



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:03 PM GMT

PDB ID : 1II9
Title : CRYSTAL STRUCTURE OF THE ESCHERICHIA COLI ARSENITE-TRANSLOCATING ATPASE IN COMPLEX WITH AMP-PNP
Authors : Zhou, T.; Radaev, S.; Gatti, D.L.; Rosen, B.P.
Deposited on : 2001-04-21
Resolution : 2.60 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
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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

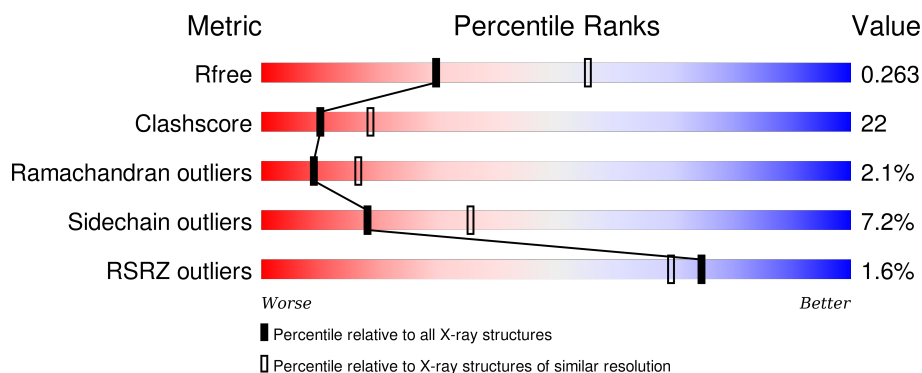
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.60 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}	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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 ≥ 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	589	 56% 32% • 8%
1	B	589	 3% 55% 34% • 7%

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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CL	B	1599	-	-	-	X
7	TAS	A	701	-	-	X	X
7	TAS	B	1701	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 8786 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 ARSENICAL PUMP-DRIVING ATPASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	544	Total	C	N	O	S	0	0	0
			4163	2620	738	790	15			
1	B	550	Total	C	N	O	S	0	0	0
			4202	2641	744	802	15			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	ASN	ILE	SEE REMARK 999	UNP P08690
A	584	HIS	-	EXPRESSION TAG	UNP P08690
A	585	HIS	-	EXPRESSION TAG	UNP P08690
A	586	HIS	-	EXPRESSION TAG	UNP P08690
A	587	HIS	-	EXPRESSION TAG	UNP P08690
A	588	HIS	-	EXPRESSION TAG	UNP P08690
A	589	HIS	-	EXPRESSION TAG	UNP P08690
B	1060	ASN	ILE	SEE REMARK 999	UNP P08690
B	1584	HIS	-	EXPRESSION TAG	UNP P08690
B	1585	HIS	-	EXPRESSION TAG	UNP P08690
B	1586	HIS	-	EXPRESSION TAG	UNP P08690
B	1587	HIS	-	EXPRESSION TAG	UNP P08690
B	1588	HIS	-	EXPRESSION TAG	UNP P08690
B	1589	HIS	-	EXPRESSION TAG	UNP P08690

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Mg	0	0
			2	2		
2	A	2	Total	Mg	0	0
			2	2		

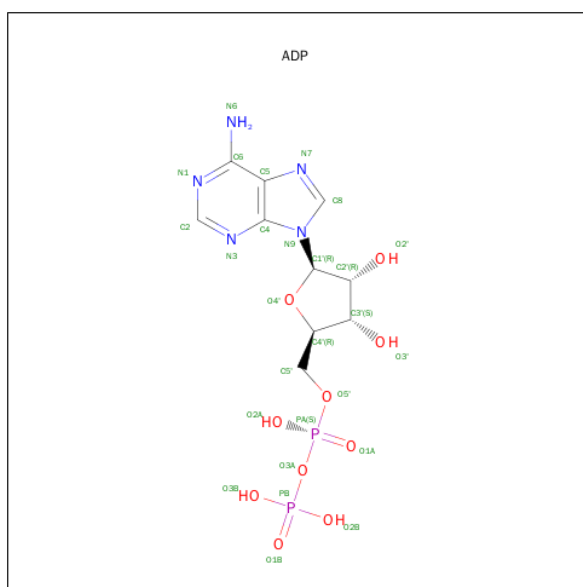
- Molecule 3 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	9	Total	Cd	0	0
			9	9		
3	A	9	Total	Cd	0	0
			9	9		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

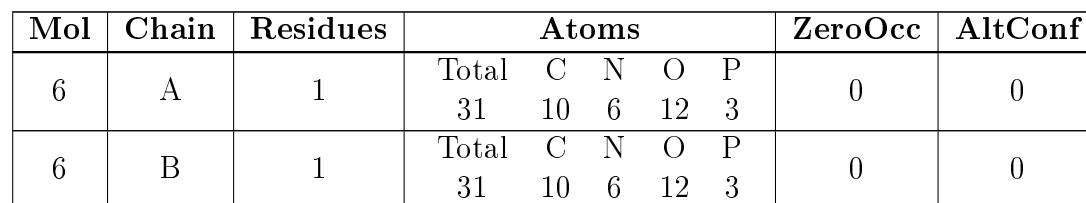
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	3	Total	Cl	0	0
			3	3		
4	A	4	Total	Cl	0	0
			4	4		

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
5	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 6 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



- TAS
-
- The diagram shows the chemical structure of Arsenic acid (H₃AsO₄). The central atom is Arsenic (As), labeled in green as 'AS'. It is bonded to four oxygen atoms. One oxygen atom is part of a hydroxyl group (OH) on the left, labeled in green as '01'. The other three oxygen atoms are part of hydroxyl groups (OH) at the top-right, bottom-right, and bottom-left positions, labeled in green as '02', '03', and '04' respectively. The hydrogen atoms (H) are labeled in red. The bonds are shown as lines, with the bond to the left oxygen atom being a single line, and the bonds to the other three oxygen atoms being single lines with a slight angle.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total 4	As 1	O 3	0	0
7	B	1	Total 4	As 1	O 3	0	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	143	Total 143	O 143	0	0
8	B	125	Total 125	O 125	0	0

K1555	R1556	Q1557	S1560	L1564	V1565	P1566	V1567	L1568	A1569	S1570	E1571	P1572	T1573	G1574	I1575	D1576	K1577	L1578	K1579	Q1580	L1581	A1582	H1585	H1588	H1589																																
ARG	GLU	ILE	ALA	LYS	MET	GLY	LYS	GLY	HIS	PHE	T1479	T1480	P1481	M1482		Q1486	D1487	P1488	E1489		L1495	V1496	T1497	L1498		T1502	P1503	V1504	L1505	L1510	R1516	A1517		I1526	L1530	S1531	I1532	T1535	R1536	S1537		M1542		Q1545	Q1546	E1547	L1548	P1549	Q1550	I1551	E1552	S1553	V1554				
SER	L1377	M1378	N1379	L1380	Q1381	R1384	I1385	Y1394	R1395	Q1396	H1397	V1398	L1399	E1400	T1401	K1402	G1403	K1404	E1405	L1406		K1411		L1414	E1415	E1416	D1417	L1418	R1419	S1420		T1426		Q1430	A1431	F1432		V1435	I1436	R1437		K1441	R1442	F1443		M1446		L1455	L1456	L1457		A1460	T1461	GLY	ALA	TYR	HIS
L1291	L1292	S1293	T1294	Q1295	PRO	VAL	ALA	SER	PRO	SER	SER	ASP	GLU	TYR	LEU	Q1307	Q1308		I1312	L1315		L1318	V1319		I1322		I1330	M1331	L1332		M1343	A1344		V1349	R1350	L1351		M1354		D1357	V1358	H1359	L1360	T1361		D1364	F1365	A1366	A1367	HIS	LEU	SER	MET	THR	ASN	GLY	

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	76.62Å 222.53Å 74.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.52 – 2.60 37.02 – 2.60	Depositor EDS
% Data completeness (in resolution range)	93.5 (36.52-2.60) 93.4 (37.02-2.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.61Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.191 , 0.265 0.190 , 0.263	Depositor DCC
R_{free} test set	3728 reflections (11.11%)	DCC
Wilson B-factor (Å ²)	43.1	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 60.7	EDS
Estimated twinning fraction	0.023 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 38395 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8786	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, ADP, CL, TAS, CD, ANP

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	0.41	0/4233	0.69	0/5752
1	B	0.42	0/4271	0.66	1/5803 (0.0%)
All	All	0.41	0/8504	0.68	1/11555 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1406	LEU	N-CA-C	-5.56	95.98	111.00

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	4163	0	4226	200	0
1	B	4202	0	4259	175	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	9	0	0	0	0
3	B	9	0	0	0	0
4	A	4	0	0	1	0
4	B	3	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	27	0	12	5	0
5	B	27	0	12	2	0
6	A	31	0	13	2	0
6	B	31	0	13	0	0
7	A	4	0	0	2	0
7	B	4	0	0	0	0
8	A	143	0	0	3	0
8	B	125	0	0	6	0
All	All	8786	0	8535	375	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 22.

The worst 5 of 375 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:27:ALA:HB1	1:A:292:LEU:HD21	1.27	1.10
1:A:248:LEU:HD23	1:A:535:THR:HB	1.38	1.02
1:B:1322:ILE:HD13	1:B:1330:ILE:HD11	1.42	1.01
1:B:1209:LYS:HG2	1:B:1213:GLN:HE21	1.26	0.99
1:A:235:ASN:HD21	5:A:590:ADP:HN61	1.02	0.95

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	534/589 (91%)	488 (91%)	35 (7%)	11 (2%)	9	16
1	B	540/589 (92%)	495 (92%)	33 (6%)	12 (2%)	8	15
All	All	1074/1178 (91%)	983 (92%)	68 (6%)	23 (2%)	9	16

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	283	VAL
1	A	570	SER
1	B	1262	ASN
1	B	1293	SER
1	A	404	LYS

5.3.2 Protein sidechains ⓘ

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	451/487 (93%)	420 (93%)	31 (7%)	19	38
1	B	455/487 (93%)	421 (92%)	34 (8%)	17	33
All	All	906/974 (93%)	841 (93%)	65 (7%)	18	35

5 of 65 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	566	PRO
1	B	1126	LEU
1	B	1510	LEU
1	A	571	GLU
1	B	1040	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	528	ASN
1	B	1079	GLN
1	B	1486	GLN
1	B	1035	GLN
1	B	1052	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 35 ligands modelled in this entry, 29 are monoatomic - leaving 6 for Mogul analysis.

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	$\# Z > 2$
5	ADP	A	590	2	22,29,29	1.24	2 (9%)	27,45,45	6.34	16 (59%)
6	ANP	A	591	2	27,33,33	1.59	5 (18%)	30,52,52	4.37	14 (46%)
7	TAS	A	701	-	0,3,3	0.00	-	0,3,3	0.00	-
5	ADP	B	1590	2	22,29,29	1.22	2 (9%)	27,45,45	5.34	15 (55%)
6	ANP	B	1591	2	27,33,33	1.43	6 (22%)	30,52,52	4.51	12 (40%)
7	TAS	B	1701	-	0,3,3	0.00	-	0,3,3	0.00	-

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
5	ADP	A	590	2	-	0/12/32/32	0/3/3/3
6	ANP	A	591	2	-	0/12/38/38	0/3/3/3
7	TAS	A	701	-	-	0/0/0/0	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ADP	B	1590	2	-	0/12/32/32	0/3/3/3
6	ANP	B	1591	2	-	0/12/38/38	0/3/3/3
7	TAS	B	1701	-	-	0/0/0/0	0/0/0/0

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	590	ADP	C8-N7	-3.29	1.28	1.34
5	B	1590	ADP	C8-N7	-3.18	1.28	1.34
6	A	591	ANP	PB-O2B	-2.69	1.49	1.56
6	B	1591	ANP	PG-O2G	-2.68	1.49	1.56
6	A	591	ANP	PG-O2G	-2.42	1.49	1.56

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1590	ADP	N3-C2-N1	-15.63	116.93	128.89
6	A	591	ANP	N3-C2-N1	-14.01	118.17	128.89
6	B	1591	ANP	N3-C2-N1	-13.36	118.67	128.89
5	A	590	ADP	N3-C2-N1	-12.07	119.65	128.89
6	B	1591	ANP	O1B-PB-N3B	-10.92	95.15	111.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	590	ADP	5	0
6	A	591	ANP	2	0
7	A	701	TAS	2	0
5	B	1590	ADP	2	0

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, 95th 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 ²)	Q<0.9
1	A	544/589 (92%)	-0.18	2 (0%) 93 91	21, 42, 76, 94	0
1	B	550/589 (93%)	-0.13	15 (2%) 58 51	20, 42, 77, 100	0
All	All	1094/1178 (92%)	-0.15	17 (1%) 74 69	20, 42, 76, 100	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1307	GLN	4.8
1	B	1308	GLN	4.4
1	B	1162	PHE	4.0
1	B	1168	GLU	3.5
1	A	245	ASN	3.3

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 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, 95th 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(\AA^2)	Q<0.9
7	TAS	A	701	4/4	0.79	0.52	9.20	80,81,83,90	4
7	TAS	B	1701	4/4	0.81	0.51	6.98	72,74,74,85	4
4	CL	B	1599	1/1	0.95	0.21	3.90	75,75,75,75	0
5	ADP	A	590	27/27	0.97	0.18	0.21	37,45,56,59	0
5	ADP	B	1590	27/27	0.96	0.17	-0.04	35,44,51,52	0
3	CD	A	595	1/1	1.00	0.12	-0.62	34,34,34,34	0
6	ANP	A	591	31/31	0.98	0.14	-0.75	27,41,52,54	0
3	CD	B	1596	1/1	1.00	0.11	-1.01	36,36,36,36	0
4	CL	A	599	1/1	1.00	0.11	-1.29	69,69,69,69	0
3	CD	A	596	1/1	1.00	0.10	-1.36	34,34,34,34	0
4	CL	A	598	1/1	1.00	0.10	-1.46	35,35,35,35	0
3	CD	B	1595	1/1	1.00	0.11	-1.49	30,30,30,30	0
6	ANP	B	1591	31/31	0.98	0.12	-1.55	23,35,48,50	0
4	CL	B	1598	1/1	0.99	0.09	-2.22	32,32,32,32	0
4	CL	A	2000	1/1	0.99	0.08	-2.44	27,27,27,27	0
4	CL	B	1597	1/1	0.99	0.10	-2.78	28,28,28,28	0
4	CL	A	597	1/1	1.00	0.06	-4.78	28,28,28,28	0
3	CD	B	1607	1/1	0.99	0.03	-	84,84,84,84	0
3	CD	B	1605	1/1	0.91	0.17	-	89,89,89,89	1
3	CD	A	594	1/1	1.00	0.11	-	40,40,40,40	0
3	CD	A	605	1/1	0.94	0.09	-	60,60,60,60	1
2	MG	B	1592	1/1	0.99	0.15	-	24,24,24,24	0
3	CD	A	604	1/1	0.98	0.08	-	46,46,46,46	0
3	CD	A	600	1/1	1.00	0.10	-	29,29,29,29	0
2	MG	B	1593	1/1	0.98	0.12	-	14,14,14,14	0
3	CD	A	601	1/1	1.00	0.12	-	31,31,31,31	0
3	CD	B	1603	1/1	0.96	0.08	-	78,78,78,78	0
3	CD	B	1606	1/1	0.80	0.08	-	118,118,118,118	1
3	CD	B	1602	1/1	0.99	0.09	-	38,38,38,38	0
2	MG	A	592	1/1	0.97	0.19	-	17,17,17,17	0
2	MG	A	593	1/1	0.98	0.14	-	21,21,21,21	0
3	CD	A	603	1/1	0.96	0.07	-	98,98,98,98	0
3	CD	A	602	1/1	1.00	0.09	-	39,39,39,39	0
3	CD	B	1601	1/1	1.00	0.09	-	32,32,32,32	0
3	CD	B	1594	1/1	1.00	0.10	-	35,35,35,35	0

6.5 Other polymers ⓘ

There are no such residues in this entry.