Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 01:37 AM BST

PDB ID	:	1CLZ
Title	:	IGG FAB (IGG3, KAPPA) FRAGMENT (MBR96) COMPLEXED WITH LEWIS Y NONOATE METHYL ESTER
Authors	:	Sheriff, S.; Bajorath, J.
Deposited on	:	1995-03-15
Resolution	:	2.80 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 ⓘ symbol.

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

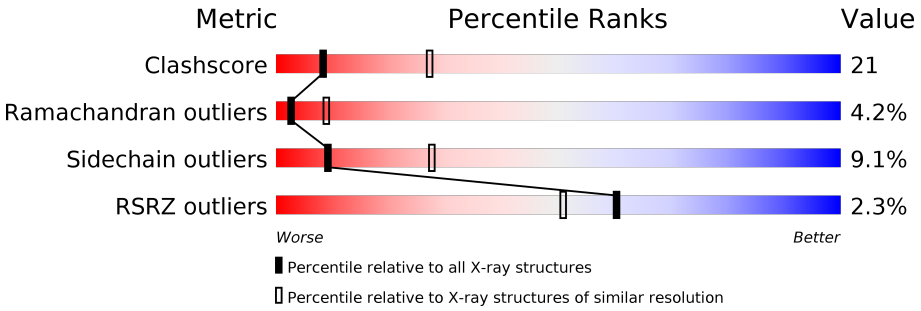
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
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	L	219	2% 54% 38% 7%
2	H	218	3% 55% 41% 5%
3	A	4	25% 50% 25%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3431 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 IGG FAB (IGG3, KAPPA).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	219	1705	1067	288	343	7	0	0	0

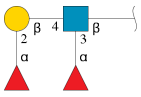
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	7	ILE	THR	conflict	PIR PC4203
L	9	VAL	LEU	conflict	PIR PC4203
L	27A	ILE	SER	conflict	PIR PC4203
L	27E	ASN	THR	conflict	PIR PC4203
L	45	GLN	LYS	conflict	PIR PC4203
L	96	PHE	ARG	conflict	PIR PC4203
L	100	SER	GLY	conflict	PIR PC4203

- Molecule 2 is a protein called IGG FAB (IGG3, KAPPA).

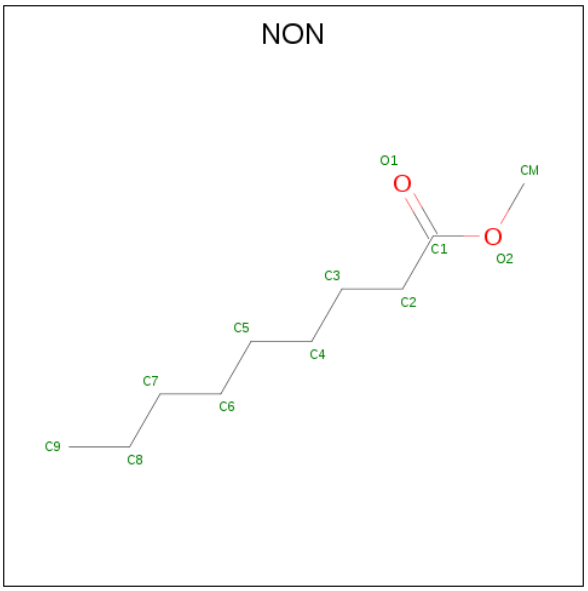
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	218	1668	1062	274	324	8	0	0	0

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	A	4	46	26	1	19	0	0	0

- Molecule 4 is METHYL NONANOATE (ESTER) (three-letter code: NON) (formula: $C_{10}H_{20}O_2$).



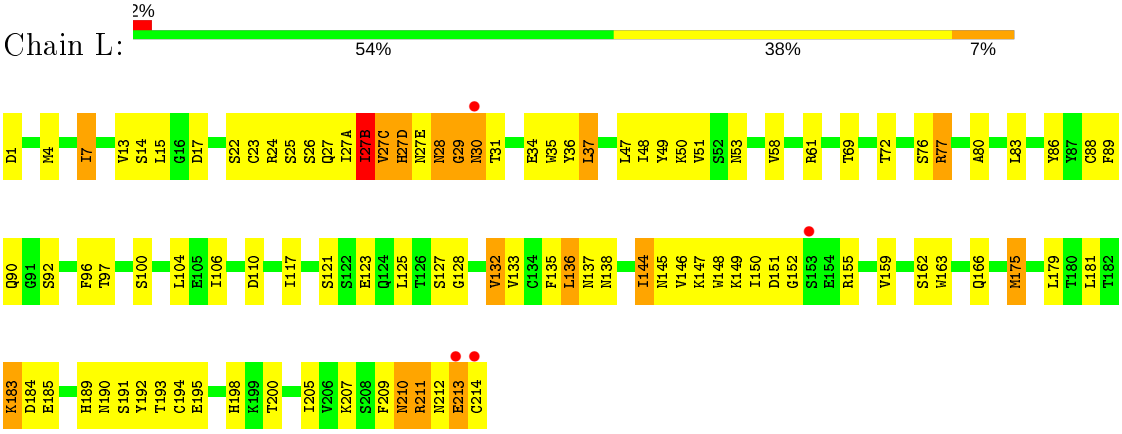
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total C O 12 10 2	0	0

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.

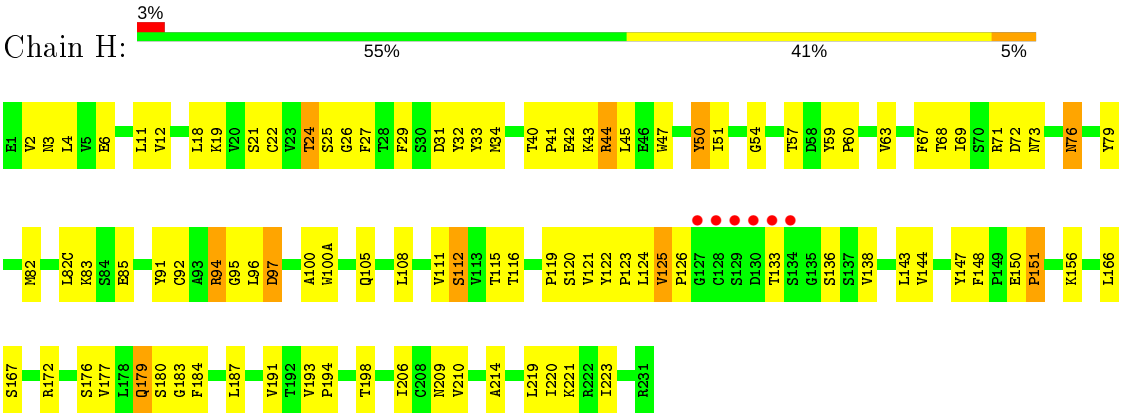
- Molecule 1: IGG FAB (IGG3, KAPPA)

Chain L:



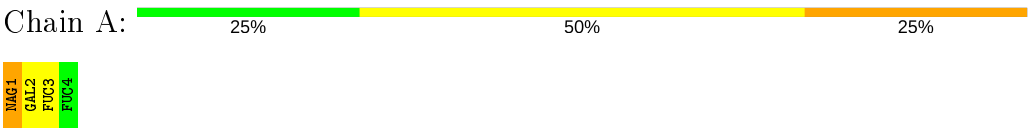
- Molecule 2: IGG FAB (IGG3, KAPPA)

Chain H:



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

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	69.40Å 84.90Å 86.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.80 42.45 – 2.80	Depositor EDS
% Data completeness (in resolution range)	70.0 (8.00-2.80) 73.5 (42.45-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.50 (at 2.81Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.197 , 0.295 0.195 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	27.9	Xtriage
Anisotropy	0.436	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 81.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.035 for -h,l,k	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	3431	wwPDB-VP
Average B, all atoms (Å^2)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NON, GAL, NAG, 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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	L	0.44	0/1744	0.73	0/2366
2	H	0.47	0/1711	0.75	0/2335
All	All	0.45	0/3455	0.74	0/4701

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

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	L	1705	0	1642	75	0
2	H	1668	0	1631	72	0
3	A	46	0	41	3	0
4	H	12	0	19	2	0
All	All	3431	0	3333	142	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 21.

All (142) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:27(B):ILE:HG22	1:L:92:SER:HB2	1.46	0.96
1:L:136:LEU:HD22	1:L:175:MET:HE2	1.60	0.82
2:H:18:LEU:HD23	2:H:82:MET:HE1	1.66	0.78
1:L:149:LYS:HD3	1:L:155:ARG:NH1	2.00	0.76
2:H:156:LYS:HB2	2:H:209:ASN:HB2	1.68	0.76
2:H:125:VAL:HG12	2:H:126:PRO:HD2	1.69	0.74
1:L:37:LEU:HB2	1:L:47:LEU:HD11	1.68	0.73
1:L:147:LYS:HB2	1:L:195:GLU:HG3	1.68	0.72
1:L:76:SER:O	1:L:77:ARG:HG2	1.89	0.72
1:L:47:LEU:HA	1:L:58:VAL:HG21	1.71	0.70
2:H:71:ARG:HD3	2:H:73:ASN:OD1	1.92	0.70
2:H:95:GLY:HA2	2:H:100(A):TRP:O	1.92	0.70
1:L:144:ILE:HD12	1:L:198:HIS:HB2	1.74	0.69
1:L:34:GLU:HG2	1:L:49:TYR:HA	1.76	0.68
2:H:119:PRO:HB3	2:H:147:TYR:HB3	1.76	0.67
1:L:27(C):VAL:H	1:L:31:THR:HG23	1.59	0.67
1:L:159:VAL:HG22	1:L:179:LEU:HD13	1.77	0.66
1:L:123:GLU:HG2	2:H:122:TYR:HD1	1.60	0.65
2:H:206:ILE:HD13	2:H:220:ILE:HD12	1.79	0.65
1:L:147:LYS:HB2	1:L:195:GLU:CG	2.28	0.64
2:H:32:TYR:CD2	3:A:1:NAG:H81	2.32	0.63
2:H:29:PHE:CD2	2:H:76:ASN:HA	2.34	0.63
2:H:47:TRP:CE3	2:H:60:PRO:HG3	2.34	0.62
1:L:148:TRP:O	1:L:155:ARG:HA	2.01	0.61
2:H:12:VAL:O	2:H:111:VAL:HA	2.03	0.59
1:L:190:ASN:O	1:L:210:ASN:HA	2.03	0.58
2:H:4:LEU:HD23	2:H:92:CYS:SG	2.44	0.57
1:L:25:SER:O	1:L:69:THR:HG23	2.05	0.56
1:L:89:PHE:CZ	1:L:96:PHE:HB3	2.41	0.56
2:H:24:THR:HG23	2:H:27:PHE:CE1	2.41	0.56
1:L:149:LYS:HD2	1:L:155:ARG:HG2	1.87	0.55
2:H:121:VAL:HG21	2:H:219:LEU:HD21	1.89	0.55
1:L:27(B):ILE:CG2	1:L:92:SER:HB2	2.30	0.55
1:L:138:ASN:HD21	2:H:172:ARG:NH2	2.05	0.55
2:H:150:GLU:HG3	2:H:151:PRO:HA	1.89	0.54
2:H:144:VAL:O	2:H:144:VAL:HG23	2.08	0.54
1:L:83:LEU:HD22	1:L:166:GLN:HG2	1.89	0.54
2:H:63:VAL:HG13	2:H:67:PHE:CG	2.43	0.53
2:H:19:LYS:HE2	2:H:79:TYR:CD2	2.43	0.53
2:H:96:LEU:HB2	2:H:100:ALA:HB3	1.89	0.53
2:H:123:PRO:HD3	2:H:221:LYS:HE2	1.90	0.52
2:H:63:VAL:CG1	2:H:67:PHE:HB2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:144:ILE:CD1	1:L:198:HIS:HB2	2.39	0.52
2:H:63:VAL:HG13	2:H:67:PHE:HB2	1.92	0.52
1:L:162:SER:HB3	2:H:177:VAL:CG1	2.40	0.52
2:H:59:TYR:OH	2:H:68:THR:HA	2.10	0.52
1:L:136:LEU:HD23	1:L:144:ILE:HG12	1.92	0.51
2:H:31:ASP:HB3	4:H:236:NON:H31	1.93	0.51
1:L:27:GLN:HG3	1:L:27(A):ILE:N	2.26	0.51
2:H:2:VAL:HA	2:H:26:GLY:HA3	1.92	0.50
1:L:36:TYR:O	1:L:86:TYR:HA	2.11	0.50
1:L:210:ASN:ND2	1:L:212:ASN:OD1	2.44	0.50
2:H:220:ILE:O	2:H:220:ILE:HG13	2.12	0.50
1:L:163:TRP:CD1	1:L:175:MET:HB3	2.47	0.50
2:H:71:ARG:HG2	2:H:72:ASP:N	2.25	0.50
2:H:210:VAL:HB	2:H:219:LEU:HD21	1.93	0.50
1:L:189:HIS:O	1:L:211:ARG:HD3	2.11	0.50
1:L:27(B):ILE:HB	1:L:31:THR:CG2	2.41	0.50
2:H:83:LYS:HG3	2:H:85:GLU:HG2	1.94	0.49
2:H:11:LEU:CD1	2:H:148:PHE:HE1	2.26	0.49
2:H:179:GLN:N	2:H:184:PHE:O	2.45	0.49
2:H:136:SER:O	2:H:194:PRO:HA	2.11	0.49
1:L:28:ASN:O	1:L:30:ASN:N	2.46	0.49
1:L:195:GLU:HA	1:L:205:ILE:O	2.13	0.49
1:L:123:GLU:HG2	2:H:122:TYR:CD1	2.44	0.48
2:H:51:ILE:CG1	2:H:54:GLY:HA2	2.42	0.48
1:L:183:LYS:HG3	1:L:184:ASP:N	2.28	0.48
2:H:50:TYR:C	2:H:50:TYR:CD1	2.86	0.48
2:H:33:TYR:HA	2:H:51:ILE:O	2.13	0.48
1:L:14:SER:O	1:L:17:ASP:HB2	2.13	0.48
2:H:82:MET:HB3	2:H:82(C):LEU:HD21	1.94	0.48
1:L:149:LYS:HB3	1:L:152:GLY:HA2	1.96	0.48
2:H:96:LEU:CB	2:H:100:ALA:HB3	2.44	0.48
1:L:146:VAL:HG21	1:L:175:MET:CE	2.44	0.48
2:H:3:ASN:C	2:H:4:LEU:HD12	2.34	0.47
2:H:210:VAL:HB	2:H:219:LEU:CD2	2.43	0.47
1:L:117:ILE:HB	1:L:207:LYS:CG	2.44	0.47
1:L:121:SER:O	1:L:125:LEU:HD23	2.15	0.47
1:L:49:TYR:O	1:L:50:LYS:HB2	2.13	0.47
2:H:63:VAL:HG13	2:H:67:PHE:CD2	2.51	0.46
1:L:192:TYR:HB2	1:L:209:PHE:CE2	2.50	0.46
2:H:51:ILE:HG12	2:H:54:GLY:HA2	1.98	0.46
2:H:47:TRP:HZ2	2:H:50:TYR:CD2	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:27(B):ILE:HB	1:L:31:THR:HG23	1.98	0.46
1:L:80:ALA:HA	1:L:106:ILE:CD1	2.45	0.46
2:H:3:ASN:OD1	2:H:25:SER:HB3	2.16	0.46
2:H:111:VAL:O	2:H:112:SER:HB3	2.16	0.46
2:H:138:VAL:HG12	2:H:193:VAL:O	2.16	0.46
2:H:40:THR:OG1	2:H:44:ARG:HB3	2.16	0.46
1:L:144:ILE:HG22	1:L:163:TRP:HZ2	1.81	0.46
2:H:123:PRO:CD	2:H:221:LYS:HE2	2.46	0.45
1:L:191:SER:HA	1:L:209:PHE:O	2.17	0.45
1:L:61:ARG:HB2	1:L:76:SER:O	2.16	0.45
2:H:11:LEU:HD12	2:H:148:PHE:HE1	1.82	0.45
2:H:166:LEU:HD13	2:H:191:VAL:HG21	1.99	0.45
2:H:4:LEU:HB3	2:H:92:CYS:SG	2.57	0.45
1:L:49:TYR:O	1:L:53:ASN:HB2	2.17	0.45
2:H:83:LYS:HG3	2:H:85:GLU:CG	2.46	0.44
2:H:179:GLN:O	2:H:183:GLY:N	2.51	0.44
1:L:110:ASP:HB3	1:L:200:THR:HG22	1.98	0.44
1:L:146:VAL:HG21	1:L:175:MET:HE2	1.99	0.44
1:L:27(D):HIS:CD2	1:L:27(E):ASN:H	2.35	0.44
1:L:162:SER:HB3	2:H:177:VAL:HG13	2.00	0.43
1:L:193:THR:HG22	1:L:194:CYS:N	2.33	0.43
1:L:24:ARG:HA	1:L:69:THR:O	2.18	0.43
2:H:31:ASP:HB3	4:H:236:NON:C3	2.47	0.43
1:L:7:ILE:HG13	1:L:22:SER:HB2	2.01	0.43
2:H:223:ILE:HD12	2:H:223:ILE:N	2.32	0.43
1:L:37:LEU:HG	1:L:86:TYR:CE2	2.54	0.43
1:L:34:GLU:O	1:L:88:CYS:HA	2.18	0.43
2:H:176:SER:HB3	2:H:187:LEU:HD23	2.00	0.43
2:H:119:PRO:CB	2:H:147:TYR:HB3	2.47	0.43
2:H:108:LEU:CD2	2:H:150:GLU:HB3	2.49	0.43
1:L:135:PHE:CE2	1:L:137:ASN:HB2	2.53	0.43
1:L:4:MET:HG2	1:L:97:THR:HG22	2.01	0.43
2:H:42:GLU:CD	2:H:42:GLU:H	2.22	0.43
1:L:117:ILE:HB	1:L:207:LYS:HG3	2.01	0.43
1:L:181:LEU:HD23	1:L:185:GLU:HG2	2.01	0.42
1:L:132:VAL:HG13	1:L:179:LEU:HB3	2.01	0.42
2:H:51:ILE:HG13	2:H:57:THR:HG22	2.01	0.42
2:H:97:ASP:HA	3:A:1:NAG:H83	2.02	0.42
1:L:27(D):HIS:CD2	1:L:27(E):ASN:N	2.88	0.42
1:L:37:LEU:HG	1:L:86:TYR:CZ	2.54	0.42
1:L:27(E):ASN:O	1:L:29:GLY:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:149:LYS:CD	1:L:155:ARG:HG2	2.49	0.41
1:L:213:GLU:O	1:L:214:CYS:SG	2.78	0.41
1:L:213:GLU:C	1:L:214:CYS:SG	2.99	0.41
2:H:29:PHE:CE1	2:H:34:MET:HG3	2.56	0.41
1:L:150:ILE:O	1:L:151:ASP:HB2	2.21	0.41
2:H:27:PHE:CE2	2:H:94:ARG:HG3	2.56	0.41
1:L:23:CYS:HB2	1:L:35:TRP:CH2	2.56	0.41
1:L:27(D):HIS:CE1	3:A:2:GAL:O3	2.74	0.41
2:H:123:PRO:N	2:H:221:LYS:HE2	2.35	0.41
1:L:13:VAL:O	1:L:106:ILE:HA	2.21	0.41
1:L:48:ILE:HG22	1:L:49:TYR:N	2.36	0.41
2:H:51:ILE:HB	2:H:69:ILE:HD13	2.03	0.40
2:H:3:ASN:HB2	2:H:25:SER:HB3	2.03	0.40
2:H:6:GLU:OE2	2:H:91:TYR:HA	2.21	0.40
1:L:15:LEU:HD21	1:L:106:ILE:HD13	2.03	0.40
1:L:144:ILE:HG13	1:L:145:ASN:H	1.86	0.40
1:L:117:ILE:HD12	1:L:117:ILE:HA	1.89	0.40
2:H:40:THR:O	2:H:43:LYS:N	2.54	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	L	217/219 (99%)	192 (88%)	16 (7%)	9 (4%)	3 9
2	H	216/218 (99%)	190 (88%)	17 (8%)	9 (4%)	3 9
All	All	433/437 (99%)	382 (88%)	33 (8%)	18 (4%)	3 9

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	29	GLY
1	L	211	ARG
2	H	112	SER
1	L	27(C)	VAL
2	H	115	THR
2	H	179	GLN
2	H	180	SER
2	H	198	THR
1	L	28	ASN
2	H	76	ASN
2	H	214	ALA
1	L	27(D)	HIS
1	L	30	ASN
1	L	27(B)	ILE
2	H	41	PRO
1	L	128	GLY
1	L	51	VAL
2	H	151	PRO

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	L	197/197 (100%)	178 (90%)	19 (10%)	8 24
2	H	187/188 (100%)	171 (91%)	16 (9%)	10 30
All	All	384/385 (100%)	349 (91%)	35 (9%)	9 27

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	1	ASP
1	L	7	ILE
1	L	26	SER
1	L	27(B)	ILE
1	L	37	LEU
1	L	72	THR

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Mol	Chain	Res	Type
1	L	77	ARG
1	L	90	GLN
1	L	100	SER
1	L	104	LEU
1	L	127	SER
1	L	132	VAL
1	L	133	VAL
1	L	136	LEU
1	L	144	ILE
1	L	175	MET
1	L	183	LYS
1	L	210	ASN
1	L	213	GLU
2	H	21	SER
2	H	22	CYS
2	H	24	THR
2	H	44	ARG
2	H	45	LEU
2	H	50	TYR
2	H	94	ARG
2	H	97	ASP
2	H	105	GLN
2	H	116	THR
2	H	120	SER
2	H	124	LEU
2	H	125	VAL
2	H	133	THR
2	H	143	LEU
2	H	167	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	18	GLN
1	L	27(D)	HIS
1	L	27(E)	ASN
1	L	138	ASN
1	L	157	ASN
1	L	190	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

4 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	NAG	A	1	3,4	15,15,15	0.52	0	21,21,21	0.85	1 (4%)
3	GAL	A	2	3	11,11,12	0.38	0	15,15,17	0.58	0
3	FUC	A	3	3	10,10,11	0.48	0	14,14,16	0.79	1 (7%)
3	FUC	A	4	3	10,10,11	0.43	0	14,14,16	0.53	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
3	NAG	A	1	3,4	-	0/6/26/26	0/1/1/1
3	GAL	A	2	3	-	2/2/19/22	0/1/1/1
3	FUC	A	3	3	-	-	0/1/1/1
3	FUC	A	4	3	-	-	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	3	FUC	C1-C2-C3	2.50	112.75	109.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1	NAG	C1-C2-N2	-2.23	108.14	110.73

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2	GAL	C4-C5-C6-O6
3	A	2	GAL	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2	GAL	1	0
3	A	1	NAG	2	0

5.6 Ligand geometry

1 ligand is 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	$\#\|Z\| > 2$
4	NON	H	236	3	11,11,11	0.36	0	11,11,11	0.49	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	NON	H	236	3	-	2/10/10/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	236	NON	C2-C1-O2-CM
4	H	236	NON	O1-C1-O2-CM

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	236	NON	2	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

6.1 Protein, DNA and RNA chains

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			OWAB(Å^2)	Q<0.9
1	L	219/219 (100%)	-0.39	4 (1%)	68	61	2, 13, 47, 69	0
2	H	218/218 (100%)	-0.40	6 (2%)	53	43	2, 8, 38, 57	0
All	All	437/437 (100%)	-0.40	10 (2%)	60	51	2, 11, 44, 69	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	133	THR	5.9
2	H	128	CYS	5.5
2	H	130	ASP	5.2
1	L	214	CYS	4.3
2	H	129	SER	4.1
2	H	134	SER	3.3
1	L	153	SER	2.3
2	H	127	GLY	2.1
1	L	30	ASN	2.1
1	L	213	GLU	2.1

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

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

6.3 Carbohydrates

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	B-factors(Å^2)	Q<0.9
3	FUC	A	3	10/11	0.94	0.16	13,14,14,14	0
3	GAL	A	2	11/12	0.96	0.16	7,10,12,13	0
3	NAG	A	1	15/15	0.97	0.12	8,11,14,14	0
3	FUC	A	4	10/11	0.98	0.10	7,9,10,10	0

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	B-factors(Å^2)	Q<0.9
4	NON	H	236	12/12	0.93	0.26	14,19,26,26	0

6.5 Other polymers (i)

There are no such residues in this entry.