



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:53 AM GMT

PDB ID : 2OLV
Title : Structural Insight Into the Transglycosylation Step Of Bacterial Cell Wall Biosynthesis : Donor Ligand Complex
Authors : Lovering, A.L.; De Castro, L.; Lim, D.; Strynadka, N.C.J.
Deposited on : 2007-01-19
Resolution : 2.80 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

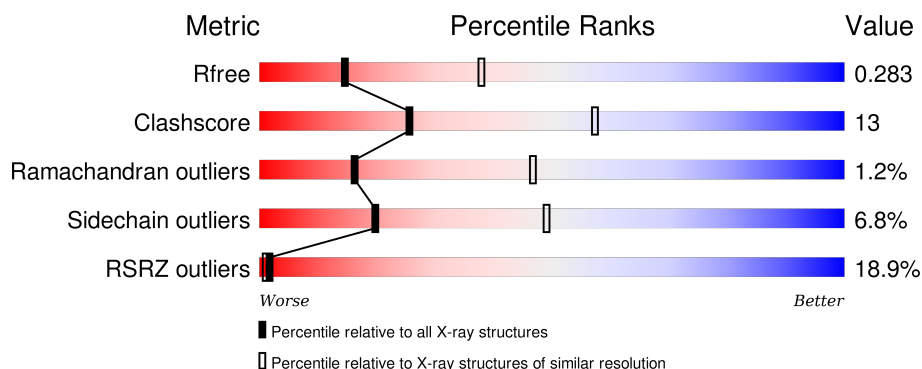
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	669	<div> <div>19%</div> <div>66%</div> <div>24%</div> <div>•</div> <div>8%</div> </div>
1	B	669	<div> <div>16%</div> <div>69%</div> <div>21%</div> <div>•</div> <div>8%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9878 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 Penicillin-binding protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	617	Total	C	N	O	Se	0	0	0
			4851	3038	837	964	12			
1	B	618	Total	C	N	O	Se	0	0	0
			4859	3042	839	966	12			

There are 30 discrepancies between the modelled and reference sequences:

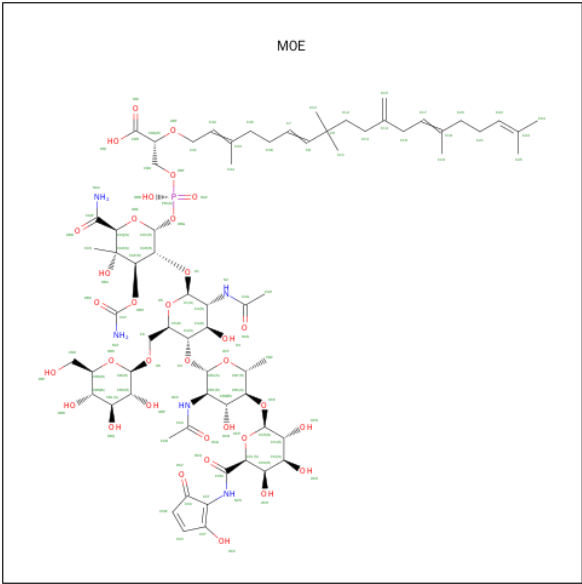
Chain	Residue	Modelled	Actual	Comment	Reference
A	59	MSE	-	SEE REMARK 999	UNP Q2YY56
A	106	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
A	257	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
A	285	PRO	ALA	VARIANT	UNP Q2YY56
A	311	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
A	335	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
A	413	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
A	439	THR	VAL	VARIANT	UNP Q2YY56
A	548	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
A	555	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
A	559	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
A	580	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
A	618	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
A	622	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
A	652	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
B	59	MSE	-	SEE REMARK 999	UNP Q2YY56
B	106	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
B	257	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
B	285	PRO	ALA	VARIANT	UNP Q2YY56
B	311	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
B	335	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
B	413	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
B	439	THR	VAL	VARIANT	UNP Q2YY56
B	548	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
B	555	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56

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Chain	Residue	Modelled	Actual	Comment	Reference
B	559	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
B	580	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
B	618	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
B	622	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56
B	652	MSE	MET	MODIFIED RESIDUE	UNP Q2YY56

- Molecule 2 is MOENOMYCIN (three-letter code: M0E) (formula: C₆₉H₁₀₆N₅O₃₄P).

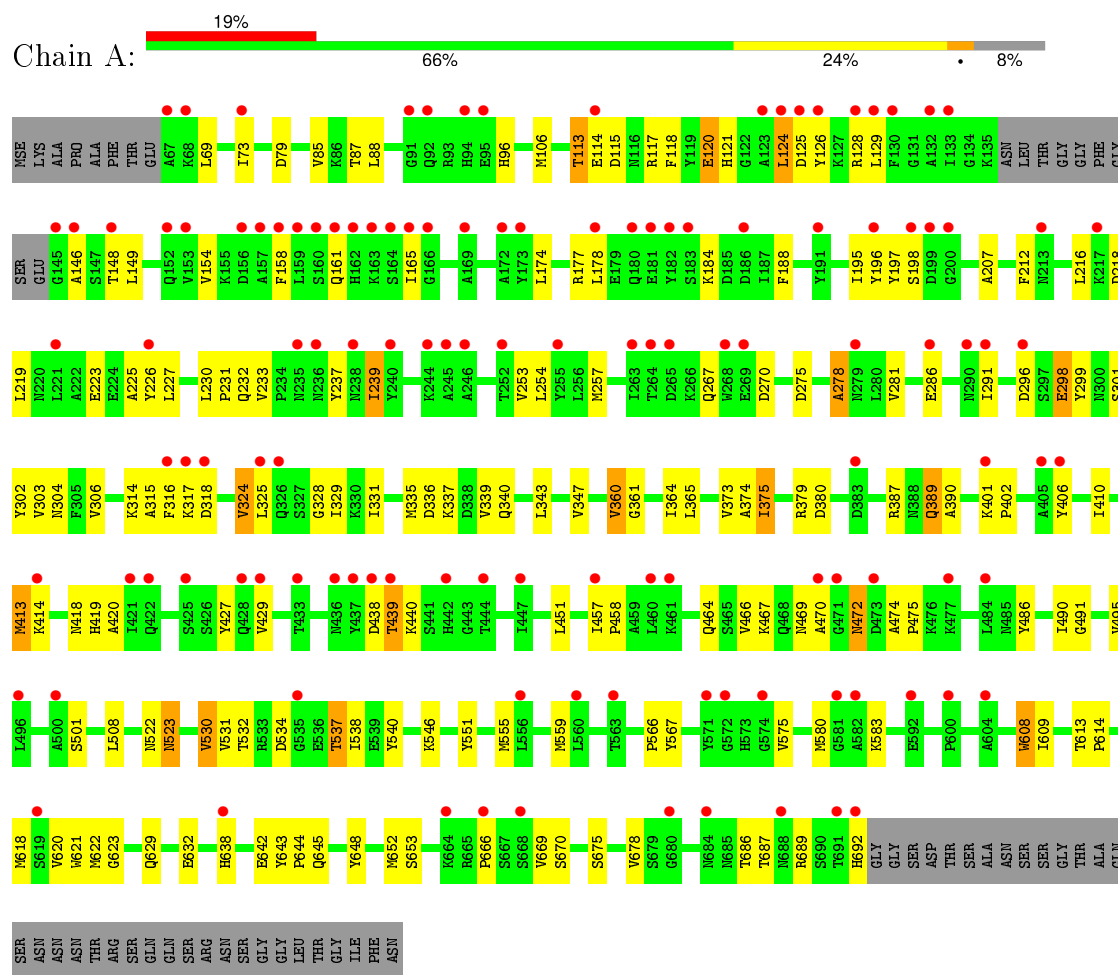


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	84	44	5	34	1	0	0
2	B	1	84	44	5	34	1	0	0

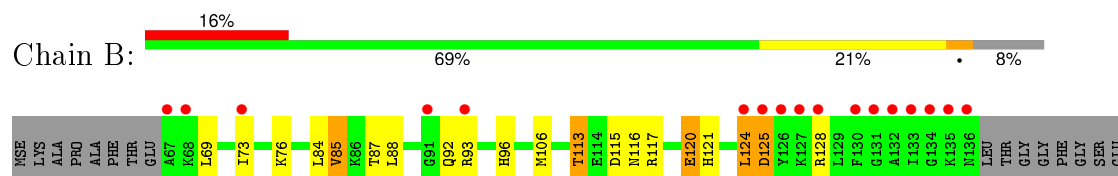
3 Residue-property plots

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 ($RSRZ > 2$). 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: Penicillin-binding protein 2



• Molecule 1: Penicillin-binding protein 2



ASN	A570	T439	M335	V233	G145
SER	G574	I447	D336	P234	A146
SER	V575	Y448	K337	N235	S147
GLY	S576	D449	I364	N236	T148
ALA	M580	A450	L365	Y237	L149
GLN	G581	L451	K368	N238	T150
SER	G585	S454	L372	I239	Q151
ASN	M598	F455	V373	K244	V154
ASN	M598	I457	A374	A246	K155
THR	V607	P458	I375	R249	D156
ARG	M608	A459	R379	K250	A157
SER	M609	W463	D380	V253	F158
GLN	M613	Q464	D383	L254	L159
SER	T613	S465	V384	M257	S160
ARG	M621	V466	V385	R261	Q161
ASN	G629	A470	N386	R262	H162
SER	G629	G471	R387	K265	K163
GLY	T635	N472	N388	K266	S164
THR	T635	D473	Q389	Q267	I165
GLY	S639	A474	A390	K272	G166
TLE	V651	P475	I391	D275	R167
PHE	M652	Y486	D392	L280	K168
ASN	M652	E487	S398	V281	A172
	D659	I490	K401	N290	Y173
	F663	G491	P402	I291	L174
	M664	E494	Y406	A278	Y176
	M665	S501	A409	N279	R177
	P666	S504	M413	L280	L178
	V669	T520	K414	Y302	E179
	S675	Y521	W415	V303	Q180
	I676	T537	A416	N304	E181
	M677	D541	T417	Y299	Y182
	V678	M555	N418	Y302	S183
	M684	D550	H419	V302	I187
	M685	Y551	A420	V303	F188
	T686	M555	I421	N304	I195
	T687	L556	Q422	N313	Y196
	M688	A557	D423	K314	Y197
	M689	E558	E424	A315	S198
	S690	T691	S425	F316	D199
	T691	M559	Y427	K317	G200
	M692	T563	Q428	D318	Y210
GLY	GLY	Y567	S432	L321	Y211
GLY	SER	G568	M436	Q326	F212
SER	THR	S569	Y437	S327	L219
THR	THR		S327	G328	N220
ALA	ALA		D438		E223

4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	79.56 Å 212.21 Å 91.64 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.15 – 2.80 44.14 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (44.15-2.80) 99.9 (44.14-2.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.81 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.231 , 0.280 0.236 , 0.283	Depositor DCC
R_{free} test set	1955 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	58.9	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 74.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 39038 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	9878	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.35% 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: M0E

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	0.56	0/4943	0.63	0/6662
1	B	0.54	0/4951	0.65	1/6673 (0.0%)
All	All	0.55	0/9894	0.64	1/13335 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
All	All	0	3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	372	LEU	CB-CG-CD1	-5.87	101.03	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	120	GLU	Peptide
1	A	608	TRP	Peptide
1	B	120	GLU	Peptide

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	4851	0	4666	124	1
1	B	4859	0	4672	109	0
2	A	84	0	62	6	0
2	B	84	0	62	5	0
All	All	9878	0	9462	242	1

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 13.

The worst 5 of 242 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:253:VAL:HG12	1:A:257:MSE:HE2	1.18	1.14
1:A:254:LEU:HA	1:A:257:MSE:HE3	1.45	0.97
1:B:253:VAL:HG12	1:B:257:MSE:HE2	1.52	0.89
1:B:254:LEU:HA	1:B:257:MSE:HE3	1.56	0.88
1:A:551:TYR:HB2	1:A:555:MSE:HE3	1.55	0.87

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:TYR:OH	1:A:126:TYR:OH[2_465]	2.15	0.05

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	613/669 (92%)	538 (88%)	67 (11%)	8 (1%)	15	44
1	B	614/669 (92%)	554 (90%)	53 (9%)	7 (1%)	17	50
All	All	1227/1338 (92%)	1092 (89%)	120 (10%)	15 (1%)	16	47

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	158	PHE
1	A	278	ALA
1	A	317	LYS
1	A	337	LYS
1	A	439	THR

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	520/546 (95%)	486 (94%)	34 (6%)	21	52
1	B	521/546 (95%)	484 (93%)	37 (7%)	18	46
All	All	1041/1092 (95%)	970 (93%)	71 (7%)	20	49

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	670	SER
1	B	188	PHE
1	B	559	MSE
1	A	689	ARG
1	B	124	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	692	HIS

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Mol	Chain	Res	Type
1	B	282	ASN
1	B	151	GLN
1	A	629	GLN
1	B	92	GLN

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	$\# Z > 2$
2	M0E	A	901	-	81,89,114	1.63	8 (9%)	101,134,166	1.70	19 (18%)
2	M0E	B	901	-	81,89,114	1.59	6 (7%)	101,134,166	1.73	20 (19%)

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	M0E	A	901	-	-	0/52/175/206	0/6/6/6
2	M0E	B	901	-	-	0/52/175/206	0/6/6/6

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	M0E	CCT-CCU	-5.24	1.39	1.50
2	A	901	M0E	CCT-CCU	-4.88	1.40	1.50
2	B	901	M0E	CCT-NCS	-3.35	1.33	1.41
2	A	901	M0E	CCT-NCS	-2.69	1.35	1.41
2	A	901	M0E	O4-CBU	2.11	1.47	1.41

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	M0E	CCW-CCX-CCY	-6.17	103.45	108.22
2	A	901	M0E	CCW-CCX-CCY	-5.68	103.82	108.22
2	A	901	M0E	CAP-OBH-CAV	-4.94	106.28	117.30
2	B	901	M0E	OCP-CCH-CCI	-4.79	100.44	110.28
2	A	901	M0E	C6-O6-CBJ	-4.06	105.29	113.82

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	M0E	6	0
2	B	901	M0E	5	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	605/669 (90%)	1.32	125 (20%) 1 1	31, 71, 107, 127	0
1	B	606/669 (90%)	1.17	104 (17%) 2 1	33, 72, 108, 127	0
All	All	1211/1338 (90%)	1.25	229 (18%) 2 1	31, 72, 108, 127	0

The worst 5 of 229 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	126	TYR	14.2
1	B	164	SER	13.0
1	A	162	HIS	11.8
1	A	164	SER	10.1
1	A	124	LEU	10.0

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](#)

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
2	M0E	B	901	84/109	0.64	0.34	-0.43	113,116,124,124	0
2	M0E	A	901	84/109	0.66	0.31	-0.46	113,116,124,125	0

6.5 Other polymers [i](#)

There are no such residues in this entry.