



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:32 PM GMT

PDB ID : 1KQP  
Title : NH<sub>3</sub>-DEPENDENT NAD<sup>+</sup> SYNTHETASE FROM BACILLUS SUBTILIS  
AT 1 Å RESOLUTION  
Authors : Symersky, J.; Devedjiev, Y.; Moore, K.; Brouillette, C.; DeLucas, L.  
Deposited on : 2002-01-07  
Resolution : 1.03 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 (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

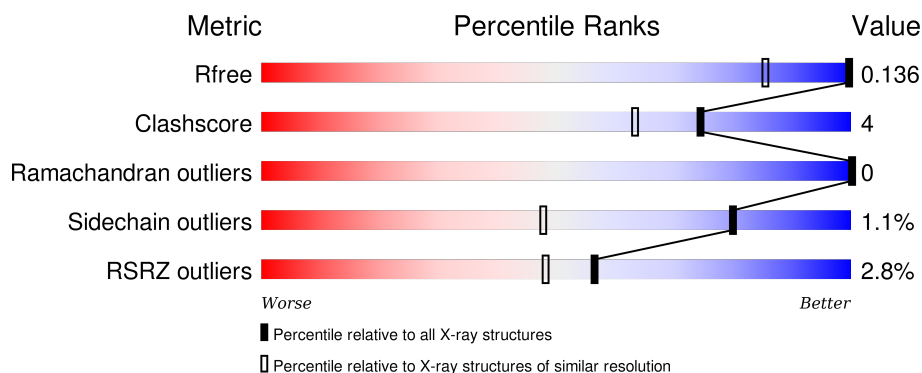
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.03 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	1032 (1.10-0.98)
Clashscore	102246	1109 (1.10-0.98)
Ramachandran outliers	100387	1041 (1.10-0.98)
Sidechain outliers	100360	1039 (1.10-0.98)
RSRZ outliers	91569	1034 (1.10-0.98)

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 style="width: 90%;"></div> <div style="width: 9%;"></div> <div style="width: 1%;"></div> </div> <div> <div style="width: 5%;"></div> <div style="width: 85%;"></div> <div style="width: 10%;"></div> </div>
1	B	271	<div> <div style="width: 5%;"></div> <div style="width: 85%;"></div> <div style="width: 10%;"></div> </div> <div> <div style="width: 85%;"></div> <div style="width: 14%;"></div> <div style="width: 1%;"></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
3	EDO	A	2008	-	-	-	X
3	EDO	B	2006	-	-	-	X
3	EDO	B	2007	-	-	-	X
3	EDO	B	2009	-	-	-	X
3	EDO	B	2010	-	-	-	X
4	ADJ	A	3001	X	-	-	-
4	ADJ	B	3002	X	-	-	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9587 atoms, of which 4355 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 NH(3)-dependent NAD(+) synthetase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	271	Total	C	H	N	O	S	0	11	0
			4316	1358	2150	367	435	6			
1	B	271	Total	C	H	N	O	S	0	7	0
			4296	1352	2139	364	433	8			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

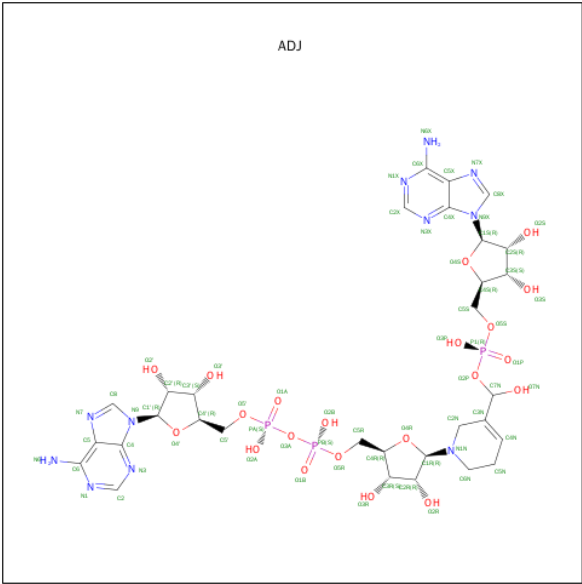
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	Mg	0	0
			3	3		
2	A	2	Total	Mg	0	0
			2	2		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 4 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE-ADENYLATE INTERMEDIATE (three-letter code: ADJ) (formula: C<sub>31</sub>H<sub>44</sub>N<sub>11</sub>O<sub>21</sub>P<sub>3</sub>).



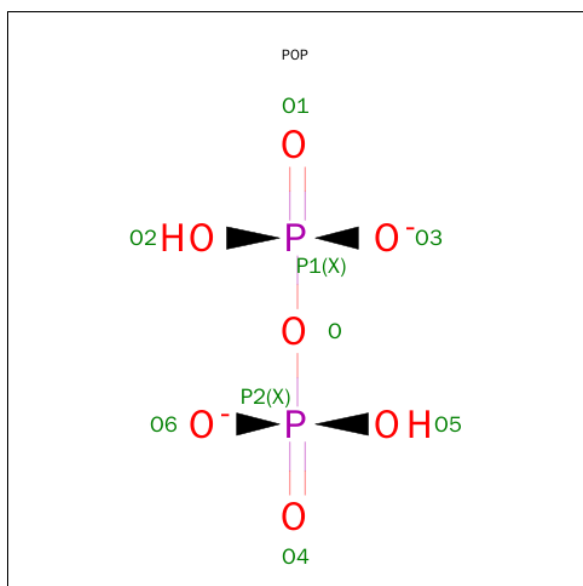
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C H N O P 99 31 33 11 21 3	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	H	N	O	P	
			99	31	33	11	21	3	
								0	0

- Molecule 5 is PYROPHOSPHATE 2- (three-letter code: POP) (formula:  $\text{H}_2\text{O}_7\text{P}_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P		
			9	7	2	0	0
5	B	1	Total	O	P		
			9	7	2	0	0


- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	352	Total	O		
			352	352	0	0
6	B	362	Total	O		
			362	362	0	0

### 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.

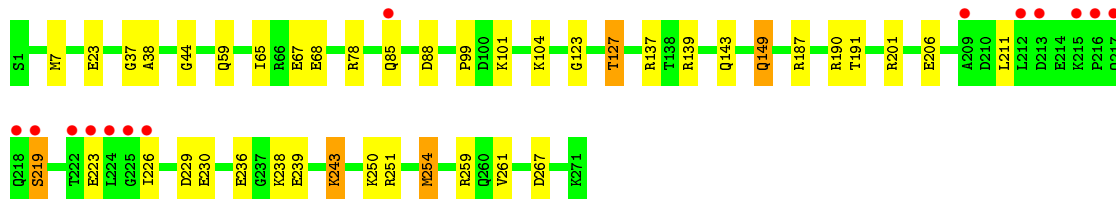
- Molecule 1: NH(3)-dependent NAD(+) synthetase

Chain A:  90% 9% •



- Molecule 1: NH(3)-dependent NAD(+) synthetase

Chain B:  5% 85% 14% •



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.28Å 84.79Å 59.64Å 90.00° 110.50° 90.00°	Depositor
Resolution (Å)	10.00 – 1.03 27.46 – 1.03	Depositor EDS
% Data completeness (in resolution range)	83.0 (10.00-1.03) 86.1 (27.46-1.03)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.02 (at 1.03Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.106 , 0.135 0.109 , 0.136	Depositor DCC
$R_{free}$ test set	10772 reflections (5.49%)	DCC
Wilson B-factor (Å <sup>2</sup> )	11.1	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.44 , 69.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 216278 reflections	Xtriage
$F_o, F_c$ correlation	0.99	EDS
Total number of atoms	9587	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.47% 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: MG, ADJ, EDO, POP

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	0.74	2/2255 (0.1%)	1.20	22/3032 (0.7%)
1	B	0.73	2/2235 (0.1%)	1.28	24/3004 (0.8%)
All	All	0.73	4/4490 (0.1%)	1.24	46/6036 (0.8%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	259	ARG	CZ-NH1	-5.78	1.25	1.33
1	B	219	SER	CB-OG	-5.24	1.35	1.42
1	A	149	GLN	CD-NE2	-5.18	1.19	1.32
1	B	149	GLN	CD-NE2	-5.11	1.20	1.32

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	259	ARG	NE-CZ-NH1	-11.98	114.31	120.30
1	B	88	ASP	CB-CG-OD1	11.73	128.86	118.30
1	B	78	ARG	NE-CZ-NH1	11.06	125.83	120.30
1	A	190	ARG	NE-CZ-NH2	-10.51	115.04	120.30
1	A	187	ARG	NE-CZ-NH1	10.09	125.34	120.30

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	2166	2150	2141	11	0
1	B	2157	2139	2131	25	0
2	A	2	0	0	0	0
2	B	3	0	0	0	0
3	A	12	0	18	0	0
3	B	28	0	42	7	0
4	A	66	33	39	3	0
4	B	66	33	40	2	0
5	A	9	0	0	0	0
5	B	9	0	0	0	0
6	A	352	0	0	6	0
6	B	362	0	0	5	0
All	All	5232	4355	4411	36	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 36 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:B:250:LYS:O	1:B:254[B]:MET:HG2	1.86	0.76
1:B:211:LEU:HD11	4:B:3002:ADJ:H5N	1.67	0.76
1:A:250:LYS:HG3	6:A:6117:HOH:O	1.92	0.70
1:B:206:GLU:OE2	1:B:219:SER:HB3	1.97	0.65
1:A:34:LYS:HD3	1:A:34:LYS:N	2.10	0.64

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	280/271 (103%)	279 (100%)	1 (0%)	0	100	100
1	B	278/271 (103%)	278 (100%)	0	0	100	100
All	All	558/542 (103%)	557 (100%)	1 (0%)	0	100	100

There are no Ramachandran outliers to report.

### 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	237/226 (105%)	236 (100%)	1 (0%)	93	74
1	B	235/226 (104%)	231 (98%)	4 (2%)	68	31
All	All	472/452 (104%)	467 (99%)	5 (1%)	80	48

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LYS
1	B	85	GLN
1	B	104	LYS
1	B	229	ASP
1	B	243	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	260	GLN
1	B	20	GLN
1	B	130	ASN
1	A	149	GLN
1	B	143	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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 5 are monoatomic - leaving 14 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	EDO	A	2001	-	3,3,3	0.40	0	2,2,2	0.37	0
3	EDO	A	2002	-	3,3,3	0.56	0	2,2,2	0.59	0
3	EDO	A	2008	-	3,3,3	0.88	0	2,2,2	1.09	0
4	ADJ	A	3001	2	59,73,73	2.34	12 (20%)	68,112,112	1.66	6 (8%)
5	POP	A	4001	2	8,8,8	0.78	0	13,13,13	1.06	1 (7%)
3	EDO	B	2003	-	3,3,3	0.43	0	2,2,2	0.73	0
3	EDO	B	2004	-	3,3,3	0.53	0	2,2,2	0.30	0
3	EDO	B	2005	-	3,3,3	0.26	0	2,2,2	0.57	0
3	EDO	B	2006	-	3,3,3	0.78	0	2,2,2	0.45	0
3	EDO	B	2007	-	3,3,3	0.94	0	2,2,2	0.72	0
3	EDO	B	2009	-	3,3,3	0.79	0	2,2,2	0.47	0
3	EDO	B	2010	-	3,3,3	0.37	0	2,2,2	3.26	1 (50%)
4	ADJ	B	3002	2	59,73,73	2.21	9 (15%)	68,112,112	2.02	11 (16%)
5	POP	B	4002	2	8,8,8	0.94	1 (12%)	13,13,13	1.06	1 (7%)

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	EDO	A	2001	-	-	0/1/1/1	0/0/0/0
3	EDO	A	2002	-	-	0/1/1/1	0/0/0/0
3	EDO	A	2008	-	-	0/1/1/1	0/0/0/0
4	ADJ	A	3001	2	1/1/19/19	0/32/103/103	0/8/8/8
5	POP	A	4001	2	-	0/6/6/6	0/0/0/0
3	EDO	B	2003	-	-	0/1/1/1	0/0/0/0
3	EDO	B	2004	-	-	0/1/1/1	0/0/0/0
3	EDO	B	2005	-	-	0/1/1/1	0/0/0/0
3	EDO	B	2006	-	-	0/1/1/1	0/0/0/0
3	EDO	B	2007	-	-	0/1/1/1	0/0/0/0
3	EDO	B	2009	-	-	0/1/1/1	0/0/0/0
3	EDO	B	2010	-	-	0/1/1/1	0/0/0/0
4	ADJ	B	3002	2	1/1/19/19	0/32/103/103	0/8/8/8
5	POP	B	4002	2	-	0/6/6/6	0/0/0/0

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	3001	ADJ	C6N-N1N	-8.42	1.29	1.47
4	B	3002	ADJ	C2N-N1N	-8.12	1.29	1.47
4	A	3001	ADJ	C5N-C4N	-7.80	1.34	1.50
4	A	3001	ADJ	C2N-N1N	-7.29	1.31	1.47
4	B	3002	ADJ	C2N-C3N	-7.21	1.36	1.51

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	3002	ADJ	O7N-C7N-C3N	-5.75	95.85	110.54
5	A	4001	POP	P2-O-P1	-3.33	123.38	132.73
4	A	3001	ADJ	C1'-N9-C4	-3.16	122.17	126.94
5	B	4002	POP	P2-O-P1	-3.15	123.88	132.73
4	B	3002	ADJ	N3-C2-N1	-2.84	126.72	128.89

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	3002	ADJ	C7N
4	A	3001	ADJ	C7N

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	3001	ADJ	3	0
3	B	2005	EDO	2	0
3	B	2006	EDO	2	0
3	B	2009	EDO	3	0
4	B	3002	ADJ	2	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	271/271 (100%)	-0.47	1 (0%) 93 87	8, 12, 25, 33	2 (0%)
1	B	271/271 (100%)	-0.13	14 (5%) 31 26	9, 12, 27, 36	3 (1%)
All	All	542/542 (100%)	-0.30	15 (2%) 56 48	8, 12, 26, 36	5 (0%)

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	216	PRO	5.1
1	B	212	LEU	3.8
1	B	215	LYS	3.8
1	B	222	THR	3.5
1	B	209	ALA	3.0

### 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, 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
3	EDO	B	2007	4/4	0.91	0.12	6.34	16,17,20,21	0
3	EDO	B	2009	4/4	0.87	0.13	4.55	24,30,34,42	0
3	EDO	B	2006	4/4	0.75	0.18	4.02	26,29,34,34	0
3	EDO	A	2008	4/4	0.94	0.12	3.10	14,21,26,30	0
3	EDO	B	2010	4/4	0.92	0.10	2.72	17,18,28,28	0
4	ADJ	A	3001	66/66	0.94	0.09	1.98	9,13,20,40	0
3	EDO	B	2005	4/4	0.82	0.12	1.64	23,23,24,44	0
3	EDO	A	2001	4/4	0.97	0.06	0.41	16,19,29,29	0
3	EDO	A	2002	4/4	0.98	0.05	0.25	14,15,17,21	0
5	POP	A	4001	9/9	1.00	0.05	0.19	8,8,8,9	0
4	ADJ	B	3002	66/66	0.98	0.07	-0.16	9,12,46,82	0
3	EDO	B	2004	4/4	0.98	0.05	-0.44	15,21,25,29	0
5	POP	B	4002	9/9	1.00	0.05	-0.81	9,9,10,10	0
2	MG	B	5005	1/1	1.00	0.04	-1.82	12,12,12,12	0
2	MG	A	5001	1/1	1.00	0.05	-	9,9,9,9	0
3	EDO	B	2003	4/4	0.85	0.15	-	21,29,34,39	0
2	MG	B	5004	1/1	1.00	0.03	-	10,10,10,10	0
2	MG	A	5002	1/1	1.00	0.03	-	9,9,9,9	0
2	MG	B	5003	1/1	1.00	0.04	-	10,10,10,10	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.