



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 17, 2018 – 01:38 am GMT

PDB ID : 2DSF
Title : Structure of the complex of C-terminal lobe of bovine lactoferrin with xylose at 2.8Å resolution
Authors : Mir, R.; Singh, N.; Sinha, M.; Sharma, S.; Bhushan, A.; Singh, T.P.
Deposited on : 2006-06-29
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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30686

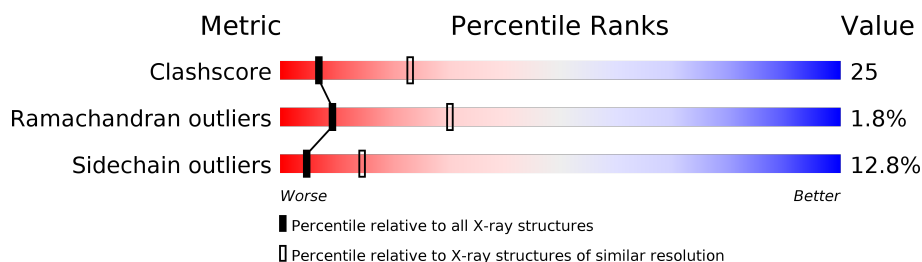
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	122078	3207 (2.80-2.80)
Ramachandran outliers	120005	3156 (2.80-2.80)
Sidechain outliers	119972	3158 (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 $\leq 5\%$. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	345	

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
6	LXC	A	3937	X	-	-	-

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 2921 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.

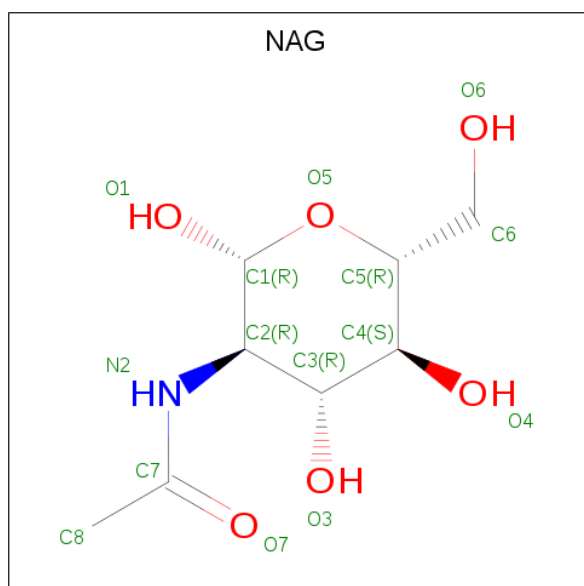
- Molecule 1 is a protein called Lactotransferrin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	0	0
			2604	1622	454	507	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	565	LYS	ASN	SEE REMARK 999	UNP P24627
A	608	GLU	LYS	SEE REMARK 999	UNP P24627

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



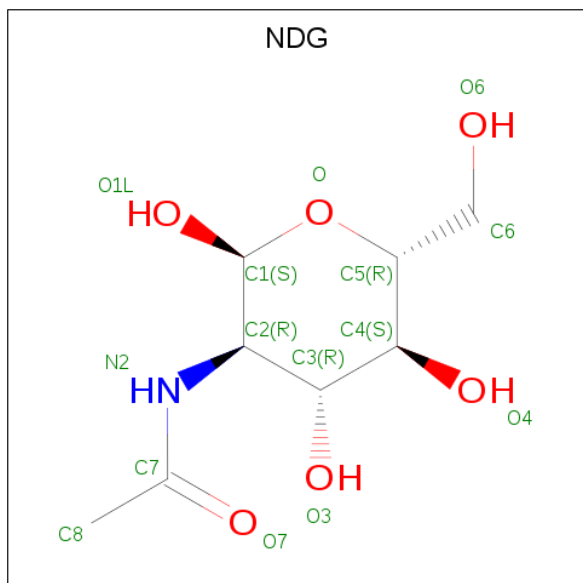
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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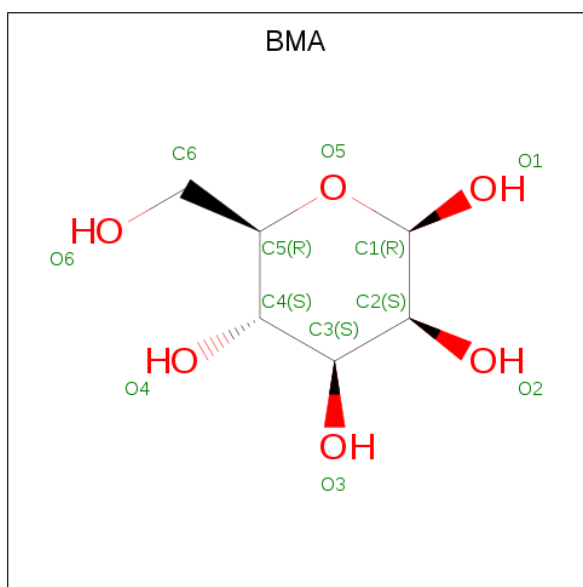
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is 2-(ACETYLAMINO)-2-DEOXY-A-D-GLUCOPYRANOSE (three-letter code: NDG) (formula: $C_8H_{15}NO_6$).



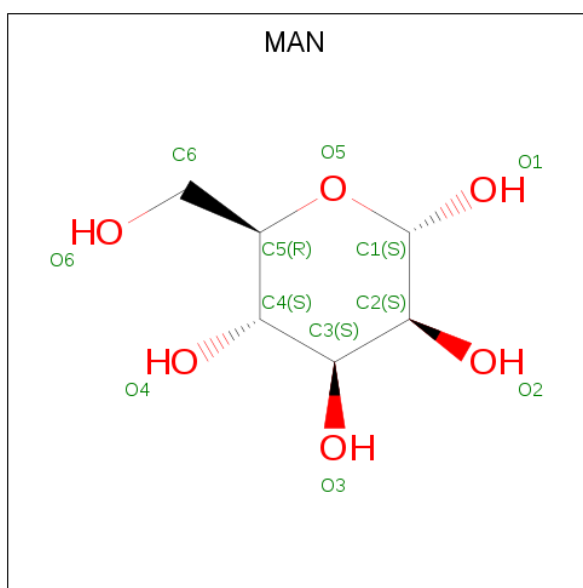
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is BETA-D-MANNOSE (three-letter code: BMA) (formula: $C_6H_{12}O_6$).



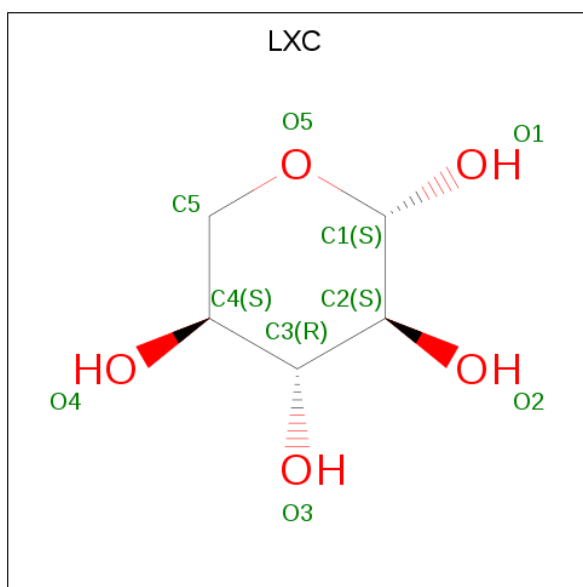
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 5 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 6 is BETA-L-XYLOPYRANOSE (three-letter code: LXC) (formula: $C_5H_{10}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			10	5	5		

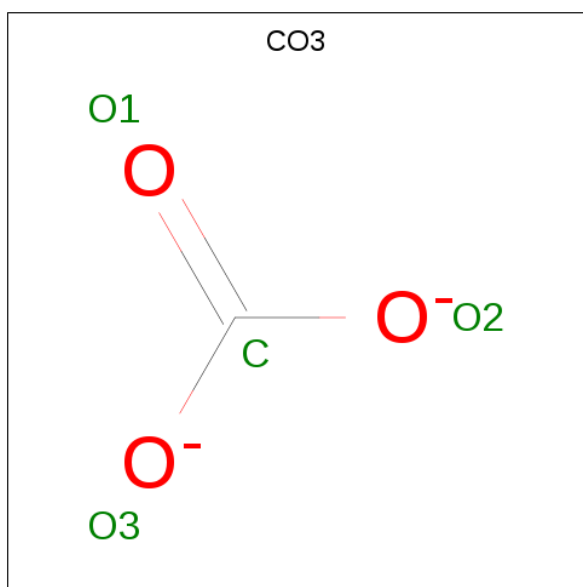
- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	2	Total	Zn	0	0
			2	2		

- Molecule 8 is FE (III) ION (three-letter code: FE) (formula: Fe).

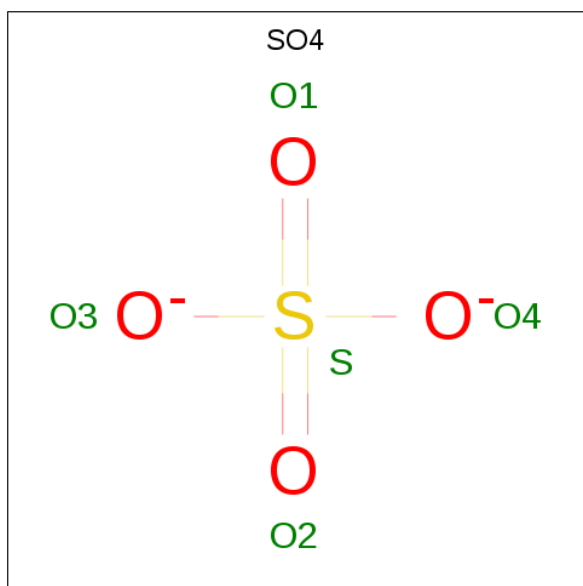
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Fe	0	0
			1	1		

- Molecule 9 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			4	1	3		

- Molecule 10 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 11 is water.

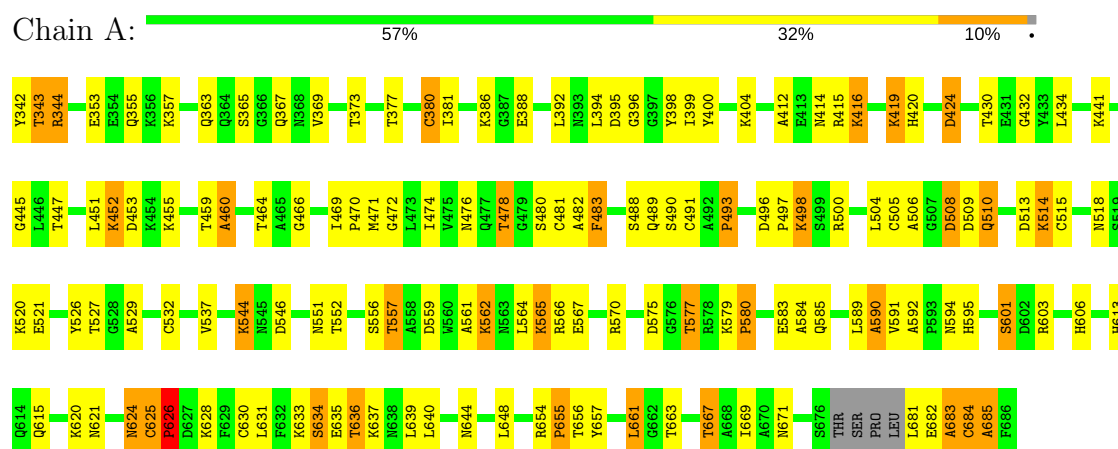
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	192	Total 192	O 192	0	0

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 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.

Note EDS was not executed.

• Molecule 1: Lactotransferrin



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.45 Å 50.44 Å 65.87 Å 90.00° 107.80° 90.00°	Depositor
Resolution (Å)	19.94 – 2.80	Depositor
% Data completeness (in resolution range)	92.9 (19.94-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.201 , 0.231	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2921	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, BMA, NAG, CO3, NDG, LXC, SO4, MAN, FE

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	0.57	2/2652 (0.1%)	1.07	14/3591 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	683	ALA	CA-CB	-5.56	1.40	1.52
1	A	510	GLN	CA-CB	-5.01	1.43	1.53

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	625	CYS	C-N-CD	-22.02	72.15	120.60
1	A	683	ALA	N-CA-C	13.13	146.44	111.00
1	A	625	CYS	C-N-CA	8.49	157.66	122.00
1	A	656	THR	N-CA-C	-8.45	88.20	111.00
1	A	626	PRO	CA-N-CD	-6.66	102.18	111.50
1	A	682	GLU	N-CA-CB	6.58	122.45	110.60
1	A	681	LEU	CA-CB-CG	6.35	129.91	115.30
1	A	684	CYS	N-CA-C	-6.28	94.04	111.00
1	A	683	ALA	N-CA-CB	-6.05	101.63	110.10
1	A	683	ALA	CB-CA-C	-5.82	101.37	110.10
1	A	625	CYS	N-CA-C	-5.74	95.51	111.00
1	A	682	GLU	CA-CB-CG	-5.71	100.84	113.40
1	A	682	GLU	C-N-CA	-5.50	107.94	121.70
1	A	419	LYS	N-CA-C	-5.14	97.12	111.00

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	2604	0	2518	131	0
2	A	56	0	49	2	0
3	A	14	0	12	1	0
4	A	22	0	20	1	0
5	A	11	0	9	0	0
6	A	10	0	7	0	0
7	A	2	0	0	0	0
8	A	1	0	0	0	0
9	A	4	0	0	0	0
10	A	5	0	0	0	0
11	A	192	0	0	22	0
All	All	2921	0	2615	132	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 25.

All (132) 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:625:CYS:SG	1:A:626:PRO:HD3	1.71	1.28
1:A:395:ASP:HA	1:A:595:HIS:CD2	2.00	0.96
1:A:625:CYS:SG	1:A:626:PRO:CD	2.62	0.88
1:A:685:ALA:HB2	11:A:4026:HOH:O	1.75	0.85
1:A:474:ILE:O	1:A:478:THR:HB	1.76	0.85
1:A:620:LYS:C	1:A:621:ASN:HD22	1.86	0.78
1:A:355:GLN:HG3	1:A:373:THR:OG1	1.87	0.74
1:A:635:GLU:O	1:A:637:LYS:HG3	1.89	0.73
1:A:419:LYS:NZ	1:A:420:HIS:NE2	2.36	0.71
1:A:404:LYS:HD3	1:A:683:ALA:HB3	1.72	0.71
1:A:419:LYS:HZ2	1:A:420:HIS:CD2	2.08	0.71
1:A:552:THR:OG1	1:A:566:ARG:HG2	1.90	0.71
1:A:472:GLY:O	1:A:476:ASN:HB2	1.91	0.70
1:A:478:THR:HG22	1:A:480:SER:H	1.57	0.69
1:A:342:TYR:O	1:A:606:HIS:NE2	2.28	0.67
1:A:565:LYS:NZ	1:A:567:GLU:HB2	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:ASP:HB2	11:A:4020:HOH:O	1.94	0.66
1:A:343:THR:HA	1:A:606:HIS:NE2	2.11	0.66
1:A:584:ALA:HB3	2:A:5:NAG:H82	1.76	0.66
1:A:603:ARG:NH2	11:A:4036:HOH:O	2.27	0.66
1:A:685:ALA:CB	11:A:4026:HOH:O	2.38	0.66
1:A:585:GLN:HG2	11:A:3958:HOH:O	1.98	0.64
1:A:419:LYS:HZ2	1:A:420:HIS:CE1	2.15	0.63
1:A:606:HIS:HD2	11:A:4036:HOH:O	1.82	0.63
1:A:357:LYS:HG3	11:A:4022:HOH:O	1.99	0.62
1:A:478:THR:CG2	1:A:480:SER:H	2.12	0.62
1:A:478:THR:CG2	1:A:480:SER:HB3	2.30	0.61
1:A:471:MET:HE1	1:A:474:ILE:HD12	1.82	0.60
1:A:404:LYS:HB3	1:A:684:CYS:H	1.64	0.60
1:A:380:CYS:HB3	1:A:392:LEU:HD13	1.83	0.60
1:A:363:GLN:HA	11:A:4068:HOH:O	2.00	0.60
4:A:4:BMA:H4	11:A:4085:HOH:O	2.01	0.60
1:A:626:PRO:HD3	1:A:630:CYS:SG	2.42	0.59
1:A:601:SER:C	1:A:603:ARG:H	2.04	0.59
1:A:488:SER:HA	1:A:500:ARG:NH2	2.19	0.58
1:A:529:ALA:O	1:A:532:CYS:HB3	2.03	0.58
1:A:565:LYS:HZ2	1:A:567:GLU:HB2	1.68	0.58
1:A:654:ARG:N	1:A:655:PRO:HD3	2.19	0.57
1:A:489:GLN:HB3	1:A:504:LEU:HD13	1.85	0.57
1:A:513:ASP:OD2	1:A:520:LYS:HD3	2.04	0.57
1:A:518:ASN:OD1	1:A:520:LYS:HB2	2.04	0.57
1:A:399:ILE:CG2	1:A:661:LEU:HD11	2.35	0.56
1:A:685:ALA:HA	11:A:4080:HOH:O	2.06	0.56
1:A:430:THR:HB	1:A:594:ASN:ND2	2.19	0.56
1:A:654:ARG:NH2	11:A:4042:HOH:O	2.39	0.56
1:A:575:ASP:OD1	1:A:577:THR:HB	2.06	0.55
1:A:399:ILE:HG22	1:A:661:LEU:HD11	1.87	0.55
1:A:452:LYS:O	1:A:453:ASP:HB2	2.07	0.55
1:A:357:LYS:HD3	1:A:640:LEU:HG	1.88	0.55
1:A:532:CYS:O	1:A:537:VAL:HB	2.07	0.54
1:A:565:LYS:HZ3	1:A:567:GLU:H	1.56	0.54
1:A:589:LEU:O	1:A:590:ALA:HB2	2.09	0.53
1:A:394:LEU:O	1:A:595:HIS:HA	2.09	0.52
1:A:445:GLY:O	1:A:447:THR:HG23	2.10	0.52
1:A:469:ILE:N	1:A:470:PRO:HD2	2.25	0.52
1:A:478:THR:HG23	1:A:480:SER:HB3	1.91	0.52
1:A:496:ASP:OD1	1:A:498:LYS:HD3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:357:LYS:O	1:A:357:LYS:HG2	2.10	0.51
1:A:556:SER:C	1:A:557:THR:HG23	2.30	0.51
1:A:654:ARG:N	1:A:655:PRO:CD	2.74	0.51
1:A:464:THR:HG21	1:A:592:ALA:CB	2.41	0.51
1:A:459:THR:OG1	1:A:466:GLY:HA3	2.12	0.50
1:A:634:SER:OG	1:A:639:LEU:HG	2.10	0.50
1:A:526:TYR:CE2	1:A:544:LYS:HE2	2.45	0.50
1:A:455:LYS:HB3	1:A:504:LEU:HD21	1.95	0.49
1:A:570:ARG:NH1	1:A:580:PRO:HA	2.27	0.49
1:A:464:THR:HG21	1:A:592:ALA:HB1	1.94	0.49
1:A:367:GLN:HB2	11:A:4056:HOH:O	2.13	0.49
1:A:601:SER:C	1:A:603:ARG:N	2.66	0.49
1:A:639:LEU:O	1:A:640:LEU:HB2	2.13	0.49
1:A:657:TYR:O	1:A:661:LEU:HD12	2.13	0.48
1:A:419:LYS:HD3	1:A:420:HIS:N	2.28	0.48
1:A:482:ALA:HA	11:A:4097:HOH:O	2.13	0.48
1:A:342:TYR:O	1:A:606:HIS:CD2	2.66	0.48
1:A:544:LYS:HG3	1:A:546:ASP:H	1.79	0.48
1:A:490:SER:C	1:A:504:LEU:HB2	2.34	0.48
1:A:667:THR:O	1:A:671:ASN:ND2	2.47	0.48
1:A:415:ARG:HH11	1:A:415:ARG:HG2	1.78	0.47
1:A:551:ASN:HA	1:A:556:SER:HB2	1.96	0.47
1:A:620:LYS:O	1:A:621:ASN:ND2	2.41	0.47
1:A:505:CYS:HB3	1:A:521:GLU:OE1	2.15	0.47
1:A:559:ASP:HB3	11:A:3962:HOH:O	2.14	0.47
1:A:344:ARG:HB2	11:A:4032:HOH:O	2.13	0.47
1:A:506:ALA:HA	1:A:514:LYS:HE2	1.96	0.47
1:A:483:PHE:C	1:A:483:PHE:CD2	2.88	0.47
1:A:434:LEU:HD12	1:A:584:ALA:HB1	1.96	0.46
1:A:634:SER:C	1:A:635:GLU:HG3	2.36	0.46
1:A:505:CYS:O	1:A:514:LYS:HE2	2.14	0.46
1:A:546:ASP:HA	2:A:5:NAG:H62	1.96	0.46
1:A:353:GLU:OE1	1:A:637:LYS:HE2	2.15	0.46
1:A:671:ASN:ND2	3:A:2:NDG:H3	2.31	0.46
1:A:498:LYS:HE2	1:A:498:LYS:HB2	1.63	0.46
1:A:459:THR:O	1:A:460:ALA:HB2	2.15	0.46
1:A:377:THR:HG21	1:A:398:TYR:CD2	2.52	0.45
1:A:419:LYS:O	1:A:420:HIS:HB2	2.14	0.45
1:A:377:THR:O	1:A:381:ILE:HG12	2.16	0.45
1:A:416:LYS:HG2	1:A:416:LYS:H	1.47	0.45
1:A:559:ASP:HA	1:A:562:LYS:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:624:ASN:HB3	1:A:628:LYS:HB2	1.98	0.45
1:A:671:ASN:HB3	11:A:4019:HOH:O	2.16	0.45
1:A:633:LYS:HA	1:A:633:LYS:HD3	1.88	0.44
1:A:561:ALA:HA	1:A:564:LEU:HG	1.98	0.44
1:A:577:THR:HG21	1:A:579:LYS:HZ3	1.82	0.44
1:A:396:GLY:HA2	1:A:399:ILE:HD12	2.00	0.44
1:A:400:TYR:CD2	1:A:669:ILE:HG21	2.53	0.43
1:A:451:LEU:HD12	11:A:3994:HOH:O	2.18	0.43
1:A:464:THR:O	1:A:469:ILE:HG12	2.18	0.43
1:A:395:ASP:HA	1:A:595:HIS:CG	2.52	0.43
1:A:685:ALA:CB	11:A:4080:HOH:O	2.65	0.43
1:A:365:SER:C	1:A:367:GLN:N	2.71	0.43
1:A:565:LYS:C	1:A:565:LYS:HD3	2.39	0.43
1:A:367:GLN:C	1:A:369:VAL:N	2.71	0.43
1:A:481:CYS:C	1:A:483:PHE:H	2.23	0.42
1:A:471:MET:HE1	1:A:474:ILE:CD1	2.49	0.42
1:A:636:THR:HG22	11:A:3971:HOH:O	2.18	0.42
1:A:613:HIS:HD2	11:A:4015:HOH:O	2.01	0.42
1:A:491:CYS:SG	1:A:493:PRO:HD3	2.59	0.42
1:A:518:ASN:C	1:A:518:ASN:OD1	2.59	0.42
1:A:565:LYS:HZ3	1:A:567:GLU:HB2	1.83	0.41
1:A:469:ILE:H	1:A:470:PRO:HD2	1.85	0.41
1:A:412:ALA:O	1:A:648:LEU:HA	2.20	0.41
1:A:367:GLN:C	1:A:369:VAL:H	2.20	0.41
1:A:480:SER:OG	1:A:481:CYS:N	2.53	0.41
1:A:526:TYR:CZ	1:A:544:LYS:HE2	2.56	0.41
1:A:386:LYS:HD2	1:A:388:GLU:OE1	2.19	0.41
1:A:683:ALA:HB1	1:A:684:CYS:O	2.21	0.41
1:A:577:THR:CG2	1:A:579:LYS:HZ3	2.34	0.41
1:A:415:ARG:NH2	1:A:432:GLY:O	2.48	0.41
1:A:644:ASN:N	11:A:3952:HOH:O	2.53	0.40
1:A:508:ASP:OD1	1:A:508:ASP:N	2.53	0.40
1:A:606:HIS:CD2	11:A:4036:HOH:O	2.66	0.40
1:A:544:LYS:HD2	1:A:546:ASP:OD1	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	337/345 (98%)	302 (90%)	29 (9%)	6 (2%)	9	30

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	508	ASP
1	A	626	PRO
1	A	685	ALA
1	A	590	ALA
1	A	636	THR
1	A	460	ALA

5.3.2 Protein sidechains

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	282/286 (99%)	246 (87%)	36 (13%)	5	14

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	343	THR
1	A	344	ARG
1	A	380	CYS
1	A	414	ASN
1	A	416	LYS

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Mol	Chain	Res	Type
1	A	424	ASP
1	A	441	LYS
1	A	452	LYS
1	A	478	THR
1	A	483	PHE
1	A	493	PRO
1	A	497	PRO
1	A	498	LYS
1	A	509	ASP
1	A	510	GLN
1	A	514	LYS
1	A	515	CYS
1	A	527	THR
1	A	544	LYS
1	A	557	THR
1	A	562	LYS
1	A	565	LYS
1	A	577	THR
1	A	580	PRO
1	A	583	GLU
1	A	591	VAL
1	A	601	SER
1	A	615	GLN
1	A	624	ASN
1	A	626	PRO
1	A	631	LEU
1	A	634	SER
1	A	655	PRO
1	A	661	LEU
1	A	663	THR
1	A	667	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	355	GLN
1	A	363	GLN
1	A	414	ASN
1	A	458	HIS
1	A	510	GLN
1	A	585	GLN
1	A	621	ASN

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Mol	Chain	Res	Type
1	A	671	ASN

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](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 3 are monoatomic - leaving 11 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	$\# Z > 2$
2	NAG	A	1001	1	14,14,15	0.62	0	17,19,21	1.91	5 (29%)
9	CO3	A	1999	8	0,3,3	0.00	-	0,3,3	0.00	-
3	NDG	A	2	1,2	14,14,15	1.29	2 (14%)	17,19,21	1.37	4 (23%)
2	NAG	A	3	3,4	14,14,15	0.95	1 (7%)	17,19,21	1.55	5 (29%)
6	LXC	A	3937	-	10,10,10	1.22	1 (10%)	14,14,14	5.08	13 (92%)
10	SO4	A	3938	-	4,4,4	0.31	0	6,6,6	0.09	0
4	BMA	A	4	2	11,11,12	0.90	1 (9%)	15,15,17	0.87	0
2	NAG	A	5	1,2	14,14,15	0.89	0	17,19,21	0.72	0
2	NAG	A	6	2,5	14,14,15	0.97	0	17,19,21	1.05	1 (5%)
5	MAN	A	7	2,4	11,11,12	1.10	1 (9%)	15,15,17	1.83	3 (20%)
4	BMA	A	8	5	11,11,12	0.75	0	15,15,17	1.37	2 (13%)

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
2	NAG	A	1001	1	-	0/6/23/26	0/1/1/1
9	CO3	A	1999	8	-	0/0/0/0	0/0/0/0
3	NDG	A	2	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	3	3,4	-	0/6/23/26	0/1/1/1
6	LXC	A	3937	-	3/3/4/4	0/0/17/17	0/1/1/1
10	SO4	A	3938	-	-	0/0/0/0	0/0/0/0
4	BMA	A	4	2	-	0/2/19/22	0/1/1/1
2	NAG	A	5	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	6	2,5	-	0/6/23/26	0/1/1/1
5	MAN	A	7	2,4	-	0/2/19/22	0/1/1/1
4	BMA	A	8	5	-	0/2/19/22	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	3937	LXC	O5-C1	-2.22	1.40	1.43
2	A	3	NAG	C1-C2	2.04	1.55	1.52
5	A	7	MAN	C2-C3	2.30	1.55	1.52
4	A	4	BMA	C2-C3	2.41	1.56	1.52
3	A	2	NDG	O-C5	2.56	1.48	1.43
3	A	2	NDG	C1-C2	2.66	1.56	1.52

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	NAG	C6-C5-C4	-3.40	104.95	112.99
2	A	1001	NAG	C2-N2-C7	-3.16	118.33	122.94
2	A	3	NAG	C4-C3-C2	-2.95	106.69	111.02
2	A	1001	NAG	O5-C1-C2	-2.87	107.56	111.52
2	A	3	NAG	C2-N2-C7	-2.69	119.02	122.94
2	A	3	NAG	O5-C1-C2	-2.57	107.97	111.52
5	A	7	MAN	C6-C5-C4	-2.43	107.25	112.99
3	A	2	NDG	C3-C4-C5	-2.38	105.97	110.24
4	A	8	BMA	O5-C1-C2	-2.38	107.07	110.78
2	A	6	NAG	C3-C4-C5	-2.15	106.39	110.24
3	A	2	NDG	C2-N2-C7	-2.09	119.89	122.94
2	A	3	NAG	C6-C5-C4	-2.04	108.17	112.99
3	A	2	NDG	O7-C7-C8	-2.00	118.45	122.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	3937	LXC	C5-O5-C1	2.00	116.27	112.80
2	A	1001	NAG	C1-O5-C5	2.06	115.03	112.19
2	A	3	NAG	C1-O5-C5	2.39	115.47	112.19
6	A	3937	LXC	O1-C1-C2	2.42	115.92	109.02
3	A	2	NDG	C1-O-C5	2.61	115.78	112.19
6	A	3937	LXC	C4-C3-C2	2.95	115.98	110.87
6	A	3937	LXC	O2-C2-C3	3.28	118.00	110.34
6	A	3937	LXC	O3-C3-C2	3.38	118.25	110.34
5	A	7	MAN	C3-C4-C5	3.79	117.02	110.24
6	A	3937	LXC	C1-C2-C3	3.92	118.19	110.36
4	A	8	BMA	C3-C4-C5	3.92	117.26	110.24
2	A	1001	NAG	C3-C4-C5	4.06	117.50	110.24
6	A	3937	LXC	O4-C4-C3	4.31	118.60	110.19
6	A	3937	LXC	O1-C1-O5	4.32	121.33	109.74
5	A	7	MAN	O5-C1-C2	4.65	118.03	110.78
6	A	3937	LXC	O4-C4-C5	5.30	119.87	109.17
6	A	3937	LXC	O2-C2-C1	6.25	123.80	109.14
6	A	3937	LXC	C5-C4-C3	7.36	118.97	109.66
6	A	3937	LXC	O3-C3-C4	7.47	123.94	110.04
6	A	3937	LXC	O5-C1-C2	9.46	122.00	109.31

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	3937	LXC	C3
6	A	3937	LXC	C2
6	A	3937	LXC	C1

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2	NDG	1	0
4	A	4	BMA	1	0
2	A	5	NAG	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.