



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 05:16 pm GMT

PDB ID : 3Q2V  
Title : Crystal structure of mouse E-cadherin ectodomain  
Authors : Jin,X.; Harrison, O.J.; Shapiro, L.  
Deposited on : 2010-12-20  
Resolution : 3.40 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	:	1.7.2 (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

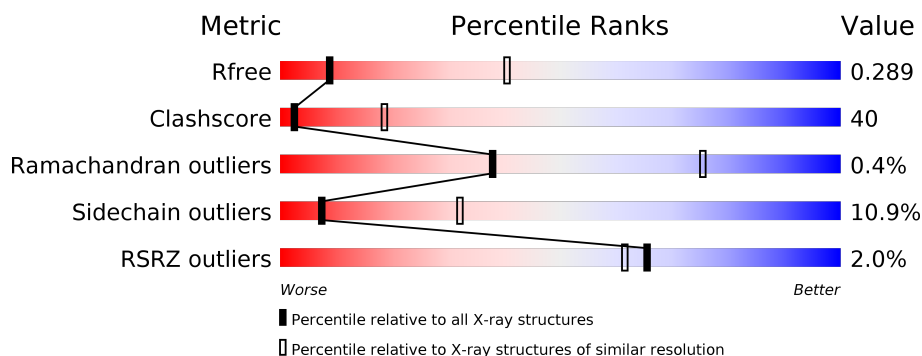
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 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	1679 (3.50-3.30)
Clashscore	112137	1832 (3.50-3.30)
Ramachandran outliers	110173	1789 (3.50-3.30)
Sidechain outliers	110143	1789 (3.50-3.30)
RSRZ outliers	101464	1709 (3.50-3.30)

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	550	<div> <div>2%</div> <div>41%</div> <div>48%</div> <div>8%</div> <div>.</div> </div>
1	B	550	<div> <div>2%</div> <div>33%</div> <div>41%</div> <div>5%</div> <div>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
2	CA	A	601	-	-	-	X
2	CA	B	601	-	-	-	X
4	MAN	A	802	X	-	-	X
4	MAN	A	804	X	-	-	-
4	MAN	A	805	X	-	-	X
4	MAN	A	806	X	-	-	-
4	MAN	A	807	X	-	-	-
4	MAN	A	809	-	-	-	X
4	MAN	B	801	X	-	-	-
4	MAN	B	803	X	-	-	-
4	MAN	B	804	X	-	-	X
4	MAN	B	805	X	-	-	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7871 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 Cadherin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	532	Total	C	N	O	S	0	1	0
			4113	2581	683	838	11			
1	B	440	Total	C	N	O	S	0	0	0
			3399	2138	553	701	7			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	545	HIS	-	EXPRESSION TAG	UNP P09803
A	546	HIS	-	EXPRESSION TAG	UNP P09803
A	547	HIS	-	EXPRESSION TAG	UNP P09803
A	548	HIS	-	EXPRESSION TAG	UNP P09803
A	549	HIS	-	EXPRESSION TAG	UNP P09803
A	550	HIS	-	EXPRESSION TAG	UNP P09803
B	545	HIS	-	EXPRESSION TAG	UNP P09803
B	546	HIS	-	EXPRESSION TAG	UNP P09803
B	547	HIS	-	EXPRESSION TAG	UNP P09803
B	548	HIS	-	EXPRESSION TAG	UNP P09803
B	549	HIS	-	EXPRESSION TAG	UNP P09803
B	550	HIS	-	EXPRESSION TAG	UNP P09803

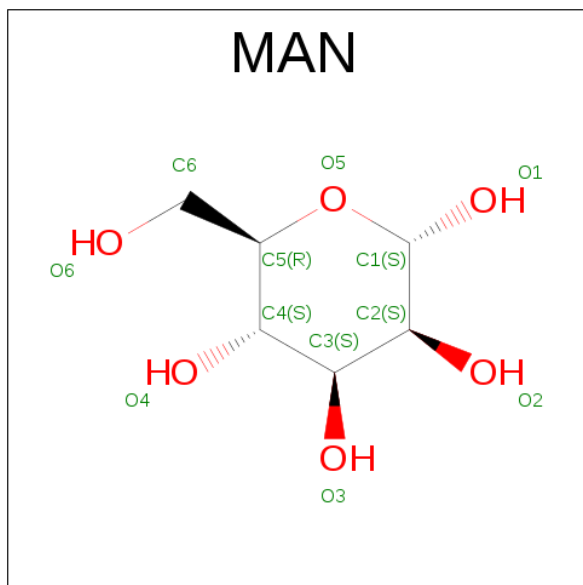
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	12	Total	Ca	0	0
			12	12		
2	A	12	Total	Ca	0	0
			12	12		

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mn	0	0
			1	1		
3	A	1	Total	Mn	0	0
			1	1		

- Molecule 4 is SUGAR (ALPHA-D-MANNOSE) (three-letter code: MAN) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).



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		
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		

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

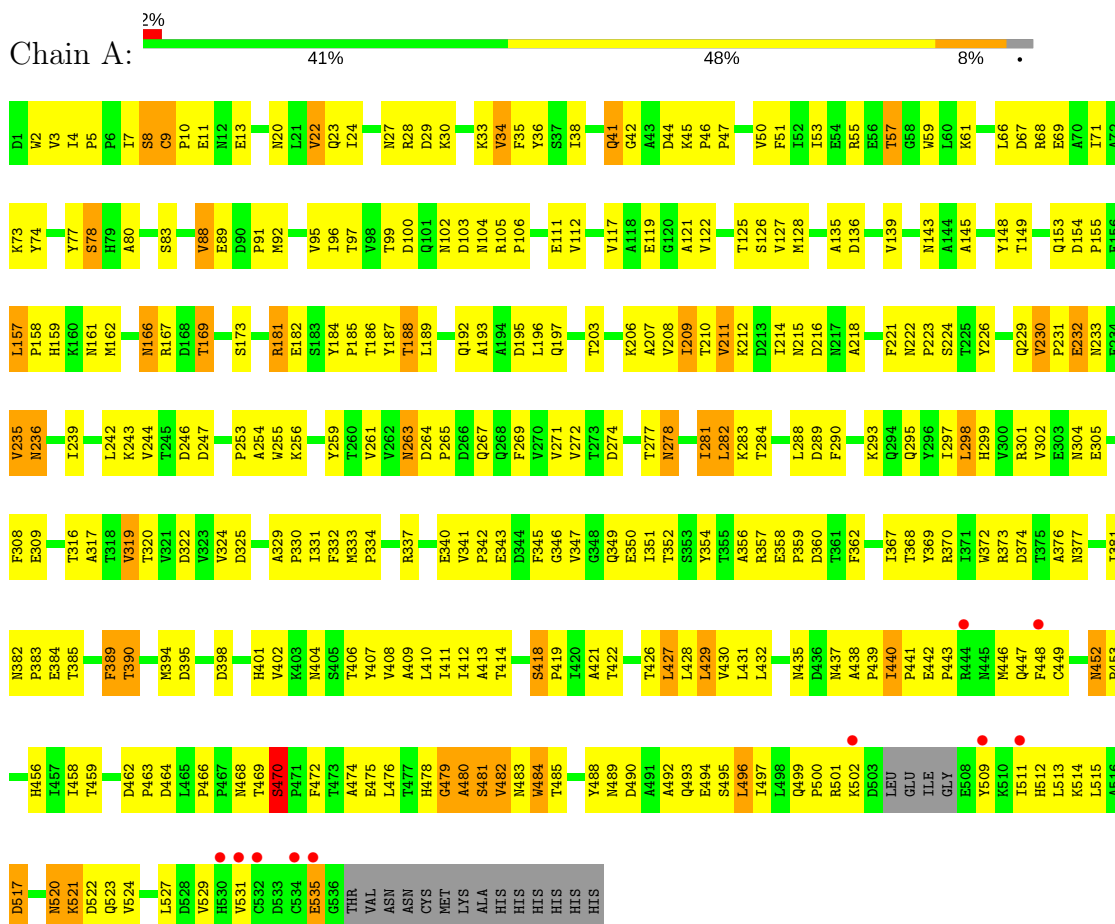
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	55	Total	O	0	0
			55	55		
5	B	80	Total	O	0	0
			80	80		

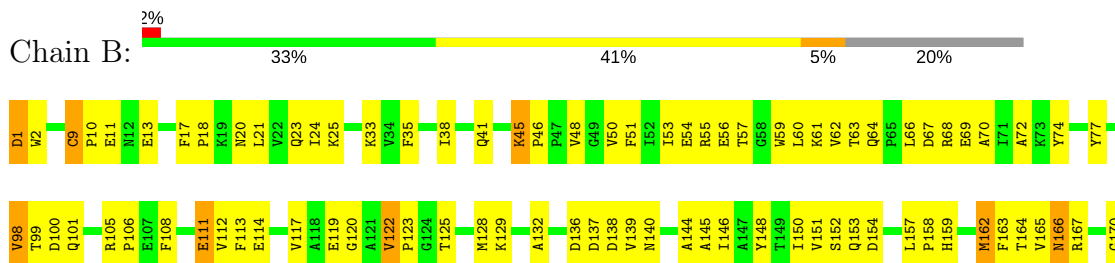
### 3 Residue-property plots

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: Cadherin-1



#### • Molecule 1: Cadherin-1



LEU	PRO	E380	V313	R238	V171
LYS	GLN	I381	P314	I239	
LEU	PRO	N382	S315	A240	L175
ALA	HIS	F383	T316	T241	T176
ASP	ILE	E384	A317	L242	S177
ASN	ILE	T385		K243	
GLN	THR	G386	T320	V244	D180
ASN	ILE	A387	V321	T245	R181
LEU	LEU	I388	D322	D246	E182
	D462	F389	V323	D247	S183
	P463	T390	V324	D248	Y184
	D464	R391	D325	A249	P185
	L465	A392	V326	P250	T186
	P466	E393	N327	N251	Y187
	P467	R394	E328	T252	T189
LEU	ASN	D395	A329	P253	L189
ASP	THR	R396	P330	A254	V190
VAL	HIS	E397	I331	W255	V191
HIS	SER	D398	F332	K256	Q192
VAL	PRO				A193
CYS	PHE	T406	R337	T260	A194
ASP	THR		R338	V261	D195
ASP	ALA	L410	V339	V262	L196
CYS	GLU	I411	E340	N263	Q197
GLU	LEU	I412	V341		G198
GLY	THR		P342	V271	
THR	HIS	A413	E343		E199
VAL	GLY	T414	D344	D274	G200
ASN	ALA	D415	F345		L201
ASN	ALA	D416	G346	T277	S202
CYS	SER	G417	V347	N278	T203
MET	VAL	S418	Q348	D279	
LYS	ASN	P419	Q349	G280	K206
ALA	TRP	I420	E350	I281	A207
HIS	THR	A421	I351	L282	V208
HIS	ILE	T422	T352		I209
HIS	GLU		T353	G287	T210
HIS	TYR		S353		V211
HIS	ASN	L429	V354	L288	K212
HIS	ASP	V430	T355	D289	D213
	ALA	L431	A356	P290	I214
	ALA	L432	R357		N215
	GLN	D433	E358	K293	D216
	GLU	V434	P359	Q294	N217
	SER	ASN	D360	Q295	A218
	LEU	ASP	T361	Y296	P219
	ILE	ASN	F362	L297	V220
	LEU	ALA	M363	L298	F221
	GLN	PRO	D364	H299	N222
	PRO	ILE	Q365	V300	P223
	ARG	PRO		R301	
	ARG	GLU		V302	
	LYS	PRO	T368	E303	Y226
	ASP	ARG	Y369	N304	Q227
	LEU	ASN	R370	E305	G228
	GLU	ILE	I371	Q229	
	GLY	GLN	A372	E306	V230
	GLY	R373	D374	P307	P231
	TYR	PHE		F308	E232
	LYS	GLN		E309	
	ILE	ARG	W378		V235
	HIS	ASN	L379	L312	



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	119.14Å 79.70Å 176.00Å 90.00° 98.56° 90.00°	Depositor
Resolution (Å)	19.92 – 3.40 29.78 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.92-3.40) 99.6 (29.78-3.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.40 (at 3.31Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.6_289)	Depositor
R, $R_{free}$	0.230 , 0.293 0.229 , 0.289	Depositor DCC
$R_{free}$ test set	1140 reflections (5.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	69.5	Xtriage
Anisotropy	0.638	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 71.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	7871	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.30% 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, 0.333 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: CA, MN, 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	0.45	0/4200	0.71	10/5755 (0.2%)
1	B	0.47	1/3469 (0.0%)	0.67	3/4752 (0.1%)
All	All	0.46	1/7669 (0.0%)	0.69	13/10507 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	419	PRO	N-CD	5.03	1.54	1.47

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	492	ALA	N-CA-CB	-11.52	93.98	110.10
1	A	452	ASN	N-CA-CB	7.71	124.47	110.60
1	A	452	ASN	N-CA-C	-7.34	91.18	111.00
1	B	419	PRO	N-CA-C	-6.72	94.62	112.10
1	B	418	SER	C-N-CD	-5.80	107.84	120.60

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	4113	0	3949	353	0
1	B	3399	0	3284	269	0
2	A	12	0	0	0	0
2	B	12	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	99	0	90	1	0
4	B	99	0	90	5	0
5	A	55	0	0	1	0
5	B	80	0	0	0	0
All	All	7871	0	7413	612	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 40.

The worst 5 of 612 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:483:ASN:CG	1:A:502:LYS:HB2	1.46	1.33
1:A:483:ASN:OD1	1:A:502:LYS:HB2	1.23	1.31
1:B:418:SER:HB2	1:B:419:PRO:CD	1.61	1.30
1:A:483:ASN:OD1	1:A:502:LYS:CB	1.81	1.29
1:B:418:SER:CB	1:B:419:PRO:HD3	1.76	1.15

There are no symmetry-related clashes.

## 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	529/550 (96%)	454 (86%)	72 (14%)	3 (1%)	28	68
1	B	436/550 (79%)	387 (89%)	48 (11%)	1 (0%)	51	84
All	All	965/1100 (88%)	841 (87%)	120 (12%)	4 (0%)	38	75

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	480	ALA
1	A	481	SER
1	A	482	VAL
1	B	419	PRO

### 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	458/482 (95%)	410 (90%)	48 (10%)	8	34
1	B	381/482 (79%)	337 (88%)	44 (12%)	6	29
All	All	839/964 (87%)	747 (89%)	92 (11%)	7	31

5 of 92 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	484	TRP
1	B	56	GLU
1	B	385	THR
1	A	496	LEU
1	A	531	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	299	HIS
1	A	489	ASN
1	B	263	ASN
1	A	382	ASN
1	A	452	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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 44 ligands modelled in this entry, 26 are monoatomic - leaving 18 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	$\# Z  > 2$
4	MAN	A	801	1	11,11,12	0.54	0	13,15,17	1.18	1 (7%)
4	MAN	A	802	1	11,11,12	0.62	0	13,15,17	0.88	0
4	MAN	A	803	1	11,11,12	0.71	0	13,15,17	0.84	1 (7%)
4	MAN	A	804	1	11,11,12	0.55	0	13,15,17	0.94	1 (7%)
4	MAN	A	805	1	11,11,12	0.59	0	13,15,17	0.75	0
4	MAN	A	806	1	11,11,12	0.55	0	13,15,17	0.88	1 (7%)
4	MAN	A	807	1	11,11,12	0.57	0	13,15,17	1.11	2 (15%)
4	MAN	A	808	1	11,11,12	0.56	0	13,15,17	0.97	1 (7%)
4	MAN	A	809	1	11,11,12	0.57	0	13,15,17	0.92	1 (7%)
4	MAN	B	801	1	11,11,12	0.63	0	13,15,17	0.69	0
4	MAN	B	802	1	11,11,12	0.56	0	13,15,17	0.90	1 (7%)
4	MAN	B	803	1	11,11,12	0.68	0	13,15,17	0.77	1 (7%)
4	MAN	B	804	1	11,11,12	0.73	0	13,15,17	1.26	1 (7%)
4	MAN	B	805	1	11,11,12	0.60	0	13,15,17	0.73	0
4	MAN	B	806	1	11,11,12	0.62	0	13,15,17	0.92	1 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	MAN	B	807	1	11,11,12	0.65	0	13,15,17	0.80	0
4	MAN	B	808	1	11,11,12	0.61	0	13,15,17	0.73	0
4	MAN	B	809	1	11,11,12	0.58	0	13,15,17	0.79	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
4	MAN	A	801	1	-	0/2/19/22	0/1/1/1
4	MAN	A	802	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	A	803	1	-	0/2/19/22	0/1/1/1
4	MAN	A	804	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	A	805	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	A	806	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	A	807	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	A	808	1	-	0/2/19/22	0/1/1/1
4	MAN	A	809	1	-	0/2/19/22	0/1/1/1
4	MAN	B	801	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	B	802	1	-	0/2/19/22	0/1/1/1
4	MAN	B	803	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	B	804	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	B	805	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	B	806	1	-	0/2/19/22	0/1/1/1
4	MAN	B	807	1	-	0/2/19/22	0/1/1/1
4	MAN	B	808	1	-	0/2/19/22	0/1/1/1
4	MAN	B	809	1	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	803	MAN	C1-C2-C3	2.06	112.26	109.65
4	B	806	MAN	C1-C2-C3	2.07	112.28	109.65
4	A	807	MAN	C3-C4-C5	2.16	114.02	110.22
4	A	804	MAN	C1-O5-C5	2.23	115.23	112.17
4	A	807	MAN	C1-O5-C5	2.25	115.26	112.17

5 of 9 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	801	MAN	C1
4	B	805	MAN	C1
4	A	805	MAN	C1
4	A	802	MAN	C1
4	B	804	MAN	C1

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	804	MAN	1	0
4	B	804	MAN	4	0
4	B	805	MAN	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	532/550 (96%)	-0.22	10 (1%) 67 63	25, 59, 123, 157	0
1	B	440/550 (80%)	-0.16	9 (2%) 65 61	32, 61, 112, 131	0
All	All	972/1100 (88%)	-0.19	19 (1%) 65 61	25, 60, 116, 157	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	509	TYR	4.9
1	A	448	PHE	3.2
1	A	532	CYS	3.0
1	A	534	CYS	3.0
1	B	467	PRO	2.9

### 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
4	MAN	A	802	11/12	0.88	0.42	6.47	59,63,79,91	0
4	MAN	B	804	11/12	0.69	0.46	5.97	91,100,120,132	0
2	CA	B	601	1/1	0.93	0.18	4.33	44,44,44,44	0
4	MAN	A	809	11/12	0.89	0.37	2.81	87,91,98,112	0
2	CA	A	601	1/1	0.96	0.22	2.54	41,41,41,41	0
4	MAN	A	805	11/12	0.85	0.28	2.52	66,69,89,95	0
2	CA	A	604	1/1	0.95	0.20	1.49	35,35,35,35	0
4	MAN	A	803	11/12	0.88	0.21	0.98	50,69,77,78	0
4	MAN	B	805	11/12	0.85	0.27	0.89	79,84,96,96	0
4	MAN	A	804	11/12	0.95	0.18	0.61	47,60,76,80	0
4	MAN	B	807	11/12	0.83	0.33	0.46	106,117,122,129	0
3	MN	B	901	1/1	0.98	0.22	0.25	54,54,54,54	0
4	MAN	A	808	11/12	0.81	0.23	0.21	72,85,90,98	0
2	CA	A	612	1/1	0.91	0.16	0.08	74,74,74,74	0
2	CA	A	605	1/1	0.83	0.16	-0.01	31,31,31,31	0
4	MAN	B	801	11/12	0.91	0.19	-0.09	55,60,72,73	0
4	MAN	A	807	11/12	0.83	0.26	-0.11	74,85,90,91	0
2	CA	A	610	1/1	0.82	0.16	-0.18	74,74,74,74	0
4	MAN	B	809	11/12	0.88	0.19	-0.68	95,99,112,113	0
2	CA	A	602	1/1	0.98	0.13	-0.75	35,35,35,35	0
4	MAN	B	802	11/12	0.88	0.18	-0.82	67,71,81,83	0
2	CA	A	607	1/1	0.89	0.10	-0.91	72,72,72,72	0
2	CA	B	605	1/1	0.93	0.14	-0.96	38,38,38,38	0
2	CA	A	611	1/1	0.97	0.09	-1.36	81,81,81,81	0
2	CA	B	602	1/1	0.92	0.12	-1.60	38,38,38,38	0
2	CA	A	603	1/1	0.94	0.11	-1.72	39,39,39,39	0
2	CA	B	609	1/1	0.80	0.12	-1.75	105,105,105,105	0
2	CA	B	606	1/1	0.93	0.07	-1.86	55,55,55,55	0
2	CA	A	606	1/1	0.94	0.09	-1.86	35,35,35,35	0
2	CA	A	608	1/1	0.84	0.10	-1.88	58,58,58,58	0
2	CA	A	609	1/1	0.96	0.04	-1.96	87,87,87,87	0
2	CA	B	603	1/1	0.98	0.09	-2.09	38,38,38,38	0
2	CA	B	607	1/1	0.85	0.07	-3.38	87,87,87,87	0
4	MAN	A	801	11/12	0.94	0.20	-	44,48,59,71	0
2	CA	B	604	1/1	0.97	0.12	-	37,37,37,37	0
4	MAN	B	806	11/12	0.79	0.28	-	99,109,124,129	0
4	MAN	B	808	11/12	0.87	0.21	-	114,123,126,127	0
4	MAN	A	806	11/12	0.80	0.32	-	73,88,105,107	0
4	MAN	B	803	11/12	0.90	0.31	-	72,93,114,121	0
2	CA	B	610	1/1	0.81	0.09	-	93,93,93,93	0
2	CA	B	611	1/1	0.81	0.17	-	104,104,104,104	0
3	MN	A	901	1/1	0.99	0.27	-	59,59,59,59	0
2	CA	B	608	1/1	0.93	0.10	-	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CA	B	612	1/1	0.82	0.09	-	89,89,89,89	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.