

Full wwPDB X-ray Structure Validation Report (i)

Sep 9, 2023 – 07:02 PM EDT

PDB ID	:	4ITG
Title	:	P113S mutant of E. coli Cystathionine beta-lyase MetC
Authors	:	Squire, C.J.; Yosaatmadja, Y.; Soo, V.W.C.; Patrick, W.M.
Deposited on		
Resolution	:	1.74 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:

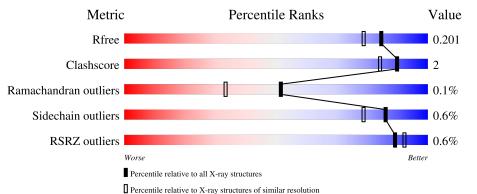
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.74 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	3764(1.76-1.72)
Clashscore	141614	3923 (1.76-1.72)
Ramachandran outliers	138981	3878 (1.76-1.72)
Sidechain outliers	138945	3878 (1.76-1.72)
RSRZ outliers	127900	3705 (1.76-1.72)

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	А	395	93%	5% ••						
1	В	395	% 92%	7% ••						



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6492 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.

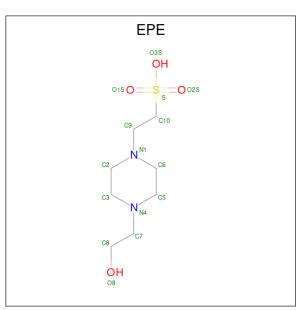
• Molecule 1 is a protein called Cystathionine beta-lyase MetC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	А	391	Total 3065	C 1943	N 533	0 574	Р 1	S 14	0	5	0
1	В	392	Total 3020	C 1914	N 526	O 565	Р 1	S 14	0	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	113	SER	PRO	engineered mutation	UNP P06721
В	113	SER	PRO	engineered mutation	UNP P06721

• Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	А	1	Total 15	C 8	N 2	0 4	S 1	0	0



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
0	Р	1	Total	С	Ν	0	S	0	0
	D	1	15	8	2	4	1	0	0

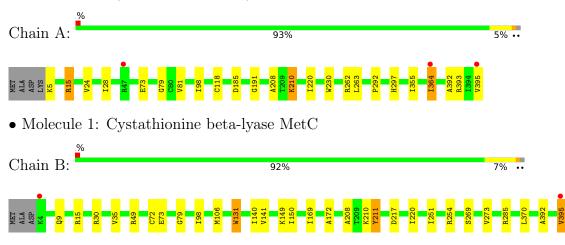
• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	193	Total O 193 193	0	0
3	В	184	Total O 184 184	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 MetC



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	59.93Å 152.77Å 150.85Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.40 - 1.74	Depositor
Resolution (A)	19.40 - 1.74	EDS
% Data completeness	99.5 (19.40-1.74)	Depositor
(in resolution range)	99.5(19.40-1.74)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$4.80 (at 1.74 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
D D.	0.160 , 0.198	Depositor
R, R_{free}	0.165 , 0.201	DCC
R_{free} test set	3587 reflections $(5.06%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	16.1	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.37, 38.6	EDS
L-test for twinning ²	$ < L >=0.43, < L^2>=0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6492	wwPDB-VP
Average B, all atoms $(Å^2)$	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 20.34 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.8812e-03.

²Theoretical 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.



¹Intensities 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: EPE, 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	Bo	nd lengths	Bond angles		
	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	1.04	4/3113~(0.1%)	0.96	6/4220~(0.1%)	
1	В	1.00	3/3060~(0.1%)	0.95	9/4151~(0.2%)	
All	All	1.02	7/6173~(0.1%)	0.95	15/8371~(0.2%)	

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	73	GLU	CG-CD	6.74	1.62	1.51
1	А	73	GLU	CD-OE2	6.00	1.32	1.25
1	В	35	VAL	CB-CG1	5.74	1.64	1.52
1	В	211	TYR	CE2-CZ	-5.54	1.31	1.38
1	В	131	TRP	CB-CG	-5.44	1.40	1.50
1	А	81	VAL	CB-CG2	5.36	1.64	1.52
1	А	118	CYS	CB-SG	-5.13	1.73	1.81

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	15	ARG	NE-CZ-NH1	10.22	125.41	120.30
1	В	285	ARG	NE-CZ-NH2	-9.62	115.49	120.30
1	В	285	ARG	NE-CZ-NH1	9.20	124.90	120.30
1	В	15	ARG	NE-CZ-NH1	8.72	124.66	120.30
1	В	15	ARG	NE-CZ-NH2	-8.69	115.96	120.30
1	А	15	ARG	NE-CZ-NH2	-8.23	116.19	120.30
1	В	254	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	В	49	ARG	NE-CZ-NH1	6.27	123.44	120.30
1	А	393	ARG	NE-CZ-NH2	-6.11	117.25	120.30
1	А	393	ARG	NE-CZ-NH1	6.05	123.33	120.30
1	В	254	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	А	262	ARG	NE-CZ-NH1	5.64	123.12	120.30



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	149	LYS	CD-CE-NZ	5.38	124.06	111.70
1	В	217	ASP	CB-CG-OD1	5.24	123.01	118.30
1	А	263	LEU	CB-CG-CD1	-5.01	102.47	111.00

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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	А	3065	0	3020	11	0
1	В	3020	0	2965	13	0
2	А	15	0	18	0	0
2	В	15	0	18	0	0
3	А	193	0	0	0	0
3	В	184	0	0	1	0
All	All	6492	0	6021	22	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 (22) 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:A:355:ILE:HG22	1:A:364:ILE:HD11	1.75	0.68
1:B:9:GLN:NE2	1:B:73:GLU:OE2	2.29	0.61
1:B:211:TYR:HB2	3:B:589:HOH:O	2.01	0.60
1:A:355:ILE:CG2	1:A:364:ILE:HD11	2.33	0.58
1:B:269:SER:O	1:B:273:VAL:HG23	2.12	0.49
1:A:208:ALA:HB3	1:A:220:ILE:HG23	1.94	0.48
1:A:185:ASP:OD2	1:A:210:LLP:N1	2.47	0.47
1:B:208:ALA:HB3	1:B:220:ILE:HG23	1.97	0.46
1:A:28:ILE:CD1	1:B:30:ARG:CZ	2.94	0.46
1:A:15:ARG:HD2	1:A:24:VAL:O	2.16	0.45
1:B:72:CYS:SG	1:B:79:GLY:HA2	2.56	0.45



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:140:ILE:HD13	1:B:169:ILE:HG23	1.97	0.45
1:A:79:GLY:HA3	1:A:230:TRP:CE2	2.52	0.43
1:A:292:PRO:HA	1:A:297:HIS:CD2	2.54	0.42
1:B:370:LEU:C	1:B:370:LEU:HD23	2.39	0.42
1:B:141:VAL:HG13	1:B:172:ALA:HB1	2.01	0.41
1:B:106:MET:O	1:B:131:TRP:HA	2.20	0.41
1:A:98:ILE:C	1:A:98:ILE:HD12	2.41	0.41
1:B:98:ILE:HG23	1:B:150:ILE:HD12	2.02	0.41
1:A:28:ILE:HD11	1:B:30:ARG:NH1	2.35	0.40
1:B:392:ALA:HA	1:B:395:VAL:HG22	2.03	0.40
1:A:392:ALA:HA	1:A:395:VAL:HG23	2.04	0.40

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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	А	393/395~(100%)	$381 \ (97\%)$	11 (3%)	1 (0%)	41	23
1	В	390/395~(99%)	379~(97%)	11 (3%)	0	100	100
All	All	783/790~(99%)	760~(97%)	22 (3%)	1 (0%)	51	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	191	GLY

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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.



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	А	322/321~(100%)	320~(99%)	2(1%)	86 79		
1	В	314/321~(98%)	312~(99%)	2(1%)	86 79		
All	All	636/642~(99%)	632~(99%)	4 (1%)	86 79		

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	5	LYS
1	А	364	ILE
1	В	251	ILE
1	В	395	VAL

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)

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	Bo	ond leng	\mathbf{ths}	B	ond ang	gles
IVIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	LLP	В	210	1	$23,\!24,\!25$	2.08	6 (26%)	25,32,34	2.69	13 (52%)
1	LLP	А	210	1	23,24,25	2.52	6 (26%)	25,32,34	2.62	11 (44%)

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



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings				
1	LLP	В	210	1	-	7/16/17/19	0/1/1/1				
1	LLP	А	210	1	-	5/16/17/19	0/1/1/1				

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	210	LLP	C4'-NZ	8.38	1.55	1.27
1	В	210	LLP	C4'-NZ	6.82	1.50	1.27
1	А	210	LLP	C6-N1	4.39	1.43	1.34
1	А	210	LLP	CB-CA	3.67	1.58	1.53
1	А	210	LLP	C2'- $C2$	-3.54	1.44	1.50
1	В	210	LLP	C6-N1	3.44	1.41	1.34
1	А	210	LLP	CD-CE	3.08	1.62	1.51
1	В	210	LLP	C2'- $C2$	-2.77	1.45	1.50
1	В	210	LLP	C4-C5	-2.54	1.38	1.42
1	А	210	LLP	C3-C2	-2.32	1.38	1.40
1	В	210	LLP	CB-CA	2.17	1.56	1.53
1	В	210	LLP	O-C	2.14	1.28	1.19

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	А	210	LLP	C4-C3-C2	6.62	124.28	120.19
1	В	210	LLP	C4-C3-C2	6.33	124.11	120.19
1	А	210	LLP	C4-C4'-NZ	-4.33	104.44	124.31
1	В	210	LLP	C3-C2-N1	-4.30	115.22	120.77
1	В	210	LLP	C4-C4'-NZ	-4.20	105.03	124.31
1	В	210	LLP	OP2-P-OP1	4.00	126.35	110.68
1	А	210	LLP	C3-C2-N1	-3.79	115.87	120.77
1	А	210	LLP	C3-C4-C4'	-3.57	113.76	120.41
1	А	210	LLP	OP4-P-OP1	-3.52	96.61	106.47
1	В	210	LLP	OP4-P-OP1	-3.45	96.80	106.47
1	В	210	LLP	OP2-P-OP4	-3.38	97.74	106.73
1	А	210	LLP	CE-NZ-C4'	3.32	129.08	118.90
1	В	210	LLP	CE-NZ-C4'	3.15	128.58	118.90
1	В	210	LLP	CD-CE-NZ	-3.11	103.31	110.93
1	А	210	LLP	C5-C4-C4'	3.08	126.62	121.56
1	А	210	LLP	OP2-P-OP1	2.94	122.19	110.68
1	В	210	LLP	CG-CD-CE	-2.85	103.65	113.57
1	В	210	LLP	C2'-C2-C3	2.55	124.04	120.89



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	210	LLP	OP3-P-OP4	-2.35	100.49	106.73
1	А	210	LLP	CD-CG-CB	2.29	121.72	113.62
1	В	210	LLP	C3-C4-C5	2.27	120.00	118.26
1	А	210	LLP	C2'-C2-C3	2.17	123.57	120.89
1	А	210	LLP	C6-N1-C2	2.17	123.18	119.17
1	В	210	LLP	OP4-C5'-C5	2.05	113.27	109.35

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There are no chirality outliers.

Mol	Chain	Res	Type	Atoms
1	А	210	LLP	O-C-CA-CB
1	В	210	LLP	C4-C4'-NZ-CE
1	В	210	LLP	O-C-CA-CB
1	А	210	LLP	C4-C4'-NZ-CE
1	В	210	LLP	CG-CD-CE-NZ
1	А	210	LLP	CA-CB-CG-CD
1	А	210	LLP	C3-C4-C4'-NZ
1	А	210	LLP	C5-C4-C4'-NZ
1	В	210	LLP	C3-C4-C4'-NZ
1	В	210	LLP	CD-CE-NZ-C4'
1	В	210	LLP	CA-CB-CG-CD
1	В	210	LLP	C5-C4-C4'-NZ

All (12) torsion outliers are listed below:

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	А	210	LLP	1	0

5.5 Carbohydrates (i)

There are no monosaccharides 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).

Mal	Mol Type	Chain	Dec	Res Link	Bo	Bond lengths			Bond angles		
Moi Type	Unain	Res		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2		
2	EPE	В	401	-	$15,\!15,\!15$	1.11	1 (6%)	18,20,20	2.01	4 (22%)	
2	EPE	А	401	-	15,15,15	1.14	1 (6%)	18,20,20	2.59	6 (33%)	

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	EPE	В	401	-	-	4/9/19/19	0/1/1/1
2	EPE	А	401	-	-	0/9/19/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	401	EPE	C10-S	3.59	1.82	1.77
2	В	401	EPE	C10-S	3.11	1.81	1.77

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	А	401	EPE	O1S-S-C10	-8.25	96.98	106.92
2	В	401	EPE	C6-N1-C2	4.33	118.57	108.83
2	В	401	EPE	C9-N1-C2	4.14	121.82	111.23
2	А	401	EPE	C6-C5-N4	3.74	118.33	110.64
2	В	401	EPE	C9-N1-C6	3.13	119.25	111.23
2	А	401	EPE	C5-N4-C3	3.06	115.71	108.83
2	А	401	EPE	O3S-S-O1S	2.83	118.18	111.27
2	В	401	EPE	O3S-S-C10	2.61	109.98	105.77
2	А	401	EPE	C2-C3-N4	2.33	115.43	110.64
2	А	401	EPE	C6-N1-C2	2.21	113.81	108.83

There are no chirality outliers.

All (4) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
2	В	401	EPE	C10-C9-N1-C2
2	В	401	EPE	C8-C7-N4-C5
2	В	401	EPE	C9-C10-S-O3S
2	В	401	EPE	C9-C10-S-O1S

There are no ring outliers.

No monomer is involved in short contacts.

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		$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	А	390/395~(98%)	-0.31	3 (0%) 86	90	8, 14, 24, 34	0
1	В	391/395~(98%)	-0.26	2 (0%) 91	93	9,15,25,34	0
All	All	781/790 (98%)	-0.28	5 (0%) 89	92	8, 14, 25, 34	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	395	VAL	4.7
1	В	4	LYS	3.3
1	А	395	VAL	2.7
1	А	364	ILE	2.6
1	А	47[A]	ARG	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. 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	$B-factors(Å^2)$	$\mathbf{Q} \! < \! 0.9$
1	LLP	А	210	24/25	0.98	0.07	7,11,21,22	0
1	LLP	В	210	24/25	0.98	0.07	9,12,23,24	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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
2	EPE	В	401	15/15	0.95	0.12	$18,\!33,\!45,\!46$	0
2	EPE	А	401	15/15	0.96	0.11	19,32,41,42	0

6.5 Other polymers (i)

There are no such residues in this entry.

