31-N32-C35
6	С	304	LSC	C12-C13-C14-C15
6	С	304	LSC	C30-C31-N32-C33
6	А	305	LSC	C3-C4-C5-C6
6	А	305	LSC	C12-C13-C14-C15
9	А	310	GOL	O1-C1-C2-O2
9	С	308	GOL	O1-C1-C2-O2
9	D	103	GOL	O1-C1-C2-O2
10	А	312	UND	C1-C2-C3-C4
6	С	304	LSC	C1-C2-C3-C4
6	А	305	LSC	C13-C14-C15-C16
6	С	304	LSC	O19-C20-C21-C22
6	А	305	LSC	O19-C20-C21-C22
9	В	3000	GOL	O2-C2-C3-O3
9	D	105	GOL	O1-C1-C2-O2
6	С	304	LSC	C30-O35-P24-O34
6	А	305	LSC	C22-O23-P24-O25
6	А	305	LSC	C22-O23-P24-O34
6	С	304	LSC	C13-C14-C15-C16
6	С	304	LSC	O35-C30-C31-N32
6	С	304	LSC	C21-C22-O23-P24
6	А	305	LSC	C30-C31-N32-C33
6	С	304	LSC	C14-C15-C16-C17
6	A	305	LSC	C16-C17-C18-O19
9	В	3000	GOL	O1-C1-C2-C3
10	A	312	UND	C4-C5-C6-C7
6	A	305	LSC	C30-C31-N32-C34
6	С	304	LSC	C9-C10-C11-C12
6	A	305	LSC	C30-C31-N32-C35
9	В	3000	GOL	O1-C1-C2-O2
6	С	304	LSC	O19-C20-C21-O33
6	C	304	LSC	C7-C8-C9-C10
9	В	3000	GOL	C1-C2-C3-O3
9	D	105	GOL	O1-C1-C2-C3
6	A	305	LSC	C2-C3-C4-C5
6	С	304	LSC	C15-C16-C17-C18

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There are no ring outliers.

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	А	310	GOL	2	0
9	В	3001	GOL	3	0
9	D	103	GOL	1	0
8	С	306	SO4	1	0
8	А	307	SO4	2	0
9	С	308	GOL	1	0
8	F	3000	SO4	1	0
8	D	104	SO4	1	0
6	С	304	LSC	3	0
9	А	311	GOL	2	0
6	А	305	LSC	20	0
9	В	3000	GOL	3	0
9	D	105	GOL	1	0
11	Е	303	NBU	1	0

14 monomers are involved in 42 short contacts:

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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	$\mathbf{OWAB}(\mathbf{\AA}^2)$	$Q{<}0.9$
1	А	273/284~(96%)	-0.28	2 (0%) 87 84	31, 52, 100, 140	7(2%)
1	С	273/284~(96%)	-0.16	1 (0%) 92 91	33,60,115,138	11 (4%)
1	E	226/284~(79%)	0.09	11 (4%) 29 20	47, 100, 140, 174	24 (10%)
2	В	99/102~(97%)	-0.28	1 (1%) 82 77	34, 45, 77, 89	2 (2%)
2	D	100/102~(98%)	-0.29	0 100 100	42,63,97,113	3~(3%)
2	F	82/102~(80%)	1.34	27 (32%) 0 0	67, 122, 152, 168	3 (3%)
All	All	1053/1158~(90%)	-0.04	42 (3%) 38 28	31,65,133,174	50~(4%)

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	23	LEU	4.8
2	F	82	VAL	4.7
2	F	7	ILE	4.6
2	F	70	PHE	4.2
1	Е	217	TRP	4.1
1	Е	276	TYR	4.0
2	F	80	CYS	3.9
2	F	95	TRP	3.8
1	Е	263	VAL	3.7
2	В	1	ILE	3.5
1	С	63	TRP	3.5
2	F	87	LEU	3.2
2	F	35	ILE	3.0
2	F	88	SER	3.0
2	F	91	LYS	2.9
2	F	22	PHE	2.9
2	F	72	PRO	2.9
2	F	71	THR	2.8
2	F	9	VAL	2.8



Mol	Chain	Res	Type	RSRZ
1	А	57	THR	2.8
2	F	20	SER	2.8
2	F	92	ILE	2.8
2	F	81	ARG	2.8
1	Ε	63	TRP	2.7
1	Ε	208	VAL	2.7
1	Ε	57	THR	2.6
1	Ε	189	ALA	2.6
1	А	198	GLY	2.6
2	F	37	VAL	2.5
2	F	46	ILE	2.5
2	F	73	THR	2.4
1	Е	216	VAL	2.4
2	F	84	HIS	2.4
1	Е	58	PHE	2.3
1	Е	191	LEU	2.3
2	F	17	ASN	2.2
2	F	39	LEU	2.2
2	F	45	ARG	2.2
1	Е	65	THR	2.2
2	F	86	THR	2.2
2	F	15	ALA	2.1
2	F	4	THR	2.1

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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, 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	${f B} ext{-factors}({ m \AA}^2)$	Q<0.9
4	FUC	Н	2	10/11	0.62	0.34	$148,\!150,\!154,\!156$	0
5	NAG	Ι	1	14/15	0.67	0.28	$123,\!140,\!147,\!149$	0
3	NAG	G	1	14/15	0.79	0.16	$76,\!100,\!127,\!129$	0
3	FUC	G	2	10/11	0.79	0.33	$121,\!141,\!155,\!163$	0
3	NAG	G	3	14/15	0.84	0.27	117,124,127,129	0



Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B}$ -factors(${ m \AA}^2$)	Q<0.9
3	FUC	G	4	10/11	0.86	0.28	96,108,124,124	0
4	NAG	Н	1	14/15	0.88	0.27	$104,\!121,\!135,\!139$	0
4	FUC	Н	3	10/11	0.89	0.15	$98,\!106,\!109,\!114$	0
5	FUC	Ι	2	10/11	0.91	0.29	$127,\!138,\!143,\!143$	0

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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
8	SO4	С	307	5/5	0.70	0.33	172,174,175,177	0
8	SO4	D	104	5/5	0.78	0.24	162, 164, 167, 171	0
11	NBU	Е	303	4/4	0.78	0.34	$64,\!73,\!76,\!77$	0
8	SO4	А	309	5/5	0.80	0.37	178, 180, 181, 181	0
8	SO4	С	306	5/5	0.85	0.25	$131,\!134,\!137,\!138$	0
9	GOL	D	103	6/6	0.86	0.21	82,94,97,101	0
6	LSC	С	304	35/35	0.87	0.47	51,104,183,190	0
9	GOL	С	308	6/6	0.87	0.18	72,82,88,89	0
8	SO4	D	101	5/5	0.89	0.23	$150,\!153,\!155,\!160$	0
6	LSC	А	305	35/35	0.89	0.29	48,82,149,158	0
8	SO4	F	3000	5/5	0.91	0.11	124,129,132,134	0
10	UND	А	312	11/11	0.92	0.38	$46,\!53,\!59,\!64$	0
9	GOL	В	3001	6/6	0.92	0.21	61,73,83,85	0
9	GOL	А	311	6/6	0.92	0.21	$46,\!55,\!58,\!58$	0
9	GOL	В	3000	6/6	0.93	0.25	42,66,82,87	0
9	GOL	D	105	6/6	0.93	0.18	68,76,92,101	0
9	GOL	А	310	6/6	0.94	0.43	$53,\!68,\!80,\!88$	0
8	SO4	А	307	5/5	0.94	0.17	$126,\!129,\!134,\!136$	0
7	HEX	А	306	6/6	0.94	0.34	47,49,58,63	0
8	SO4	D	102	5/5	0.95	0.14	92,95,103,114	0
8	SO4	С	305	5/5	0.95	0.17	$98,\!103,\!108,\!121$	0
8	SO4	А	308	5/5	0.95	0.17	106, 110, 113, 120	0
8	SO4	С	309	5/5	0.96	0.27	82,89,91,94	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.







6.5 Other polymers (i)

There are no such residues in this entry.

