

# Full wwPDB X-ray Structure Validation Report (i)

#### Mar 26, 2024 – 10:31 AM EDT

PDB ID : 6VJU

Title : Crystal Structure of Cystathionine beta synthase from Legionella pneumophila

with LLP, PLP, and homocysteine

Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)

Deposited on : 2020-01-17

Resolution : 1.30 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*A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

 $Mol Probity \quad : \quad 4.02b\text{--}467$ 

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36.1

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac : 5.8.0158

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

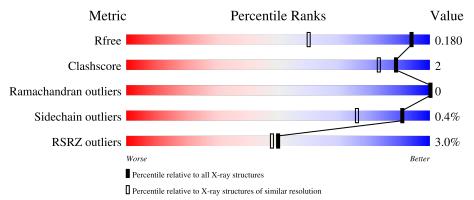
Validation Pipeline (wwPDB-VP) : 2.36.1

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 1.30 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	Similar resolution
Metric	$(\#  ext{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	1058 (1.30-1.30)
Clashscore	141614	1101 (1.30-1.30)
Ramachandran outliers	138981	1058 (1.30-1.30)
Sidechain outliers	138945	1058 (1.30-1.30)
RSRZ outliers	127900	1029 (1.30-1.30)

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 of the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	324	93% •	-
2	В	324	94%	



# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5581 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 Cystathionine beta-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	317	Total 2433	C 1553	N 405	O 461	P 1	S 13	0	7	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A2S6F0T8
A	2	ALA	-	expression tag	UNP A0A2S6F0T8
A	3	HIS	-	expression tag	UNP A0A2S6F0T8
A	4	HIS	-	expression tag	UNP A0A2S6F0T8
A	5	HIS	-	expression tag	UNP A0A2S6F0T8
A	6	HIS	-	expression tag	UNP A0A2S6F0T8
A	7	HIS	-	expression tag	UNP A0A2S6F0T8
A	8	HIS	-	expression tag	UNP A0A2S6F0T8

• Molecule 2 is a protein called Cystathionine beta-lyase.

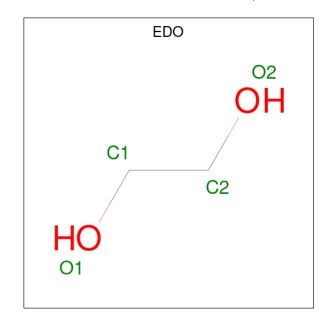
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	317	Total 2439	C 1554	N 405	O 467	S 13	0	8	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual Comment		Reference	
В	1	MET	-	initiating methionine	UNP A0A2S6F0T8	
В	2	ALA	-	expression tag	UNP A0A2S6F0T8	
В	3	HIS	-	expression tag	UNP A0A2S6F0T8	
В	4	HIS	-	expression tag	UNP A0A2S6F0T8	
В	5	HIS	-	expression tag	UNP A0A2S6F0T8	
В	6	HIS	-	expression tag	UNP A0A2S6F0T8	
В	7	HIS	-	expression tag	UNP A0A2S6F0T8	
В	8	HIS	-	expression tag	UNP A0A2S6F0T8	



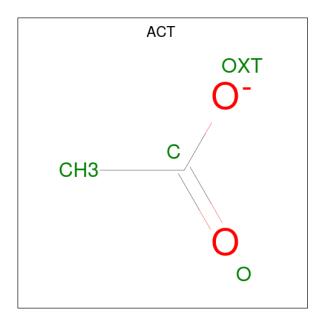
• Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	В	1	Total C O 4 2 2	0	0
3	В	1	Total C O 4 2 2	0	0
3	В	1	Total C O 4 2 2	0	0
3	В	1	Total C O 4 2 2	0	0
3	В	1	Total C O 4 2 2	0	0
3	В	1	Total C O 4 2 2	0	0

• Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).

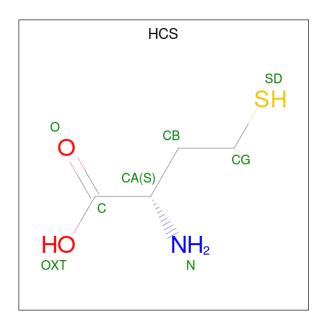




Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 8 4 4	0	1
4	В	1	Total C O 4 2 2	0	1
4	В	1	Total C O 4 2 2	0	0

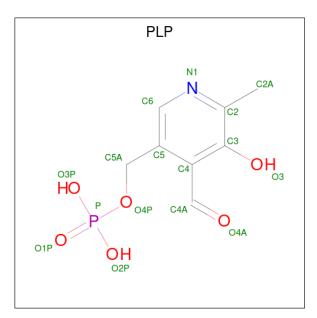
 $\bullet$  Molecule 5 is 2-AMINO-4-MERCAPTO-BUTYRIC ACID (three-letter code: HCS) (formula: C\_4H\_9NO\_2S).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
5	Λ	1	Total	С	N	О	S	0	0
9	А	1	8	4	1	2	1	0	U

 $\bullet \ \ \mathrm{Molecule} \ 6 \ \mathrm{is} \ \mathrm{PYRIDOXAL-5'-PHOSPHATE} \ (\mathrm{three-letter} \ \mathrm{code} \colon \mathrm{PLP}) \ (\mathrm{formula:} \ \mathrm{C_8H_{10}NO_6P}).$ 



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
6	B	1	Total	С	N	О	Р	0	1
	ט	1	31	16	2	11	2	U	1

• Molecule 7 is water.



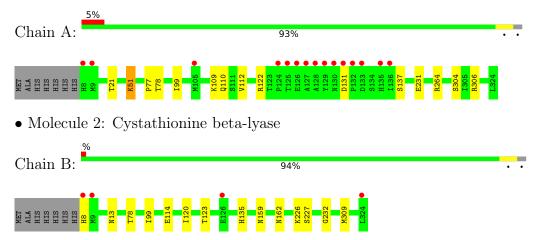
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	272	Total O 272 272	0	0
7	В	326	Total O 326 326	0	0



# 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: Cystathionine beta-lyase





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	65.35Å 91.79Å 93.77Å	Donositon
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	41.22 - 1.30	Depositor
Resolution (A)	41.22 - 1.30	EDS
% Data completeness	99.7 (41.22-1.30)	Depositor
(in resolution range)	99.7 (41.22-1.30)	EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.53 (at 1.30Å)	Xtriage
Refinement program	PHENIX 1.17.1-3660	Depositor
D D.	0.148 , 0.180	Depositor
$R, R_{free}$	0.148 , $0.180$	DCC
$R_{free}$ test set	1955 reflections (1.41%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	13.4	Xtriage
Anisotropy	0.683	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36 , 47.0	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	0.017 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	5581	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.05% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: HCS, PLP, LLP, EDO, ACT

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		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.30	0/2475	0.53	0/3345	
2	В	0.30	0/2509	0.55	0/3392	
All	All	0.30	0/4984	0.54	0/6737	

There are no bond length outliers.

There are no bond angle outliers.

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	2433	0	2439	11	0
2	В	2439	0	2451	9	0
3	A	16	0	24	0	0
3	В	24	0	36	2	0
4	A	24	0	18	1	0
4	В	8	0	6	0	0
5	A	8	0	8	0	0
6	В	31	0	15	0	0
7	A	272	0	0	4	0
7	В	326	0	0	2	0
All	All	5581	0	4997	19	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 2.

All (19) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance } (\text{\AA}) \end{array}$	Clash overlap (Å)
1:A:112:VAL:HG23	2:B:309[B]:MET:HE1	1.79	0.65
1:A:264:ARG:NH1	7:A:605:HOH:O	2.30	0.63
1:A:21:THR:HA	4:A:507:ACT:H1	1.84	0.58
2:B:114:GLU:HG3	2:B:120:ILE:HD13	1.89	0.54
1:A:77:PRO:O	7:A:601:HOH:O	2.19	0.53
2:B:8:HIS:N	7:B:606:HOH:O	2.42	0.52
1:A:51:LLP:OP2	1:A:51:LLP:H4'1	2.10	0.50
1:A:131:ASP:O	7:A:602:HOH:O	2.20	0.49
2:B:232:GLY:H	3:B:502:EDO:H22	1.80	0.47
1:A:109:LYS:NZ	1:A:231:GLU:OE1	2.31	0.47
2:B:159:ASN:HA	2:B:162:ASN:HB2	1.96	0.47
2:B:13:ASN:HD21	3:B:504:EDO:H12	1.81	0.44
1:A:306:ARG:HD3	7:B:716:HOH:O	2.18	0.43
2:B:123:THR:HG21	2:B:135:HIS:HA	2.00	0.43
1:A:78:THR:HG22	1:A:99[B]:ILE:HG23	2.02	0.42
2:B:226:LYS:HE3	2:B:226:LYS:HB3	1.85	0.42
1:A:137[A]:SER:OG	7:A:602:HOH:O	2.21	0.41
2:B:78:THR:CG2	2:B:99[A]:ILE:HG23	2.51	0.41
1:A:110:GLN:OE1	1:A:122:ARG:NH2	2.45	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	Perce	entiles
1	A	321/324 (99%)	314 (98%)	7 (2%)	0	100	100
2	В	323/324 (100%)	316 (98%)	7 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	644/648 (99%)	630 (98%)	14 (2%)	0	100 100

There are no Ramachandran outliers to report.

#### 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	252/261 (97%)	251 (100%)	1 (0%)	91 76		
2	В	259/262 (99%)	257 (99%)	2 (1%)	81 58		
All	All	511/523 (98%)	508 (99%)	3 (1%)	91 65		

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	304	SER
2	В	227[A]	SER
2	В	227[B]	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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).

Mal	Type	Chain	Pog	Link	Bo	ond leng	$ ag{ths}$	В	ond ang	les
MIOI	туре	Chain	rtes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	LLP	A	51	1	23,24,25	1.38	2 (8%)	25,32,34	1.00	1 (4%)

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.

$\mathbf{Mol}$	$\mathbf{Type}$	Chain	Res	Link	Chirals	Torsions	Rings
1	LLP	A	51	1	-	2/16/17/19	0/1/1/1

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
1	A	51	LLP	C4'-NZ	5.29	1.45	1.27
1	A	51	LLP	C4-C4'	3.12	1.52	1.46

#### All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	51	LLP	CE-NZ-C4'	-2.54	111.09	118.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	51	LLP	CG-CD-CE-NZ
1	A	51	LLP	CE-CD-CG-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes	
1	A	51	LLP	1	0	



### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry (i)

21 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	Во	ond leng	ths	В	ond ang	les
IVIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	В	503	-	3,3,3	0.45	0	2,2,2	0.36	0
4	ACT	A	508	-	3,3,3	1.29	0	3,3,3	1.53	0
4	ACT	A	510[A]	-	3,3,3	1.24	0	3,3,3	1.40	0
3	EDO	В	505	-	3,3,3	0.45	0	2,2,2	0.35	0
3	EDO	В	502	-	3,3,3	0.42	0	2,2,2	0.17	0
3	EDO	В	504	-	3,3,3	0.46	0	2,2,2	0.35	0
4	ACT	A	504	-	3,3,3	1.30	0	3,3,3	1.49	0
3	EDO	В	501	-	3,3,3	0.44	0	2,2,2	0.33	0
3	EDO	В	508	-	3,3,3	0.43	0	2,2,2	0.48	0
4	ACT	В	509	-	3,3,3	1.33	0	3,3,3	1.35	0
6	PLP	В	507[B]	2	15,15,16	0.96	0	20,22,23	0.97	1 (5%)
3	EDO	A	503	-	3,3,3	0.44	0	2,2,2	0.43	0
6	PLP	В	507[A]	-	16,16,16	1.08	0	20,23,23	0.74	0
3	EDO	A	502	-	3,3,3	0.37	0	2,2,2	0.90	0
4	ACT	A	505	-	3,3,3	1.21	0	3,3,3	1.35	0
4	ACT	A	507	-	3,3,3	1.25	0	3,3,3	1.38	0
3	EDO	A	506	-	3,3,3	0.45	0	2,2,2	0.40	0
3	EDO	A	501	-	3,3,3	0.42	0	2,2,2	0.48	0
4	ACT	В	506[B]	-	3,3,3	1.29	0	3,3,3	1.29	0
4	ACT	A	510[B]	-	3,3,3	1.24	0	3,3,3	1.40	0
5	HCS	A	509	-	6,7,7	1.26	1 (16%)	7,8,8	3.27	4 (57%)

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	В	503	-	-	1/1/1/1	-
6	PLP	В	507[A]	-	-	0/8/8/8	0/1/1/1
3	EDO	A	501	-	-	0/1/1/1	-
3	EDO	A	502	-	-	1/1/1/1	-
3	EDO	В	505	-	-	0/1/1/1	_
3	EDO	В	502	-	-	1/1/1/1	-
6	PLP	В	507[B]	2	-	0/6/6/8	0/1/1/1
3	EDO	В	504	-	-	1/1/1/1	-
5	HCS	A	509	-	-	1/7/7/7	-
3	EDO	A	506	-	-	0/1/1/1	-
3	EDO	В	501	-	-	0/1/1/1	-
3	EDO	A	503	-	-	1/1/1/1	-
3	EDO	В	508	-	-	0/1/1/1	-

### All (1) bond length outliers are listed below:

]	Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
	5	A	509	HCS	CB-CG	-2.04	1.50	1.52

### All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
5	A	509	HCS	CB-CG-SD	-5.67	107.83	113.74
5	A	509	HCS	CG-CB-CA	-4.69	105.49	113.14
5	A	509	HCS	OXT-C-O	-2.92	117.45	124.09
6	В	507[B]	PLP	O4P-C5A-C5	2.13	113.41	109.35
5	A	509	HCS	CB-CA-C	-2.08	105.35	110.30

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	509	HCS	CA-CB-CG-SD
3	В	504	EDO	O1-C1-C2-O2
3	В	502	EDO	O1-C1-C2-O2
3	A	502	EDO	O1-C1-C2-O2
3	В	503	EDO	O1-C1-C2-O2
3	A	503	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 3 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	502	EDO	1	0
3	В	504	EDO	1	0
4	A	507	ACT	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,  $95^{th}$  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	$OWAB(A^2)$	Q<0.9
1	A	316/324 (97%)	-0.09	15 (4%) 31 29	11, 17, 40, 66	0
2	В	317/324 (97%)	-0.27	4 (1%) 77 79	12, 17, 27, 43	0
All	All	633/648 (97%)	-0.18	19 (3%) 50 48	11, 17, 32, 66	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	128	ALA	7.9
1	A	129	TYR	4.4
2	В	8	HIS	4.3
1	A	124	PRO	4.1
1	A	132	PRO	4.1
1	A	8	HIS	4.1
1	A	127	ALA	3.4
1	A	9	MET	3.3
1	A	131	ASP	3.2
2	В	9	MET	3.1
1	A	126	GLU	2.9
1	A	133	ASP	2.9
1	A	136	ILE	2.8
1	A	125	THR	2.7
2	В	126	GLU	2.3
1	A	105	MET	2.2
2	В	324	LEU	2.1
1	A	130	ASN	2.1
1	A	135	HIS	2.0

## 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. The B-factors column lists the minimum,



median,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	LLP	A	51	24/25	0.98	0.07	12,13,17,17	0

## 6.3 Carbohydrates (i)

There are no monosaccharides 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,  $95^{th}$  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	$ extbf{B-factors}( extbf{A}^2)$	Q<0.9
4	ACT	В	509	4/4	0.54	0.26	40,41,42,43	0
4	ACT	A	507	4/4	0.56	0.17	37,40,40,41	0
3	EDO	В	505	4/4	0.66	0.24	60,60,61,61	0
4	ACT	A	504	4/4	0.75	0.13	53,54,55,56	0
3	EDO	A	506	4/4	0.78	0.17	60,61,61,62	0
3	EDO	В	503	4/4	0.78	0.15	50,51,51,51	0
4	ACT	A	508	4/4	0.80	0.14	54,54,55,55	0
3	EDO	В	508	4/4	0.81	0.12	50,50,51,51	0
3	EDO	A	501	4/4	0.83	0.12	49,50,50,50	0
3	EDO	A	503	4/4	0.84	0.14	39,40,41,42	0
5	HCS	A	509	8/8	0.85	0.18	52,59,62,62	0
3	EDO	В	504	4/4	0.86	0.09	59,59,60,60	0
4	ACT	A	510[A]	4/4	0.87	0.28	27,28,28,30	4
4	ACT	A	510[B]	4/4	0.87	0.28	29,30,31,31	4
3	EDO	A	502	4/4	0.88	0.11	59,59,59,60	0
3	EDO	В	502	4/4	0.90	0.16	20,24,26,26	0
3	EDO	В	501	4/4	0.90	0.13	47,48,48,48	0
4	ACT	A	505	4/4	0.93	0.10	27,27,27,27	0
4	ACT	В	506[B]	4/4	0.97	0.08	19,20,20,21	4
6	PLP	В	507[A]	16/16	0.98	0.06	11,12,15,18	16
6	PLP	В	507[B]	15/16	0.98	0.06	14,15,17,20	15

## 6.5 Other polymers (i)

There are no such residues in this entry.

