



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:40 AM GMT

PDB ID : 2DW0  
Title : Crystal structure of VAP2 from Crotalus atrox venom (Form 2-1 crystal)  
Authors : Takeda, S.; Igarashi, T.; Araki, S.  
Deposited on : 2006-08-02  
Resolution : 2.15 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](mailto: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.

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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

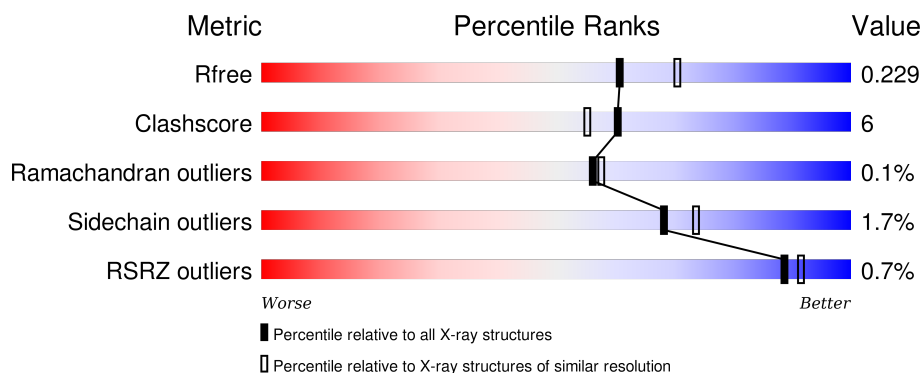
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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	1045 (2.16-2.16)
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)
RSRZ outliers	91569	1050 (2.16-2.16)

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  $\geq 3$ , 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	419	<div> <div></div> <div>87% 11% .</div> </div>
1	B	419	<div> <div></div> <div>87% 11% ..</div> </div>

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7292 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 Catrocollastatin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	S	0	0	0
			3211	1986	543	635	47			
1	B	414	Total	C	N	O	S	0	0	0
			3211	1986	543	635	47			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	203	VAL	PHE	SEE REMARK 999	UNP Q90282
B	203	VAL	PHE	SEE REMARK 999	UNP Q90282

- Molecule 2 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	5	Total	C	N	O	0	0
			64	36	3	25		

- Molecule 3 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	6	Total	C	N	O	0	0
			75	42	3	30		

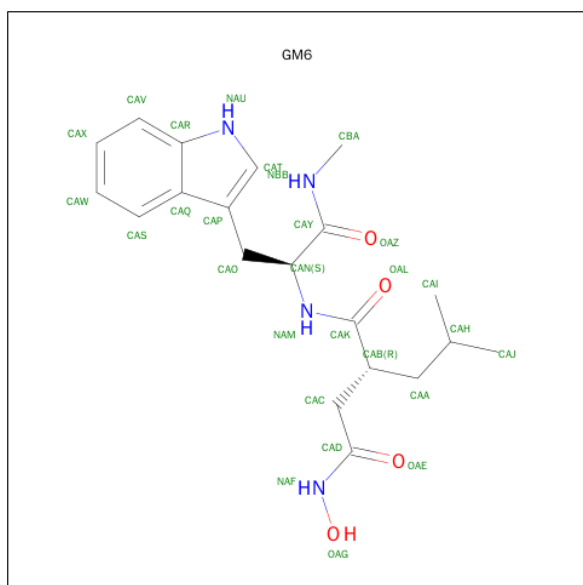
- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 6 is 3-(N-HYDROXYCARBOXAMIDO)-2-ISOBUTYLPROPANOYL-TRP-METHYLAMIDE (three-letter code: GM6) (formula:  $C_{20}H_{28}N_4O_4$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C N O 28 20 4 4	0	0
6	B	1	Total C N O 28 20 4 4	0	0

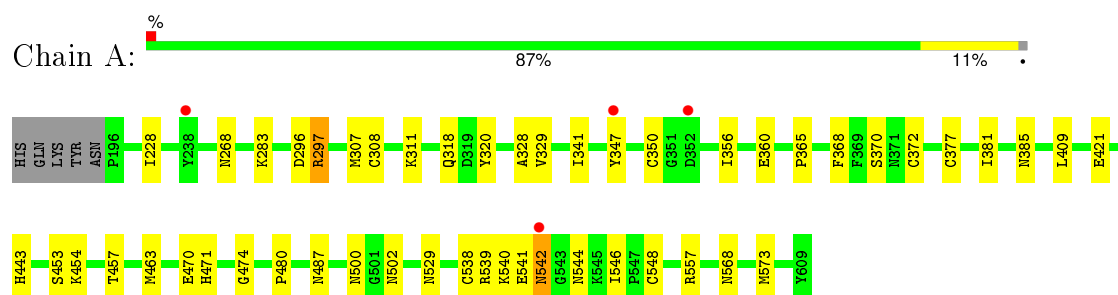
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	315	Total O 315 315	0	0
7	B	352	Total O 352 352	0	0

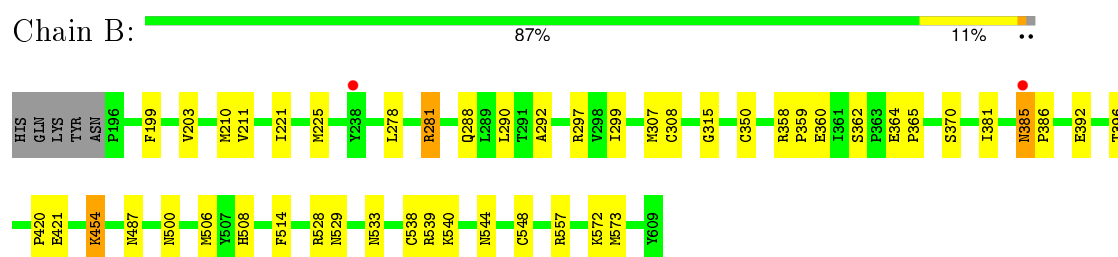
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ( $RSRZ > 2$ ). 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: Catrocollastatin



#### • Molecule 1: Catrocollastatin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.91Å 137.95Å 59.24Å 90.00° 91.52° 90.00°	Depositor
Resolution (Å)	50.00 – 2.15 44.93 – 2.15	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.15) 98.0 (44.93-2.15)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.48 (at 2.16Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.175 , 0.228 0.179 , 0.229	Depositor DCC
$R_{free}$ test set	2418 reflections (4.97%)	DCC
Wilson B-factor (Å <sup>2</sup> )	16.9	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 50.5	EDS
Estimated twinning fraction	0.003 for l,k,-h 0.045 for h,-k,-l 0.020 for l,-k,h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 48635 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7292	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.24% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, BMA, NAG, CA, GM6, 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	0.40	0/3283	0.65	0/4441
1	B	0.41	0/3283	0.65	0/4441
All	All	0.41	0/6566	0.65	0/8882

There are no bond length outliers.

There are no bond angle outliers.

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	3211	0	2981	38	0
1	B	3211	0	2981	34	0
2	A	64	0	55	2	0
3	B	75	0	64	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	3	0	0	0	0
5	B	3	0	0	0	0
6	A	28	0	27	0	0
6	B	28	0	27	3	0
7	A	315	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	352	0	0	4	0
All	All	7292	0	6135	72	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 6.

All (72) 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:B:487:ASN:HD21	1:B:500:ASN:H	1.35	0.74
1:A:487:ASN:HD21	1:A:500:ASN:H	1.34	0.74
1:B:529:ASN:HD21	1:B:557:ARG:HB3	1.55	0.71
1:A:454:LYS:O	1:A:457:THR:HG23	1.90	0.71
1:A:529:ASN:HD21	1:A:557:ARG:HB3	1.58	0.69
1:A:296:ASP:O	1:A:297:ARG:HG3	1.94	0.67
1:B:225:MET:SD	1:B:290:LEU:HD22	2.38	0.63
1:A:470:GLU:HB3	1:A:480:PRO:HG2	1.79	0.63
1:B:487:ASN:ND2	1:B:500:ASN:H	1.96	0.63
1:A:372:CYS:SG	2:A:801:NAG:H82	2.39	0.62
1:B:281:ARG:HH11	1:B:281:ARG:HG2	1.68	0.59
1:A:350:CYS:HB3	1:A:370:SER:HA	1.83	0.59
1:A:487:ASN:ND2	1:A:500:ASN:H	2.03	0.56
1:A:341:ILE:HD11	1:A:377:CYS:HB2	1.87	0.56
1:B:396:THR:HG23	7:B:1055:HOH:O	2.07	0.55
1:B:454:LYS:HD2	1:B:454:LYS:O	2.06	0.55
1:A:421:GLU:HG2	7:A:1119:HOH:O	2.07	0.55
1:B:203:VAL:HG11	1:B:278:LEU:HD21	1.89	0.54
1:A:471:HIS:HD2	7:A:1118:HOH:O	1.92	0.52
1:A:529:ASN:HB3	1:A:548:CYS:SG	2.50	0.52
1:B:299:ILE:HG12	6:B:901:GM6:OAL	2.10	0.52
1:A:463:MET:HE2	1:A:502:ASN:OD1	2.10	0.51
1:A:540:LYS:HA	1:A:544:ASN:O	2.10	0.51
1:B:454:LYS:C	1:B:454:LYS:HD2	2.31	0.51
1:B:514:PHE:CD2	1:B:572:LYS:HE3	2.45	0.51
1:A:268:ASN:HD21	1:A:311:LYS:NZ	2.09	0.50
1:B:381:ILE:O	1:B:385:ASN:HA	2.12	0.50
1:A:487:ASN:HD21	1:A:500:ASN:N	2.07	0.50
1:A:356:ILE:HG12	1:A:368:PHE:O	2.12	0.50
1:B:308:CYS:SG	1:B:386:PRO:HB2	2.52	0.49
1:A:541:GLU:HB2	1:A:546:ILE:HD11	1.95	0.49
1:A:453:SER:O	1:A:474:GLY:HA2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:MET:O	1:A:308:CYS:HB2	2.13	0.49
1:B:364:GLU:O	1:B:364:GLU:HG3	2.12	0.49
1:B:540:LYS:HA	1:B:544:ASN:O	2.13	0.49
1:A:541:GLU:CB	1:A:546:ILE:HD11	2.43	0.48
1:B:211:VAL:HA	1:B:221:ILE:HD11	1.94	0.48
1:A:268:ASN:HD21	1:A:311:LYS:HZ1	1.62	0.47
1:A:318:GLN:O	1:A:320:TYR:N	2.48	0.47
1:B:529:ASN:HB3	1:B:548:CYS:SG	2.54	0.47
1:B:533:ASN:HB2	7:B:990:HOH:O	2.13	0.47
1:A:381:ILE:O	1:A:385:ASN:HA	2.15	0.47
1:B:288:GLN:HE22	1:B:315:GLY:HA3	1.80	0.47
1:A:409:LEU:HD22	1:A:443:HIS:CG	2.50	0.46
1:B:539:ARG:HH11	1:B:539:ARG:HG2	1.80	0.46
1:A:541:GLU:HG3	1:A:546:ILE:CD1	2.46	0.46
1:B:528:ARG:NH1	7:B:1187:HOH:O	2.49	0.46
1:A:541:GLU:HG3	1:A:546:ILE:HD11	1.99	0.45
1:B:362:SER:O	1:B:365:PRO:HD3	2.16	0.45
1:B:297:ARG:HE	6:B:901:GM6:HAX	1.81	0.45
1:B:307:MET:O	1:B:308:CYS:HB2	2.16	0.45
1:A:296:ASP:O	1:A:297:ARG:CG	2.62	0.45
1:B:514:PHE:CE2	1:B:572:LYS:HE3	2.52	0.45
1:A:296:ASP:C	1:A:297:ARG:CG	2.85	0.45
1:A:347:TYR:CD2	2:A:802:NAG:H2	2.52	0.44
1:A:268:ASN:ND2	1:A:311:LYS:NZ	2.66	0.44
1:B:508:HIS:HD2	7:B:943:HOH:O	2.01	0.44
1:A:454:LYS:HG2	1:A:457:THR:CG2	2.48	0.44
1:B:358:ARG:NE	1:B:359:PRO:HD2	2.33	0.44
1:B:281:ARG:HH11	1:B:281:ARG:CG	2.31	0.43
1:A:329:VAL:HG21	1:A:365:PRO:HB2	1.99	0.43
1:B:350:CYS:HB3	1:B:370:SER:HA	2.00	0.43
1:A:283:LYS:O	1:A:283:LYS:HG3	2.19	0.42
1:B:297:ARG:NE	6:B:901:GM6:HAX	2.33	0.42
1:B:420:PRO:HB2	1:B:421:GLU:OE2	2.19	0.42
1:B:210:MET:HA	1:B:292:ALA:HB2	2.02	0.42
1:A:228:ILE:HG23	1:A:328:ALA:HA	2.02	0.42
1:A:541:GLU:CG	1:A:546:ILE:HD11	2.51	0.41
1:B:421:GLU:CD	1:B:421:GLU:H	2.23	0.41
1:A:542:ASN:HD22	1:A:542:ASN:HA	1.65	0.40
1:A:539:ARG:HD2	7:A:1107:HOH:O	2.20	0.40
1:B:199:PHE:CE1	1:B:392:GLU:HG3	2.55	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	412/419 (98%)	394 (96%)	17 (4%)	1 (0%)	52	51
1	B	412/419 (98%)	393 (95%)	19 (5%)	0	100	100
All	All	824/838 (98%)	787 (96%)	36 (4%)	1 (0%)	56	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	297	ARG

### 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	360/365 (99%)	355 (99%)	5 (1%)	74	80
1	B	360/365 (99%)	353 (98%)	7 (2%)	65	69
All	All	720/730 (99%)	708 (98%)	12 (2%)	68	74

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	360	GLU
1	A	538	CYS
1	A	542	ASN
1	A	568	ASN
1	A	573	MET

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Mol	Chain	Res	Type
1	B	281	ARG
1	B	360	GLU
1	B	385	ASN
1	B	454	LYS
1	B	506	MET
1	B	538	CYS
1	B	573	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	230	ASN
1	A	268	ASN
1	A	288	GLN
1	A	449	GLN
1	A	471	HIS
1	A	487	ASN
1	A	529	ASN
1	A	542	ASN
1	A	568	ASN
1	B	288	GLN
1	B	383	ASN
1	B	385	ASN
1	B	422	ASN
1	B	449	GLN
1	B	487	ASN
1	B	500	ASN
1	B	508	HIS
1	B	529	ASN
1	B	568	ASN
1	B	599	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 ⓘ

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	801	1,2	14,14,15	0.53	0	15,19,21	0.85	1 (6%)
2	NAG	A	802	2	14,14,15	0.48	0	15,19,21	0.83	1 (6%)
2	BMA	A	803	2	11,11,12	0.56	0	14,15,17	0.51	0
2	NAG	A	804	2	14,14,15	0.44	0	15,19,21	0.74	1 (6%)
2	MAN	A	805	2	11,11,12	0.57	0	14,15,17	0.55	0
3	NAG	B	801	1,3	14,14,15	0.67	0	15,19,21	1.12	1 (6%)
3	NAG	B	802	3	14,14,15	0.60	0	15,19,21	0.68	0
3	BMA	B	803	3	11,11,12	0.56	0	14,15,17	0.33	0
3	NAG	B	804	3	14,14,15	0.55	0	15,19,21	0.71	1 (6%)
3	MAN	B	805	3	11,11,12	0.54	0	14,15,17	0.61	0
3	MAN	B	807	3	11,11,12	0.58	0	14,15,17	0.65	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	801	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	802	2	-	0/6/23/26	0/1/1/1
2	BMA	A	803	2	-	0/2/19/22	0/1/1/1
2	NAG	A	804	2	-	0/6/23/26	0/1/1/1
2	MAN	A	805	2	-	0/2/19/22	0/1/1/1
3	NAG	B	801	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	802	3	-	0/6/23/26	0/1/1/1
3	BMA	B	803	3	-	0/2/19/22	0/1/1/1
3	NAG	B	804	3	-	0/6/23/26	0/1/1/1
3	MAN	B	805	3	-	0/2/19/22	0/1/1/1
3	MAN	B	807	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	801	NAG	C2-N2-C7	-3.46	118.60	123.04
2	A	802	NAG	C2-N2-C7	-2.60	119.70	123.04
2	A	804	NAG	C2-N2-C7	-2.39	119.97	123.04
2	A	801	NAG	C2-N2-C7	-2.29	120.09	123.04
3	B	804	NAG	C2-N2-C7	-2.25	120.14	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	801	NAG	1	0
2	A	802	NAG	1	0

## 5.6 Ligand geometry

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 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	GM6	A	901	4	28,29,29	1.20	4 (14%)	25,39,39	1.15	4 (16%)
6	GM6	B	901	4	28,29,29	1.29	3 (10%)	25,39,39	1.01	1 (4%)

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	GM6	A	901	4	-	0/27/28/28	0/2/2/2
6	GM6	B	901	4	-	0/27/28/28	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	901	GM6	OAG-NAF	-2.13	1.36	1.39
6	A	901	GM6	CAT-CAP	-2.04	1.34	1.38
6	B	901	GM6	CAW-CAX	2.03	1.43	1.38
6	B	901	GM6	CAW-CAS	2.18	1.41	1.36
6	A	901	GM6	CAW-CAS	2.37	1.42	1.36
6	A	901	GM6	CAX-CAV	2.57	1.42	1.36
6	B	901	GM6	CAX-CAV	2.72	1.42	1.36

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	901	GM6	CAO-CAP-CAT	-2.87	124.43	127.97
6	B	901	GM6	CAN-CAY-NBB	-2.80	112.82	116.99
6	A	901	GM6	CAB-CAK-NAM	-2.61	112.18	116.30
6	A	901	GM6	CBA-NBB-CAY	-2.14	118.35	122.23
6	A	901	GM6	CAN-NAM-CAK	2.40	127.00	121.62

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	901	GM6	3	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	414/419 (98%)	-0.38	4 (0%) 84 88	8, 17, 31, 51	0
1	B	414/419 (98%)	-0.42	2 (0%) 91 93	8, 16, 30, 42	0
All	All	828/838 (98%)	-0.40	6 (0%) 89 91	8, 17, 31, 51	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	238	TYR	3.2
1	A	347	TYR	2.8
1	B	238	TYR	2.8
1	B	385	ASN	2.5
1	A	352	ASP	2.3
1	A	542	ASN	2.0

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	NAG	A	801	14/15	0.87	0.19	0.72	38,42,45,48	0
3	NAG	B	801	14/15	0.93	0.13	0.42	27,30,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	BMA	A	803	11/12	0.64	0.23	-	59,60,61,62	0
2	MAN	A	805	11/12	0.73	0.32	-	62,63,64,65	0
3	BMA	B	803	11/12	0.84	0.22	-	54,58,62,63	0
3	MAN	B	807	11/12	0.68	0.35	-	64,65,66,66	0
3	NAG	B	804	14/15	0.73	0.28	-	57,58,60,60	0
2	NAG	A	804	14/15	0.77	0.24	-	61,63,64,64	0
3	NAG	B	802	14/15	0.93	0.17	-	37,39,43,49	0
3	MAN	B	805	11/12	0.74	0.26	-	66,68,70,70	0
2	NAG	A	802	14/15	0.83	0.19	-	50,51,53,56	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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
6	GM6	A	901	28/28	0.94	0.13	1.28	10,14,29,30	0
6	GM6	B	901	28/28	0.96	0.10	0.21	10,12,14,16	0
5	CA	B	712	1/1	1.00	0.07	-0.24	12,12,12,12	0
5	CA	A	702	1/1	0.99	0.08	-0.59	17,17,17,17	0
5	CA	B	711	1/1	1.00	0.07	-0.96	12,12,12,12	0
5	CA	A	703	1/1	0.99	0.06	-1.47	15,15,15,15	0
5	CA	A	701	1/1	1.00	0.05	-2.08	15,15,15,15	0
5	CA	B	713	1/1	0.99	0.04	-2.80	13,13,13,13	0
4	ZN	B	700	1/1	1.00	0.08	-	13,13,13,13	0
4	ZN	A	700	1/1	1.00	0.09	-	13,13,13,13	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.