



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 11:53 PM GMT

PDB ID : 1YTV
Title : Maltose-binding protein fusion to a C-terminal fragment of the V1a vasopressin receptor
Authors : Adikesavan, N.V; Mahmood, S.S.; Stanley, S.; Xu, Z.; Wu, N.; Thibonnier, M.; Shoham, M.
Deposited on : 2005-02-11
Resolution : 1.80 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

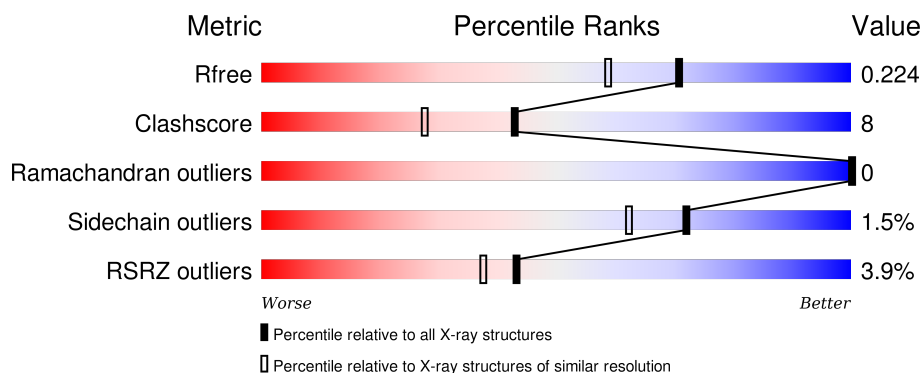
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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	366	<div> <div>3%</div> <div>86%</div> <div>14%</div> </div>
1	B	366	<div> <div>4%</div> <div>80%</div> <div>19%</div> <div>.</div> </div>
2	M	84	<div> <div>4%</div> <div>7%</div> <div>93%</div> </div>
2	N	84	<div> <div>4%</div> <div>6%</div> <div>94%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6445 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 Maltose-binding periplasmic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	366	Total	C	N	O	S	0	0	0
			2842	1831	461	544	6			
1	B	366	Total	C	N	O	S	0	0	0
			2842	1831	461	544	6			

- Molecule 2 is a protein called Vasopressin V1a receptor.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	M	6	Total	C	N	O	0	0	0
			42	21	9	12			
2	N	5	Total	C	N	O	0	0	0
			34	17	7	10			

There are 50 discrepancies between the modelled and reference sequences:

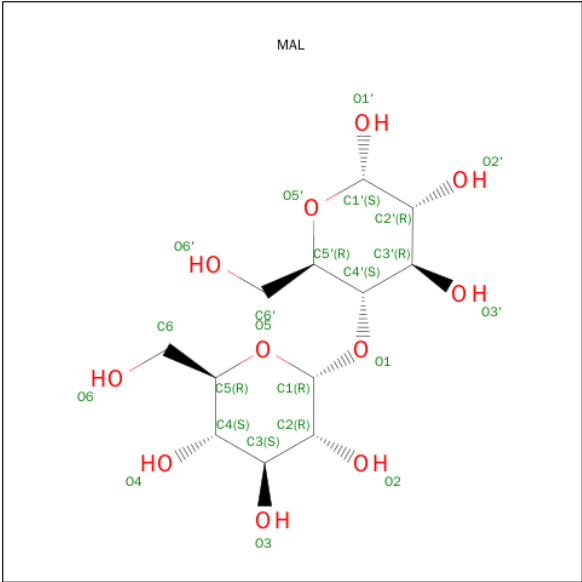
Chain	Residue	Modelled	Actual	Comment	Reference
M	381	ASN	-	LINKER SEQUENCE	UNP P37288
M	382	SER	-	LINKER SEQUENCE	UNP P37288
M	383	SER	-	LINKER SEQUENCE	UNP P37288
M	384	SER	-	LINKER SEQUENCE	UNP P37288
M	385	ASN	-	LINKER SEQUENCE	UNP P37288
M	386	ASN	-	LINKER SEQUENCE	UNP P37288
M	387	ASN	-	LINKER SEQUENCE	UNP P37288
M	388	ASN	-	LINKER SEQUENCE	UNP P37288
M	389	ASN	-	LINKER SEQUENCE	UNP P37288
M	390	ASN	-	LINKER SEQUENCE	UNP P37288
M	391	ASN	-	LINKER SEQUENCE	UNP P37288
M	392	ASN	-	LINKER SEQUENCE	UNP P37288
M	393	ASN	-	LINKER SEQUENCE	UNP P37288
M	394	ASN	-	LINKER SEQUENCE	UNP P37288
M	395	LEU	-	LINKER SEQUENCE	UNP P37288
M	396	GLY	-	LINKER SEQUENCE	UNP P37288

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Chain	Residue	Modelled	Actual	Comment	Reference
M	397	ILE	-	LINKER SEQUENCE	UNP P37288
M	398	GLU	-	LINKER SEQUENCE	UNP P37288
M	399	GLU	-	LINKER SEQUENCE	UNP P37288
M	400	ASN	-	LINKER SEQUENCE	UNP P37288
M	401	LEU	-	LINKER SEQUENCE	UNP P37288
M	402	TYR	-	LINKER SEQUENCE	UNP P37288
M	403	PHE	-	LINKER SEQUENCE	UNP P37288
M	404	GLN	-	LINKER SEQUENCE	UNP P37288
M	405	GLY	-	LINKER SEQUENCE	UNP P37288
N	381	ASN	-	LINKER SEQUENCE	UNP P37288
N	382	SER	-	LINKER SEQUENCE	UNP P37288
N	383	SER	-	LINKER SEQUENCE	UNP P37288
N	384	SER	-	LINKER SEQUENCE	UNP P37288
N	385	ASN	-	LINKER SEQUENCE	UNP P37288
N	386	ASN	-	LINKER SEQUENCE	UNP P37288
N	387	ASN	-	LINKER SEQUENCE	UNP P37288
N	388	ASN	-	LINKER SEQUENCE	UNP P37288
N	389	ASN	-	LINKER SEQUENCE	UNP P37288
N	390	ASN	-	LINKER SEQUENCE	UNP P37288
N	391	ASN	-	LINKER SEQUENCE	UNP P37288
N	392	ASN	-	LINKER SEQUENCE	UNP P37288
N	393	ASN	-	LINKER SEQUENCE	UNP P37288
N	394	ASN	-	LINKER SEQUENCE	UNP P37288
N	395	LEU	-	LINKER SEQUENCE	UNP P37288
N	396	GLY	-	LINKER SEQUENCE	UNP P37288
N	397	ILE	-	LINKER SEQUENCE	UNP P37288
N	398	GLU	-	LINKER SEQUENCE	UNP P37288
N	399	GLU	-	LINKER SEQUENCE	UNP P37288
N	400	ASN	-	LINKER SEQUENCE	UNP P37288
N	401	LEU	-	LINKER SEQUENCE	UNP P37288
N	402	TYR	-	LINKER SEQUENCE	UNP P37288
N	403	PHE	-	LINKER SEQUENCE	UNP P37288
N	404	GLN	-	LINKER SEQUENCE	UNP P37288
N	405	GLY	-	LINKER SEQUENCE	UNP P37288

- Molecule 3 is SUGAR (MALTOSE) (three-letter code: MAL) (formula: C₁₂H₂₂O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			22	12	10		
3	B	1	Total	C	O	0	0
			22	12	10		

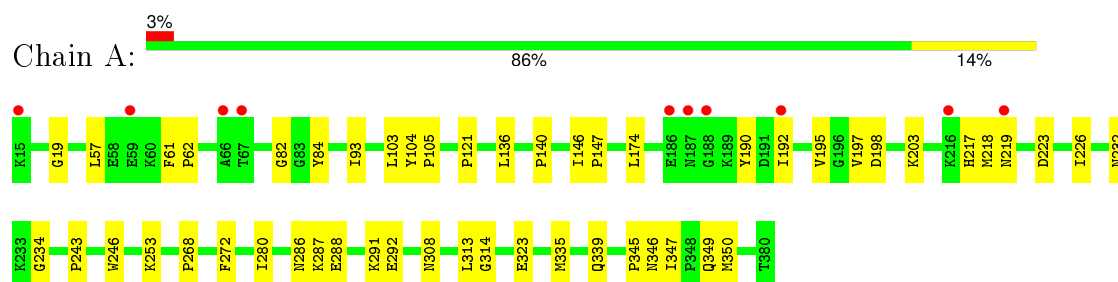
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	337	Total	O	0	0
			337	337		
4	B	296	Total	O	0	0
			296	296		
4	M	6	Total	O	0	0
			6	6		
4	N	2	Total	O	0	0
			2	2		

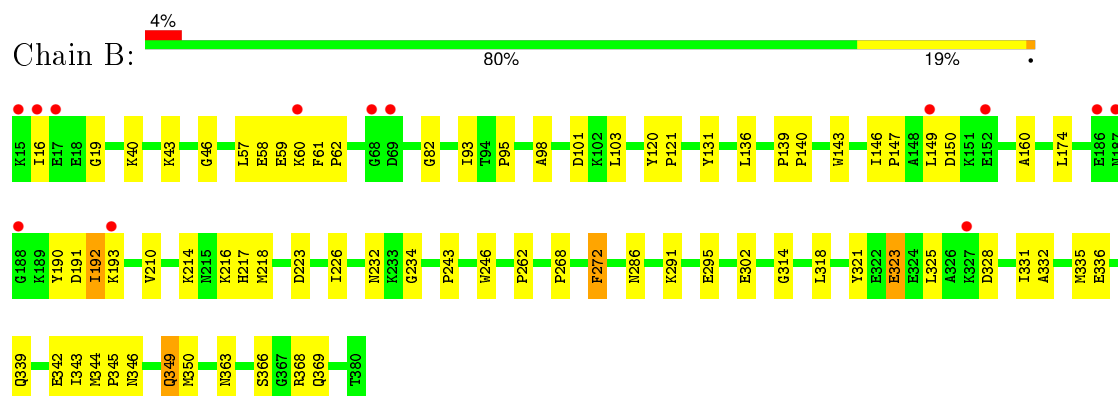
3 Residue-property plots [i](#)

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.

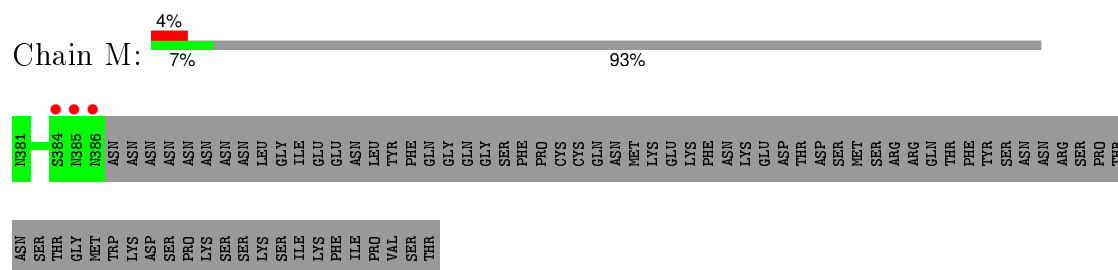
- Molecule 1: Maltose-binding periplasmic protein



- Molecule 1: Maltose-binding periplasmic protein



- Molecule 2: Vasopressin V1a receptor



- Molecule 2: Vasopressin V1a receptor



S381	ASN
S382	ASN
S383	ASN
S384	ASN
S385	ASN
S386	ASN
S387	ASN
S388	ASN
S389	ASN
S390	ASN
S391	ASN
S392	ASN
S393	ASN
S394	ASN
S395	ASN
S396	ASN
S397	ASN
S398	ASN
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S586	ASN
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S588	ASN
S589	ASN
S590	ASN
S591	ASN
S592	ASN
S593	ASN
S594	ASN
S595	ASN
S5	

THR	ASN	SER	THR	GLY	MET	TRP	LYS	ASP	SER	PRO	LYS	SER	SER	LYS	SER	ILE	LYS	PHE	ILE	PRO	VAL	SER	THR
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.10 Å 66.56 Å 115.72 Å 90.00° 95.99° 90.00°	Depositor
Resolution (Å)	34.43 – 1.80 34.43 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.5 (34.43-1.80) 99.6 (34.43-1.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 1.81 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.199 , 0.225 0.199 , 0.224	Depositor DCC
R_{free} test set	3609 reflections (5.07%)	DCC
Wilson B-factor (Å ²)	18.7	Xtriage
Anisotropy	0.532	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 56.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 71204 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6445	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MAL

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	0.32	0/2911	0.54	0/3952
1	B	0.32	0/2911	0.53	0/3952
2	M	0.30	0/41	0.45	0/54
2	N	0.44	0/33	0.74	0/43
All	All	0.32	0/5896	0.54	0/8001

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 [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	2842	0	2812	39	0
1	B	2842	0	2812	59	0
2	M	42	0	32	0	0
2	N	34	0	26	0	0
3	A	22	0	20	0	0
3	B	22	0	20	0	0
4	A	337	0	0	8	0
4	B	296	0	0	10	0
4	M	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	N	2	0	0	0	0
All	All	6445	0	5722	95	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 8.

The worst 5 of 95 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:93:ILE:HG22	1:A:291:LYS:HE3	1.40	1.02
1:B:16:ILE:H	1:B:16:ILE:HD12	1.35	0.89
1:A:314:GLY:HA3	4:A:892:HOH:O	1.79	0.81
1:A:136:LEU:HD21	1:A:140:PRO:HD3	1.68	0.76
1:A:345:PRO:HG2	1:A:350:MET:SD	2.26	0.76

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	364/366 (100%)	360 (99%)	4 (1%)	0	100	100
1	B	364/366 (100%)	357 (98%)	7 (2%)	0	100	100
2	M	4/84 (5%)	2 (50%)	2 (50%)	0	100	100
2	N	3/84 (4%)	3 (100%)	0	0	100	100
All	All	735/900 (82%)	722 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	293/293 (100%)	290 (99%)	3 (1%)	82	77
1	B	293/293 (100%)	287 (98%)	6 (2%)	63	49
2	M	6/80 (8%)	6 (100%)	0	100	100
2	N	5/80 (6%)	5 (100%)	0	100	100
All	All	597/746 (80%)	588 (98%)	9 (2%)	72	62

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	192	ILE
1	B	349	GLN
1	B	272	PHE
1	A	323	GLU
1	B	216	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	339	GLN
1	A	349	GLN
1	B	296	ASN
1	A	296	ASN
1	A	308	ASN

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](#)

2 ligands 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	$\# Z > 2$
3	MAL	A	401	-	23,23,24	0.93	1 (4%)	33,33,35	1.52	5 (15%)
3	MAL	B	402	-	23,23,24	0.98	2 (8%)	33,33,35	1.48	5 (15%)

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	MAL	A	401	-	-	0/8/45/48	0/2/2/2
3	MAL	B	402	-	-	0/8/45/48	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	402	MAL	C2'-C3'	2.02	1.55	1.52
3	B	402	MAL	O5'-C5'	2.16	1.48	1.43
3	A	401	MAL	O5'-C5'	2.20	1.48	1.43

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	402	MAL	O2'-C2'-C3'	-3.77	102.54	110.12
3	A	401	MAL	O2'-C2'-C3'	-3.68	102.71	110.12
3	B	402	MAL	O6'-C6'-C5'	-3.09	101.12	111.33
3	A	401	MAL	C2'-C3'-C4'	-3.08	104.19	110.56

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	B	402	MAL	C2'-C3'-C4'	-2.95	104.44	110.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	366/366 (100%)	0.09	10 (2%) 58 53	11, 19, 35, 50	0
1	B	366/366 (100%)	0.14	13 (3%) 46 40	11, 19, 36, 56	0
2	M	6/84 (7%)	2.59	3 (50%) 0 0	22, 36, 63, 68	0
2	N	5/84 (5%)	2.84	3 (60%) 0 0	26, 27, 50, 54	0
All	All	743/900 (82%)	0.15	29 (3%) 43 37	11, 19, 36, 68	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	15	LYS	10.7
1	B	16	ILE	9.6
2	N	385	ASN	7.7
2	M	386	ASN	6.5
1	B	68	GLY	6.4

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, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	MAL	B	402	22/23	0.95	0.10	-0.27	8,12,16,17	0
3	MAL	A	401	22/23	0.94	0.10	-0.40	10,13,17,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.