



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 09:08 PM GMT

PDB ID : 4ZLP  
Title : Crystal Structure of Notch3 Negative Regulatory Region  
Authors : Xu, X.; Blacklow, S.C.  
Deposited on : 2015-05-01  
Resolution : 2.48 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](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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
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) : rb-20026982

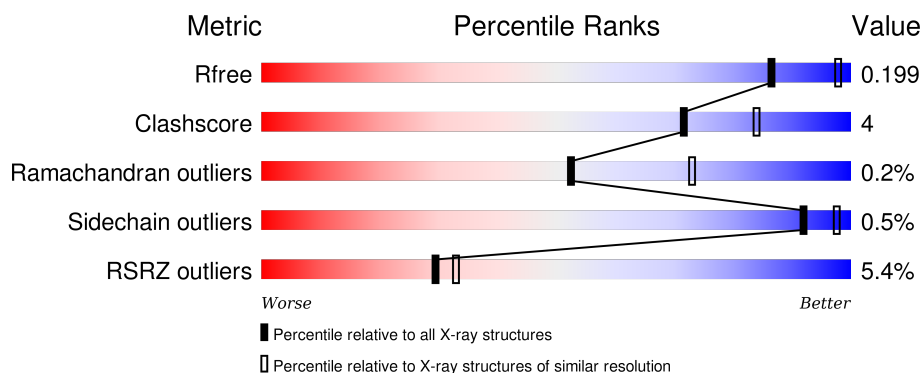
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.48 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	4309 (2.50-2.46)
Clashscore	102246	5050 (2.50-2.46)
Ramachandran outliers	100387	4961 (2.50-2.46)
Sidechain outliers	100360	4963 (2.50-2.46)
RSRZ outliers	91569	4319 (2.50-2.46)

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	271	<div> <div></div> <div>81% 8% 11%</div> </div>
1	B	271	<div> <div>8%</div> <div>72% 8% 20%</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	GOL	A	5008	-	-	-	X
5	GOL	A	5009	-	-	-	X
5	GOL	B	5005	-	-	-	X
6	ACT	A	5010	-	-	-	X
6	ACT	A	5011	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 3694 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 Neurogenic locus notch homolog protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	241	Total	C	N	O	S	0	0	0
			1848	1139	333	354	22			
1	B	218	Total	C	N	O	S	0	0	0
			1602	987	283	311	21			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1641	GLY	-	expression tag	UNP Q9UM47
A	1642	SER	-	expression tag	UNP Q9UM47
A	1643	HIS	-	expression tag	UNP Q9UM47
A	1644	HIS	-	expression tag	UNP Q9UM47
A	1645	HIS	-	expression tag	UNP Q9UM47
A	1646	HIS	-	expression tag	UNP Q9UM47
A	1647	HIS	-	expression tag	UNP Q9UM47
A	1648	HIS	-	expression tag	UNP Q9UM47
B	1641	GLY	-	expression tag	UNP Q9UM47
B	1642	SER	-	expression tag	UNP Q9UM47
B	1643	HIS	-	expression tag	UNP Q9UM47
B	1644	HIS	-	expression tag	UNP Q9UM47
B	1645	HIS	-	expression tag	UNP Q9UM47
B	1646	HIS	-	expression tag	UNP Q9UM47
B	1647	HIS	-	expression tag	UNP Q9UM47
B	1648	HIS	-	expression tag	UNP Q9UM47

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

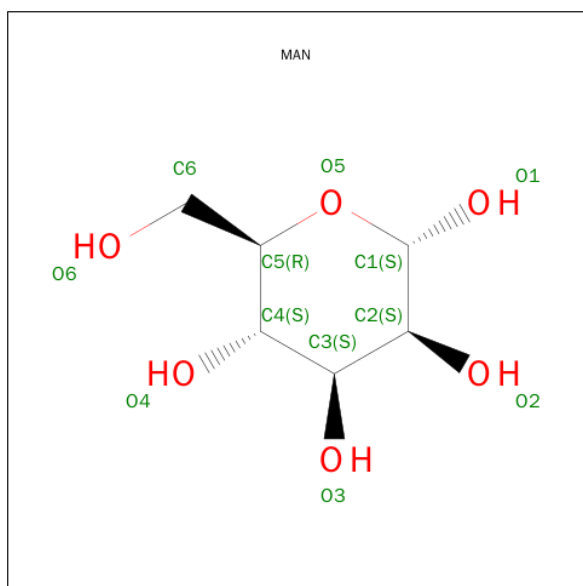
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	Ca	0	0
			3	3		
2	A	3	Total	Ca	0	0
			3	3		

- Molecule 3 is 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	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula:  $C_6H_{12}O_6$ ).



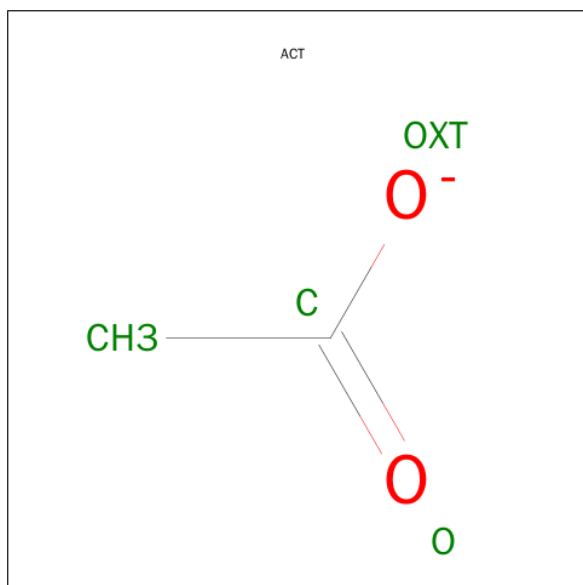
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



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

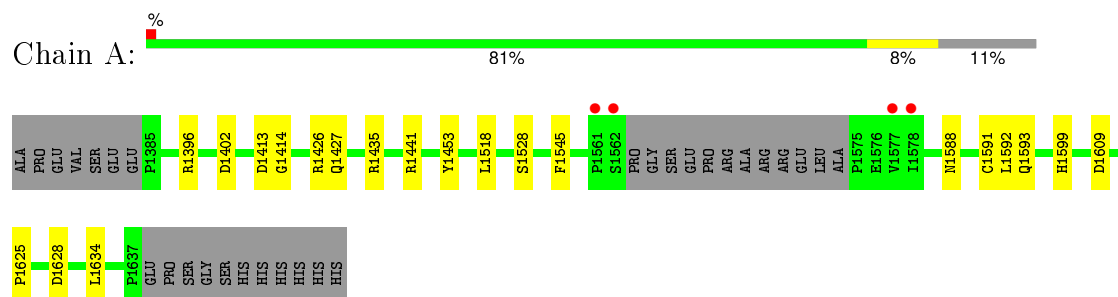
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	126	Total	O	0	0
			126	126		
7	B	22	Total	O	0	0
			22	22		

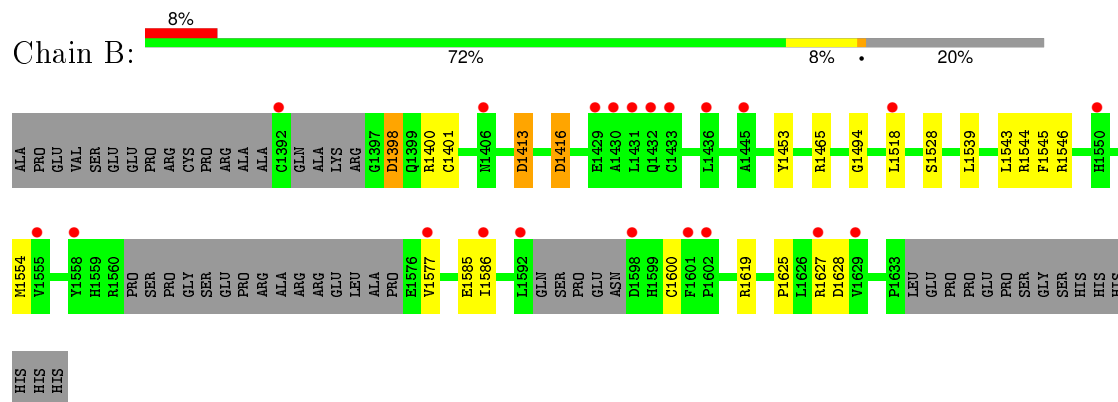
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Neurogenic locus notch homolog protein 3



- Molecule 1: Neurogenic locus notch homolog protein 3





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	122.48Å 64.31Å 83.09Å 90.00° 105.23° 90.00°	Depositor
Resolution (Å)	49.18 – 2.48 49.18 – 2.48	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.18-2.48) 95.5 (49.18-2.48)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.42 (at 2.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.178 , 0.204 0.174 , 0.199	Depositor DCC
$R_{free}$ test set	1089 reflections (5.11%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.1	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 54.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 22317 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3694	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.65% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CA, MAN, NAG, ACT

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	0.42	0/1893	0.57	0/2573
1	B	0.34	0/1635	0.56	3/2224 (0.1%)
All	All	0.39	0/3528	0.57	3/4797 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1416	ASP	CB-CG-OD1	-5.98	112.92	118.30
1	B	1413	ASP	CB-CG-OD2	-5.61	113.25	118.30
1	B	1398	ASP	CB-CG-OD1	-5.00	113.80	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	1848	0	1708	13	0
1	B	1602	0	1424	15	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	28	0	24	0	0
3	B	14	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	22	0	19	1	0
5	A	12	0	16	1	0
5	B	6	0	8	0	0
6	A	8	0	6	0	0
7	A	126	0	0	5	0
7	B	22	0	0	1	0
All	All	3694	0	3218	29	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 4.

The worst 5 of 29 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:1628:ASP:OD1	7:A:5101:HOH:O	1.94	0.86
1:B:1465:ARG:HH12	1:B:1619:ARG:HH21	1.26	0.82
1:B:1627:ARG:NH1	1:B:1628:ASP:OD2	2.16	0.78
1:B:1539:LEU:HD12	1:B:1543:LEU:HD11	1.67	0.76
1:A:1426:ARG:NH1	1:A:1609:ASP:OD1	2.29	0.65

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	237/271 (88%)	230 (97%)	7 (3%)	0	100	100
1	B	211/271 (78%)	202 (96%)	8 (4%)	1 (0%)	34	53
All	All	448/542 (83%)	432 (96%)	15 (3%)	1 (0%)	52	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1577	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	199/228 (87%)	197 (99%)	2 (1%)	82	94
1	B	165/228 (72%)	165 (100%)	0	100	100
All	All	364/456 (80%)	362 (100%)	2 (0%)	92	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1592	LEU
1	A	1634	LEU

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 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 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	$\# Z  > 2$
3	NAG	A	5004	1,3	14,14,15	0.24	0	15,19,21	0.90	1 (6%)
3	NAG	A	5005	3,4	14,14,15	0.64	1 (7%)	15,19,21	0.30	0
4	MAN	A	5006	3,4	11,11,12	0.87	1 (9%)	15,15,17	1.52	2 (13%)
4	MAN	A	5007	4	11,11,12	0.93	1 (9%)	15,15,17	1.26	2 (13%)
5	GOL	A	5008	-	5,5,5	0.24	0	5,5,5	0.72	0
5	GOL	A	5009	-	5,5,5	0.36	0	5,5,5	0.33	0
6	ACT	A	5010	-	0,3,3	0.00	-	0,3,3	0.00	-
6	ACT	A	5011	-	0,3,3	0.00	-	0,3,3	0.00	-
3	NAG	B	5004	1	14,14,15	0.16	0	15,19,21	0.26	0
5	GOL	B	5005	-	5,5,5	0.37	0	5,5,5	0.19	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
3	NAG	A	5004	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	5005	3,4	-	0/6/23/26	0/1/1/1
4	MAN	A	5006	3,4	-	0/2/19/22	1/1/1/1
4	MAN	A	5007	4	-	0/2/19/22	0/1/1/1
5	GOL	A	5008	-	-	0/4/4/4	0/0/0/0
5	GOL	A	5009	-	-	0/4/4/4	0/0/0/0
6	ACT	A	5010	-	-	0/0/0/0	0/0/0/0
6	ACT	A	5011	-	-	0/0/0/0	0/0/0/0
3	NAG	B	5004	1	-	0/6/23/26	0/1/1/1
5	GOL	B	5005	-	-	0/4/4/4	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	5005	NAG	O5-C1	-2.33	1.39	1.43
4	A	5007	MAN	C1-C2	2.19	1.57	1.52
4	A	5006	MAN	O5-C5	2.63	1.49	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	5007	MAN	O2-C2-C3	-2.35	105.46	110.19
4	A	5006	MAN	O5-C1-C2	2.26	114.50	110.89
3	A	5004	NAG	C1-O5-C5	2.32	115.56	112.14
4	A	5007	MAN	C1-O5-C5	3.29	116.97	112.14
4	A	5006	MAN	C1-O5-C5	4.48	118.73	112.14

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	5006	MAN	C1-C2-C3-C4-C5-O5

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	5006	MAN	1	0
5	A	5008	GOL	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 [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	241/271 (88%)	0.13	4 (1%)	73 76	20, 31, 63, 101	0
1	B	218/271 (80%)	0.70	21 (9%)	10 11	29, 73, 109, 137	0
All	All	459/542 (84%)	0.40	25 (5%)	29 33	20, 45, 103, 137	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1445	ALA	5.6
1	B	1555	VAL	3.8
1	B	1601	PHE	3.8
1	B	1598	ASP	3.7
1	B	1430	ALA	3.7

### 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](#)

There are no carbohydrates in this entry.

### 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
5	GOL	A	5009	6/6	0.88	0.32	10.97	59,61,61,62	0
6	ACT	A	5011	4/4	0.73	0.38	8.57	82,83,85,87	0
6	ACT	A	5010	4/4	0.85	0.25	4.95	60,61,62,63	0
5	GOL	A	5008	6/6	0.86	0.27	3.97	35,43,47,50	0
5	GOL	B	5005	6/6	0.89	0.28	2.35	71,73,73,75	0
3	NAG	A	5004	14/15	0.97	0.15	-1.27	16,30,39,53	0
2	CA	A	5003	1/1	0.98	0.12	-1.71	21,21,21,21	0
2	CA	A	5001	1/1	0.90	0.09	-1.72	52,52,52,52	0
2	CA	B	5002	1/1	0.94	0.11	-1.87	72,72,72,72	0
2	CA	A	5002	1/1	0.99	0.14	-2.10	25,25,25,25	0
2	CA	B	5003	1/1	0.98	0.11	-3.32	31,31,31,31	0
2	CA	B	5001	1/1	0.91	0.09	-5.11	204,204,204,204	0
3	NAG	B	5004	14/15	0.81	0.26	-	72,83,90,91	0
4	MAN	A	5006	11/12	0.69	0.20	-	102,109,112,112	0
3	NAG	A	5005	14/15	0.88	0.16	-	61,69,82,93	0
4	MAN	A	5007	11/12	0.66	0.25	-	114,117,118,118	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.