



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 22, 2024 – 06:49 AM EDT

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

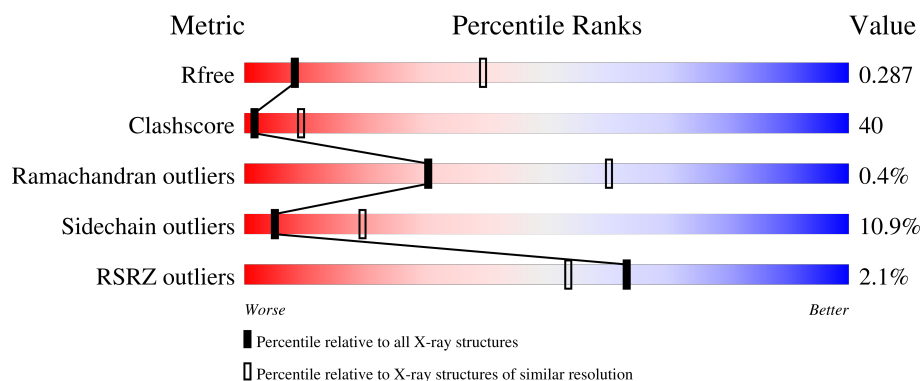
1 Overall quality at a glance

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}	164625	1140 (3.46-3.34)
Clashscore	180529	1172 (3.46-3.34)
Ramachandran outliers	177936	1172 (3.46-3.34)
Sidechain outliers	177891	1172 (3.46-3.34)
RSRZ outliers	164620	1140 (3.46-3.34)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	
1	B	550	

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
4	MAN	A	802	X	-	-	-
4	MAN	A	804	X	-	-	-
4	MAN	A	805	X	-	-	-
4	MAN	A	806	X	-	-	-
4	MAN	A	807	X	-	-	-
4	MAN	B	801	X	-	-	-
4	MAN	B	803	X	-	-	-
4	MAN	B	804	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

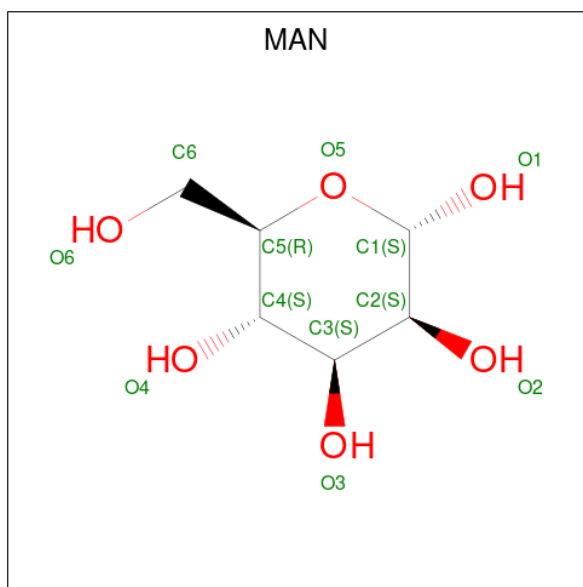
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	12	Total	Ca	0	0
			12	12		
2	B	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	A	1	Total	Mn	0	0
			1	1		
3	B	1	Total	Mn	0	0
			1	1		

- Molecule 4 is alpha-D-mannopyranose (three-letter code: MAN) (formula: C₆H₁₂O₆).



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		

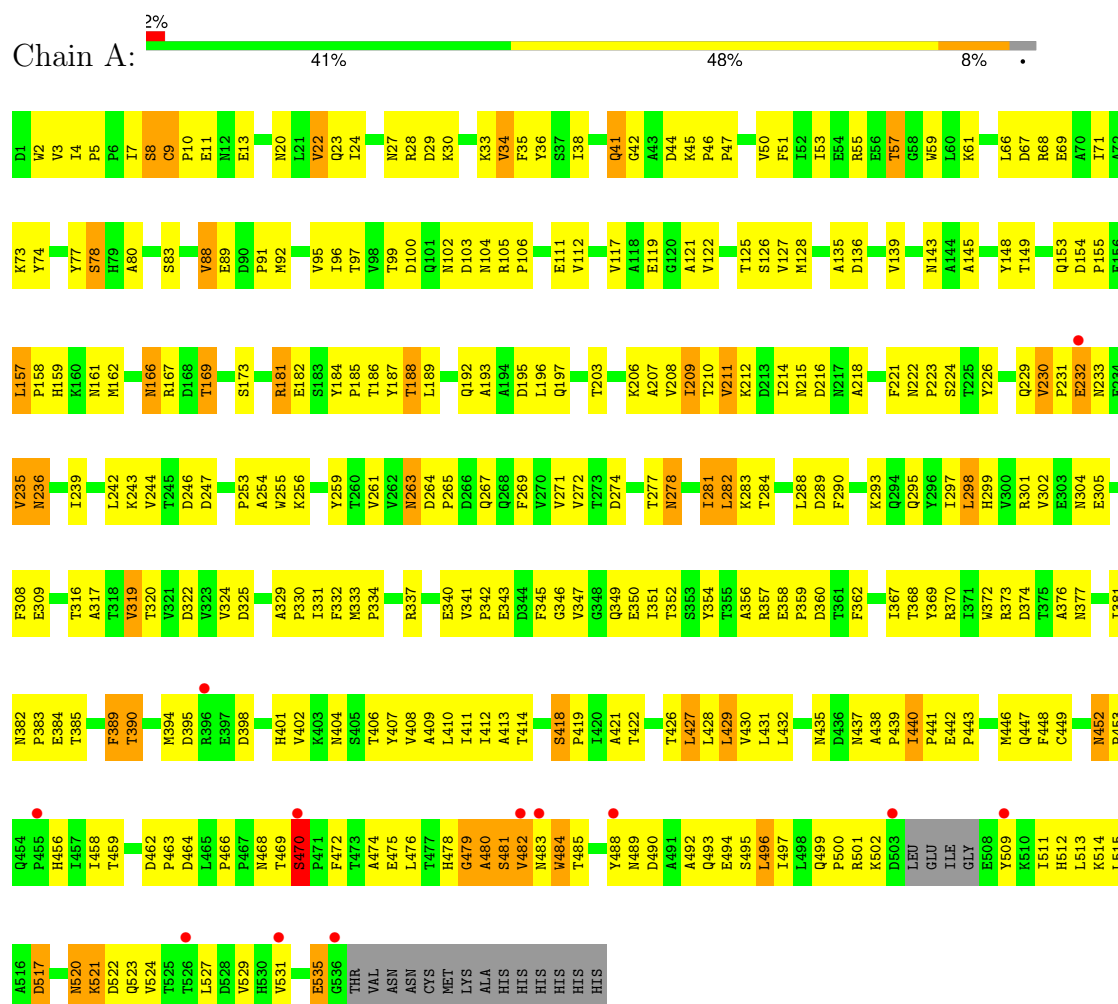
- Molecule 5 is water.

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

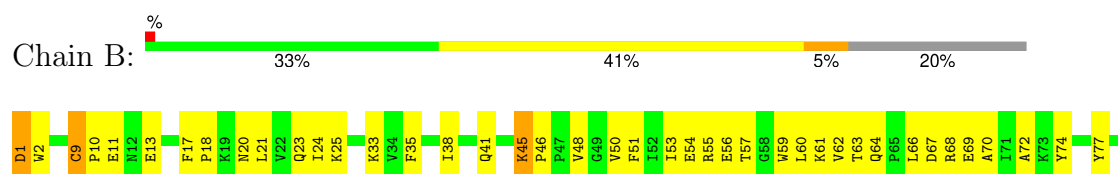
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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	V98
LYS	GLN	I381	P314	I239	L175	T99
LEU	PRO	N382	S315	A240	T176	D100
ALA	HIS	E384	T316	T241	S177	Q101
ASP	ILE	T385	A317	L242	●	R105
ASN	THR	G386	K243	P250		P106
GLN	THR	T388	T320	V244	E107	F108
ASN	LEU	I387	V321	T245	E182	●
LYS	LEU	I388	D322	D246	S183	
ASP	D462	F389	V323	D247	Y184	E111
GLN	P463	T390	V324	D248	P185	V112
VAL	D464	R391	D325	A249	T186	F113
THR	L465	A392	V326	P250	Y187	E114
THR	P466	E393	N327	N251	T188	●
LEU	P467	M394	E328	T252	L189	
ASP	ASN	D395	A329	P253	V190	V117
VAL	THR	R396	P330	A254	V191	A118
HIS	SER	E397	I331	W255	Q192	E119
HIS	PRO	D398	F332	K256	A193	G120
CYS	PHE	●	●	●	A194	A121
ASP	THR	T406	R337	T260	A194	V122
CYS	ALA	R338	V261	D195	P123	V122
GLU	GLU	L410	V339	V262	L196	G124
GLY	LEU	I411	E340	N263	Q197	T125
THR	THR	I412	V341	●	G198	●
VAL	HIS	A413	P342	V271	E199	
ASN	GLY	T414	E343	G200	M128	K129
ASN	ALA	D415	D344	D274	L201	●
CYS	SER	D416	F345	●	S202	
MET	VAL	G417	G346	T277	T203	●
LYS	ASN	N378	V347	N278	K206	D136
ALA	TRP	P419	Q348	D279	A207	D137
THR	THR	I420	Q349	G280	V208	D138
HIS	ILE	A421	E350	I281	L209	V139
HIS	GLU	T422	I351	L282	T210	N140
HIS	TYR	●	T352	●	●	●
HIS	ASN	L429	S353	G287	V211	A144
ASP	ASP	V430	Y354	L288	K212	A145
ALA	ALA	L431	T355	D289	D213	I146
ALA	ALA	L432	A356	F290	T214	I147
GLN	GLN	D433	E357	N215	A147	Y148
GLU	GLU	V434	E358	K293	D216	T149
SER	SER	ASN	P359	Q294	N217	I150
LEU	LEU	ASP	D360	Q295	A218	V151
ILE	ILE	ASN	T361	Y296	P219	S152
LEU	LEU	ALA	F362	I297	V220	Q153
GLN	PRO	PRO	M363	L298	F221	D154
PRO	PRO	ILE	D364	H299	N222	●
ARG	ARG	PRO	Q365	V300	P223	L157
LYS	LYS	GLU	●	R301	●	P158
ASP	ASP	PRO		V302		H159
LEU	LEU	ARG	T366	E303	Y226	●
GLU	GLU	ASN	R370	N304	Q227	M162
ILE	ILE	MET	I371	E305	Q229	F163
GLY	GLY	GLN	A372	E306	V230	T164
GLU	GLU	PHE	R373	F307	T231	V165
TYR	TYR	CYS	D374	F308	E232	M166
LYS	LYS	GLN	●	E309	●	R167
ILE	ILE	ARG	W378	V235		G170
HIS	HIS	ASN	L379	L312	●	●

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	119.14Å 79.70Å 176.00Å 90.00° 98.56° 90.00°	Depositor
Resolution (Å)	19.92 – 3.40 19.92 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.92-3.40) 99.3 (19.92-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 3.31Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6_289)	Depositor
R, R_{free}	0.230 , 0.293 0.229 , 0.287	Depositor DCC
R_{free} test set	1137 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	69.5	Xtriage
Anisotropy	0.638	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 61.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	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 ²)	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.*

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: MN, MAN, CA

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:HB2	1:B:419:PRO:HD2	1.23	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%)	22	50
1	B	436/550 (79%)	387 (89%)	48 (11%)	1 (0%)	44	72
All	All	965/1100 (88%)	841 (87%)	120 (12%)	4 (0%)	30	60

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%)	5	21
1	B	381/482 (79%)	337 (88%)	44 (12%)	4	17
All	All	839/964 (87%)	747 (89%)	92 (11%)	5	19

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

Mol	Chain	Res	Type
1	B	154	ASP
1	B	260	THR
1	B	166	ASN
1	B	222	ASN
1	B	290	PHE

Sometimes 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	489	ASN
1	B	64	GLN
1	B	263	ASN
1	A	520	ASN
1	B	110	GLN

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 oligosaccharides 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	808	1	11,11,12	0.55	0	15,15,17	0.90	1 (6%)
4	MAN	A	809	1	11,11,12	0.56	0	15,15,17	0.86	1 (6%)
4	MAN	B	807	1	11,11,12	0.64	0	15,15,17	0.72	0
4	MAN	A	803	1	11,11,12	0.70	0	15,15,17	0.80	1 (6%)
4	MAN	A	805	1	11,11,12	0.58	0	15,15,17	0.68	0
4	MAN	A	802	1	11,11,12	0.62	0	15,15,17	0.76	0
4	MAN	A	804	1	11,11,12	0.54	0	15,15,17	0.87	1 (6%)
4	MAN	A	807	1	11,11,12	0.56	0	15,15,17	1.03	2 (13%)
4	MAN	B	809	1	11,11,12	0.57	0	15,15,17	0.73	0
4	MAN	B	802	1	11,11,12	0.55	0	15,15,17	0.85	1 (6%)
4	MAN	A	801	1	11,11,12	0.53	0	15,15,17	1.12	1 (6%)
4	MAN	A	806	1	11,11,12	0.55	0	15,15,17	0.81	1 (6%)
4	MAN	B	801	1	11,11,12	0.62	0	15,15,17	0.61	0
4	MAN	B	803	1	11,11,12	0.67	0	15,15,17	0.72	0
4	MAN	B	805	1	11,11,12	0.59	0	15,15,17	0.65	0
4	MAN	B	806	1	11,11,12	0.61	0	15,15,17	0.80	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MAN	B	804	1	11,11,12	0.71	0	15,15,17	1.17	1 (6%)
4	MAN	B	808	1	11,11,12	0.61	0	15,15,17	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
4	MAN	A	808	1	-	0/2/19/22	0/1/1/1
4	MAN	A	809	1	-	2/2/19/22	0/1/1/1
4	MAN	B	807	1	-	2/2/19/22	0/1/1/1
4	MAN	A	803	1	-	2/2/19/22	0/1/1/1
4	MAN	A	805	1	1/1/4/5	2/2/19/22	0/1/1/1
4	MAN	A	802	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	A	804	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	B	809	1	-	2/2/19/22	0/1/1/1
4	MAN	B	802	1	-	2/2/19/22	0/1/1/1
4	MAN	B	805	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	A	806	1	1/1/4/5	2/2/19/22	0/1/1/1
4	MAN	B	801	1	1/1/4/5	2/2/19/22	0/1/1/1
4	MAN	B	803	1	1/1/4/5	2/2/19/22	0/1/1/1
4	MAN	A	801	1	-	2/2/19/22	0/1/1/1
4	MAN	B	806	1	-	2/2/19/22	0/1/1/1
4	MAN	B	804	1	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	B	808	1	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	801	MAN	C1-O5-C5	3.77	117.24	112.19
4	B	804	MAN	C1-C2-C3	3.27	114.41	109.64
4	A	808	MAN	C1-O5-C5	2.57	115.63	112.19
4	A	809	MAN	C1-O5-C5	2.52	115.57	112.19
4	B	802	MAN	C1-O5-C5	2.38	115.37	112.19

5 of 9 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	802	MAN	C1
4	A	804	MAN	C1
4	A	805	MAN	C1
4	A	806	MAN	C1
4	A	807	MAN	C1

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	806	MAN	O5-C5-C6-O6
4	B	807	MAN	O5-C5-C6-O6
4	A	806	MAN	C4-C5-C6-O6
4	A	805	MAN	C4-C5-C6-O6
4	B	806	MAN	O5-C5-C6-O6

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	805	MAN	1	0
4	B	804	MAN	4	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	532/550 (96%)	-0.04	12 (2%) 61 51	17, 59, 123, 157	1 (0%)
1	B	440/550 (80%)	0.07	8 (1%) 67 58	32, 61, 112, 131	0
All	All	972/1100 (88%)	0.01	20 (2%) 63 53	17, 60, 116, 157	1 (0%)

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	509	TYR	4.9
1	B	432	LEU	3.6
1	B	433	ASP	3.2
1	A	531	VAL	3.0
1	B	368	THR	2.8

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 monosaccharides 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. 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	B-factors(\AA^2)	Q<0.9
4	MAN	B	808	11/12	0.48	0.13	114,123,126,127	0
4	MAN	B	804	11/12	0.49	0.25	91,100,120,132	0
4	MAN	B	807	11/12	0.55	0.19	106,117,122,129	0
4	MAN	B	806	11/12	0.57	0.13	99,109,124,129	0
2	CA	B	611	1/1	0.63	0.12	104,104,104,104	0
4	MAN	B	802	11/12	0.70	0.15	67,71,81,83	0
4	MAN	A	809	11/12	0.71	0.20	87,91,98,112	0
4	MAN	B	805	11/12	0.72	0.13	79,84,96,96	0
4	MAN	A	806	11/12	0.72	0.16	73,88,105,107	0
4	MAN	A	805	11/12	0.76	0.15	66,69,89,95	0
4	MAN	A	808	11/12	0.77	0.15	72,85,90,98	0
4	MAN	B	803	11/12	0.78	0.18	72,93,114,121	0
4	MAN	B	809	11/12	0.79	0.12	95,99,112,113	0
4	MAN	A	802	11/12	0.80	0.18	59,63,79,91	0
2	CA	B	609	1/1	0.81	0.09	105,105,105,105	0
4	MAN	A	803	11/12	0.82	0.11	50,69,77,78	0
2	CA	B	612	1/1	0.83	0.12	89,89,89,89	0
4	MAN	B	801	11/12	0.83	0.11	55,60,72,73	0
4	MAN	A	807	11/12	0.84	0.14	74,85,90,91	0
4	MAN	A	804	11/12	0.88	0.18	47,60,76,80	0
2	CA	B	608	1/1	0.89	0.12	81,81,81,81	0
4	MAN	A	801	11/12	0.91	0.09	44,48,59,71	0
2	CA	A	608	1/1	0.91	0.08	58,58,58,58	0
2	CA	B	610	1/1	0.92	0.10	93,93,93,93	0
2	CA	B	604	1/1	0.93	0.09	37,37,37,37	0
2	CA	B	601	1/1	0.93	0.14	44,44,44,44	0
2	CA	B	606	1/1	0.94	0.07	55,55,55,55	0
2	CA	A	605	1/1	0.94	0.07	31,31,31,31	0
2	CA	B	605	1/1	0.94	0.07	38,38,38,38	0
2	CA	B	602	1/1	0.95	0.07	38,38,38,38	0
2	CA	A	610	1/1	0.95	0.10	74,74,74,74	0
2	CA	A	604	1/1	0.95	0.09	35,35,35,35	0
2	CA	A	606	1/1	0.96	0.07	35,35,35,35	0
2	CA	A	607	1/1	0.96	0.09	72,72,72,72	0
3	MN	B	901	1/1	0.96	0.14	54,54,54,54	0
3	MN	A	901	1/1	0.97	0.14	59,59,59,59	0
2	CA	A	601	1/1	0.97	0.18	41,41,41,41	0
2	CA	A	603	1/1	0.97	0.07	39,39,39,39	0
2	CA	B	607	1/1	0.97	0.07	87,87,87,87	0
2	CA	A	611	1/1	0.97	0.06	81,81,81,81	0
2	CA	B	603	1/1	0.98	0.05	38,38,38,38	0
2	CA	A	609	1/1	0.98	0.03	87,87,87,87	0
2	CA	A	612	1/1	0.98	0.09	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CA	A	602	1/1	0.99	0.08	35,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.