Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:38 PM GMT

PDB ID	:	1XZ0
Title	:	Crystal structure of CD1a in complex with a synthetic mycobactin lipopeptide
Authors	:	Zajonc, D.M.; Crispin, M.D.; Bowden, T.A.; Young, D.C.; Cheng, T.Y.; Hu, J.; Costello, C.E.; Miller, M.J.; Moody, D.B.; Wilson, I.A.
Deposited on	:	2004-11-11
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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ①) were used in the production of this report:

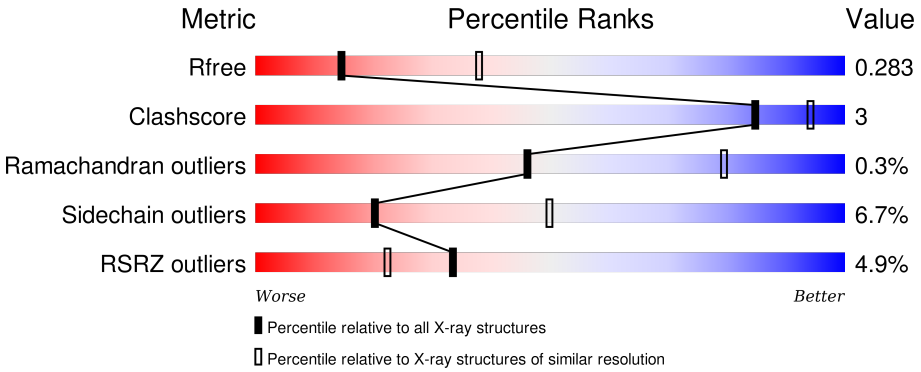
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (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. 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	A	279	3% 82% 13%
1	C	279	7% 85% 11%
2	B	99	2% 80% 19%
2	D	99	7% 89% 10%

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	A	501	-	-	-	X
5	JH0	A	601	-	-	-	X
5	JH0	C	602	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6209 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 T-cell surface glycoprotein CD1a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	271	Total	C	N	O	S	0	0	0
			2198	1410	384	396	8			
1	C	270	Total	C	N	O	S	0	0	0
			2191	1405	383	395	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	278	VAL	-	CLONING ARTIFACT	UNP P06126
A	279	ASP	-	CLONING ARTIFACT	UNP P06126
C	278	VAL	-	CLONING ARTIFACT	UNP P06126
C	279	ASP	-	CLONING ARTIFACT	UNP P06126

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	98	Total	C	N	O	S	0	0	0
			820	523	139	156	2			
2	D	98	Total	C	N	O	S	0	0	0
			820	523	139	156	2			

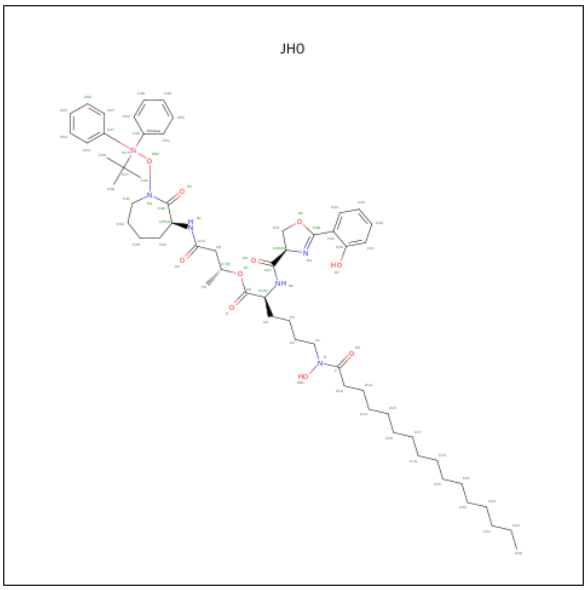
- Molecule 3 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	2	Total	C	N	O	0	0
			24	14	1	9		

- Molecule 5 is 6-(HYDROXY-HEXADECANOYL-AMINO)-2-{[(4S)-2-(2-HYDROXY-PHENYL)-4,5-DIHYDRO-OXAZOLE-4-CARBONYL]-AMINO}-HEXANOIC ACID 2-[(3S)-1-(TERT-BUTYL-DIPHENYL-SILANYLOXY)-2-OXO-AZEPAN-3-YLCARBAMOYL]-(1S)-1-METHYL-ETHYL ESTER (three-letter code: JH0) (formula: $C_{58}H_{85}N_5O_{10}Si$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O Si 58 42 5 10 1	0	0
5	C	1	Total C N O 41 30 4 7	0	0

- Molecule 6 is water.

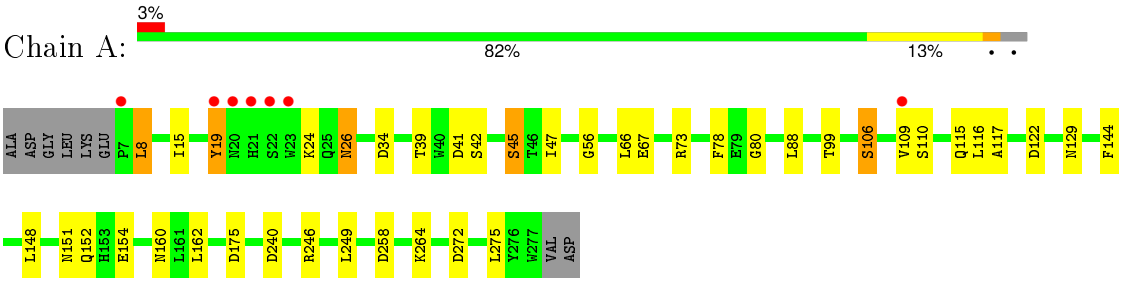
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	11	Total O 11 11	0	0
6	B	4	Total O 4 4	0	0
6	C	3	Total O 3 3	0	0
6	D	1	Total O 1 1	0	0

3 Residue-property plots

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

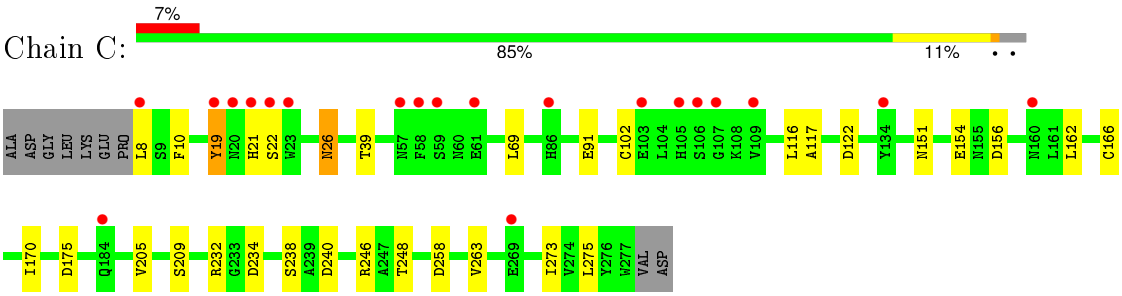
- Molecule 1: T-cell surface glycoprotein CD1a

Chain A:



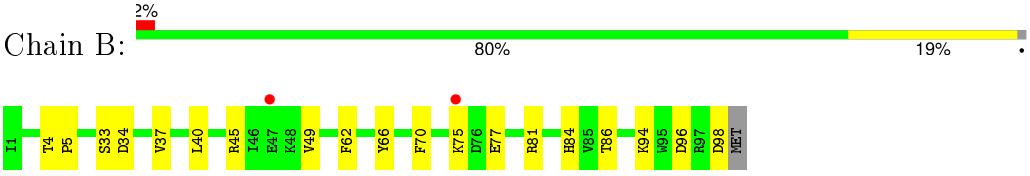
- Molecule 1: T-cell surface glycoprotein CD1a

Chain C:



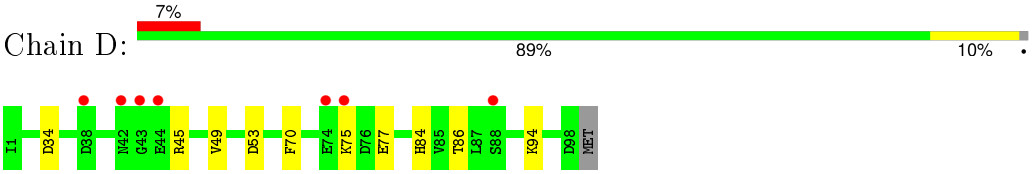
- Molecule 2: Beta-2-microglobulin

Chain B:



- Molecule 2: Beta-2-microglobulin

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	55.96Å 43.23Å 209.94Å 90.00° 91.04° 90.00°	Depositor
Resolution (Å)	38.63 – 2.80 38.63 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.3 (38.63-2.80) 94.3 (38.63-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	2.94 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.217 , 0.277 0.225 , 0.283	Depositor DCC
R_{free} test set	1157 reflections (5.08%)	DCC
Wilson B-factor (Å^2)	53.8	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 76.5	EDS
Estimated twinning fraction	0.035 for h,-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 23923 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	6209	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.54% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: JH0, 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	A	0.68	1/2271 (0.0%)	0.81	7/3091 (0.2%)
1	C	0.55	0/2263	0.75	6/3080 (0.2%)
2	B	0.73	0/843	0.83	3/1142 (0.3%)
2	D	0.56	0/843	0.74	2/1142 (0.2%)
All	All	0.63	1/6220 (0.0%)	0.79	18/8455 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	19	TYR	CD1-CE1	5.12	1.47	1.39

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	258	ASP	CB-CG-OD2	6.97	124.57	118.30
2	B	34	ASP	CB-CG-OD2	6.93	124.54	118.30
1	C	234	ASP	CB-CG-OD2	6.83	124.44	118.30
1	A	34	ASP	CB-CG-OD2	6.76	124.38	118.30
1	A	19	TYR	CA-CB-CG	6.61	125.95	113.40
2	D	34	ASP	CB-CG-OD2	6.21	123.89	118.30
1	A	258	ASP	CB-CG-OD2	6.20	123.88	118.30
2	D	53	ASP	CB-CG-OD2	6.07	123.76	118.30
1	A	240	ASP	CB-CG-OD2	5.93	123.64	118.30
2	B	98	ASP	CB-CG-OD2	5.77	123.49	118.30
1	C	156	ASP	CB-CG-OD2	5.76	123.48	118.30
1	C	240	ASP	CB-CG-OD2	5.68	123.42	118.30
1	C	122	ASP	CB-CG-OD2	5.60	123.34	118.30
1	A	122	ASP	CB-CG-OD2	5.58	123.32	118.30
2	B	96	ASP	CB-CG-OD2	5.52	123.27	118.30
1	A	41	ASP	CB-CG-OD2	5.46	123.22	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	19	TYR	CB-CG-CD1	5.43	124.26	121.00
1	C	19	TYR	CA-CB-CG	5.17	123.23	113.40

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	A	2198	0	2084	16	0
1	C	2191	0	2076	9	0
2	B	820	0	785	5	0
2	D	820	0	785	1	0
3	A	38	0	34	0	0
4	C	24	0	22	0	0
5	A	58	0	65	4	0
5	C	41	0	51	2	0
6	A	11	0	0	2	0
6	B	4	0	0	0	0
6	C	3	0	0	0	0
6	D	1	0	0	0	0
All	All	6209	0	5902	35	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 3.

All (35) 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:A:151:ASN:ND2	1:A:154:GLU:HB2	2.17	0.60
5:C:602:JH0:N2	5:C:602:JH0:H93	2.17	0.59
1:A:80:GLY:HA3	5:A:601:JH0:H342	1.83	0.59
1:C:102:CYS:HG	1:C:166:CYS:HG	1.52	0.56
1:A:106:SER:OG	1:A:106:SER:O	2.22	0.55
1:A:116:LEU:HD23	1:A:117:ALA:N	2.23	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:116:LEU:HD23	1:C:117:ALA:N	2.26	0.51
1:A:47:ILE:HG13	1:A:67:GLU:HG2	1.93	0.51
5:A:601:JH0:H341	5:A:601:JH0:O2	2.11	0.50
1:A:264:LYS:NZ	1:A:272:ASP:OD1	2.45	0.49
1:A:144:PHE:O	1:A:148:LEU:HG	2.12	0.49
1:A:249:LEU:HA	6:A:609:HOH:O	2.12	0.49
1:A:56:GLY:HA3	6:A:603:HOH:O	2.13	0.47
5:C:602:JH0:H93	5:C:602:JH0:N4	2.31	0.46
1:C:26:ASN:C	1:C:26:ASN:OD1	2.54	0.46
5:A:601:JH0:H92	5:A:601:JH0:C38	2.47	0.44
1:C:151:ASN:ND2	1:C:154:GLU:HB2	2.32	0.44
1:C:8:LEU:HD12	1:C:8:LEU:O	2.18	0.44
1:A:88:LEU:HD11	1:A:144:PHE:CD2	2.53	0.44
1:C:263:VAL:HB	1:C:273:ILE:HB	2.00	0.44
1:C:102:CYS:SG	1:C:166:CYS:SG	3.09	0.43
1:A:24:LYS:HB2	1:A:78:PHE:HZ	1.83	0.43
2:D:84:HIS:CE1	2:D:86:THR:HG23	2.53	0.43
2:B:37:VAL:HG21	2:B:66:TYR:CE1	2.54	0.43
2:B:33:SER:HB3	2:B:62:PHE:CE2	2.54	0.43
2:B:4:THR:OG1	2:B:5:PRO:HD2	2.19	0.43
1:A:88:LEU:HD11	1:A:144:PHE:HD2	1.83	0.43
1:C:10:PHE:HB3	1:C:170:ILE:HD12	2.00	0.42
1:C:205:VAL:HG22	1:C:248:THR:HG22	2.01	0.42
2:B:40:LEU:HD11	2:B:81:ARG:HB2	2.01	0.41
1:A:99:THR:HG23	1:A:99:THR:O	2.19	0.41
1:A:80:GLY:CA	5:A:601:JH0:H342	2.48	0.41
1:A:15:ILE:O	1:A:26:ASN:HA	2.21	0.41
1:A:73:ARG:NH2	1:A:154:GLU:HG3	2.36	0.41
2:B:84:HIS:CE1	2:B:86:THR:HG23	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	269/279 (96%)	257 (96%)	10 (4%)	2 (1%)	26 62
1	C	268/279 (96%)	257 (96%)	11 (4%)	0	100 100
2	B	96/99 (97%)	93 (97%)	3 (3%)	0	100 100
2	D	96/99 (97%)	92 (96%)	4 (4%)	0	100 100
All	All	729/756 (96%)	699 (96%)	28 (4%)	2 (0%)	46 79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	LEU
1	A	45	SER

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	236/242 (98%)	218 (92%)	18 (8%)	16 42
1	C	235/242 (97%)	221 (94%)	14 (6%)	24 56
2	B	93/94 (99%)	87 (94%)	6 (6%)	21 52
2	D	93/94 (99%)	87 (94%)	6 (6%)	21 52
All	All	657/672 (98%)	613 (93%)	44 (7%)	20 50

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LEU
1	A	19	TYR
1	A	26	ASN
1	A	39	THR
1	A	42	SER
1	A	45	SER
1	A	66	LEU
1	A	106	SER
1	A	109	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	110	SER
1	A	115	GLN
1	A	129	ASN
1	A	152	GLN
1	A	160	ASN
1	A	162	LEU
1	A	175	ASP
1	A	246	ARG
1	A	275	LEU
2	B	45	ARG
2	B	49	VAL
2	B	70	PHE
2	B	75	LYS
2	B	77	GLU
2	B	94	LYS
1	C	19	TYR
1	C	21	HIS
1	C	22	SER
1	C	26	ASN
1	C	39	THR
1	C	69	LEU
1	C	91	GLU
1	C	162	LEU
1	C	175	ASP
1	C	209	SER
1	C	232	ARG
1	C	238	SER
1	C	246	ARG
1	C	275	LEU
2	D	45	ARG
2	D	49	VAL
2	D	70	PHE
2	D	75	LYS
2	D	77	GLU
2	D	94	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	151	ASN
1	C	228	GLN

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

5 carbohydrates are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	NAG	A	501	1,3	14,14,15	0.67	0	15,19,21	1.44	2 (13%)
3	NAG	A	502	3	14,14,15	0.50	0	15,19,21	0.81	0
3	FUC	A	531	3	10,10,11	0.60	0	14,14,16	1.18	1 (7%)
4	NAG	C	501	1,4	14,14,15	0.59	0	15,19,21	2.28	1 (6%)
4	FUC	C	532	4	10,10,11	0.62	0	14,14,16	1.34	2 (14%)

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	501	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	502	3	-	0/6/23/26	0/1/1/1
3	FUC	A	531	3	-	0/0/17/20	0/1/1/1
4	NAG	C	501	1,4	-	0/6/23/26	0/1/1/1
4	FUC	C	532	4	-	0/0/17/20	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	501	NAG	O7-C7-C8	-2.79	116.95	122.06
4	C	532	FUC	O5-C1-C2	-2.59	106.66	110.86
4	C	532	FUC	O5-C5-C6	2.03	109.48	106.13
3	A	531	FUC	O5-C5-C6	2.55	110.35	106.13
3	A	501	NAG	C1-O5-C5	3.00	116.06	112.25
4	C	501	NAG	C1-O5-C5	7.99	122.38	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	JH0	A	601	-	56,60,78	1.81	4 (7%)	63,76,104	2.00	14 (22%)
5	JH0	C	602	-	40,41,78	1.28	3 (7%)	41,49,104	1.97	8 (19%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	JH0	A	601	-	-	2/51/80/104	1/3/3/5
5	JH0	C	602	-	-	0/45/53/104	0/1/1/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	601	JH0	ON2-N3	-9.93	1.36	1.48
5	C	602	JH0	C-N	2.02	1.37	1.34
5	A	601	JH0	ON1-N	2.48	1.40	1.29
5	C	602	JH0	O6-C38	4.30	1.45	1.36
5	C	602	JH0	O1-C6	5.11	1.46	1.34
5	A	601	JH0	O6-C38	5.15	1.44	1.36
5	A	601	JH0	O1-C6	5.38	1.47	1.34

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	601	JH0	O6-C38-N4	-6.43	111.12	118.13
5	C	602	JH0	O1-C6-O	-3.54	116.59	123.89
5	A	601	JH0	O2-C10-C8	-3.20	116.63	121.30
5	C	602	JH0	C37-C39-N4	-2.96	101.10	103.65
5	A	601	JH0	C37-C39-N4	-2.74	101.29	103.65
5	A	601	JH0	O1-C6-O	-2.67	118.38	123.89
5	C	602	JH0	C37-O6-C38	2.10	108.81	105.52
5	A	601	JH0	C33-C34-C35	2.23	118.91	114.23
5	A	601	JH0	C37-O6-C38	2.42	107.90	105.53
5	A	601	JH0	C7-O1-C6	2.68	121.32	118.23
5	A	601	JH0	O1-C6-C5	2.92	119.86	111.74
5	A	601	JH0	O1-C7-C9	2.94	114.51	107.88
5	C	602	JH0	O1-C6-C5	3.10	120.37	111.74
5	C	602	JH0	C7-O1-C6	3.25	121.98	118.23
5	A	601	JH0	C5-N2-C11	3.43	129.31	121.62
5	A	601	JH0	C4-C5-N2	3.44	117.42	110.87
5	A	601	JH0	C34-C35-N1	3.45	116.52	109.98
5	A	601	JH0	O6-C38-C45	4.09	123.65	115.91
5	C	602	JH0	C39-C11-N2	4.58	121.36	115.76
5	C	602	JH0	C11-C39-N4	5.00	118.87	111.78
5	C	602	JH0	O1-C7-C8	6.40	117.15	105.94
5	A	601	JH0	C39-N4-C38	7.48	113.83	107.11

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	601	JH0	O3-C11-C39-C37
5	A	601	JH0	C37-C39-C11-N2

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	601	JH0	C31-C32-C33-C34-C35-C36-N3

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	601	JH0	4	0
5	C	602	JH0	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	A	271/279 (97%)	0.48	7 (2%) 59 47	49, 54, 58, 59	0
1	C	270/279 (96%)	0.67	20 (7%) 17 9	50, 54, 57, 59	0
2	B	98/99 (98%)	0.37	2 (2%) 68 58	51, 54, 58, 60	0
2	D	98/99 (98%)	0.54	7 (7%) 19 10	52, 54, 58, 59	0
All	All	737/756 (97%)	0.54	36 (4%) 33 22	49, 54, 58, 60	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	22	SER	8.4
1	C	23	TRP	7.0
1	C	8	LEU	5.5
1	A	21	HIS	5.4
1	C	106	SER	5.3
1	C	105	HIS	4.6
1	A	22	SER	4.1
1	C	20	ASN	4.0
1	C	59	SER	3.7
1	A	19	TYR	3.6
1	C	19	TYR	3.6
2	D	75	LYS	3.4
1	A	7	PRO	3.4
1	C	160	ASN	3.3
2	B	75	LYS	3.1
1	A	109	VAL	2.9
1	C	61	GLU	2.8
1	C	107	GLY	2.7
2	D	42	ASN	2.7
2	D	38	ASP	2.6
1	C	21	HIS	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	D	44	GLU	2.4
1	C	86	HIS	2.4
1	C	57	ASN	2.4
1	C	103	GLU	2.4
1	C	134	TYR	2.4
2	D	74	GLU	2.3
1	C	109	VAL	2.3
1	C	184	GLN	2.3
2	D	43	GLY	2.2
1	A	23	TRP	2.1
1	A	20	ASN	2.1
2	D	88	SER	2.1
1	C	58	PHE	2.1
1	C	269	GLU	2.0
2	B	47	GLU	2.0

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

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

6.3 Carbohydrates (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å^2)	Q<0.9
3	NAG	A	501	14/15	0.83	0.25	2.34	48,52,57,58	0
4	NAG	C	501	14/15	0.83	0.28	0.01	54,55,56,57	0
3	FUC	A	531	10/11	0.83	0.34	-	58,59,60,61	0
3	NAG	A	502	14/15	0.72	0.31	-	46,49,51,51	0
4	FUC	C	532	10/11	0.76	0.43	-	56,57,58,58	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å^2)	Q<0.9
5	JH0	C	602	41/74	0.61	0.35	4.20	59,88,100,101	0
5	JH0	A	601	58/74	0.74	0.35	3.99	43,86,100,100	0

6.5 Other polymers (i)

There are no such residues in this entry.