



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 02:29 am GMT

PDB ID : 1TOG  
Title : Hydrocinnamic acid-bound structure of SRHEPT + A293D mutant of E. coli aspartate aminotransferase  
Authors : Chow, M.A.; McElroy, K.E.; Corbett, K.D.; Berger, J.M.; Kirsch, J.F.  
Deposited on : 2004-06-14  
Resolution : 2.31 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.

---

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 : trunk28620  
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) : recalc28949

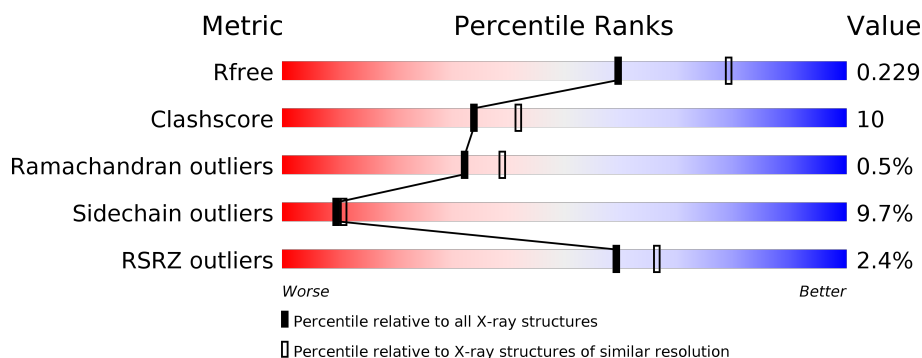
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.31 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	4787 (2.34-2.30)
Clashscore	112137	5439 (2.34-2.30)
Ramachandran outliers	110173	5386 (2.34-2.30)
Sidechain outliers	110143	5385 (2.34-2.30)
RSRZ outliers	101464	4814 (2.34-2.30)

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	396	<div> <div>3%</div> <div> <div></div> <div>81%</div> <div>16%</div> <div>.</div> </div> </div>
1	B	396	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>21%</div> <div>..</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6329 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.

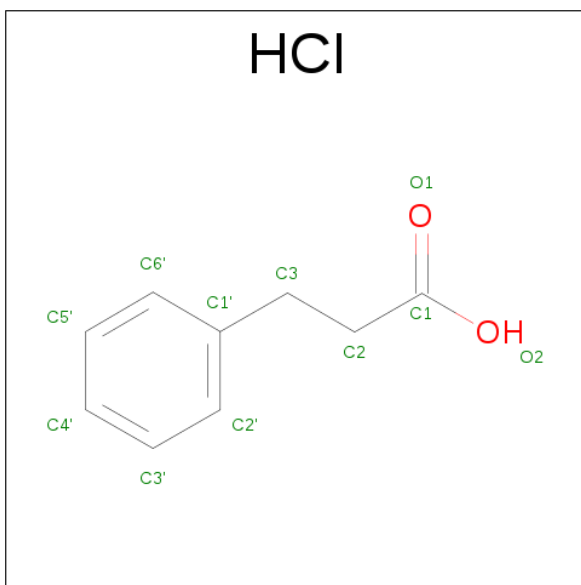
- Molecule 1 is a protein called Aspartate aminotransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	396	Total	C	N	O	P	S	0	0	0
			3085	1943	535	593	1	13			
1	B	396	Total	C	N	O	P	S	0	0	0
			3085	1943	535	593	1	13			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	THR	ALA	ENGINEERED	UNP P00509
A	13	THR	PRO	ENGINEERED	UNP P00509
A	34	ASP	ASN	ENGINEERED	UNP P00509
A	109	SER	THR	ENGINEERED	UNP P00509
A	258	LLP	LYS	MODIFIED RESIDUE	UNP P00509
A	261	ALA	GLY	ENGINEERED	UNP P00509
A	285	GLY	SER	ENGINEERED	UNP P00509
A	293	ASP	ALA	ENGINEERED	UNP P00509
A	297	SER	ASN	ENGINEERED	UNP P00509
B	12	THR	ALA	ENGINEERED	UNP P00509
B	13	THR	PRO	ENGINEERED	UNP P00509
B	34	ASP	ASN	ENGINEERED	UNP P00509
B	109	SER	THR	ENGINEERED	UNP P00509
B	258	LLP	LYS	MODIFIED RESIDUE	UNP P00509
B	261	ALA	GLY	ENGINEERED	UNP P00509
B	285	GLY	SER	ENGINEERED	UNP P00509
B	293	ASP	ALA	ENGINEERED	UNP P00509
B	297	SER	ASN	ENGINEERED	UNP P00509

- Molecule 2 is HYDROCINNAMIC ACID (three-letter code: HCI) (formula: C<sub>9</sub>H<sub>10</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			11	9	2		
2	B	1	Total	C	O	0	0
			11	9	2		

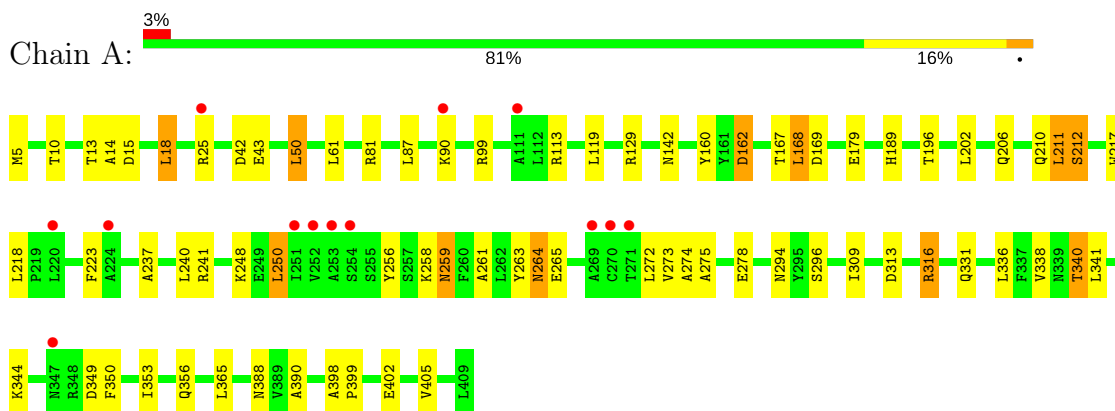
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	60	Total	O	0	0
			60	60		
3	B	77	Total	O	0	0
			77	77		

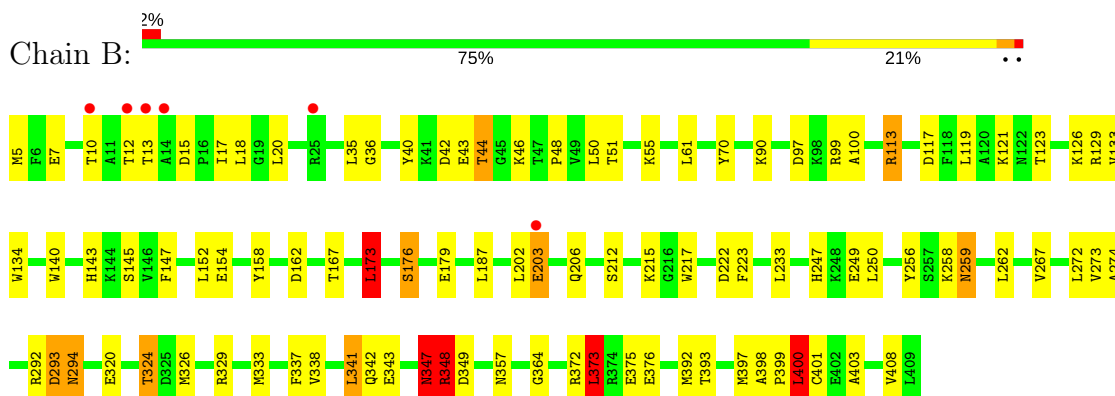
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Aspartate aminotransferase



#### • Molecule 1: Aspartate aminotransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	151.38Å 151.38Å 79.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.31 29.45 – 2.31	Depositor EDS
% Data completeness (in resolution range)	96.6 (30.00-2.31) 96.6 (29.45-2.31)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	11.74 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, $R_{free}$	0.185 , 0.232 0.185 , 0.229	Depositor DCC
$R_{free}$ test set	2247 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.7	Xtriage
Anisotropy	0.168	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 36.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.023 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6329	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.16% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HCl, LLP

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	0.64	0/3120	0.81	4/4225 (0.1%)
1	B	0.73	0/3120	0.90	11/4225 (0.3%)
All	All	0.69	0/6240	0.86	15/8450 (0.2%)

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	400	LEU	CA-CB-CG	8.03	133.78	115.30
1	B	97	ASP	CB-CG-OD2	6.87	124.48	118.30
1	B	293	ASP	CB-CG-OD2	6.51	124.16	118.30
1	B	222	ASP	CB-CG-OD2	6.30	123.97	118.30
1	B	173	LEU	CA-CB-CG	6.21	129.59	115.30

There are no chirality outliers.

There are no planarity outliers.

### 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	3085	0	3017	40	0
1	B	3085	0	3017	84	0
2	A	11	0	9	0	0
2	B	11	0	9	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	60	0	0	4	0
3	B	77	0	0	4	0
All	All	6329	0	6052	118	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 10.

The worst 5 of 118 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:333:MET:HE2	1:B:393:THR:CA	1.88	1.03
1:B:347:ASN:N	1:B:347:ASN:HD22	1.61	0.96
1:B:333:MET:HE2	1:B:393:THR:HA	1.48	0.94
1:B:397:MET:HE2	1:B:401:CYS:SG	2.15	0.87
1:A:336:LEU:O	1:A:340:THR:HG22	1.75	0.85

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	393/396 (99%)	378 (96%)	14 (4%)	1 (0%)	44	54
1	B	393/396 (99%)	377 (96%)	13 (3%)	3 (1%)	22	26
All	All	786/792 (99%)	755 (96%)	27 (3%)	4 (0%)	32	39

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	14	ALA
1	B	348	ARG

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	B	347	ASN
1	B	364	GLY

### 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	A	320/320 (100%)	289 (90%)	31 (10%)	9	11
1	B	320/320 (100%)	289 (90%)	31 (10%)	9	11
All	All	640/640 (100%)	578 (90%)	62 (10%)	9	11

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	340	THR
1	B	18	LEU
1	B	348	ARG
1	B	10	THR
1	B	50	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	388	ASN
1	B	175	ASN
1	B	328	GLN
1	A	357	ASN
1	B	339	ASN

### 5.3.3 RNA [i](#)

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	LLP	A	258	1	24,24,25	1.82	5 (20%)	28,32,34	1.90	6 (21%)
1	LLP	B	258	1	24,24,25	1.69	6 (25%)	28,32,34	2.12	8 (28%)

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	LLP	A	258	1	-	0/15/17/19	0/1/1/1
1	LLP	B	258	1	-	0/15/17/19	0/1/1/1

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	258	LLP	O3-C3	-5.33	1.24	1.37
1	B	258	LLP	O3-C3	-4.85	1.25	1.37
1	B	258	LLP	P-OP3	-2.03	1.46	1.54
1	B	258	LLP	C4'-NZ	2.04	1.33	1.27
1	B	258	LLP	C4-C4'	2.25	1.50	1.46

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	258	LLP	C4-C3-C2	-4.28	117.52	120.15
1	B	258	LLP	C5-C4-C4'	-3.96	115.45	121.36
1	B	258	LLP	CE-NZ-C4'	-3.72	108.23	119.03
1	B	258	LLP	C5-C6-N1	-2.81	119.11	123.87
1	A	258	LLP	CE-NZ-C4'	-2.78	110.95	119.03

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	258	LLP	1	0
1	B	258	LLP	2	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	$\# Z  > 2$
2	HCI	A	410	-	8,11,11	0.87	0	10,13,13	0.78	0
2	HCI	B	410	-	8,11,11	1.29	0	10,13,13	0.49	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
2	HCI	A	410	-	-	0/3/5/5	0/1/1/1
2	HCI	B	410	-	-	0/3/5/5	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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, 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	395/396 (99%)	-0.18	13 (3%) 47 54	18, 26, 38, 46	0
1	B	395/396 (99%)	-0.45	6 (1%) 74 79	15, 24, 41, 51	0
All	All	790/792 (99%)	-0.31	19 (2%) 59 66	15, 25, 39, 51	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	14	ALA	5.2
1	A	347	ASN	4.0
1	B	12	THR	3.0
1	A	252	VAL	2.9
1	A	270	CYS	2.8

### 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(Å <sup>2</sup> )	Q<0.9
1	LLP	A	258	24/25	0.98	0.18	-	18,23,25,26	0
1	LLP	B	258	24/25	0.98	0.10	-	15,18,19,22	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(Å <sup>2</sup> )	Q<0.9
2	HCI	A	410	11/11	0.96	0.13	0.02	20,22,24,26	0
2	HCI	B	410	11/11	0.97	0.08	-0.91	14,18,20,20	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.