



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:45 AM UTC

PDB ID : 2RTN / pdb\_00002rtn  
Title : STREPTAVIDIN-2-IMINOBIOTIN COMPLEX, PH 2.0, SPACE GROUP I222  
Authors : Katz, B.A.  
Deposited on : 1997-09-11  
Resolution : 1.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

<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>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

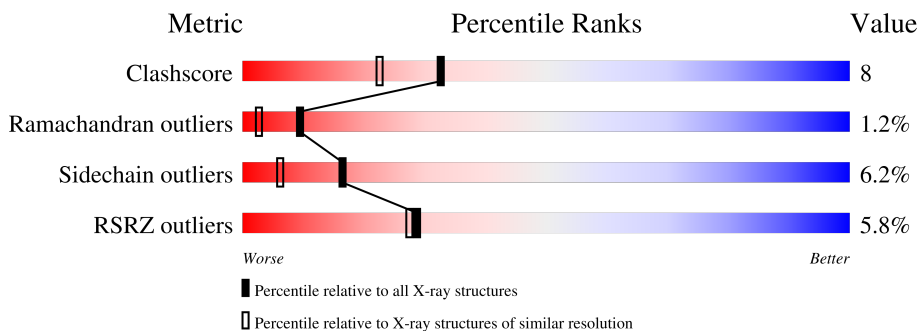
# 1 Overall quality at a glance

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))
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	B	135	 4% 57% 24% 10% 9%
1	D	135	 6% 59% 27% 10% 10%

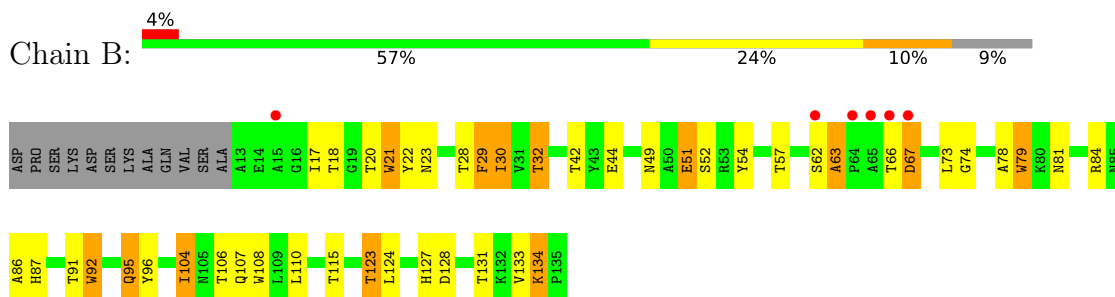


<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>			<b>ZeroOcc</b>	<b>AltConf</b>
3	B	51	Total	H	O	0	0
			143	92	51		
3	D	52	Total	H	O	0	2
			156	104	52		

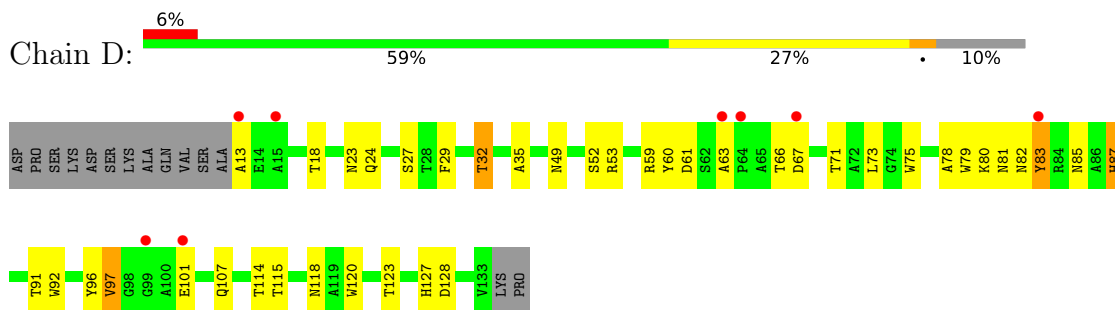
### 3 Residue-property plots [i](#)

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: STREPTAVIDIN



- Molecule 1: STREPTAVIDIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.41Å 106.54Å 48.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.50 – 1.80 7.50 – 1.80	Depositor EDS
% Data completeness (in resolution range)	69.0 (7.50-1.80) 67.5 (7.50-1.80)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.81 (at 1.80Å)	Xtrriage
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.276 , 0.200 0.222 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.7	Xtrriage
Anisotropy	0.176	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.20 , 55.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2615	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.65% 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: IMI

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	B	1.09	2/970 (0.2%)	1.86	27/1327 (2.0%)
1	D	1.03	4/938 (0.4%)	1.93	32/1284 (2.5%)
All	All	1.06	6/1908 (0.3%)	1.90	59/2611 (2.3%)

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	B	0	2
1	D	0	1
All	All	0	3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	127	HIS	CD2-NE2	-6.79	1.30	1.37
1	D	87	HIS	CD2-NE2	-6.45	1.30	1.37
1	B	87	HIS	CD2-NE2	-6.25	1.30	1.37
1	D	71	THR	CA-CB	5.56	1.60	1.53
1	B	127	HIS	CD2-NE2	-5.46	1.31	1.37
1	D	61	ASP	CG-OD2	-5.01	1.23	1.33

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	81	ASN	CA-CB-CG	11.58	124.18	112.60
1	D	63	ALA	N-CA-C	10.48	120.19	108.14
1	B	67	ASP	CA-CB-CG	9.93	122.53	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	81	ASN	CA-CB-CG	9.86	122.46	112.60
1	D	29	PHE	CA-CB-CG	9.65	123.45	113.80
1	B	128	ASP	CA-CB-CG	8.88	121.48	112.60
1	B	29	PHE	CA-CB-CG	8.69	122.49	113.80
1	B	123	THR	N-CA-C	8.27	122.38	109.07
1	D	123	THR	N-CA-C	8.01	121.58	108.52
1	D	23	ASN	CA-CB-CG	7.72	120.32	112.60
1	D	78	ALA	N-CA-C	-7.60	96.84	109.46
1	B	49	ASN	OD1-CG-ND2	-7.54	115.06	122.60
1	B	78	ALA	N-CA-C	-6.87	98.06	109.46
1	B	30	ILE	N-CA-C	-6.81	97.81	107.75
1	D	107[A]	GLN	N-CA-C	-6.55	98.72	109.40
1	D	107[B]	GLN	N-CA-C	-6.55	98.72	109.40
1	B	104	ILE	N-CA-C	-6.53	98.22	107.75
1	D	29	PHE	N-CA-CB	-6.50	100.51	110.65
1	D	92	TRP	CB-CG-CD1	-6.43	117.25	126.90
1	B	29	PHE	CB-CA-C	6.42	120.02	110.14
1	D	92	TRP	CG-CD2-CE3	6.41	140.31	133.90
1	B	92	TRP	CG-CD2-CE3	6.33	140.23	133.90
1	B	29	PHE	N-CA-CB	-6.31	100.48	110.77
1	B	92	TRP	CB-CG-CD1	-6.30	117.45	126.90
1	D	82	ASN	CA-CB-CG	6.21	118.81	112.60
1	D	83	TYR	CA-CB-CG	-6.04	103.04	113.90
1	D	87	HIS	CB-CG-CD2	-5.92	123.51	131.20
1	B	23	ASN	CA-CB-CG	5.91	118.51	112.60
1	B	23	ASN	OD1-CG-ND2	-5.89	116.71	122.60
1	B	95	GLN	OE1-CD-NE2	-5.87	116.73	122.60
1	B	87	HIS	CB-CG-CD2	-5.82	123.64	131.20
1	D	49	ASN	CA-CB-CG	5.79	118.39	112.60
1	D	81	ASN	OD1-CG-ND2	-5.75	116.85	122.60
1	D	97	VAL	CB-CA-C	-5.72	101.70	110.50
1	D	35	ALA	N-CA-C	5.71	119.35	112.38
1	D	92	TRP	CE2-CD2-CG	-5.71	100.35	107.20
1	D	115	THR	O-C-N	-5.65	116.06	122.68
1	D	85	ASN	OD1-CG-ND2	-5.64	116.95	122.60
1	B	108	TRP	CG-CD2-CE3	5.64	139.54	133.90
1	B	79	TRP	CG-CD2-CE3	5.59	139.49	133.90
1	B	107	GLN	N-CA-C	-5.57	99.94	109.24
1	D	115	THR	N-CA-C	-5.55	102.55	110.59
1	D	75	TRP	CE2-CD2-CG	-5.49	100.61	107.20
1	B	87	HIS	CA-CB-CG	5.48	119.28	113.80
1	B	115	THR	N-CA-C	-5.33	103.65	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	92	TRP	CD1-CG-CD2	5.30	114.78	106.30
1	B	49	ASN	CB-CG-ND2	5.27	124.31	116.40
1	D	79	TRP	CE2-CD2-CG	-5.26	100.89	107.20
1	B	92	TRP	CE2-CD2-CG	-5.25	100.90	107.20
1	B	32	THR	N-CA-C	-5.25	99.89	108.76
1	B	107	GLN	CA-CB-CG	-5.20	103.69	114.10
1	D	127	HIS	CB-CG-CD2	-5.19	124.45	131.20
1	D	120	TRP	CG-CD2-CE3	5.16	139.06	133.90
1	D	92	TRP	CG-CD1-NE1	-5.16	103.50	110.20
1	D	67	ASP	CA-CB-CG	5.15	117.75	112.60
1	D	60	TYR	N-CA-C	-5.08	101.36	109.23
1	D	79	TRP	CD1-CG-CD2	5.07	114.41	106.30
1	D	80	LYS	CA-CB-CG	-5.06	103.97	114.10
1	B	21	TRP	CG-CD2-CE3	5.06	138.96	133.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	134	LYS	Peptide
1	B	63	ALA	Peptide
1	D	83	TYR	Sidechain

## 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	B	934	218	878	23	0
1	D	908	216	844	9	0
2	B	16	4	15	0	0
2	D	16	4	15	1	0
3	B	51	92	0	1	0
3	D	52	104	0	0	0
All	All	1977	638	1752	28	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.

All (28) 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:22[B]:TYR:CE1	1:B:131:THR:HB	2.15	0.81
1:B:22[B]:TYR:HE2	1:B:133:VAL:HB	1.48	0.79
1:B:21:TRP:HB2	1:B:29:PHE:HD2	1.61	0.66
1:D:13:ALA:N	1:D:96:TYR:HH	1.96	0.64
1:B:91:THR:HB	1:D:91:THR:HB	1.84	0.59
1:B:57:THR:HG22	1:D:59:ARG:HG2	1.92	0.52
1:B:110[A]:LEU:HD23	1:B:124:LEU:HD12	1.92	0.51
1:B:95:GLN:NE2	1:D:114:THR:H	2.08	0.50
1:B:22[B]:TYR:CE2	1:B:133:VAL:HB	2.38	0.48
1:B:51:GLU:HG2	1:B:84:ARG:HG3	1.96	0.48
1:B:79:TRP:HB2	1:B:86:ALA:HB3	1.94	0.48
1:B:22[A]:TYR:HE2	1:B:133:VAL:HG11	1.77	0.48
1:D:24:GLN:HE22	1:D:128:ASP:HA	1.79	0.47
1:B:22[B]:TYR:HD1	3:B:525:HOH:O	1.98	0.46
1:B:28:THR:HB	1:B:44:GLU:HB3	1.99	0.45
1:B:42:THR:HA	1:B:54:TYR:O	2.17	0.44
1:B:63:ALA:HB1	1:D:87:HIS:HD2	1.82	0.44
1:B:133:VAL:HG13	1:B:134:LYS:H	1.83	0.43
1:B:17:ILE:HD13	1:B:73[A]:LEU:HD23	2.00	0.43
1:B:73[B]:LEU:HD11	1:B:96:TYR:HB2	2.01	0.42
1:B:74:GLY:HA2	1:B:92:TRP:O	2.19	0.42
1:D:27:SER:OG	2:D:300:IMI:N3	2.39	0.42
1:B:20:THR:HB	1:B:133:VAL:HG13	2.02	0.42
1:D:18:THR:HG23	1:D:32:THR:HA	2.02	0.42
1:D:114:THR:HB	1:D:118:ASN:HB2	2.02	0.41
1:B:18:THR:HG23	1:B:32:THR:HA	2.02	0.41
1:B:104:ILE:HG22	1:B:106:THR:HG23	2.02	0.41
1:B:133:VAL:HG22	1:B:134:LYS:HG3	2.03	0.40

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	B	124/135 (92%)	119 (96%)	3 (2%)	2 (2%)	7	2
1	D	121/135 (90%)	115 (95%)	5 (4%)	1 (1%)	16	6
All	All	245/270 (91%)	234 (96%)	8 (3%)	3 (1%)	9	3

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	52	SER
1	B	62	SER
1	B	52	SER

### 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	B	93/100 (93%)	88 (95%)	5 (5%)	20	8
1	D	90/100 (90%)	84 (93%)	6 (7%)	15	5
All	All	183/200 (92%)	172 (94%)	11 (6%)	16	7

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	30	ILE
1	B	51	GLU
1	B	66	THR
1	B	67	ASP
1	B	123	THR
1	D	32	THR
1	D	53	ARG
1	D	66	THR
1	D	73	LEU
1	D	97	VAL

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Mol	Chain	Res	Type
1	D	101	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	95	GLN
1	D	49	ASN
1	D	87	HIS
1	D	118	ASN
1	D	127	HIS

### 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 oligosaccharides 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	IMI	D	300	-	16,17,17	1.13	2 (12%)	19,23,23	2.16	3 (15%)
2	IMI	B	300	-	16,17,17	0.92	1 (6%)	19,23,23	2.34	7 (36%)

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	IMI	D	300	-	-	2/7/28/28	0/2/2/2
2	IMI	B	300	-	-	0/7/28/28	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	300	IMI	C3-N2	-2.37	1.31	1.35
2	B	300	IMI	O12-C11	-2.13	1.23	1.30
2	D	300	IMI	C3-N1	-2.06	1.31	1.35

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	300	IMI	C4-C2-S1	6.50	112.42	105.03
2	D	300	IMI	C4-C2-S1	6.32	112.20	105.03
2	D	300	IMI	C5-C6-S1	4.82	112.70	106.06
2	B	300	IMI	C2-C4-N2	-3.51	109.63	113.34
2	B	300	IMI	C5-C6-S1	3.37	110.71	106.06
2	B	300	IMI	C6-C5-N1	-3.37	108.84	113.18
2	B	300	IMI	C2-C4-C5	-2.73	105.56	108.89
2	D	300	IMI	C7-C2-S1	2.46	119.89	112.78
2	B	300	IMI	C6-S1-C2	-2.26	85.29	89.98
2	B	300	IMI	O12-C11-C10	2.02	120.39	114.00

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	300	IMI	C9-C10-C11-O12
2	D	300	IMI	C9-C10-C11-O11

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	300	IMI	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	B	121/135 (89%)	0.11	6 (4%) 34 33	5, 21, 38, 63	19 (15%)
1	D	119/135 (88%)	0.22	8 (6%) 24 22	4, 24, 39, 60	19 (15%)
All	All	240/270 (88%)	0.16	14 (5%) 29 27	4, 22, 39, 63	38 (15%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	64	PRO	6.1
1	B	65	ALA	5.6
1	D	15	ALA	4.8
1	D	64	PRO	4.7
1	B	15	ALA	3.7
1	D	99	GLY	3.3
1	B	66	THR	3.2
1	D	67	ASP	3.2
1	B	67	ASP	3.0
1	D	63	ALA	2.9
1	D	83	TYR	2.4
1	D	101	GLU	2.3
1	B	62	SER	2.1
1	D	13	ALA	2.1

### 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 oligosaccharides 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, 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	IMI	D	300	16/16	0.96	0.05	0,21,35,38	0
2	IMI	B	300	16/16	0.97	0.05	0,23,29,29	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.