



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 12:52 am GMT

PDB ID : 4BTW
Title : Crystal structure of human vascular adhesion protein-1 in complex with pyridazinone inhibitors
Authors : Bligt-Linden, E.; Pihlavisto, M.; Szatmari, I.; Otwinowski, Z.; Smith, D.J.; Lazar, L.; Fulop, F.; Salminen, T.A.
Deposited on : 2013-06-19
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

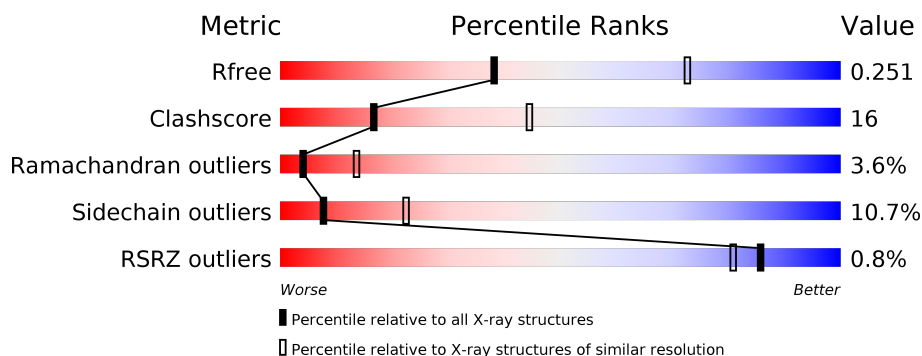
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
R_{free}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (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.

Mol	Chain	Length	Quality of chain
1	A	737	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 59%, yellow 30%, orange 6%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 60% 30% 6% • </div> </div>
1	B	737	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 59%, yellow 30%, orange 6%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 59% 30% 6% • </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
6	NAG	A	1770	X	-	-	-
6	NAG	A	1771	X	-	-	-
6	NAG	B	1774	X	-	-	-
7	JW7	A	2000	-	-	-	X

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 11573 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 MEMBRANE PRIMARY AMINE OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	711	Total	C	N	O	S	0	0	0
			5609	3599	970	1020	20			
1	B	705	Total	C	N	O	S	0	0	0
			5562	3571	959	1012	20			

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cu	0	0
			1	1		
2	A	1	Total	Cu	0	0
			1	1		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Ca	0	0
			2	2		
3	A	2	Total	Ca	0	0
			2	2		

- 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 (2-MER).

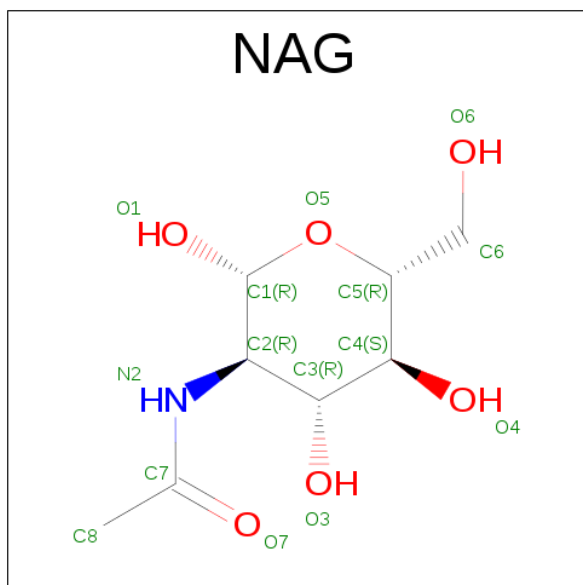
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	2	Total	C	N	O	0	0
			28	16	2	10		

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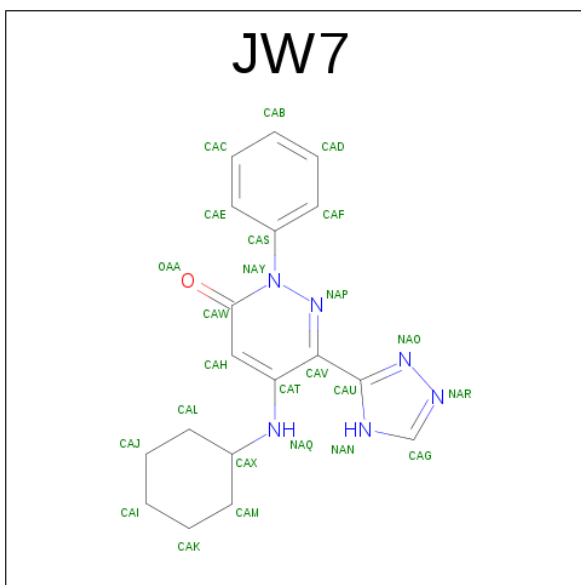
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is 5-(CYCLOHEXYLAMINO)-2-PHENYL-6-(1H-1,2,4-TRIAZOL-5-YL)-3(2H)-PYRIDAZINONE (three-letter code: JW7) (formula: $C_{18}H_{20}N_6O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			25	18	6	1		
7	B	1	Total	C	N	O	0	0
			25	18	6	1		

- Molecule 8 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	5	Total	C	N	O	0	0
			61	34	2	25		

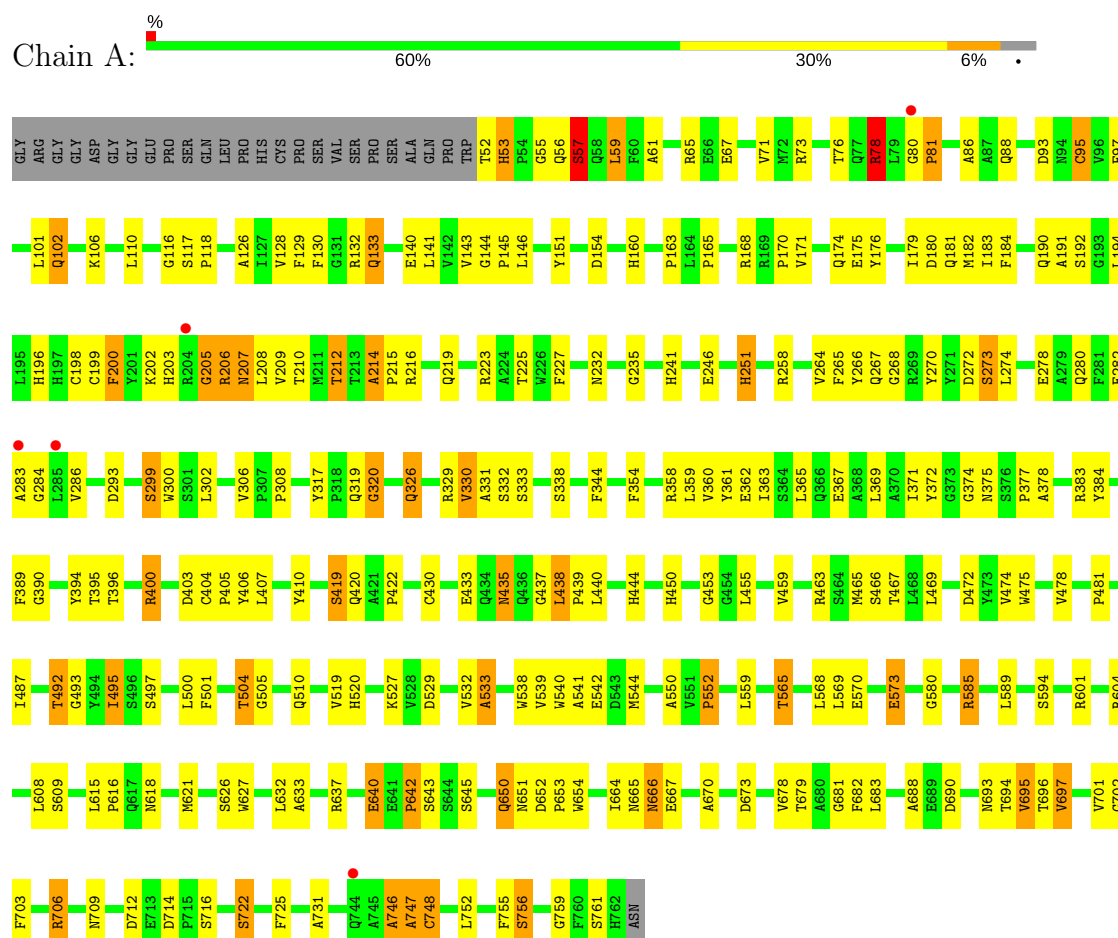
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	64	Total	O	0	0
			64	64		
9	B	42	Total	O	0	0
			42	42		

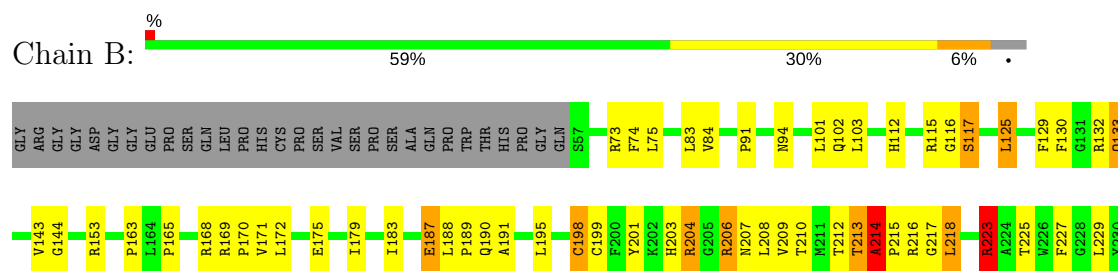
3 Residue-property plots

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.

• Molecule 1: MEMBRANE PRIMARY AMINE OXIDASE



• Molecule 1: MEMBRANE PRIMARY AMINE OXIDASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	226.47Å 226.47Å 219.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.39 – 2.80 49.34 – 2.80	Depositor EDS
% Data completeness (in resolution range)	77.9 (49.39-2.80) 77.9 (49.34-2.80)	Depositor EDS
R_{merge}	0.32	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.205 , 0.260 0.199 , 0.251	Depositor DCC
R_{free} test set	3176 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	53.3	Xtriage
Anisotropy	0.531	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 43.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11573	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, CA, JW7, TPQ, CU, 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	0.73	1/5774 (0.0%)	0.95	6/7874 (0.1%)
1	B	0.73	2/5724 (0.0%)	0.93	8/7805 (0.1%)
All	All	0.73	3/11498 (0.0%)	0.94	14/15679 (0.1%)

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	3
1	B	0	4
All	All	0	7

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	641	GLU	CG-CD	6.26	1.61	1.51
1	B	641	GLU	CD-OE2	5.39	1.31	1.25
1	A	540	TRP	CB-CG	-5.39	1.40	1.50

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	223	ARG	NE-CZ-NH1	7.22	123.91	120.30
1	A	78	ARG	NE-CZ-NH1	6.41	123.51	120.30
1	A	529	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	B	531	ASP	CB-CG-OD1	5.96	123.66	118.30
1	B	223	ARG	NE-CZ-NH2	-5.91	117.34	120.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	198	CYS	Peptide
1	A	205	GLY	Peptide
1	A	437	GLY	Peptide
1	B	213	THR	Peptide
1	B	214	ALA	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	5609	0	5351	171	1
1	B	5562	0	5313	197	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	39	0	34	1	0
5	A	28	0	25	0	0
5	B	28	0	25	0	0
6	A	28	0	26	0	0
6	B	56	0	52	2	0
7	A	25	0	20	4	0
7	B	25	0	20	6	0
8	B	61	0	52	3	0
9	A	64	0	0	1	0
9	B	42	0	0	8	0
All	All	11573	0	10918	353	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 16.

The worst 5 of 353 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:367:GLU:OE2	1:A:645:SER:OG	1.75	1.04
1:A:492:THR:HG21	1:B:441:ARG:HA	1.42	1.01
1:A:80:GLY:O	1:A:81:PRO:O	1.90	0.90
1:B:620:SER:HG	1:B:654:TRP:HD1	1.11	0.90
1:A:495:ILE:HB	9:A:2046:HOH:O	1.70	0.89

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:326:GLN:OE1	1:A:326:GLN:OE1[10_665]	1.91	0.29

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	708/737 (96%)	599 (85%)	82 (12%)	27 (4%)	4	12
1	B	702/737 (95%)	607 (86%)	71 (10%)	24 (3%)	4	15
All	All	1410/1474 (96%)	1206 (86%)	153 (11%)	51 (4%)	4	13

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	81	PRO
1	A	116	GLY
1	A	206	ARG
1	A	214	ALA
1	A	267	GLN

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	590/610 (97%)	530 (90%)	60 (10%)	8	25
1	B	585/610 (96%)	519 (89%)	66 (11%)	7	20
All	All	1175/1220 (96%)	1049 (89%)	126 (11%)	8	22

5 of 126 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	722	SER
1	B	206	ARG
1	B	646	SER
1	A	756	SER
1	B	125	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	HIS
1	A	102	GLN
1	B	112	HIS
1	B	593	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	TPQ	A	471	1	14,14,15	1.57	3 (21%)	17,19,21	1.54	3 (17%)
1	TPQ	B	471	1	14,14,15	1.37	2 (14%)	17,19,21	1.68	3 (17%)

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
1	TPQ	A	471	1	-	0/4/22/24	0/1/1/1
1	TPQ	B	471	1	-	0/4/22/24	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	471	TPQ	CA-C	-2.04	1.47	1.50
1	B	471	TPQ	C6-C1	2.46	1.41	1.34
1	A	471	TPQ	C6-C1	2.56	1.41	1.34
1	B	471	TPQ	C3-C4	2.88	1.40	1.35
1	A	471	TPQ	C3-C4	3.70	1.41	1.35

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	471	TPQ	CB-CA-C	-4.22	103.29	111.41
1	A	471	TPQ	CB-CA-C	-3.08	105.47	111.41
1	B	471	TPQ	O5-C5-C4	2.32	123.27	119.32
1	A	471	TPQ	C6-C1-C2	2.77	120.77	118.54
1	A	471	TPQ	O5-C5-C4	3.46	125.22	119.32

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
1	B	471	TPQ	1	0

5.5 Carbohydrates [i](#)

12 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$
4	NAG	A	1765	1,4	14,14,15	0.72	0	15,19,21	1.65	4 (26%)
4	NAG	A	1766	4	14,14,15	0.82	1 (7%)	15,19,21	1.79	4 (26%)
4	BMA	A	1767	4	11,11,12	0.61	0	13,15,17	1.42	2 (15%)
5	NAG	A	1768	1,5	14,14,15	0.60	0	15,19,21	1.57	3 (20%)
5	NAG	A	1769	5	14,14,15	0.78	1 (7%)	15,19,21	1.39	2 (13%)
8	NAG	B	1765	1,8	14,14,15	0.57	0	15,19,21	1.15	1 (6%)
8	NAG	B	1766	8	14,14,15	0.48	0	15,19,21	1.71	3 (20%)
8	BMA	B	1767	8	11,11,12	0.79	0	13,15,17	2.23	3 (23%)
8	BMA	B	1768	8	11,11,12	0.68	0	13,15,17	2.32	5 (38%)
8	MAN	B	1769	8	11,11,12	0.53	0	13,15,17	2.62	3 (23%)
5	NAG	B	1770	1,5	14,14,15	0.83	0	15,19,21	2.21	5 (33%)
5	NAG	B	1771	5	14,14,15	0.64	0	15,19,21	1.59	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
4	NAG	A	1765	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1766	4	-	0/6/23/26	0/1/1/1
4	BMA	A	1767	4	-	0/2/19/22	0/1/1/1
5	NAG	A	1768	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	1769	5	-	0/6/23/26	0/1/1/1
8	NAG	B	1765	1,8	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	NAG	B	1766	8	-	0/6/23/26	0/1/1/1
8	BMA	B	1767	8	-	0/2/19/22	0/1/1/1
8	BMA	B	1768	8	-	0/2/19/22	0/1/1/1
8	MAN	B	1769	8	-	0/2/19/22	0/1/1/1
5	NAG	B	1770	1,5	-	0/6/23/26	0/1/1/1
5	NAG	B	1771	5	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1766	NAG	O5-C1	-2.08	1.40	1.43
5	A	1769	NAG	C1-C2	2.06	1.55	1.52

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	1767	BMA	O4-C4-C3	-5.01	99.46	110.36
8	B	1766	NAG	C2-N2-C7	-4.04	117.06	122.94
5	B	1770	NAG	C1-C2-N2	-3.89	103.84	110.49
4	A	1766	NAG	O4-C4-C3	-3.74	102.22	110.36
5	B	1770	NAG	O5-C1-C2	-3.42	106.71	111.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1765	NAG	1	0
8	B	1765	NAG	1	0
8	B	1767	BMA	2	0
8	B	1768	BMA	2	0

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 6 are monoatomic - leaving 8 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
6	NAG	A	1770	1	14,14,15	1.18	2 (14%)	15,19,21	2.20	4 (26%)
6	NAG	A	1771	1	14,14,15	1.82	3 (21%)	15,19,21	3.57	8 (53%)
7	JW7	A	2000	-	23,28,28	1.83	3 (13%)	23,38,38	4.08	6 (26%)
6	NAG	B	1772	-	14,14,15	0.76	0	15,19,21	1.20	1 (6%)
6	NAG	B	1773	1	14,14,15	1.02	1 (7%)	15,19,21	2.93	5 (33%)
6	NAG	B	1774	1	14,14,15	1.50	1 (7%)	15,19,21	2.65	6 (40%)
6	NAG	B	1775	1	14,14,15	0.71	0	15,19,21	1.51	3 (20%)
7	JW7	B	2000	-	23,28,28	2.02	4 (17%)	23,38,38	4.24	8 (34%)

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
6	NAG	A	1770	1	1/1/5/7	0/6/23/26	0/1/1/1
6	NAG	A	1771	1	1/1/5/7	0/6/23/26	0/1/1/1
7	JW7	A	2000	-	-	0/10/20/20	0/4/4/4
6	NAG	B	1772	-	-	0/6/23/26	0/1/1/1
6	NAG	B	1773	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1774	1	1/1/5/7	0/6/23/26	0/1/1/1
6	NAG	B	1775	1	-	0/6/23/26	0/1/1/1
7	JW7	B	2000	-	-	0/10/20/20	0/4/4/4

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	2000	JW7	CAS-NAY	-5.22	1.33	1.44
7	B	2000	JW7	CAV-CAU	-5.11	1.39	1.49
7	A	2000	JW7	CAV-CAU	-4.61	1.40	1.49
7	A	2000	JW7	CAS-NAY	-4.46	1.34	1.44
6	A	1770	NAG	C1-C2	2.19	1.55	1.52

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	2000	JW7	NAN-CAU-NAO	-10.55	105.96	114.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	2000	JW7	NAN-CAU-NAO	-8.71	107.49	114.75
6	A	1771	NAG	O5-C1-C2	-7.06	101.64	111.47
7	B	2000	JW7	CAM-CAX-CAL	-3.87	104.62	110.85
6	B	1773	NAG	O7-C7-C8	-3.87	115.02	122.06

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	1770	NAG	C1
6	B	1774	NAG	C1
6	A	1771	NAG	C1

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	2000	JW7	4	0
6	B	1773	NAG	1	0
6	B	1774	NAG	1	0
7	B	2000	JW7	6	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	710/737 (96%)	-0.49	5 (0%) 87 83	39, 58, 82, 138	0
1	B	704/737 (95%)	-0.41	7 (0%) 82 77	38, 59, 91, 153	0
All	All	1414/1474 (95%)	-0.45	12 (0%) 86 81	38, 59, 86, 153	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	746	ALA	5.4
1	B	747	ALA	5.0
1	B	745	ALA	4.3
1	B	748	CYS	2.9
1	B	735	GLU	2.8

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TPQ	B	471	14/15	0.98	0.26	-	44,53,56,59	0
1	TPQ	A	471	14/15	0.98	0.19	-	43,48,52,54	0

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	NAG	A	1769	14/15	0.88	0.18	0.52	91,112,124,126	0
4	NAG	A	1765	14/15	0.97	0.13	-0.28	65,71,75,77	0
5	NAG	B	1770	14/15	0.95	0.11	-0.74	70,86,93,104	0
5	NAG	A	1768	14/15	0.98	0.10	-0.96	72,83,99,101	0
8	NAG	B	1765	14/15	0.98	0.09	-1.62	49,56,59,66	0
8	MAN	B	1769	11/12	0.89	0.31	-	112,126,141,142	0
5	NAG	B	1771	14/15	0.91	0.17	-	105,119,128,130	0
4	NAG	A	1766	14/15	0.94	0.18	-	63,76,95,112	0
8	BMA	B	1767	11/12	0.89	0.19	-	116,126,135,160	0
4	BMA	A	1767	11/12	0.76	0.30	-	110,116,124,128	0
8	BMA	B	1768	11/12	0.72	0.26	-	116,140,161,163	0
8	NAG	B	1766	14/15	0.91	0.18	-	67,101,115,119	0

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
7	JW7	A	2000	25/25	0.91	0.29	4.57	65,90,143,148	0
7	JW7	B	2000	25/25	0.96	0.19	1.00	46,54,97,99	0
3	CA	A	1763	1/1	0.96	0.06	-1.26	51,51,51,51	0
3	CA	B	1763	1/1	0.98	0.06	-1.41	51,51,51,51	0
3	CA	B	1764	1/1	0.98	0.03	-3.40	60,60,60,60	0
3	CA	A	1764	1/1	0.93	0.04	-4.32	59,59,59,59	0
2	CU	A	1762	1/1	1.00	0.20	-	54,54,54,54	0
6	NAG	B	1775	14/15	0.84	0.28	-	72,97,107,109	0
6	NAG	A	1770	14/15	0.84	0.31	-	74,93,115,115	0
6	NAG	B	1773	14/15	0.79	0.23	-	87,129,136,136	0
2	CU	B	1762	1/1	1.00	0.18	-	54,54,54,54	0
6	NAG	A	1771	14/15	0.82	0.24	-	77,97,104,105	0
6	NAG	B	1772	14/15	0.73	0.31	-	103,132,140,141	0
6	NAG	B	1774	14/15	0.55	0.40	-	94,121,135,136	0

6.5 Other polymers [i](#)

There are no such residues in this entry.