Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 06:56 PM GMT

PDB ID	:	4N6P
Title	:	Crystal Structure of C-lobe of Bovine lactoferrin complexed with meclofenamic acid at 1.4 A resolution
Authors	:	Gautam, L.; Dube, D.; Sinha, M.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on	:	2013-10-14
Resolution	:	1.40 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 (i) symbol.

The following versions of software and data (see references (i)) 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 ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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	Percentile Ranks	Value
Rfree		0.211
Clashscore		8
Ramachandran outliers		0
Sidechain outliers		2.8%
RSRZ outliers		9.4%

Worse   *Better*

▌ Percentile relative to all X-ray structures
◫ Percentile relative to X-ray structures of similar resolution
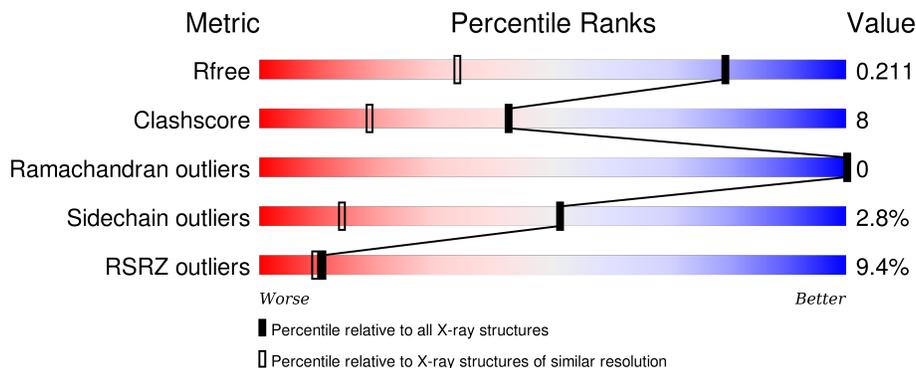
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1199 (1.40-1.40)
Clashscore	102246	1295 (1.40-1.40)
Ramachandran outliers	100387	1259 (1.40-1.40)
Sidechain outliers	100360	1258 (1.40-1.40)
RSRZ outliers	91569	1198 (1.40-1.40)

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	341	8% 80% 17% ··
2	B	6	83% 83% 17%

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
10	JMS	A	713	-	-	-	X
9	GOL	A	711	-	-	-	X
9	GOL	A	712	-	-	-	X

2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 3021 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 Lactotransferrin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total 2560	C 1593	N 448	O 499	S 20	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	565	LYS	ASN	ENGINEERED MUTATION	UNP P24627
A	608	GLU	LYS	ENGINEERED MUTATION	UNP P24627
A	677	LEU	-	EXPRESSION TAG	UNP P24627
A	678	GLU	-	EXPRESSION TAG	UNP P24627
A	679	ALA	-	EXPRESSION TAG	UNP P24627
A	680	CYS	-	EXPRESSION TAG	UNP P24627
A	681	ALA	-	EXPRESSION TAG	UNP P24627
A	682	PHE	-	EXPRESSION TAG	UNP P24627

- Molecule 2 is a protein called C-terminal peptide from Lactotransferrin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	6	Total 44	C 29	N 6	O 8	S 1	0	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Zn 1	0	0

- Molecule 4 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Fe 1	0	0

• Molecule 5 is CARBONATE ION (three-letter code: CO3) (formula: CO_3).
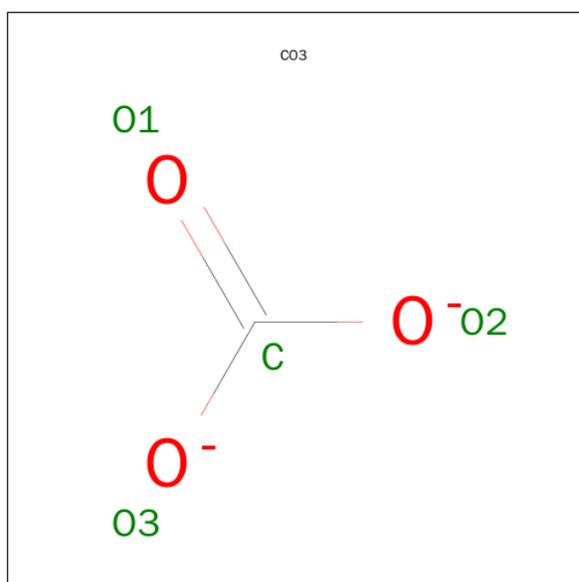
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	4	1	3	0	0

• Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).
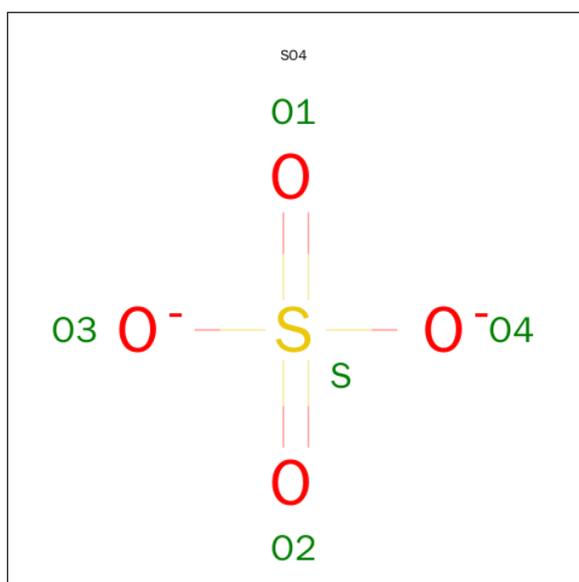
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
6	A	1	5	4	1	0	0

• Molecule 7 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:

$C_8H_{15}NO_6$).
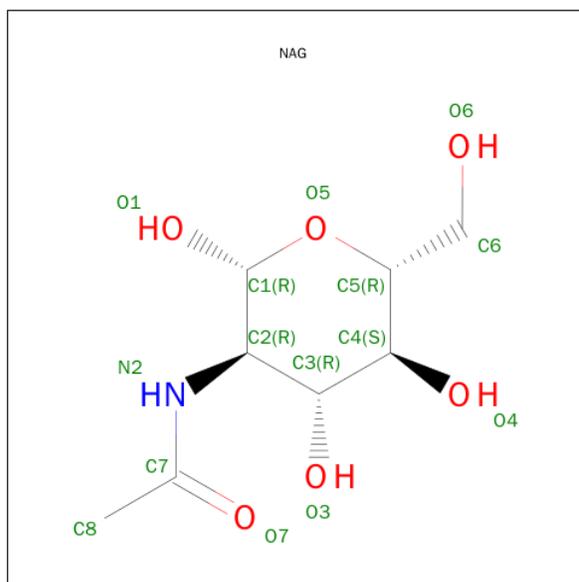
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	2	Total	C	N	O	0	0
			28	16	2	10		
8	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 9 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).
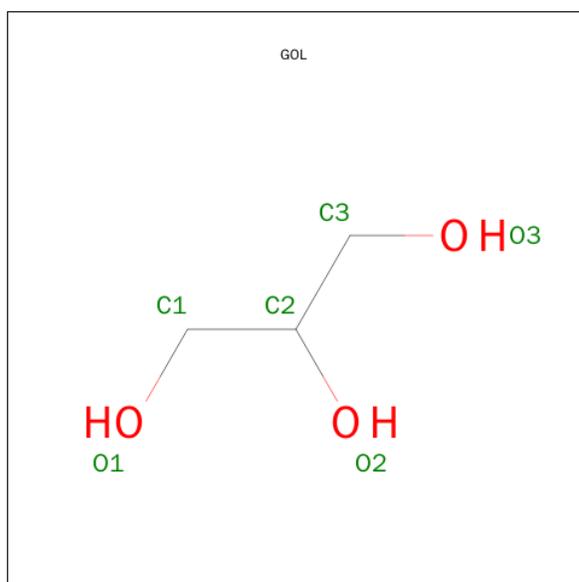
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	O		0	0
			6	3	3			
9	A	1	Total	C	O		0	0
			6	3	3			

- Molecule 10 is 2-[(2,6-DICHLORO-3-METHYL-PHENYL)AMINO]BENZOIC ACID (three-letter code: JMS) (formula: $C_{14}H_{11}Cl_2NO_2$).
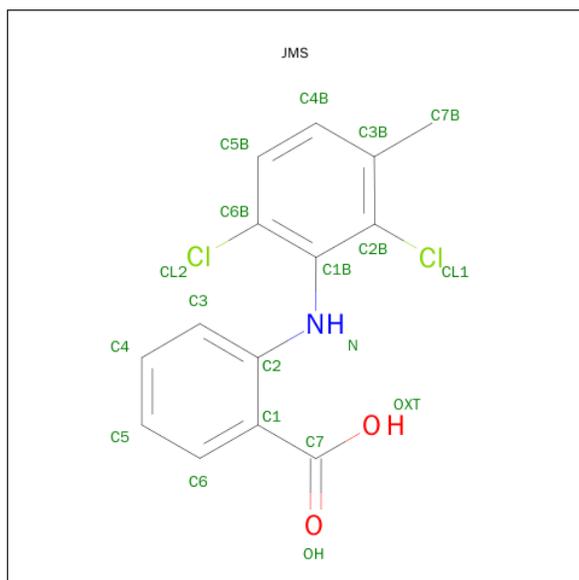
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	A	1	Total	C	Cl	N	O	0	0
			19	14	2	1	2		

• Molecule 11 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	301	Total O 301 301		0	0
11	B	4	Total O 4 4		0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Lactotransferrin
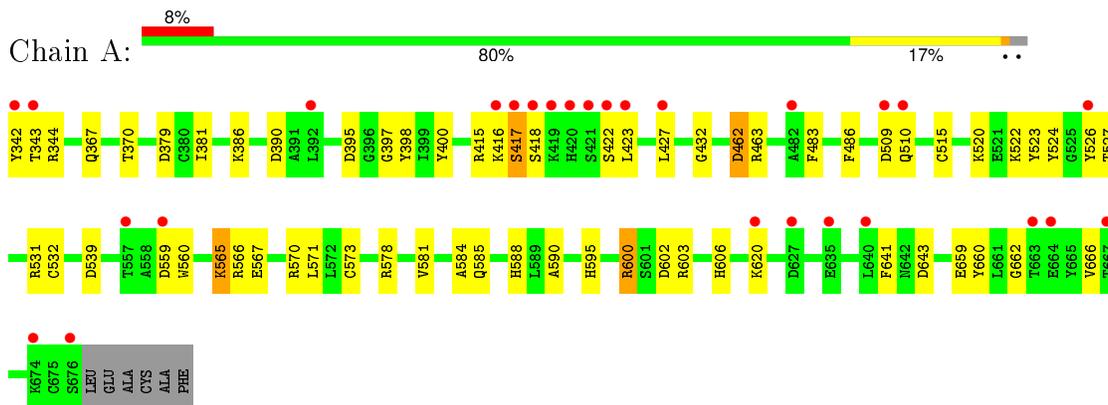
• Molecule 2: C-terminal peptide from Lactotransferrin
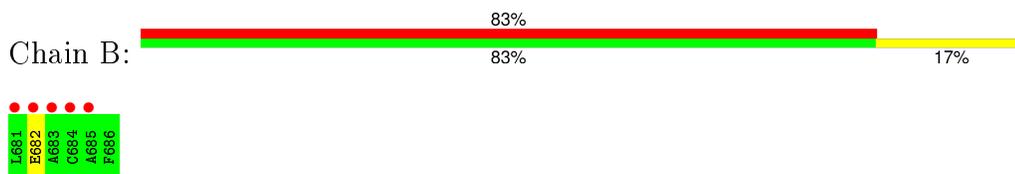
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	62.14Å 49.88Å 65.21Å 90.00° 106.83° 90.00°	Depositor
Resolution (Å)	50.00 – 1.40 31.66 – 1.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (50.00-1.40) 99.5 (31.66-1.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	4.36 (at 1.40Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.177 , 0.208 0.182 , 0.211	Depositor DCC
R_{free} test set	3781 reflections (5.31%)	DCC
Wilson B-factor (Å^2)	15.0	Xtriage
Anisotropy	0.468	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 50.9	EDS
Estimated twinning fraction	0.023 for l,-k,h	Xtriage
L-test for twinning[2]	$< |L| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	1 of 75020 reflections (0.001%)	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	3021	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.71% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, NAG, JMS, CO3, FE, SO4

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	1.47	15/2608 (0.6%)	1.40	25/3533 (0.7%)
2	B	1.43	0/44	1.02	0/58
All	All	1.47	15/2652 (0.6%)	1.40	25/3591 (0.7%)

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	573	CYS	CB-SG	-7.52	1.69	1.82
1	A	381	ILE	CG1-CD1	-7.37	0.99	1.50
1	A	463	ARG	CZ-NH1	7.01	1.42	1.33
1	A	523	TYR	CE1-CZ	-6.99	1.29	1.38
1	A	400	TYR	CE2-CZ	-6.59	1.29	1.38
1	A	660	TYR	CE1-CZ	6.59	1.47	1.38
1	A	523	TYR	CD2-CE2	6.12	1.48	1.39
1	A	486	PHE	CE2-CZ	6.07	1.48	1.37
1	A	531	ARG	CZ-NH2	5.77	1.40	1.33
1	A	603	ARG	CZ-NH1	5.72	1.40	1.33
1	A	659	GLU	CD-OE1	-5.42	1.19	1.25
1	A	398	TYR	CE2-CZ	-5.33	1.31	1.38
1	A	571	LEU	C-O	5.19	1.33	1.23
1	A	386	LYS	CE-NZ	5.08	1.61	1.49
1	A	532	CYS	CB-SG	-5.03	1.73	1.81

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	462	ASP	CB-CG-OD2	-11.67	107.80	118.30
1	A	570	ARG	NE-CZ-NH1	11.58	126.09	120.30
1	A	531	ARG	NE-CZ-NH2	-9.45	115.58	120.30
1	A	526	TYR	CB-CG-CD2	-8.42	115.95	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	570	ARG	NE-CZ-NH2	-8.22	116.19	120.30
1	A	643	ASP	CB-CG-OD1	7.75	125.28	118.30
1	A	578	ARG	NE-CZ-NH2	-7.69	116.46	120.30
1	A	462	ASP	CB-CG-OD1	7.36	124.93	118.30
1	A	641	PHE	CB-CG-CD1	-7.06	115.86	120.80
1	A	524	TYR	CZ-CE2-CD2	-7.02	113.48	119.80
1	A	660	TYR	CD1-CE1-CZ	-6.93	113.56	119.80
1	A	379	ASP	CB-CG-OD2	-6.76	112.22	118.30
1	A	390	ASP	CB-CG-OD2	-6.64	112.33	118.30
1	A	523	TYR	CG-CD2-CE2	-6.31	116.25	121.30
1	A	600	ARG	NE-CZ-NH2	-6.06	117.27	120.30
1	A	531	ARG	NE-CZ-NH1	5.91	123.25	120.30
1	A	427	LEU	CB-CG-CD1	-5.82	101.11	111.00
1	A	400	TYR	CZ-CE2-CD2	-5.77	114.61	119.80
1	A	400	TYR	CG-CD1-CE1	-5.51	116.89	121.30
1	A	524	TYR	CD1-CE1-CZ	-5.38	114.95	119.80
1	A	417	SER	CB-CA-C	-5.37	99.89	110.10
1	A	524	TYR	CB-CG-CD1	-5.36	117.78	121.00
1	A	539	ASP	CB-CG-OD1	-5.21	113.61	118.30
1	A	522	LYS	CD-CE-NZ	-5.20	99.74	111.70
1	A	532	CYS	CA-CB-SG	5.05	123.09	114.00

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	A	2560	0	2480	44	0
2	B	44	0	39	0	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	4	0	0	0	0
6	A	5	0	0	0	0
7	A	14	0	13	0	0
8	A	56	0	50	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	A	12	0	16	0	0
10	A	19	0	9	2	0
11	A	301	0	0	4	0
11	B	4	0	0	0	0
All	All	3021	0	2607	44	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 8.

All (44) 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:565:LYS:HD3	1:A:566:ARG:N	1.80	0.96
1:A:565:LYS:CD	1:A:567:GLU:H	1.82	0.92
1:A:565:LYS:HD2	1:A:567:GLU:H	1.33	0.92
1:A:559:ASP:HB3	11:A:994:HOH:O	1.67	0.92
1:A:343:THR:HA	1:A:606:HIS:NE2	1.87	0.89
1:A:343:THR:HA	1:A:606:HIS:CE1	2.11	0.84
1:A:343:THR:HG22	1:A:606:HIS:HE1	1.45	0.81
1:A:416:LYS:HE3	1:A:620:LYS:HE3	1.64	0.79
1:A:588:HIS:NE2	10:A:713:JMS:CL1	2.51	0.79
1:A:565:LYS:HD2	1:A:567:GLU:HB3	1.68	0.74
1:A:565:LYS:HD3	1:A:565:LYS:C	2.04	0.72
1:A:416:LYS:HG2	11:A:978:HOH:O	1.93	0.69
1:A:527:THR:CG2	1:A:560:TRP:HZ2	2.07	0.68
1:A:416:LYS:CE	1:A:620:LYS:HE3	2.24	0.68
1:A:343:THR:CA	1:A:606:HIS:NE2	2.59	0.64
1:A:343:THR:HG22	1:A:606:HIS:CE1	2.32	0.63
1:A:527:THR:HG21	11:A:954:HOH:O	2.01	0.61
1:A:415:ARG:NH2	1:A:432:GLY:O	2.33	0.61
1:A:416:LYS:HE3	1:A:620:LYS:CE	2.30	0.60
1:A:585:GLN:O	1:A:588:HIS:HE1	1.84	0.59
1:A:565:LYS:HD2	1:A:567:GLU:N	2.12	0.58
1:A:343:THR:CG2	1:A:606:HIS:HE1	2.15	0.58
1:A:565:LYS:HD3	1:A:567:GLU:H	1.64	0.57
1:A:527:THR:CG2	1:A:560:TRP:CZ2	2.87	0.57
1:A:590:ALA:HA	10:A:713:JMS:CL2	2.43	0.55
1:A:343:THR:CA	1:A:606:HIS:CE1	2.87	0.55
1:A:527:THR:HG23	1:A:560:TRP:HZ2	1.73	0.54
1:A:395:ASP:HA	1:A:595:HIS:CD2	2.42	0.54
1:A:600:ARG:HD3	11:A:866:HOH:O	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:527:THR:HG23	1:A:560:TRP:CZ2	2.42	0.53
1:A:565:LYS:HD2	1:A:567:GLU:CB	2.40	0.52
1:A:662:GLY:O	1:A:666:VAL:HG23	2.12	0.50
1:A:584:ALA:O	1:A:588:HIS:ND1	2.47	0.48
1:A:417:SER:OG	1:A:418:SER:N	2.46	0.48
1:A:585:GLN:O	1:A:588:HIS:CE1	2.66	0.47
1:A:566:ARG:HG2	1:A:581:VAL:CG2	2.44	0.47
1:A:520:LYS:HD2	1:A:520:LYS:HA	1.81	0.44
1:A:483:PHE:C	1:A:483:PHE:CD2	2.91	0.43
1:A:509:ASP:OD1	1:A:510:GLN:N	2.52	0.43
1:A:343:THR:CB	1:A:606:HIS:CE1	3.03	0.41
1:A:397:GLY:HA3	1:A:462:ASP:O	2.20	0.41
1:A:344:ARG:HD2	1:A:370:THR:CG2	2.51	0.41
1:A:566:ARG:HG2	1:A:581:VAL:HG21	2.02	0.40
1:A:343:THR:CB	1:A:606:HIS:HE1	2.34	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	333/341 (98%)	322 (97%)	11 (3%)	0	100	100
2	B	4/6 (67%)	3 (75%)	1 (25%)	0	100	100
All	All	337/347 (97%)	325 (96%)	12 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	278/282 (99%)	271 (98%)	7 (2%)	55	17
2	B	4/4 (100%)	3 (75%)	1 (25%)	1	0
All	All	282/286 (99%)	274 (97%)	8 (3%)	51	14

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	342	TYR
1	A	367	GLN
1	A	422	SER
1	A	423	LEU
1	A	515	CYS
1	A	565	LYS
1	A	602	ASP
2	B	682	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	359	GLN
1	A	420	HIS
1	A	613	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)

4 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	#$|Z| > 2$
8	NAG	A	706	1,8	14,14,15	1.17	2 (14%)	15,19,21	1.54	4 (26%)
8	NAG	A	707	8	14,14,15	0.71	0	15,19,21	2.18	5 (33%)
8	NAG	A	709	1,8	14,14,15	1.03	2 (14%)	15,19,21	1.99	4 (26%)
8	NAG	A	710	8	14,14,15	0.65	0	15,19,21	1.61	4 (26%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	A	706	1,8	-	0/6/23/26	0/1/1/1
8	NAG	A	707	8	-	0/6/23/26	0/1/1/1
8	NAG	A	709	1,8	-	0/6/23/26	0/1/1/1
8	NAG	A	710	8	-	0/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	706	NAG	O7-C7	2.14	1.28	1.23
8	A	709	NAG	C2-N2	2.29	1.50	1.46
8	A	709	NAG	C4-C5	2.45	1.58	1.53
8	A	706	NAG	C4-C3	2.50	1.58	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	A	709	NAG	O3-C3-C2	-4.41	100.38	109.11
8	A	707	NAG	O7-C7-C8	-4.02	114.69	122.06
8	A	707	NAG	O4-C4-C3	-2.90	103.81	110.34
8	A	706	NAG	C2-N2-C7	-2.89	119.33	123.04
8	A	706	NAG	O7-C7-C8	-2.73	117.05	122.06
8	A	709	NAG	C3-C4-C5	-2.29	106.20	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	A	710	NAG	C3-C4-C5	-2.27	106.23	110.20
8	A	710	NAG	O6-C6-C5	-2.16	104.21	111.33
8	A	710	NAG	C2-N2-C7	2.03	125.65	123.04
8	A	706	NAG	O3-C3-C4	2.05	114.96	110.34
8	A	707	NAG	O7-C7-N2	2.29	126.53	121.86
8	A	709	NAG	O7-C7-N2	2.31	126.58	121.86
8	A	706	NAG	C1-O5-C5	2.53	115.45	112.25
8	A	707	NAG	C2-N2-C7	3.08	127.00	123.04
8	A	710	NAG	C1-O5-C5	3.55	116.75	112.25
8	A	709	NAG	C1-O5-C5	3.98	117.30	112.25
8	A	707	NAG	C1-O5-C5	4.62	118.11	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 (i)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
5	CO3	A	703	4	0,3,3	0.00	-	0,3,3	0.00	-
6	SO4	A	704	-	4,4,4	0.47	0	6,6,6	0.42	0
7	NAG	A	705	1	14,14,15	1.07	1 (7%)	15,19,21	2.75	7 (46%)
9	GOL	A	711	-	5,5,5	0.59	0	5,5,5	0.65	0
9	GOL	A	712	-	5,5,5	0.45	0	5,5,5	0.65	0
10	JMS	A	713	-	17,20,20	3.69	4 (23%)	23,28,28	5.09	12 (52%)

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	CO3	A	703	4	-	0/0/0/0	0/0/0/0
6	SO4	A	704	-	-	0/0/0/0	0/0/0/0
7	NAG	A	705	1	-	0/6/23/26	0/1/1/1
9	GOL	A	711	-	-	0/4/4/4	0/0/0/0
9	GOL	A	712	-	-	0/4/4/4	0/0/0/0
10	JMS	A	713	-	-	0/4/8/8	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	713	JMS	C2B-CL1	-14.02	1.43	1.72
10	A	713	JMS	C2-N	2.14	1.45	1.39
7	A	705	NAG	O7-C7	2.44	1.28	1.23
10	A	713	JMS	C1-C2	2.86	1.44	1.40
10	A	713	JMS	C6B-CL2	3.37	1.81	1.73

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	713	JMS	C1B-C2B-C3B	-10.95	107.63	122.20
10	A	713	JMS	C7B-C3B-C4B	-7.78	104.45	120.33
10	A	713	JMS	C1B-C2B-CL1	-7.26	106.07	118.86
10	A	713	JMS	C2B-C1B-N	-4.75	110.49	120.76
7	A	705	NAG	O3-C3-C4	-3.67	102.08	110.34
10	A	713	JMS	C6-C1-C7	-3.22	115.27	120.23
10	A	713	JMS	C4B-C5B-C6B	-2.85	115.70	119.95
7	A	705	NAG	C8-C7-N2	-2.81	110.72	116.11
7	A	705	NAG	O7-C7-C8	-2.12	118.18	122.06
10	A	713	JMS	C5B-C6B-C1B	-2.01	118.15	121.86
10	A	713	JMS	C4-C3-C2	2.09	122.93	118.53
7	A	705	NAG	O5-C5-C6	2.23	112.17	107.35
10	A	713	JMS	C4B-C3B-C2B	3.78	124.31	116.85
10	A	713	JMS	C6B-C1B-C2B	4.42	129.78	117.76
7	A	705	NAG	O7-C7-N2	4.44	130.92	121.86
10	A	713	JMS	C7B-C3B-C2B	4.71	130.65	122.21
7	A	705	NAG	C1-O5-C5	4.83	118.38	112.25
7	A	705	NAG	C2-N2-C7	6.04	130.79	123.04
10	A	713	JMS	C3B-C2B-CL1	15.49	142.37	118.79

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	713	JMS	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 (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å²)	Q<0.9
1	A	335/341 (98%)	0.53	27 (8%)	15	13	9, 18, 39, 75	0
2	B	6/6 (100%)	6.84	5 (83%)	0	0	36, 42, 68, 69	0
All	All	341/347 (98%)	0.64	32 (9%)	11	9	9, 18, 41, 75	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	681	LEU	17.1
1	A	342	TYR	16.1
1	A	420	HIS	10.8
1	A	422	SER	10.1
1	A	421	SER	9.9
2	B	682	GLU	9.1
1	A	418	SER	8.1
1	A	419	LYS	7.8
1	A	343	THR	7.1
1	A	423	LEU	6.0
1	A	417	SER	5.8
2	B	683	ALA	5.4
2	B	685	ALA	4.9
1	A	676	SER	3.9
1	A	627	ASP	3.5
1	A	664	GLU	3.1
1	A	509	ASP	3.0
1	A	482	ALA	2.9
1	A	416	LYS	2.9
1	A	640	LEU	2.8
1	A	559	ASP	2.8
2	B	684	CYS	2.7
1	A	427	LEU	2.4
1	A	510	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	635	GLU	2.2
1	A	620	LYS	2.2
1	A	674	LYS	2.2
1	A	557	THR	2.2
1	A	392	LEU	2.1
1	A	663	THR	2.1
1	A	667	THR	2.1
1	A	526	TYR	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
8	NAG	A	706	14/15	0.87	0.12	-0.11	23,27,35,41	0
8	NAG	A	710	14/15	0.88	0.14	-0.53	38,40,49,53	0
8	NAG	A	709	14/15	0.95	0.07	-2.03	21,23,30,30	0
8	NAG	A	707	14/15	0.89	0.25	-	34,40,47,54	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
9	GOL	A	711	6/6	0.83	0.19	4.27	34,51,56,56	0
9	GOL	A	712	6/6	0.89	0.15	2.91	17,26,27,28	0
10	JMS	A	713	19/19	0.89	0.30	2.30	8,34,47,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
7	NAG	A	705	14/15	0.76	0.25	1.14	31,40,44,51	0
5	CO3	A	703	4/4	0.99	0.14	0.43	9,10,10,11	0
3	ZN	A	701	1/1	0.99	0.06	-0.80	15,15,15,15	0
4	FE	A	702	1/1	0.98	0.09	-2.29	10,10,10,10	0
6	SO4	A	704	5/5	0.95	0.18	-	48,48,52,52	0

6.5 Other polymers (i)

There are no such residues in this entry.