



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 12, 2017 – 05:11 PM EDT

PDB ID : 2Q7Q  
Title : Crystal structure of *Alcaligenes faecalis* AADH in complex with p-chlorobenzylamine.  
Authors : Roujeinikova, A.; Leys, D.  
Deposited on : unknown  
Resolution : 1.60 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

<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	:	rb-20030345
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)	:	rb-20030345

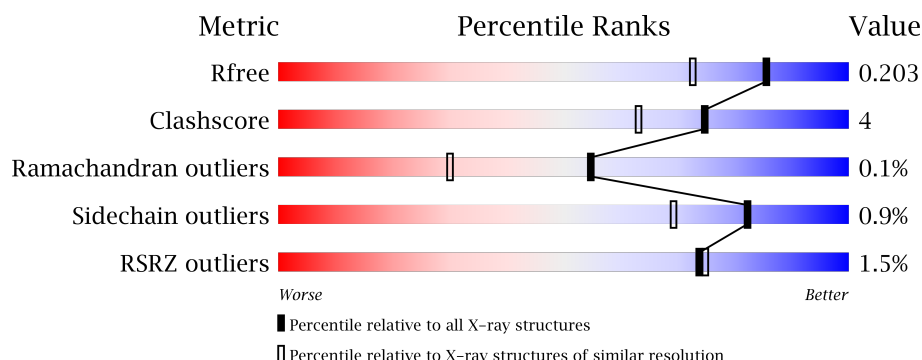
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	2696 (1.60-1.60)
Clashscore	112137	2967 (1.60-1.60)
Ramachandran outliers	110173	2887 (1.60-1.60)
Sidechain outliers	110143	2886 (1.60-1.60)
RSRZ outliers	101464	2714 (1.60-1.60)

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	D	124	<div> <div>6%</div> <div> <div></div> <div>78%</div> <div>10%</div> <div>12%</div> </div> </div>
1	H	124	<div> <div>4%</div> <div> <div></div> <div>90%</div> <div>8%</div> <div>.</div> </div> </div>
2	A	361	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>8%</div> <div>.</div> </div> </div>
2	B	361	<div> <div></div> <div> <div></div> <div>92%</div> <div>7%</div> <div>..</div> </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.

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	C2B	D	2002	-	-	-	X
3	C2B	H	2001	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8572 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 Aralkylamine dehydrogenase light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	109	Total	C	N	O	S	0	0	0
			836	510	147	164	15			
1	H	122	Total	C	N	O	S	0	0	0
			925	564	162	184	15			

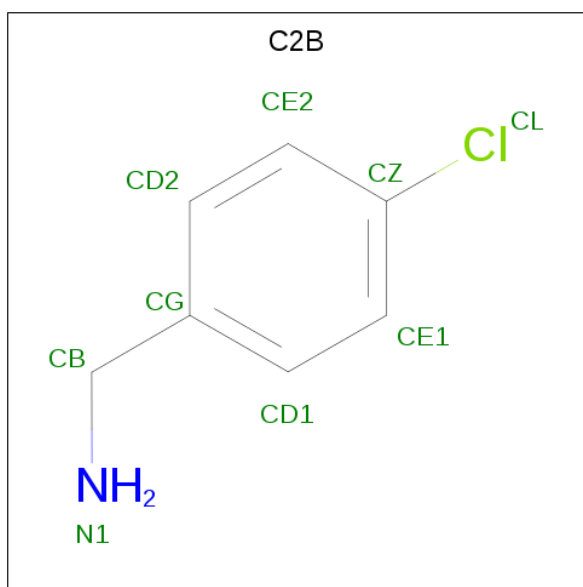
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	109	TRQ	TRP	MODIFIED RESIDUE	UNP P84887
H	109	TRQ	TRP	MODIFIED RESIDUE	UNP P84887

- Molecule 2 is a protein called Aralkylamine dehydrogenase heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	356	Total	C	N	O	S	0	1	0
			2782	1757	483	528	14			
2	B	358	Total	C	N	O	S	0	1	0
			2791	1761	486	530	14			

- Molecule 3 is 1-(4-CHLOROPHENYL)METHANAMINE (three-letter code: C2B) (formula: C<sub>7</sub>H<sub>8</sub>ClN).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	Cl	N	0	0
			9	7	1	1		
3	H	1	Total	C	Cl	N	0	0
			9	7	1	1		

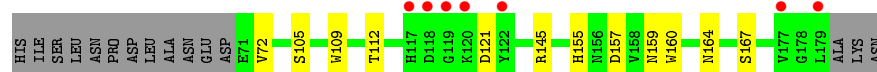
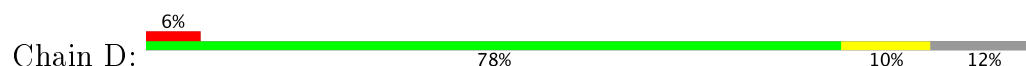
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	104	Total	O	0	0
			104	104		
4	H	120	Total	O	0	0
			120	120		
4	A	466	Total	O	0	0
			466	466		
4	B	530	Total	O	0	0
			530	530		

### 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 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.

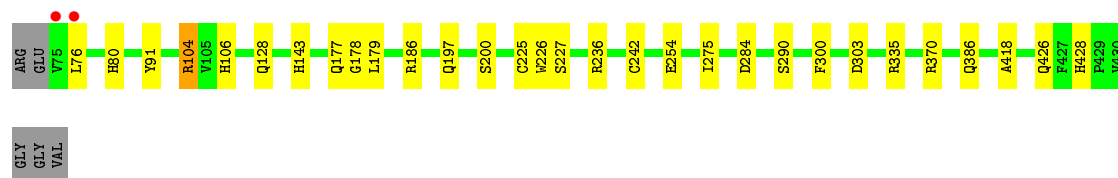
- Molecule 1: Aralkylamine dehydrogenase light chain



- Molecule 1: Aralkylamine dehydrogenase light chain



- Molecule 2: Aralkylamine dehydrogenase heavy chain



- Molecule 2: Aralkylamine dehydrogenase heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.54Å 96.76Å 120.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.60 25.12 – 1.60	Depositor EDS
% Data completeness (in resolution range)	95.5 (15.00-1.60) 95.5 (25.12-1.60)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.63 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.165 , 0.193 0.177 , 0.203	Depositor DCC
$R_{free}$ test set	6757 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.5	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 56.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8572	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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: TRQ, C2B

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	D	0.49	0/842	0.63	0/1146
1	H	0.53	0/932	0.66	0/1271
2	A	0.58	0/2850	0.74	2/3863 (0.1%)
2	B	0.58	0/2859	0.71	0/3877
All	All	0.57	0/7483	0.71	2/10157 (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
2	B	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	370	ARG	NE-CZ-NH1	7.62	124.11	120.30
2	A	370	ARG	NE-CZ-NH2	-6.28	117.16	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	200	SER	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	D	836	0	732	9	0
1	H	925	0	811	9	0
2	A	2782	0	2727	21	0
2	B	2791	0	2722	21	0
3	D	9	0	8	1	0
3	H	9	0	8	1	0
4	A	466	0	0	2	0
4	B	530	0	0	2	1
4	D	104	0	0	1	0
4	H	120	0	0	3	0
All	All	8572	0	7008	53	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 4.

All (53) 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)
2:B:91:TYR:OH	2:B:428:HIS:HD2	1.69	0.75
1:H:76:ASP:HB2	4:H:2073:HOH:O	1.89	0.72
1:D:105:SER:HA	1:D:164:ASN:HD21	1.55	0.72
1:H:105:SER:HA	1:H:164:ASN:HD21	1.55	0.71
2:A:104:ARG:HH11	2:A:106:HIS:HE1	1.39	0.71
2:B:104:ARG:HH11	2:B:106:HIS:HE1	1.39	0.69
2:A:91:TYR:OH	2:A:428:HIS:HD2	1.79	0.64
2:B:197:GLN:NE2	2:B:227:SER:H	1.97	0.62
2:A:197:GLN:NE2	2:A:227:SER:H	1.97	0.61
2:A:335:ARG:H	2:A:386:GLN:HE22	1.47	0.61
4:H:2076:HOH:O	2:B:118[B]:MET:SD	2.56	0.60
2:B:73:ARG:N	4:B:727:HOH:O	2.35	0.60
2:B:335:ARG:H	2:B:386:GLN:HE22	1.49	0.60
2:B:197:GLN:HE21	2:B:227:SER:H	1.50	0.59
1:D:109:TRQ:HB2	1:D:160:TRP:NE1	2.18	0.59
1:H:173:THR:HG21	2:B:76:LEU:HD13	1.85	0.58
2:B:335:ARG:H	2:B:386:GLN:NE2	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:159:ASN:HD22	2:B:177:GLN:NE2	2.05	0.54
2:A:106:HIS:HD2	2:A:418:ALA:O	1.91	0.54
1:H:109:TRQ:HB2	1:H:160:TRP:NE1	2.24	0.53
1:H:167:SER:HB2	2:A:177:GLN:HE22	1.74	0.53
2:A:335:ARG:H	2:A:386:GLN:NE2	2.07	0.53
1:D:109:TRQ:O6	3:D:2002:C2B:N1	2.41	0.53
1:H:159:ASN:HD22	2:A:177:GLN:NE2	2.07	0.53
2:B:124:ASN:HD21	2:B:178:GLY:H	1.57	0.53
2:A:197:GLN:HE21	2:A:227:SER:H	1.56	0.52
2:A:236:ARG:NH1	2:A:254:GLU:HA	2.25	0.52
1:D:167:SER:HB2	2:B:177:GLN:HE22	1.75	0.51
2:A:76:LEU:O	2:A:80:HIS:NE2	2.44	0.50
1:D:112:THR:HB	1:D:145:ARG:HD3	1.93	0.49
2:B:91:TYR:OH	2:B:428:HIS:CD2	2.58	0.48
1:D:109:TRQ:HB2	1:D:160:TRP:HE1	1.77	0.48
1:H:173:THR:HG21	2:B:76:LEU:CD1	2.43	0.48
2:A:91:TYR:OH	2:A:428:HIS:CD2	2.66	0.46
1:D:112:THR:HG21	1:D:145:ARG:NH1	2.31	0.46
2:B:143:HIS:HD2	4:B:751:HOH:O	1.98	0.45
2:B:106:HIS:HD2	2:B:418:ALA:O	1.99	0.45
1:H:149:GLY:HA3	2:A:226:TRP:CD1	2.52	0.45
2:A:179:LEU:HD23	4:A:775:HOH:O	2.17	0.44
2:B:200:SER:N	2:B:201:PRO:HA	2.33	0.44
2:A:128:GLN:HE22	2:A:186:ARG:C	2.22	0.43
1:D:155:HIS:CE1	1:D:157:ASP:HB2	2.54	0.43
2:B:207:ILE:HB	2:B:217:GLU:HB3	2.01	0.42
2:A:284:ASP:HA	2:A:300:PHE:CE1	2.55	0.42
2:A:225:CYS:HA	2:A:242:CYS:HA	2.02	0.42
2:A:275:ILE:HA	2:A:290:SER:HA	2.02	0.42
2:A:143:HIS:HD2	4:A:635:HOH:O	2.03	0.41
2:B:275:ILE:HA	2:B:290:SER:HA	2.03	0.41
4:D:2033:HOH:O	2:B:143:HIS:HE1	2.03	0.41
1:H:59:HIS:N	4:H:2070:HOH:O	2.53	0.41
2:A:186:ARG:HH22	2:A:426:GLN:NE2	2.17	0.41
2:B:194:ILE:HB	2:B:208:VAL:HB	2.02	0.40
3:H:2001:C2B:HE2	2:A:178:GLY:HA2	2.04	0.40

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)
4:B:761:HOH:O	4:B:950:HOH:O[4_555]	2.15	0.05

## 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	D	106/124 (86%)	103 (97%)	3 (3%)	0	100	100
1	H	119/124 (96%)	117 (98%)	2 (2%)	0	100	100
2	A	355/361 (98%)	343 (97%)	11 (3%)	1 (0%)	44	22
2	B	357/361 (99%)	343 (96%)	14 (4%)	0	100	100
All	All	937/970 (97%)	906 (97%)	30 (3%)	1 (0%)	55	30

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	200	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	D	95/108 (88%)	93 (98%)	2 (2%)	59	32
1	H	104/108 (96%)	104 (100%)	0	100	100
2	A	303/305 (99%)	301 (99%)	2 (1%)	87	77
2	B	302/305 (99%)	299 (99%)	3 (1%)	80	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	804/826 (97%)	797 (99%)	7 (1%)	82	69

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	72	VAL
1	D	121	ASP
2	A	104	ARG
2	A	303	ASP
2	B	104	ARG
2	B	218	ASP
2	B	388	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	139	GLN
1	D	143	GLN
1	D	164	ASN
1	H	139	GLN
1	H	143	GLN
1	H	164	ASN
2	A	86	GLN
2	A	106	HIS
2	A	128	GLN
2	A	143	HIS
2	A	177	GLN
2	A	180	ASN
2	A	187	GLN
2	A	197	GLN
2	A	231	GLN
2	A	261	GLN
2	A	266	GLN
2	A	386	GLN
2	A	424	GLN
2	A	426	GLN
2	A	428	HIS
2	B	86	GLN
2	B	106	HIS
2	B	124	ASN
2	B	128	GLN

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Mol	Chain	Res	Type
2	B	143	HIS
2	B	177	GLN
2	B	180	ASN
2	B	187	GLN
2	B	197	GLN
2	B	231	GLN
2	B	386	GLN
2	B	424	GLN
2	B	426	GLN
2	B	428	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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
1	TRQ	D	109	1	16,17,18	4.80	7 (43%)	15,24,26	1.38	1 (6%)
1	TRQ	H	109	1	16,17,18	4.90	7 (43%)	15,24,26	2.07	4 (26%)

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
1	TRQ	D	109	1	-	0/3/19/21	0/2/2/2
1	TRQ	H	109	1	-	0/3/19/21	0/2/2/2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	109	TRQ	CH2-CZ2	-14.59	1.36	1.53
1	H	109	TRQ	CH2-CZ2	-14.22	1.36	1.53
1	H	109	TRQ	CE2-CZ2	-8.21	1.39	1.49
1	D	109	TRQ	CE2-CZ2	-8.16	1.40	1.49
1	D	109	TRQ	CA-C	2.27	1.53	1.50
1	H	109	TRQ	CA-C	2.61	1.53	1.50
1	D	109	TRQ	CD2-CG	3.57	1.45	1.40
1	D	109	TRQ	O6-CH2	3.72	1.34	1.24
1	H	109	TRQ	O6-CH2	4.43	1.36	1.24
1	H	109	TRQ	CD2-CG	4.43	1.46	1.40
1	D	109	TRQ	O7-CZ2	4.80	1.33	1.23
1	D	109	TRQ	CZ3-CE3	4.99	1.43	1.34
1	H	109	TRQ	CZ3-CE3	5.36	1.43	1.34
1	H	109	TRQ	O7-CZ2	5.57	1.35	1.23

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	109	TRQ	O7-CZ2-CE2	-4.18	117.27	122.03
1	D	109	TRQ	CD2-CE3-CZ3	-2.84	117.52	121.09
1	H	109	TRQ	CD2-CE3-CZ3	-2.59	117.83	121.09
1	H	109	TRQ	CB-CG-CD1	-2.06	125.42	127.97
1	H	109	TRQ	O7-CZ2-CH2	5.25	124.28	119.03

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	109	TRQ	3	0
1	H	109	TRQ	1	0

## 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$
3	C2B	D	2002	-	9,9,9	3.30	2 (22%)	11,11,11	1.04	0
3	C2B	H	2001	-	9,9,9	3.30	2 (22%)	11,11,11	0.81	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
3	C2B	D	2002	-	-	0/2/2/2	0/1/1/1
3	C2B	H	2001	-	-	0/2/2/2	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	2002	C2B	CZ-CL	-2.23	1.69	1.74
3	H	2001	C2B	CE1-CZ	2.00	1.41	1.38
3	H	2001	C2B	CD2-CE2	9.34	1.55	1.38
3	D	2002	C2B	CD2-CE2	9.55	1.55	1.38

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	2002	C2B	1	0
3	H	2001	C2B	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	D	108/124 (87%)	-0.11	7 (6%) 20 19	17, 25, 48, 63	0
1	H	121/124 (97%)	-0.03	5 (4%) 38 36	16, 23, 43, 60	0
2	A	356/361 (98%)	-0.25	2 (0%) 89 89	15, 24, 37, 50	0
2	B	358/361 (99%)	-0.56	0 100 100	14, 20, 33, 52	0
All	All	943/970 (97%)	-0.32	14 (1%) 74 75	14, 22, 38, 63	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	75	VAL	5.1
2	A	76	LEU	4.5
1	D	117	HIS	3.4
1	D	119	GLY	3.2
1	H	180	ALA	3.1
1	D	179	LEU	3.1
1	H	179	LEU	3.0
1	H	59	HIS	3.0
1	D	177	VAL	3.0
1	H	68	ASN	2.6
1	H	70	ASP	2.4
1	D	118	ASP	2.3
1	D	122	TYR	2.2
1	D	120	LYS	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TRQ	H	109	16/17	0.95	0.11	-	18,23,26,35	0
1	TRQ	D	109	16/17	0.94	0.07	-	21,24,30,44	0

### 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	C2B	D	2002	9/9	0.94	0.30	14.72	14,19,26,27	9
3	C2B	H	2001	9/9	0.96	0.31	14.05	11,16,20,23	9

### 6.5 Other polymers [i](#)

There are no such residues in this entry.