



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 10:46 pm GMT

PDB ID : 5ELY
Title : X-ray structure of human glutamate carboxypeptidase II (GCPII) in complex with a hydroxamate inhibitor JHU242
Authors : Barinka, C.; Novakova, Z.; Pavlicek, J.
Deposited on : 2015-11-05
Resolution : 1.81 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

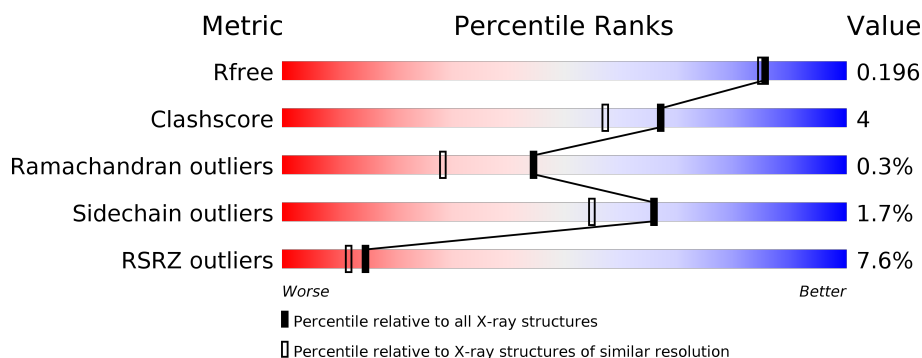
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.81 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}	100719	5868 (1.84-1.80)
Clashscore	112137	6856 (1.84-1.80)
Ramachandran outliers	110173	6780 (1.84-1.80)
Sidechain outliers	110143	6780 (1.84-1.80)
RSRZ outliers	101464	5947 (1.84-1.80)

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.

Mol	Chain	Length	Quality of chain
1	A	696	<div> <div>7%</div> <div>88%</div> <div>10%</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
5	NAG	A	806	-	-	-	X
5	NAG	A	807	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
9	ACT	A	818	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 6394 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	682	Total	C	N	O	S	0	55	0
			5738	3689	953	1072	24			

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

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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

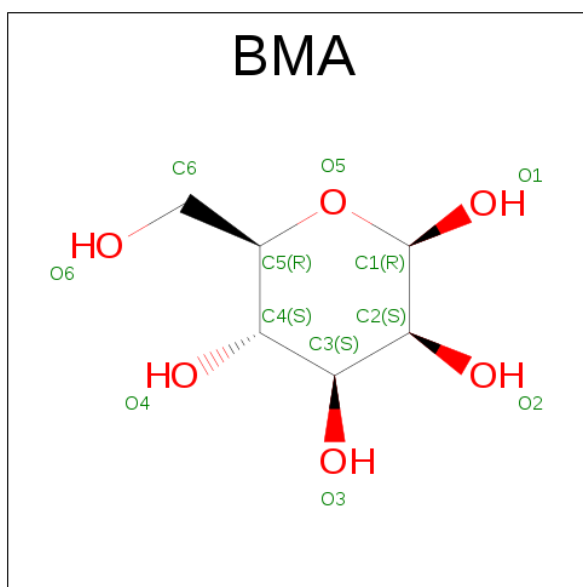
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C₈H₁₅NO₆).



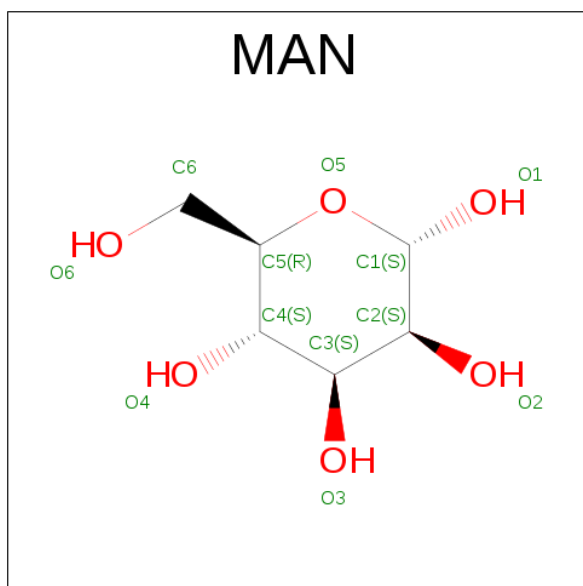
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1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

- Molecule 6 is BETA-D-MANNOSE (three-letter code: BMA) (formula: C₆H₁₂O₆).



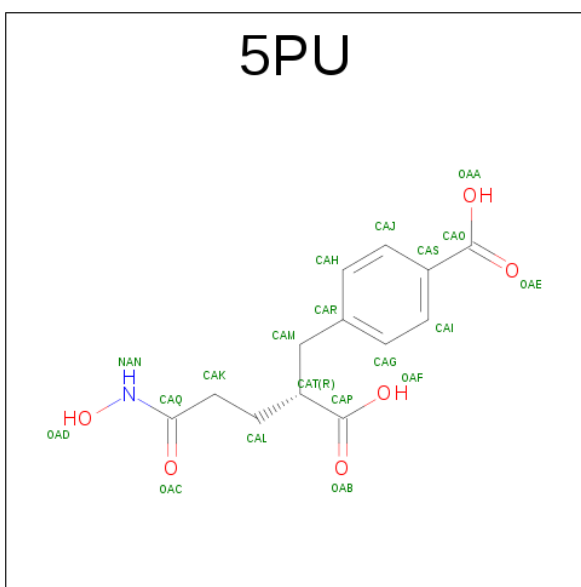
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 7 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C₆H₁₂O₆).



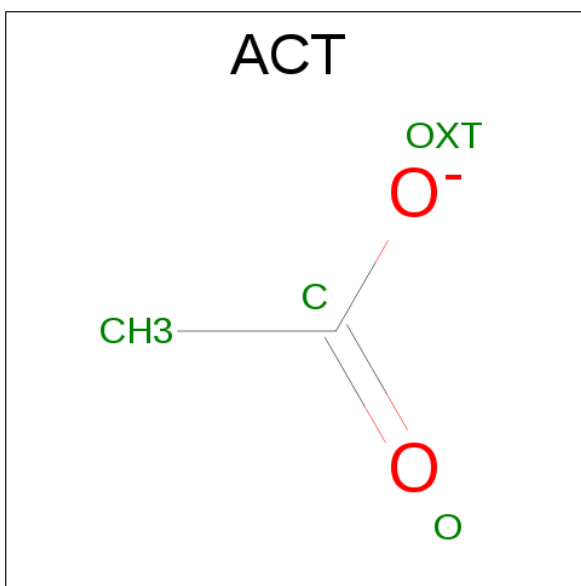
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 8 is 4-[(2 {R})-2-carboxy-5-(oxidanylamino)-5-oxidanylidene-pentyl]benzoic acid (three-letter code: 5PU) (formula: C₁₃H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			20	13	1	6		

- Molecule 9 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			4	2	2		

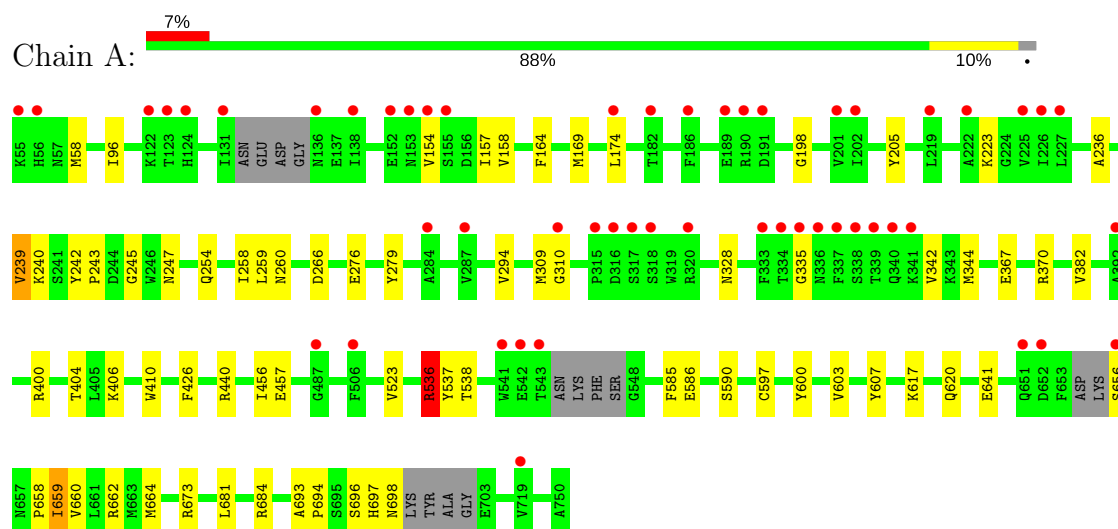
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	466	Total 466	O 466	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 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.

• 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	101.06Å 130.83Å 158.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.81 29.43 – 1.81	Depositor EDS
% Data completeness (in resolution range)	99.5 (40.00-1.81) 99.5 (29.43-1.81)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.15 (at 1.80Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.177 , 0.199 0.177 , 0.196	Depositor DCC
R_{free} test set	952 reflections (1.01%)	DCC
Wilson B-factor (Å ²)	25.2	Xtriage
Anisotropy	0.500	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 49.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6394	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.44% 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, 0.333 respectively for untwinned datasets, and 0.375, 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, BMA, NAG, CL, CA, ACT, 5PU, 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	0.93	4/6017 (0.1%)	0.81	4/8148 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	158	VAL	CB-CG1	6.34	1.66	1.52
1	A	597	CYS	CB-SG	5.47	1.91	1.82
1	A	426	PHE	CE2-CZ	5.24	1.47	1.37
1	A	523	VAL	CB-CG1	5.09	1.63	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	536[A]	ARG	NE-CZ-NH2	-6.65	116.97	120.30
1	A	536[B]	ARG	NE-CZ-NH2	-6.65	116.97	120.30
1	A	440	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	A	370	ARG	NE-CZ-NH1	5.10	122.85	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	697	HIS	Peptide

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	5738	0	5630	43	1
2	A	2	0	0	0	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	140	0	125	3	0
6	A	11	0	9	0	1
7	A	11	0	10	0	0
8	A	20	0	0	3	0
9	A	4	0	3	7	0
10	A	466	0	0	17	0
All	All	6394	0	5777	53	1

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 (53) 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)
9:A:818:ACT:CH3	10:A:1238:HOH:O	1.88	1.21
1:A:660[A]:VAL:O	1:A:664[A]:MET:HG2	1.44	1.18
9:A:818:ACT:H1	10:A:1238:HOH:O	1.53	1.03
1:A:641:GLU:HG3	10:A:1031:HOH:O	1.68	0.93
9:A:818:ACT:H2	10:A:1238:HOH:O	1.56	0.90
1:A:693:ALA:HB2	10:A:1050:HOH:O	1.69	0.89
1:A:659[A]:ILE:HD13	1:A:659[A]:ILE:N	1.91	0.84
1:A:603[B]:VAL:HG13	1:A:607:TYR:CZ	2.15	0.80
1:A:603[B]:VAL:CG1	1:A:607:TYR:CZ	2.68	0.77
1:A:603[B]:VAL:CG1	1:A:607:TYR:CE2	2.71	0.73
5:A:806:NAG:H81	10:A:1307:HOH:O	1.88	0.72
1:A:400:ARG:O	1:A:404[B]:THR:HG23	1.90	0.72
1:A:236:ALA:HB3	1:A:239[A]:VAL:HG11	1.74	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457[B]:GLU:OE1	1:A:536[B]:ARG:NH1	2.25	0.69
1:A:603[B]:VAL:HG12	1:A:607:TYR:CE2	2.28	0.68
1:A:641:GLU:CG	10:A:1031:HOH:O	2.37	0.65
1:A:457[B]:GLU:OE2	10:A:901:HOH:O	0.64	0.64
1:A:239[A]:VAL:HG13	1:A:247:ASN:ND2	2.13	0.63
9:A:818:ACT:H3	10:A:1262:HOH:O	2.00	0.61
8:A:817:5PU:CAK	9:A:818:ACT:CH3	2.82	0.57
1:A:236:ALA:HB3	1:A:239[A]:VAL:CG1	2.36	0.55
1:A:198:GLY:O	1:A:223:LYS:HE2	2.06	0.55
1:A:681[A]:LEU:HD11	1:A:693:ALA:HB3	1.91	0.53
5:A:806:NAG:H83	10:A:1265:HOH:O	2.08	0.52
1:A:658[A]:PRO:HG2	1:A:659[A]:ILE:HD13	1.92	0.51
1:A:656[B]:SER:O	1:A:658[B]:PRO:HD3	2.11	0.50
8:A:817:5PU:CAK	9:A:818:ACT:H1	2.41	0.50
1:A:96[B]:ILE:HD13	10:A:997:HOH:O	2.11	0.50
1:A:205:TYR:CE1	1:A:254:GLN:HB3	2.47	0.48
1:A:154:VAL:HA	1:A:157:ILE:HD12	1.96	0.47
1:A:266:ASP:N	10:A:914:HOH:O	2.41	0.47
8:A:817:5PU:CAK	9:A:818:ACT:H3	2.43	0.47
1:A:586[B]:GLU:HG3	1:A:590[B]:SER:OG	2.15	0.47
1:A:276[A]:GLU:HB2	10:A:1268:HOH:O	2.16	0.46
1:A:240[A]:LYS:O	1:A:245:GLY:HA3	2.15	0.45
1:A:169:MET:HA	1:A:344:MET:O	2.16	0.45
1:A:310:GLY:O	1:A:328:ASN:HB3	2.18	0.44
5:A:806:NAG:C8	10:A:1307:HOH:O	2.56	0.44
1:A:457[A]:GLU:HG3	1:A:538:THR:HA	2.00	0.43
1:A:258:ILE:HD13	1:A:294:VAL:HB	2.00	0.43
1:A:406:LYS:HA	1:A:410:TRP:O	2.17	0.43
1:A:174[A]:LEU:HD23	1:A:309[A]:MET:SD	2.59	0.42
1:A:620[A]:GLN:HG2	10:A:1025:HOH:O	2.19	0.42
1:A:260[B]:ASN:ND2	10:A:902:HOH:O	2.03	0.41
1:A:684:ARG:NH2	1:A:694:PRO:O	2.53	0.41
1:A:164:PHE:CE2	1:A:259:LEU:HD11	2.56	0.41
1:A:242:TYR:CG	1:A:243:PRO:HA	2.55	0.41
1:A:174[B]:LEU:HG	1:A:342:VAL:HG21	2.02	0.41
1:A:58[B]:MET:HG3	1:A:585:PHE:CG	2.56	0.41
1:A:367:GLU:OE1	1:A:662[B]:ARG:NH1	2.53	0.41
1:A:693:ALA:CB	10:A:1050:HOH:O	2.45	0.40

All (1) 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)
1:A:276[A]:GLU:OE1	6:A:815:BMA:O2[2_565]	2.19	0.01

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	727/696 (104%)	708 (97%)	17 (2%)	2 (0%)	44 28

All (2) Ramachandran outliers are listed below:

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

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	638/593 (108%)	625 (98%)	13 (2%)	60 47

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

Mol	Chain	Res	Type
1	A	239[A]	VAL
1	A	239[B]	VAL
1	A	456	ILE
1	A	536[A]	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	536[B]	ARG
1	A	537	TYR
1	A	600	TYR
1	A	617	LYS
1	A	659[A]	ILE
1	A	659[B]	ILE
1	A	673	ARG
1	A	696	SER
1	A	698	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 18 ligands modelled in this entry, 4 are monoatomic - leaving 14 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	NAG	A	805	1,5	14,14,15	0.47	0	15,19,21	1.05	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	806	5	14,14,15	0.70	0	15,19,21	1.40	2 (13%)
5	NAG	A	807	1	14,14,15	0.63	0	15,19,21	1.12	1 (6%)
5	NAG	A	808	1,5	14,14,15	0.77	0	15,19,21	1.28	3 (20%)
5	NAG	A	809	5	14,14,15	0.58	0	15,19,21	1.12	1 (6%)
5	NAG	A	810	1	14,14,15	0.75	0	15,19,21	2.37	3 (20%)
5	NAG	A	811	1,5	14,14,15	0.79	0	15,19,21	1.20	2 (13%)
5	NAG	A	812	5	14,14,15	0.69	0	15,19,21	1.32	3 (20%)
5	NAG	A	813	1,5	14,14,15	0.71	0	15,19,21	1.27	3 (20%)
5	NAG	A	814	5,6	14,14,15	0.56	0	15,19,21	1.40	3 (20%)
6	BMA	A	815	5,7	11,11,12	0.44	0	13,15,17	0.91	1 (7%)
7	MAN	A	816	6	11,11,12	0.67	0	13,15,17	0.76	0
8	5PU	A	817	2	14,20,20	1.28	2 (14%)	19,26,26	1.87	8 (42%)
9	ACT	A	818	-	1,3,3	0.40	0	0,3,3	0.00	-

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	NAG	A	805	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	806	5	-	0/6/23/26	0/1/1/1
5	NAG	A	807	1	-	0/6/23/26	0/1/1/1
5	NAG	A	808	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	809	5	-	0/6/23/26	0/1/1/1
5	NAG	A	810	1	-	0/6/23/26	0/1/1/1
5	NAG	A	811	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	812	5	-	0/6/23/26	0/1/1/1
5	NAG	A	813	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	814	5,6	-	0/6/23/26	0/1/1/1
6	BMA	A	815	5,7	-	0/2/19/22	0/1/1/1
7	MAN	A	816	6	-	0/2/19/22	0/1/1/1
8	5PU	A	817	2	-	0/11/19/19	0/1/1/1
9	ACT	A	818	-	-	0/0/0/0	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	817	5PU	CAM-CAR	2.28	1.56	1.51
8	A	817	5PU	CAG-CAI	2.39	1.43	1.38

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	810	NAG	O5-C1-C2	-6.54	102.37	111.47
8	A	817	5PU	CAJ-CAS-CAO	-3.75	115.42	120.45
8	A	817	5PU	CAL-CAK-CAQ	-2.76	106.94	113.18
5	A	813	NAG	C6-C5-C4	-2.75	106.56	113.00
8	A	817	5PU	CAJ-CAH-CAR	-2.74	117.23	121.02
8	A	817	5PU	CAG-CAI-CAS	-2.57	117.38	121.10
8	A	817	5PU	CAM-CAR-CAH	-2.48	115.90	120.91
5	A	808	NAG	O4-C4-C3	-2.45	105.02	110.36
5	A	812	NAG	O7-C7-C8	-2.40	117.68	122.06
5	A	807	NAG	C1-C2-N2	-2.40	106.39	110.49
5	A	808	NAG	O5-C1-C2	-2.34	108.22	111.47
5	A	813	NAG	O5-C1-C2	-2.26	108.33	111.47
8	A	817	5PU	CAM-CAT-CAP	-2.26	106.43	111.08
5	A	811	NAG	O4-C4-C3	-2.19	105.59	110.36
5	A	812	NAG	O6-C6-C5	-2.15	104.11	111.34
5	A	805	NAG	O7-C7-C8	-2.09	118.26	122.06
6	A	815	BMA	O3-C3-C2	-2.05	106.30	110.02
5	A	814	NAG	O3-C3-C2	-2.04	105.01	109.39
5	A	811	NAG	O7-C7-C8	-2.01	118.40	122.06
5	A	814	NAG	C8-C7-N2	2.02	119.75	116.11
5	A	808	NAG	O4-C4-C5	2.12	114.62	109.28
8	A	817	5PU	CAJ-CAS-CAI	2.17	121.89	117.59
5	A	806	NAG	C1-O5-C5	2.21	115.21	112.17
8	A	817	5PU	CAH-CAR-CAG	2.29	121.80	118.16
5	A	813	NAG	C1-O5-C5	2.33	115.37	112.17
5	A	809	NAG	C4-C3-C2	2.60	114.83	111.02
5	A	812	NAG	C8-C7-N2	2.61	120.81	116.11
5	A	810	NAG	C3-C4-C5	3.47	116.32	110.22
5	A	814	NAG	C1-O5-C5	3.47	116.95	112.17
5	A	806	NAG	C2-N2-C7	3.56	128.14	122.94
5	A	810	NAG	C1-O5-C5	3.87	117.50	112.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	806	NAG	3	0
6	A	815	BMA	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	817	5PU	3	0
9	A	818	ACT	7	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	682/696 (97%)	0.13	52 (7%) 15 12	16, 28, 59, 72	1 (0%)

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	541	TRP	4.8
1	A	154	VAL	4.8
1	A	543	THR	4.6
1	A	55	LYS	4.5
1	A	155	SER	4.5
1	A	219	LEU	4.3
1	A	174[A]	LEU	4.2
1	A	136	ASN	4.1
1	A	287	VAL	3.9
1	A	336	ASN	3.8
1	A	542	GLU	3.8
1	A	191	ASP	3.7
1	A	138	ILE	3.5
1	A	152	GLU	3.5
1	A	338	SER	3.5
1	A	656[A]	SER	3.5
1	A	226	ILE	3.4
1	A	334	THR	3.1
1	A	122	LYS	3.1
1	A	186	PHE	3.1
1	A	335	GLY	3.1
1	A	124	HIS	3.1
1	A	337	PHE	3.0
1	A	153	ASN	3.0
1	A	123	THR	2.9
1	A	317[A]	SER	2.9
1	A	487	GLY	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	201	VAL	2.8
1	A	202	ILE	2.7
1	A	506	PHE	2.7
1	A	190	ARG	2.6
1	A	131	ILE	2.6
1	A	341	LYS	2.5
1	A	227	LEU	2.5
1	A	284	ALA	2.5
1	A	189	GLU	2.5
1	A	652	ASP	2.4
1	A	225	VAL	2.4
1	A	320	ARG	2.4
1	A	318	SER	2.3
1	A	222	ALA	2.3
1	A	339	THR	2.3
1	A	315	PRO	2.3
1	A	316	ASP	2.3
1	A	651	GLN	2.2
1	A	182	THR	2.1
1	A	56	HIS	2.1
1	A	333	PHE	2.1
1	A	340	GLN	2.1
1	A	719	VAL	2.0
1	A	310	GLY	2.0
1	A	392	ALA	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	806	14/15	0.71	0.27	5.73	37,50,53,55	0
5	NAG	A	807	14/15	0.79	0.31	2.10	53,59,62,63	0
9	ACT	A	818	4/4	0.94	0.18	1.89	35,37,38,39	0
7	MAN	A	816	11/12	0.92	0.17	1.18	53,55,58,58	0
5	NAG	A	808	14/15	0.72	0.22	0.87	51,56,60,66	0
5	NAG	A	813	14/15	0.94	0.08	0.31	22,28,39,47	0
3	CA	A	803	1/1	1.00	0.07	-0.10	18,18,18,18	0
8	5PU	A	817	20/20	0.94	0.10	-0.12	19,26,34,39	0
5	NAG	A	811	14/15	0.91	0.10	-0.23	27,30,34,41	0
4	CL	A	804	1/1	0.99	0.11	-0.72	24,24,24,24	0
2	ZN	A	802	1/1	1.00	0.07	-1.88	20,20,20,20	0
2	ZN	A	801	1/1	1.00	0.07	-4.10	21,21,21,21	0
5	NAG	A	814	14/15	0.89	0.18	-	41,46,53,54	0
6	BMA	A	815	11/12	0.89	0.18	-	46,50,52,53	0
5	NAG	A	810	14/15	0.87	0.19	-	34,48,56,58	0
5	NAG	A	812	14/15	0.86	0.19	-	35,40,46,48	0
5	NAG	A	809	14/15	0.73	0.34	-	68,72,76,76	0
5	NAG	A	805	14/15	0.95	0.11	-	32,41,45,48	0

6.5 Other polymers

There are no such residues in this entry.