



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:04 AM GMT

PDB ID : 3D7H
Title : A high resolution crystal structure of human glutamate carboxypeptidase II (GCPII) in a complex with DCIBzL, a urea-based inhibitor
Authors : Lubkowski, J.; Barinka, C.
Deposited on : 2008-05-21
Resolution : 1.55 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

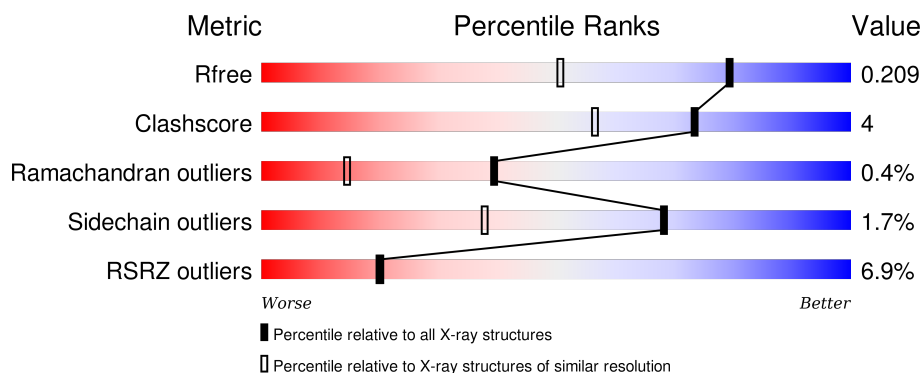
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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	1665 (1.58-1.54)
Clashscore	102246	1014 (1.56-1.56)
Ramachandran outliers	100387	1704 (1.58-1.54)
Sidechain outliers	100360	1702 (1.58-1.54)
RSRZ outliers	91569	1668 (1.58-1.54)

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	709	

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
4	NAG	A	1761	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	A	1763	-	-	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 6529 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 Glutamate carboxypeptidase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	694	Total	C	N	O	S	0	39	0
			5715	3677	955	1060	23			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	ARG	-	EXPRESSION TAG	UNP Q04609
A	43	SER	-	EXPRESSION TAG	UNP Q04609

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

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

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (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		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 5 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

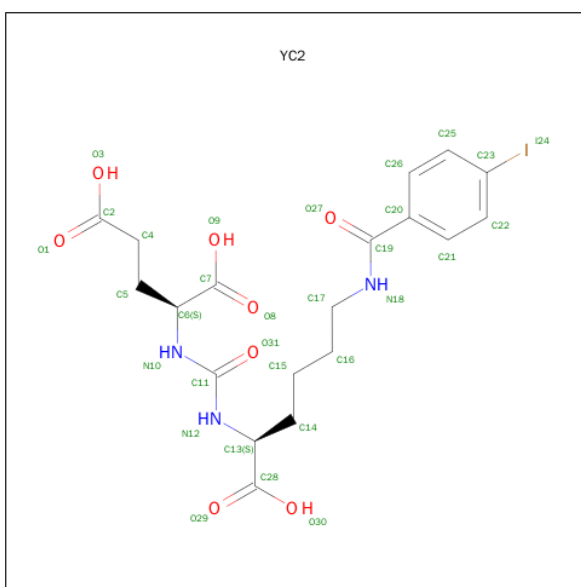
- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Ca 1 1	0	0

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 9 is N-{[(1S)-1-CARBOXY-5-{[(4-IODOPHENYL)CARBONYL]AMINO}PENTYL]CARBAMOYL}-L-GLUTAMIC ACID (three-letter code: YC2) (formula: C₁₉H₂₄IN₃O₈).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C I N O 31 19 1 3 8	0	0

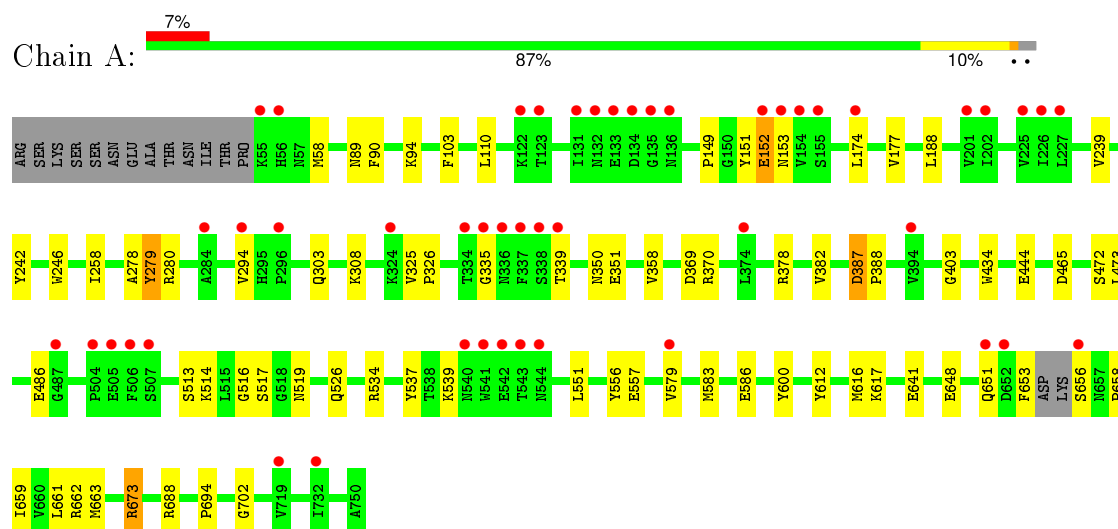
- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	592	Total O 592 592	0	1

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: Glutamate carboxypeptidase 2



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	101.27Å 130.51Å 158.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.55 28.46 – 1.55	Depositor EDS
% Data completeness (in resolution range)	94.7 (15.00-1.55) 94.6 (28.46-1.55)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 1.55Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.183 , 0.209 0.183 , 0.209	Depositor DCC
R_{free} test set	1445 reflections (1.02%)	DCC
Wilson B-factor (Å ²)	21.6	Xtriage
Anisotropy	0.514	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 55.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 143406 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6529	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, BMA, NAG, CL, YC2, CA, MAN

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	0.88	2/5997 (0.0%)	0.87	5/8119 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	557	GLU	CB-CG	-6.11	1.40	1.52
1	A	434	TRP	CE3-CZ3	5.08	1.47	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	370	ARG	NE-CZ-NH2	-9.28	115.66	120.30
1	A	370	ARG	NE-CZ-NH1	7.76	124.18	120.30
1	A	673	ARG	NE-CZ-NH2	-7.33	116.64	120.30
1	A	673	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	A	387	ASP	CB-CG-OD1	-5.01	113.79	118.30

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	5715	0	5560	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	56	0	50	2	0
3	A	42	0	39	1	0
4	A	39	0	34	0	0
5	A	50	0	43	0	0
6	A	2	0	0	0	0
7	A	1	0	0	0	0
8	A	1	0	0	0	0
9	A	31	0	21	1	0
10	A	592	0	0	9	2
All	All	6529	0	5747	48	2

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 4.

All (48) 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:TYR:O	1:A:153:ASN:N	1.99	0.95
1:A:89[B]:ASN:HD21	1:A:378:ARG:HH21	1.07	0.94
1:A:58:MET:CE	1:A:586:GLU:HG2	2.09	0.82
1:A:486:GLU:HG2	10:A:2214:HOH:O	1.79	0.81
1:A:89[B]:ASN:ND2	1:A:378:ARG:HH21	1.80	0.78
1:A:278:ALA:HB3	1:A:280[B]:ARG:NH1	2.02	0.74
1:A:58:MET:HE1	1:A:586:GLU:HG2	1.69	0.72
1:A:656[B]:SER:O	1:A:658[B]:PRO:HD3	1.90	0.72
1:A:89[B]:ASN:HD21	1:A:378:ARG:NH2	1.87	0.68
1:A:641:GLU:HG3	10:A:2350:HOH:O	1.93	0.67
2:A:1767:NAG:H83	10:A:2100:HOH:O	1.95	0.66
1:A:177:VAL:HG12	1:A:188:LEU:HD11	1.79	0.65
1:A:58:MET:HE2	1:A:586:GLU:HG2	1.86	0.56
1:A:90:PHE:CE2	1:A:94:LYS:HE2	2.41	0.56
1:A:617:LYS:NZ	10:A:2135:HOH:O	2.38	0.56
1:A:514[A]:LYS:HE2	1:A:702:GLY:O	2.06	0.55
2:A:1756:NAG:H81	10:A:2014:HOH:O	2.08	0.53
1:A:648:GLU:O	1:A:651[B]:GLN:HG2	2.09	0.53
1:A:369:ASP:OD2	1:A:662[B]:ARG:NH2	2.28	0.53
1:A:579:VAL:O	1:A:583[B]:MET:HG2	2.09	0.52
1:A:278:ALA:HB3	1:A:280[B]:ARG:CZ	2.41	0.51
1:A:472[B]:SER:OG	10:A:2329:HOH:O	2.18	0.50
1:A:517:SER:HB2	1:A:694:PRO:HG3	1.93	0.49
1:A:551:LEU:HD22	1:A:556:TYR:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:465:ASP:OD1	1:A:513:SER:HB2	2.15	0.47
1:A:473:LEU:HD23	1:A:583[B]:MET:CE	2.45	0.46
1:A:688[B]:ARG:CZ	10:A:1877:HOH:O	2.63	0.46
1:A:242:TYR:OH	10:A:2162:HOH:O	1.93	0.46
1:A:350:ASN:C	1:A:351[B]:GLU:HG2	2.36	0.45
1:A:103:PHE:O	1:A:403:GLY:HA3	2.15	0.45
1:A:325:VAL:HB	1:A:326:PRO:HD2	1.98	0.44
1:A:534:ARG:HG3	9:A:1:YC2:I24	2.88	0.44
1:A:149:PRO:HA	1:A:152:GLU:OE2	2.19	0.43
1:A:653:PHE:HZ	1:A:661[A]:LEU:HD13	1.83	0.42
1:A:246:TRP:CD1	3:A:1760:NAG:H83	2.55	0.42
1:A:551:LEU:HA	1:A:551:LEU:HD23	1.88	0.42
1:A:659[B]:ILE:O	1:A:663[B]:MET:HG3	2.20	0.42
1:A:653:PHE:HE1	1:A:661[A]:LEU:HB2	1.84	0.41
1:A:612:TYR:CZ	1:A:616:MET:HG3	2.56	0.41
1:A:308:LYS:HB2	10:A:2202:HOH:O	2.20	0.41
1:A:110:LEU:CD2	1:A:358:VAL:HG22	2.51	0.41
1:A:444:GLU:HA	1:A:444:GLU:OE1	2.21	0.40
1:A:516:GLY:O	1:A:526[B]:GLN:NE2	2.47	0.40
1:A:387:ASP:HA	1:A:388:PRO:HA	1.94	0.40
1:A:258:ILE:HD13	1:A:294:VAL:HB	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:2104:HOH:O	10:A:2273:HOH:O[2_565]	1.97	0.23
10:A:1986:HOH:O	10:A:2285:HOH:O[2_565]	1.99	0.21

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	727/709 (102%)	701 (96%)	23 (3%)	3 (0%)	39 14

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	GLU
1	A	382	VAL
1	A	335	GLY

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	629/605 (104%)	618 (98%)	11 (2%)	68 38

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	174	LEU
1	A	239	VAL
1	A	279[A]	TYR
1	A	279[B]	TYR
1	A	303	GLN
1	A	339	THR
1	A	519	ASN
1	A	537	TYR
1	A	539	LYS
1	A	600	TYR
1	A	673	ARG

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	136	ASN
1	A	618	HIS

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 ⓘ

11 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	$\# Z > 2$
2	NAG	A	1755	1,2	14,14,15	0.55	0	15,19,21	1.20	2 (13%)
2	NAG	A	1756	2	14,14,15	0.58	0	15,19,21	0.98	1 (6%)
2	NAG	A	1758	1,2	14,14,15	0.78	0	15,19,21	0.83	0
4	NAG	A	1761	1,4	14,14,15	0.87	1 (7%)	15,19,21	1.09	2 (13%)
4	NAG	A	1762	4	14,14,15	0.52	0	15,19,21	1.15	2 (13%)
5	NAG	A	1763	1,5	14,14,15	0.66	0	15,19,21	0.95	1 (6%)
5	NAG	A	1764	5	14,14,15	0.62	0	15,19,21	1.31	2 (13%)
5	BMA	A	1765	5	11,11,12	0.44	0	14,15,17	0.94	1 (7%)
5	MAN	A	1766	5	11,11,12	0.57	0	14,15,17	0.95	0
2	NAG	A	1767	2	14,14,15	0.36	0	15,19,21	1.77	4 (26%)
4	BMA	A	1768	4	11,11,12	0.53	0	14,15,17	1.04	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1755	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1756	2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1758	1,2	-	0/6/23/26	0/1/1/1
4	NAG	A	1761	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1762	4	-	0/6/23/26	0/1/1/1
5	NAG	A	1763	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	1764	5	-	0/6/23/26	0/1/1/1
5	BMA	A	1765	5	-	0/2/19/22	0/1/1/1
5	MAN	A	1766	5	-	0/2/19/22	0/1/1/1
2	NAG	A	1767	2	-	0/6/23/26	0/1/1/1
4	BMA	A	1768	4	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1761	NAG	O7-C7	2.06	1.28	1.23

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1764	NAG	C3-C4-C5	-2.91	105.12	110.20
2	A	1755	NAG	O3-C3-C4	-2.85	103.92	110.34
5	A	1763	NAG	C6-C5-C4	-2.50	106.85	113.02
2	A	1767	NAG	O7-C7-C8	-2.27	117.89	122.06
4	A	1761	NAG	O4-C4-C3	-2.15	105.51	110.34
2	A	1755	NAG	O4-C4-C3	-2.04	105.73	110.34
4	A	1762	NAG	C2-N2-C7	-2.04	120.41	123.04
5	A	1764	NAG	O5-C5-C6	2.08	111.85	107.35
5	A	1765	BMA	C1-O5-C5	2.21	115.05	112.25
4	A	1761	NAG	C2-N2-C7	2.34	126.05	123.04
4	A	1762	NAG	C1-O5-C5	2.48	115.40	112.25
2	A	1756	NAG	C2-N2-C7	2.56	126.33	123.04
2	A	1767	NAG	C1-O5-C5	2.85	115.87	112.25
2	A	1767	NAG	C8-C7-N2	3.01	121.86	116.11
2	A	1767	NAG	C2-N2-C7	4.17	128.40	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1756	NAG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1767	NAG	1	0

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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
9	YC2	A	1	-	22,31,31	1.06	1 (4%)	25,40,40	2.02	9 (36%)
3	NAG	A	1757	1	14,14,15	0.54	0	15,19,21	1.09	1 (6%)
3	NAG	A	1759	1	14,14,15	0.47	0	15,19,21	1.74	1 (6%)
3	NAG	A	1760	1	14,14,15	0.61	0	15,19,21	1.55	3 (20%)

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
9	YC2	A	1	-	-	0/23/33/33	0/1/1/1
3	NAG	A	1757	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1759	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1760	1	-	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)
9	A	1	YC2	C23-I24	2.27	2.16	2.10

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1	YC2	C25-C23-C22	-4.36	113.96	120.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1	YC2	O27-C19-N18	-2.97	116.33	122.58
9	A	1	YC2	C26-C20-C21	-2.66	114.65	118.60
9	A	1	YC2	C6-N10-C11	-2.52	115.76	120.90
3	A	1760	NAG	C2-N2-C7	-2.14	120.29	123.04
3	A	1760	NAG	O5-C5-C6	2.18	112.06	107.35
9	A	1	YC2	C25-C26-C20	2.37	123.51	120.76
9	A	1	YC2	C22-C23-I24	2.41	123.46	119.67
3	A	1757	NAG	O5-C5-C6	2.52	112.81	107.35
9	A	1	YC2	C21-C22-C23	2.97	123.94	119.53
9	A	1	YC2	C17-N18-C19	3.05	128.99	122.15
9	A	1	YC2	C20-C19-N18	3.20	124.31	117.12
3	A	1760	NAG	C1-O5-C5	3.38	116.53	112.25
3	A	1759	NAG	C1-O5-C5	5.90	119.73	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	1	YC2	1	0
3	A	1760	NAG	1	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	694/709 (97%)	0.16	48 (6%)	20 20	16, 26, 45, 59	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	541	TRP	6.6
1	A	153	ASN	5.7
1	A	719	VAL	5.6
1	A	55	LYS	5.4
1	A	335	GLY	5.1
1	A	506	PHE	4.6
1	A	135	GLY	4.4
1	A	155	SER	3.9
1	A	543	THR	3.9
1	A	507[A]	SER	3.8
1	A	542	GLU	3.6
1	A	136	ASN	3.6
1	A	134	ASP	3.5
1	A	336	ASN	3.5
1	A	123	THR	3.4
1	A	504	PRO	3.3
1	A	227	LEU	3.2
1	A	505	GLU	3.2
1	A	226	ILE	3.1
1	A	201	VAL	3.1
1	A	154	VAL	3.0
1	A	133	GLU	2.9
1	A	487	GLY	2.9
1	A	122	LYS	2.7
1	A	652	ASP	2.7
1	A	656[A]	SER	2.6
1	A	132	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	334	THR	2.6
1	A	324	LYS	2.5
1	A	131	ILE	2.5
1	A	544	ASN	2.5
1	A	152	GLU	2.5
1	A	339	THR	2.4
1	A	651[A]	GLN	2.4
1	A	56	HIS	2.4
1	A	284	ALA	2.4
1	A	394	VAL	2.3
1	A	374	LEU	2.3
1	A	202	ILE	2.3
1	A	337	PHE	2.3
1	A	294	VAL	2.2
1	A	579	VAL	2.2
1	A	338	SER	2.1
1	A	225	VAL	2.1
1	A	174	LEU	2.1
1	A	732	ILE	2.1
1	A	296	PRO	2.1
1	A	540	ASN	2.0

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

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

6.3 Carbohydrates ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
5	NAG	A	1763	14/15	0.91	0.08	2.36	22,30,41,46	0
4	NAG	A	1761	14/15	0.91	0.11	2.34	29,33,37,40	0
5	MAN	A	1766	11/12	0.90	0.19	1.44	51,52,55,56	0
2	NAG	A	1758	14/15	0.89	0.12	0.95	38,41,46,49	0
4	BMA	A	1768	11/12	0.76	0.31	-	57,59,63,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	NAG	A	1762	14/15	0.89	0.18	-	38,44,49,52	0
5	BMA	A	1765	11/12	0.82	0.24	-	46,48,49,50	0
5	NAG	A	1764	14/15	0.86	0.26	-	42,47,53,54	0
2	NAG	A	1756	14/15	0.63	0.27	-	45,53,56,58	0
2	NAG	A	1767	14/15	0.79	0.28	-	53,56,62,63	0
2	NAG	A	1755	14/15	0.93	0.09	-	34,41,44,48	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(\AA^2)	Q<0.9
3	NAG	A	1757	14/15	0.73	0.25	1.99	44,49,54,57	0
8	CL	A	1754	1/1	0.99	0.10	-0.24	24,24,24,24	0
7	CA	A	1753	1/1	1.00	0.05	-0.42	16,16,16,16	0
9	YC2	A	1	31/31	0.99	0.07	-0.53	18,23,31,35	1
6	ZN	A	1752	1/1	1.00	0.04	-2.15	21,21,21,21	0
6	ZN	A	1751	1/1	1.00	0.05	-3.93	20,20,20,20	0
3	NAG	A	1759	14/15	0.83	0.23	-	62,67,71,71	0
3	NAG	A	1760	14/15	0.84	0.16	-	32,46,52,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.