



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:58 PM GMT

PDB ID : 4NED
Title : Crystal STRUCTURE OF C-LOBE OF BOVINE LACTOFERRIN COM-
PLEXED WITH FENOPROFEN AT 2.1 ANGSTROM RESOLUTION
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Deposited on : 2013-10-29
Resolution : 2.10 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 ⓘ](#)) 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

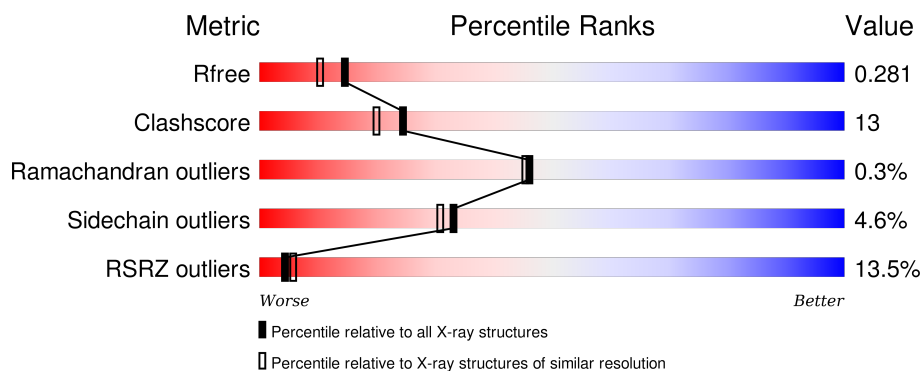
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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.

Mol	Chain	Length	Quality of chain
1	A	345	<div> <div>13%</div> <div>72%</div> <div>26%</div> <div>..</div> </div>

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
8	PFN	A	709	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 2894 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

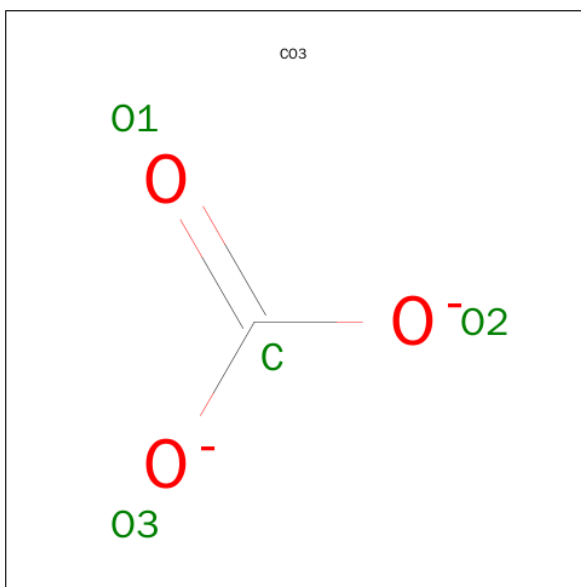
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

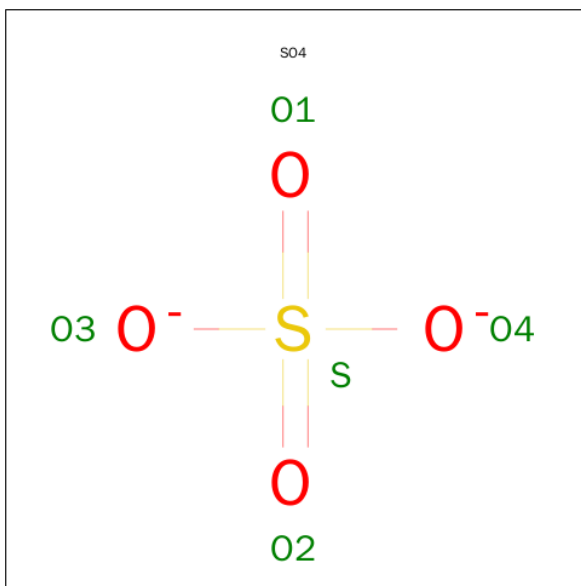
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Fe	0	0
			1	1		

- Molecule 4 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



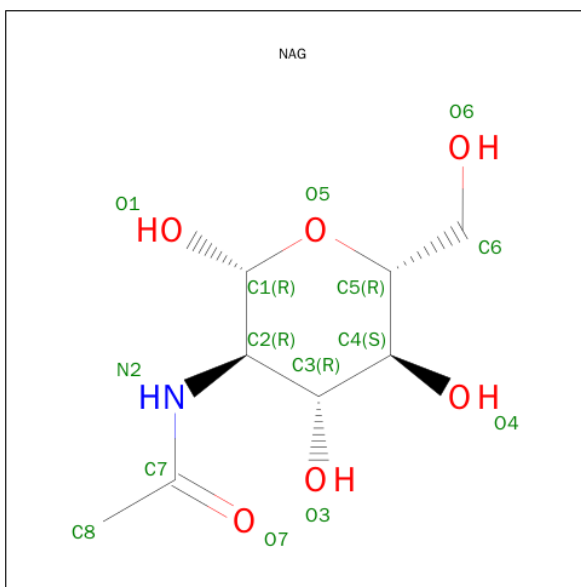
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	1	3		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 6 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).

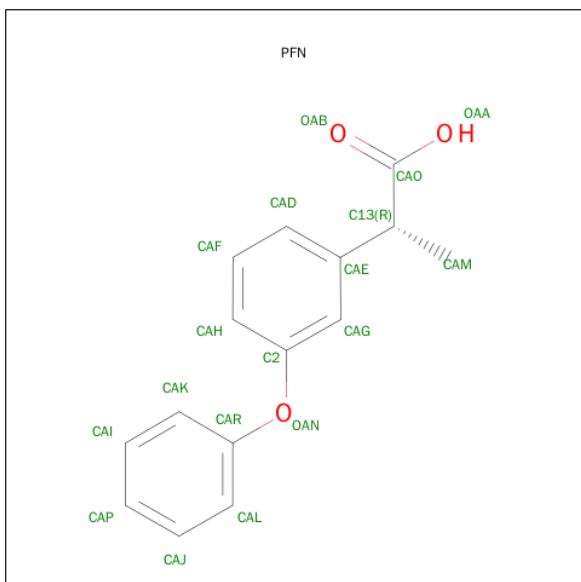


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is a polymer of unknown type called SUGAR (2-MER).

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

- Molecule 8 is FENOPROFEN (three-letter code: PFN) (formula: $C_{15}H_{14}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			18	15	3		

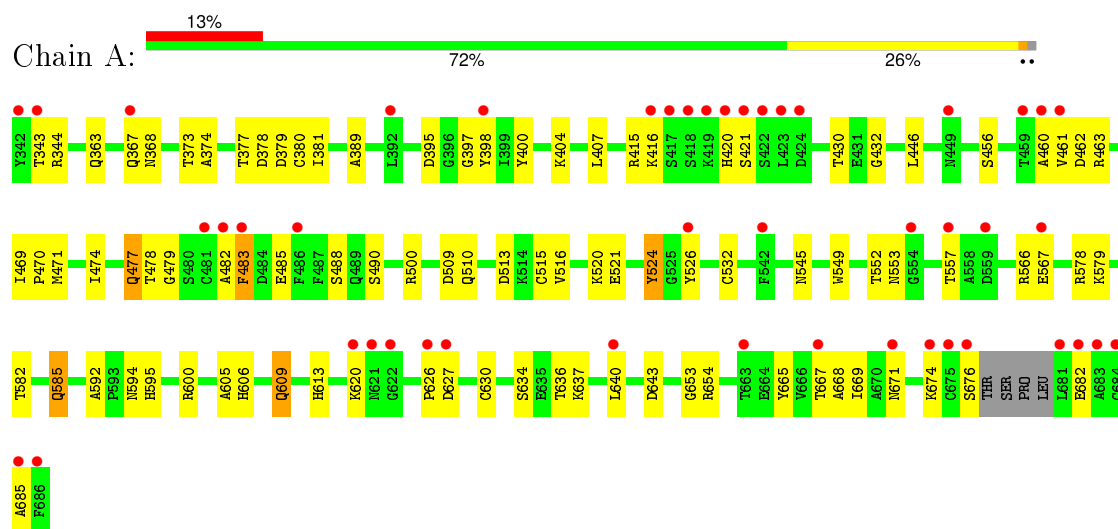
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	204	Total	O	0	0
			204	204		

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 ($\text{RSRZ} > 2$). 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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	62.47Å 50.07Å 65.49Å 90.00° 107.32° 90.00°	Depositor
Resolution (Å)	37.89 – 2.10 37.89 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.0 (37.89-2.10) 98.0 (37.89-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.10Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.223 , 0.252 0.215 , 0.281	Depositor DCC
R_{free} test set	1147 reflections (5.13%)	DCC
Wilson B-factor (Å ²)	34.6	Xtriage
Anisotropy	0.664	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 67.5	EDS
Estimated twinning fraction	0.022 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	2 of 22392 reflections (0.009%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2894	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.91% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: ZN, NAG, CO3, PFN, SO4, 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	1.04	5/2652 (0.2%)	0.92	3/3591 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	380	CYS	CB-SG	-7.25	1.70	1.82
1	A	524	TYR	CD2-CE2	6.72	1.49	1.39
1	A	526	TYR	CD2-CE2	5.27	1.47	1.39
1	A	605	ALA	CA-CB	5.10	1.63	1.52
1	A	389	ALA	CA-CB	5.09	1.63	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	379	ASP	CB-CG-OD1	6.08	123.77	118.30
1	A	640	LEU	CB-CA-C	-5.95	98.90	110.20
1	A	532	CYS	CA-CB-SG	5.28	123.51	114.00

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	2520	65	0
2	A	2	0	0	0	0
3	A	1	0	0	0	0
4	A	4	0	0	0	0
5	A	5	0	0	0	0
6	A	28	0	26	5	0
7	A	28	0	25	1	0
8	A	18	0	13	9	0
9	A	204	0	0	7	0
All	All	2894	0	2584	68	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 13.

All (68) 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:368:ASN:HD21	6:A:705:NAG:H2	1.26	0.98
1:A:685:ALA:CB	8:A:709:PFN:HAP	2.04	0.87
1:A:609:GLN:HG3	9:A:876:HOH:O	1.71	0.87
8:A:709:PFN:HAL	8:A:709:PFN:CAG	2.09	0.83
8:A:709:PFN:CAL	8:A:709:PFN:CAG	2.56	0.79
1:A:482:ALA:HB1	1:A:485:GLU:HG3	1.71	0.72
1:A:368:ASN:ND2	6:A:705:NAG:H2	2.06	0.67
1:A:636:THR:HA	1:A:643:ASP:OD2	1.95	0.66
1:A:509:ASP:HB3	9:A:933:HOH:O	1.96	0.66
1:A:415:ARG:HG3	1:A:416:LYS:N	2.13	0.64
1:A:400:TYR:CZ	1:A:404:LYS:HE3	2.33	0.62
1:A:430:THR:HB	1:A:594:ASN:ND2	2.14	0.62
1:A:553:ASN:OD1	1:A:566:ARG:HG3	2.00	0.62
1:A:685:ALA:HB1	8:A:709:PFN:HAP	1.80	0.61
1:A:676:SER:HB3	8:A:709:PFN:HAM3	1.84	0.59
1:A:585:GLN:HB2	9:A:835:HOH:O	2.03	0.58
1:A:665:TYR:CZ	1:A:669:ILE:HD11	2.38	0.58
1:A:344:ARG:HD3	1:A:367:GLN:O	2.04	0.58
1:A:368:ASN:HD21	6:A:705:NAG:C2	2.11	0.55
1:A:668:ALA:HB1	6:A:706:NAG:H83	1.88	0.55
1:A:471:MET:CE	1:A:483:PHE:HB2	2.36	0.55
1:A:421:SER:HB2	9:A:870:HOH:O	2.07	0.54
1:A:600:ARG:HB2	9:A:873:HOH:O	2.08	0.53
1:A:474:ILE:O	1:A:478:THR:HG23	2.07	0.53
1:A:626:PRO:HA	1:A:630:CYS:SG	2.49	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:685:ALA:HB2	8:A:709:PFN:HAP	1.90	0.52
1:A:416:LYS:HE3	1:A:620:LYS:HE3	1.92	0.52
1:A:415:ARG:CG	1:A:416:LYS:N	2.73	0.50
1:A:377:THR:O	1:A:381:ILE:HG12	2.12	0.50
8:A:709:PFN:HAG	8:A:709:PFN:CAL	2.41	0.50
1:A:462:ASP:OD1	8:A:709:PFN:HAH	2.13	0.49
1:A:553:ASN:CG	1:A:566:ARG:HG3	2.34	0.48
1:A:483:PHE:C	1:A:483:PHE:CD2	2.87	0.48
1:A:513:ASP:O	1:A:516:VAL:HG22	2.13	0.48
1:A:509:ASP:OD1	1:A:510:GLN:N	2.46	0.48
1:A:446:LEU:O	1:A:578:ARG:NH1	2.45	0.47
1:A:469:ILE:HB	1:A:470:PRO:HD3	1.96	0.47
1:A:471:MET:HE3	1:A:483:PHE:HB2	1.97	0.47
1:A:395:ASP:HA	1:A:595:HIS:CD2	2.50	0.47
1:A:471:MET:HE1	1:A:483:PHE:HB2	1.96	0.46
1:A:671:ASN:HA	1:A:674:LYS:HD2	1.98	0.46
1:A:671:ASN:ND2	6:A:706:NAG:H5	2.32	0.45
1:A:567:GLU:HA	1:A:567:GLU:OE1	2.16	0.45
1:A:549:TRP:HB2	7:A:707:NAG:H62	1.99	0.45
1:A:456:SER:O	1:A:490:SER:HA	2.16	0.45
1:A:415:ARG:HG3	1:A:416:LYS:H	1.82	0.44
1:A:579:LYS:NZ	9:A:959:HOH:O	2.50	0.44
1:A:520:LYS:HA	1:A:520:LYS:HD2	1.85	0.44
1:A:432:GLY:HA2	1:A:592:ALA:O	2.17	0.44
1:A:653:GLY:O	1:A:654:ARG:C	2.56	0.44
1:A:378:ASP:OD2	8:A:709:PFN:HAK	2.18	0.43
1:A:460:ALA:HB3	1:A:463:ARG:HD3	2.00	0.43
1:A:377:THR:HG21	1:A:398:TYR:CD2	2.54	0.43
1:A:415:ARG:NH2	1:A:432:GLY:O	2.46	0.43
1:A:477:GLN:NE2	9:A:817:HOH:O	2.53	0.42
1:A:343:THR:HG22	1:A:606:HIS:HB3	2.00	0.42
1:A:665:TYR:CE2	1:A:669:ILE:HD11	2.54	0.42
1:A:549:TRP:CH2	1:A:582:THR:HG22	2.53	0.42
1:A:521:GLU:HB3	1:A:524:TYR:HB2	2.03	0.41
1:A:488:SER:O	1:A:500:ARG:HD3	2.21	0.41
1:A:373:THR:HG22	1:A:374:ALA:N	2.36	0.41
1:A:469:ILE:HB	1:A:470:PRO:CD	2.51	0.41
1:A:461:VAL:O	1:A:462:ASP:HB2	2.21	0.41
1:A:397:GLY:HA3	1:A:462:ASP:O	2.21	0.41
1:A:483:PHE:C	1:A:483:PHE:HD2	2.23	0.41
1:A:407:LEU:CD2	1:A:600:ARG:HG3	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:634:SER:O	1:A:637:LYS:HE2	2.21	0.41
1:A:552:THR:OG1	1:A:566:ARG:HG2	2.21	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	337/345 (98%)	310 (92%)	26 (8%)	1 (0%)	46 45

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	479	GLY

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	282/286 (99%)	269 (95%)	13 (5%)	33 31

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	363	GLN

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Mol	Chain	Res	Type
1	A	420	HIS
1	A	477	GLN
1	A	483	PHE
1	A	515	CYS
1	A	545	ASN
1	A	557	THR
1	A	585	GLN
1	A	609	GLN
1	A	613	HIS
1	A	627	ASP
1	A	667	THR
1	A	682	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	359	GLN
1	A	367	GLN
1	A	368	ASN
1	A	613	HIS
1	A	671	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 ⓘ

2 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	$\# Z > 2$
7	NAG	A	707	1,7	14,14,15	0.72	1 (7%)	15,19,21	1.77	2 (13%)
7	NAG	A	708	7	14,14,15	0.46	0	15,19,21	2.47	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
7	NAG	A	707	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	708	7	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	707	NAG	C1-C2	2.04	1.55	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	708	NAG	C3-C4-C5	-3.71	103.72	110.20
7	A	708	NAG	C4-C3-C2	-2.46	107.41	111.23
7	A	708	NAG	O4-C4-C5	2.05	114.68	109.24
7	A	707	NAG	C2-N2-C7	2.52	126.28	123.04
7	A	707	NAG	C1-O5-C5	5.89	119.72	112.25
7	A	708	NAG	C1-O5-C5	7.66	121.97	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	707	NAG	1	0

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 3 are monoatomic - leaving 5 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	$\# Z > 2$
4	CO3	A	703	3	0,3,3	0.00	-	0,3,3	0.00	-
5	SO4	A	704	-	4,4,4	0.18	0	6,6,6	0.40	0
6	NAG	A	705	-	14,14,15	0.61	0	15,19,21	1.53	2 (13%)
6	NAG	A	706	1	14,14,15	0.61	0	15,19,21	1.56	2 (13%)
8	PFN	A	709	-	16,19,19	1.14	1 (6%)	20,25,25	1.10	1 (5%)

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	CO3	A	703	3	-	0/0/0/0	0/0/0/0
5	SO4	A	704	-	-	0/0/0/0	0/0/0/0
6	NAG	A	705	-	-	0/6/23/26	0/1/1/1
6	NAG	A	706	1	-	0/6/23/26	0/1/1/1
8	PFN	A	709	-	-	0/8/12/12	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	709	PFN	CAE-C13	-2.90	1.46	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	709	PFN	C2-OAN-CAR	-2.40	112.84	118.81
6	A	706	NAG	C2-N2-C7	2.00	125.61	123.04
6	A	705	NAG	C4-C3-C2	3.40	116.52	111.23
6	A	705	NAG	C3-C4-C5	3.47	116.24	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	706	NAG	C1-O5-C5	4.99	118.58	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	705	NAG	3	0
6	A	706	NAG	2	0
8	A	709	PFN	9	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, 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(Å ²)	Q<0.9
1	A	341/345 (98%)	0.88	46 (13%) 4 6	24, 41, 73, 93	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	423	LEU	13.5
1	A	418	SER	10.7
1	A	420	HIS	9.4
1	A	421	SER	8.3
1	A	342	TYR	7.2
1	A	419	LYS	6.4
1	A	681	LEU	5.8
1	A	482	ALA	5.8
1	A	626	PRO	5.3
1	A	682	GLU	5.3
1	A	554	GLY	5.1
1	A	422	SER	5.0
1	A	685	ALA	4.9
1	A	676	SER	4.8
1	A	667	THR	4.6
1	A	683	ALA	4.5
1	A	481	CYS	4.4
1	A	627	ASP	4.2
1	A	674	LYS	4.0
1	A	684	CYS	3.8
1	A	567	GLU	3.5
1	A	417	SER	3.4
1	A	461	VAL	3.3
1	A	620	LYS	3.1
1	A	663	THR	3.0
1	A	424	ASP	3.0
1	A	416	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	622	GLY	2.8
1	A	675	CYS	2.7
1	A	557	THR	2.6
1	A	398	TYR	2.5
1	A	459	THR	2.4
1	A	686	PHE	2.3
1	A	640	LEU	2.3
1	A	367	GLN	2.3
1	A	486	PHE	2.2
1	A	621	ASN	2.2
1	A	671	ASN	2.2
1	A	526	TYR	2.2
1	A	559	ASP	2.2
1	A	343	THR	2.1
1	A	392	LEU	2.1
1	A	460	ALA	2.1
1	A	449	ASN	2.1
1	A	542	PHE	2.1
1	A	483	PHE	2.1

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(\AA^2)	Q<0.9
7	NAG	A	707	14/15	0.82	0.14	-0.10	50,55,61,67	0
7	NAG	A	708	14/15	0.85	0.28	-	74,78,80,81	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
8	PFN	A	709	18/18	0.65	0.26	0.37	67,73,78,79	0
4	CO3	A	703	4/4	0.95	0.19	-0.08	21,24,25,26	0
6	NAG	A	706	14/15	0.84	0.15	-0.26	70,74,81,82	0
2	ZN	A	701	1/1	0.99	0.07	-1.48	41,41,41,41	0
3	FE	A	702	1/1	0.99	0.10	-2.14	27,27,27,27	0
2	ZN	A	710	1/1	0.96	0.15	-	56,56,56,56	0
6	NAG	A	705	14/15	0.63	0.24	-	98,100,101,101	0
5	SO4	A	704	5/5	0.92	0.20	-	108,108,109,109	0

6.5 Other polymers

There are no such residues in this entry.