

Full wwPDB X-ray Structure Validation Report (i)

May 26, 2020 – 02:09 pm BST

PDB ID	:	2G8S
Title	:	Crystal structure of the soluble Aldose sugar dehydrogenase (Asd) from Es-
		cherichia coli in the apo-form
Authors	:	Southall, S.M.; Doel, J.J.; Richardson, D.J.; Oubrie, A.
Deposited on	:	2006-03-03
Resolution	:	1.50 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 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 as 541 be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
$\operatorname{CCP4}$:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 1.50 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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 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	353	88%	10%	·
1	В	353	% 	11%	••

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	EDO	В	3014	-	-	Х	-



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7102 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	Δ	3/18	Total	\mathbf{C}	Ν	Ο	Se	0	46	0
	Л	040	2989	1914	523	542	10	0	40	0
1	р	247	Total	С	Ν	Ο	Se	0	49	0
	D	347	2974	1900	520	546	8	0	42	0

• Molecule 1 is a protein called Glucose/sorbosone dehydrogenases.

Chain	Residue	Modelled	Actual	$\mathbf{Comment}$	Reference
А	-2	GLY	-	CLONING ARTIFACT	UNP P75804
А	-1	ALA	-	CLONING ARTIFACT	UNP P75804
А	0	MET	-	CLONING ARTIFACT	UNP P75804
A	29	MSE	MET	MODIFIED RESIDUE	UNP P75804
А	119	MSE	MET	MODIFIED RESIDUE	UNP P75804
A	199	MSE	MET	MODIFIED RESIDUE	UNP P75804
A	201	MSE	MET	MODIFIED RESIDUE	UNP P75804
A	273	MSE	MET	MODIFIED RESIDUE	UNP P75804
A	301	MSE	MET	MODIFIED RESIDUE	UNP P75804
В	-2	GLY	-	CLONING ARTIFACT	UNP P75804
В	-1	ALA	-	CLONING ARTIFACT	UNP P75804
В	0	MET	-	CLONING ARTIFACT	UNP P75804
В	29	MSE	MET	MODIFIED RESIDUE	UNP P75804
В	119	MSE	MET	MODIFIED RESIDUE	UNP P75804
В	199	MSE	MET	MODIFIED RESIDUE	UNP P75804
В	201	MSE	MET	MODIFIED RESIDUE	UNP P75804
В	273	MSE	MET	MODIFIED RESIDUE	UNP P75804
В	301	MSE	MET	MODIFIED RESIDUE	UNP P75804

There are 18 discrepancies between the modelled and reference sequences:

• Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	Total Ca 1 1	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Ca 1 1	0	0

• Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	А	1	Total 5	0 4	Р 1	0	0

• Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).





Mol	Chain	Residues	Ate	Atoms		ZeroOcc	AltConf
4	Δ	1	Total	С	Ο	0	0
4	A	1	4	2	2	0	0
4	Δ	1	Total	С	0	0	Ο
4		T	4	2	2	0	0
4	А	1	Total	С	Ο	0	0
-		-	4	2	2	Ŭ	
4	A	1	Total	С	0	0	1
_		_	8	4	4		
4	А	1	Total	C	0	0	0
			4	2	2		
4	А	1	Total	C	0	0	1
			8 T- 4 - 1	$\frac{4}{C}$	4		
4	А	1		0 0	0	0	0
			4 Total	$\frac{2}{C}$	2		
4	A	1		0 2	0 9	0	0
			Total	$\frac{2}{C}$	<u></u>		
4	A	1	4	$\frac{1}{2}$	$\frac{1}{2}$	0	0
			Total	$\frac{1}{C}$	$\frac{1}{0}$		
4	A	1	4	2	2	0	0
			Total	С	0		
4	A	l	4	2	2	0	0
4	Δ	-1	Total	С	Ο	0	0
4	A	T	4	2	2	0	0
4	Δ	1	Total	С	Ο	0	0
4	А	T	4	2	2	0	0
1	B	1	Total	С	0	0	0
4	D	Ţ	4	2	2	0	0
4	В	1	Total	С	Ο	0	0
-			4	2	2	0	0
4	В	1	Total	С	Ο	0	0
-		-	4	2	2	Ŭ	
4	В	1	Total	С	0	0	0
			4	$\frac{2}{2}$	2		
4	В	1	Total	C	0	0	0
			4 	$\frac{2}{C}$	$\frac{2}{0}$		
4	В	1	10tal	U n	0 9	0	0
			$\frac{4}{T_{atal}}$	$\frac{2}{C}$	2		
4	В	1		し う	0 2	0	0
			Total	$\frac{2}{C}$	<u></u>		
4	В	1	10tai 4	$\frac{1}{2}$	2	0	0
			 Total	$\frac{2}{C}$	$\frac{2}{0}$		
4	В	1	4	$\frac{1}{2}$	$\frac{1}{2}$	0	0
			±	-	$\frac{-}{Co}$	ntinued on a	l



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
4	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
4	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	480	Total O 492 492	0	12
5	В	520	Total O 532 532	0	12



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: Glucose/sorbosone dehydrogenases



• Molecule 1: Glucose/sorbosone dehydrogenases





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	40.83Å 11 3.47 Å 7 5.37 Å	Deperitor
$\mathrm{a,b,c,\alpha,\beta,\gamma}$	90.00° 90.03° 90.00°	Depositor
$\mathbf{P}_{\text{assolution}}(\hat{\mathbf{A}})$	7.96 - 1.50	Depositor
Resolution (A)	7.96 - 1.50	EDS
% Data completeness	94.2 (7.96-1.50)	Depositor
(in resolution range $)$	$94.0\ (7.96-1.50)$	EDS
R _{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) > 1$	$3.21 (at 1.50 \text{\AA})$	Xtriage
Refinement program	REFMAC	Depositor
D D.	0.149 , 0.183	Depositor
Π, Π_{free}	0.147 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor $(Å^2)$	10.2	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.50 , 57.8	EDS
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.479 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7102	wwPDB-VP
Average B, all atoms $(Å^2)$	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.60% of the height of the origin peak. No significant pseudotranslation is detected.

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.



 $^{^1 {\}rm Intensities}$ 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: CA, PO4, EDO

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).

Mal	Mal Chain		nd lengths	Bond angles	
	Cham	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.41	0/3181	0.61	0/4281
1	В	0.45	3/3141~(0.1%)	0.62	0/4233
All	All	0.43	3/6322~(0.0%)	0.61	0/8514

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	В	29[A]	MSE	CG-SE	-6.16	1.74	1.95
1	В	29[B]	MSE	CG-SE	-6.16	1.74	1.95
1	В	273	MSE	SE-CE	-5.06	1.65	1.95

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	А	2989	0	3052	38	1
1	В	2974	0	3000	64	0
2	А	1	0	0	0	0
2	В	1	0	0	0	0
3	А	5	0	0	0	0
4	А	60	0	90	8	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	В	48	0	72	14	0
5	А	492	0	0	12	0
5	В	532	0	0	32	1
All	All	7102	0	6214	101	1

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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 8.

All (101) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:29[B]:MSE:CE	4:B:3014:EDO:H12	1.28	1.63
1:B:29[B]:MSE:HE2	4:B:3014:EDO:C1	1.40	1.48
1:B:108[B]:LYS:NZ	5:B:3254[B]:HOH:O	1.63	1.27
1:A:89[B]:ASP:OD2	5:A:3460:HOH:O	1.54	1.20
1:B:56[B]:ASP:OD2	5:B:3513:HOH:O	1.59	1.19
1:B:89[B]:ASP:OD2	5:B:3505:HOH:O	1.59	1.18
1:B:113[C]:ARG:NH2	5:B:3308:HOH:O	1.89	1.03
1:B:90[B]:ASP:HB3	5:B:3527[B]:HOH:O	1.60	1.01
1:B:113[C]:ARG:CZ	5:B:3474:HOH:O	2.11	0.99
1:B:89[B]:ASP:N	5:B:3520:HOH:O	1.96	0.96
1:B:113[C]:ARG:NH2	5:B:3474:HOH:O	1.96	0.95
1:B:113[C]:ARG:NH1	5:B:3474:HOH:O	1.98	0.95
1:B:52[A]:SER:HB2	5:B:3512:HOH:O	1.72	0.89
1:B:234[B]:LEU:HD11	1:B:250[B]:LYS:HG3	1.54	0.89
1:A:326[B]:ARG:HD3	5:A:3114[B]:HOH:O	1.72	0.89
1:B:90[B]:ASP:CB	5:B:3527[B]:HOH:O	2.16	0.88
1:B:157[B]:ASP:OD2	5:B:3454:HOH:O	1.90	0.88
1:B:234[B]:LEU:HD12	1:B:250[B]:LYS:HG2	1.59	0.85
1:A:143:ALA:HB2	1:A:199[B]:MSE:HE1	1.58	0.83
1:B:283:GLN:H	1:B:283:GLN:HE21	1.25	0.82
1:B:52[B]:SER:OG	5:B:3512:HOH:O	1.56	0.82
1:A:143:ALA:HB2	1:A:199[B]:MSE:CE	2.11	0.80
1:B:277[B]:ASN:ND2	5:B:3473:HOH:O	1.76	0.79
1:B:234[B]:LEU:CD1	1:B:250[B]:LYS:HG2	2.14	0.77
1:B:234[B]:LEU:HD11	1:B:250[B]:LYS:CG	2.15	0.77
1:B:29[B]:MSE:CE	4:B:3014:EDO:C1	2.22	0.77
1:A:199[B]:MSE:HG2	1:A:208:LEU:HD11	1.66	0.75
1:B:29[B]:MSE:HE1	4:B:3014:EDO:H12	1.58	0.75
1:B:199[B]:MSE:HG2	1:B:208:LEU:HD11	1.69	0.73
1:B:234[B]:LEU:CD1	1:B:250[B]:LYS:CG	2.65	0.73



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:89[B]:ASP:CG	5:A:3460:HOH:O	2.14	0.69	
1:B:89[B]:ASP:OD1	5:B:3520:HOH:O	2.09	0.69	
1:A:277[B]:ASN:OD1	5:A:3193:HOH:O	2.15	0.65	
1:B:29[B]:MSE:HE2	4:B:3014:EDO:H11	1.70	0.64	
1:B:16[B]:HIS:CD2	4:B:3009:EDO:O2	2.51	0.63	
1:B:277[B]:ASN:OD1	5:B:3228:HOH:O	2.16	0.63	
1:B:113[C]:ARG:CZ	5:B:3308:HOH:O	2.36	0.61	
1:B:117:ARG:HG3	5:B:3542:HOH:O	2.02	0.58	
1:A:225[B]:GLN:HB2	1:A:228[B]:LYS:HD2	1.87	0.57	
1:B:16[B]:HIS:HD2	4:B:3009:EDO:O2	1.88	0.56	
1:B:326[B]:ARG:HD3	5:B:3097[B]:HOH:O	2.06	0.55	
1:B:147:ASN:ND2	1:B:160:GLN:HE21	2.05	0.55	
1:B:80[B]:ILE:HD11	1:B:109:VAL:HG13	1.89	0.54	
1:B:283:GLN:H	1:B:283:GLN:NE2	2.00	0.54	
1:B:29[B]:MSE:HE2	4:B:3014:EDO:H12	0.56	0.54	
1:B:204:TRP:CD2	4:B:3008:EDO:H11	2.43	0.53	
1:B:286:GLN:HG2	4:B:3008:EDO:H12	1.89	0.53	
1:B:89[B]:ASP:CG	5:B:3520:HOH:O	2.45	0.53	
1:B:150:ARG:NH1	5:B:3334:HOH:O	2.41	0.52	
1:A:34[A]:ARG:HD3	5:A:3150[A]:HOH:O	2.10	0.52	
1:B:33[A]:LEU:HD11	4:B:3001:EDO:H11	1.92	0.51	
1:B:52[A]:SER:CB	5:B:3512:HOH:O	2.42	0.51	
1:A:33[A]:LEU:HD11	4:A:3011[A]:EDO:H22	1.93	0.51	
1:A:34[A]:ARG:NH1	5:A:3150[A]:HOH:O	2.10	0.51	
1:A:199[B]:MSE:SE	1:A:208:LEU:HD21	2.61	0.50	
1:B:206[B]:ASN:ND2	5:B:3281:HOH:O	0.65	0.50	
1:A:204:TRP:CD2	4:A:3007:EDO:H11	2.47	0.49	
1:A:143:ALA:CB	1:A:199[B]:MSE:HE1	2.37	0.49	
1:B:52[B]:SER:CB	5:B:3512:HOH:O	2.37	0.49	
1:B:90[B]:ASP:CG	5:B:3527[B]:HOH:O	2.47	0.49	
1:A:143:ALA:HB2	1:A:199[B]:MSE:HE3	1.94	0.49	
1:B:6:ASN:OD1	1:B:350[A]:ARG:HD3	2.13	0.48	
1:A:238:GLY:HA2	4:A:3021:EDO:H22	1.96	0.48	
4:B:3005:EDO:C2	5:B:3542:HOH:O	2.61	0.48	
1:A:286:GLN:HG2	4:A:3007:EDO:H12	1.94	0.48	
1:B:204:TRP:CG	4:B:3008:EDO:H11	2.48	0.48	
4:A:3016[B]:EDO:O1	5:A:3457[B]:HOH:O	2.19	0.47	
1:B:113[C]:ARG:NH2	5:B:3406:HOH:O	2.46	0.47	
1:A:58:TRP:CD1	1:A:87:VAL:HB	2.49	0.47	
1:B:113[B]:ARG:NH2	5:B:3380:HOH:O	2.37	0.47	
1:A:27[B]:HIS:CG	4:A:3016[B]:EDO:O1	2.69	0.46	



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:76[A]:GLN:NE2	5:A:3250:HOH:O	2.47	0.46
1:A:131:ARG:HG2	1:A:199[B]:MSE:HB3	1.97	0.46
1:A:323:ARG:HB2	1:A:338:ASP:HB2	1.98	0.46
1:B:238:GLY:HA2	4:B:3018:EDO:H11	1.96	0.46
1:A:131:ARG:HG2	1:A:199[A]:MSE:HB2	1.98	0.45
1:B:297:ASP:HB2	1:B:314:ILE:O	2.17	0.45
1:A:297:ASP:HB2	1:A:314:ILE:O	2.18	0.44
1:B:350[A]:ARG:HA	5:B:3518:HOH:O	2.16	0.44
1:B:326[A]:ARG:NH1	5:B:3500:HOH:O	2.50	0.44
1:A:113[B]:ARG:NH2	5:A:3333:HOH:O	2.36	0.44
1:B:34[A]:ARG:NH1	5:B:3327:HOH:O	2.50	0.44
1:A:350[A]:ARG:CD	1:B:110:THR:HG22	2.48	0.43
1:B:234[B]:LEU:HD12	1:B:250[B]:LYS:CG	2.33	0.43
1:B:131:ARG:HG2	1:B:199[B]:MSE:HB3	2.00	0.42
1:B:25[A]:ASP:HB2	1:B:27[A]:HIS:CE1	2.54	0.42
1:A:89[B]:ASP:O	1:A:90[B]:ASP:HB2	2.20	0.42
1:B:350[B]:ARG:HA	5:B:3518:HOH:O	2.18	0.42
1:B:150:ARG:HB2	1:B:151:PRO:HD3	2.02	0.42
1:A:301[B]:MSE:HE3	1:A:308:VAL:HG22	2.02	0.41
1:A:34[A]:ARG:NH1	5:A:3383:HOH:O	2.53	0.41
1:A:350[A]:ARG:HD3	1:B:110:THR:HG22	2.02	0.41
1:A:204:TRP:CG	4:A:3007:EDO:H11	2.56	0.41
1:A:26[A]:ASN:HA	1:A:26[A]:ASN:HD22	1.67	0.41
1:A:34[A]:ARG:NH2	5:A:3377:HOH:O	2.53	0.41
1:A:33[A]:LEU:CD1	4:A:3011[A]:EDO:H22	2.50	0.40
1:A:60:HIS:HE1	5:A:3332:HOH:O	2.03	0.40
1:A:350[B]:ARG:HB3	1:B:108[B]:LYS:HE3	2.03	0.40
1:B:222:ASN:ND2	1:B:260:PRO:HA	2.35	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	$\begin{array}{c} {\rm Interatomic}\\ {\rm distance}~({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:52[A]:SER:OG	5:B:3518:HOH:O[1_554]	1.95	0.25



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	392/353~(111%)	380~(97%)	11 (3%)	1 (0%)	41 18
1	В	387/353~(110%)	374 (97%)	12 (3%)	1 (0%)	41 18
All	All	779/706~(110%)	754 (97%)	23 (3%)	2(0%)	41 18

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	215	PRO
1	В	215	PRO

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	А	329/281~(117%)	320~(97%)	9~(3%)	44 15
1	В	325/281~(116%)	321~(99%)	4 (1%)	71 48
All	All	654/562~(116%)	641~(98%)	13 (2%)	62 25

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	4[A]	THR
1	А	4[B]	THR
1	А	26[A]	ASN
1	А	26[B]	ASN



Mol	Chain	Res	Type
1	А	146	GLU
1	А	179	ILE
1	А	206[A]	ASN
1	А	206[B]	ASN
1	А	245	LYS
1	В	108[A]	LYS
1	В	108[B]	LYS
1	В	146	GLU
1	В	283	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	60	HIS
1	А	197	GLN
1	В	147	ASN
1	В	222	ASN
1	В	283	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 30 ligands modelled in this entry, 2 are monoatomic - leaving 28 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



Mal	True	Chain	Dec	Timle	В	ond leng	gths	E	Bond ang	gles
	Type	Chain	Res		Counts	RMSZ	$\bar{ } \# Z > 2$	Counts	RMSZ	# Z > 2
4	EDO	А	3016[A]	-	3,3,3	0.45	0	2,2,2	0.30	0
4	EDO	В	3003	-	3,3,3	0.44	0	2,2,2	0.48	0
4	EDO	В	3008	-	3,3,3	0.39	0	2,2,2	0.20	0
4	EDO	А	3023	-	3,3,3	0.43	0	2,2,2	0.42	0
4	EDO	А	3016[B]	-	3,3,3	0.45	0	2,2,2	0.33	0
4	EDO	В	3018	-	3,3,3	0.45	0	2,2,2	0.30	0
4	EDO	В	3005	-	3,3,3	0.46	0	2,2,2	0.51	0
4	EDO	А	3025	-	3,3,3	0.45	0	2,2,2	0.41	0
4	EDO	В	3004	-	3,3,3	0.40	0	2,2,2	0.41	0
4	EDO	В	3009	-	3,3,3	0.44	0	2,2,2	0.37	0
4	EDO	А	3021	-	3,3,3	0.49	0	2,2,2	0.29	0
4	EDO	А	3002	-	3,3,3	0.50	0	2,2,2	0.40	0
4	EDO	А	3024	-	3,3,3	0.46	0	2,2,2	0.39	0
4	EDO	В	3013	-	3,3,3	0.43	0	2,2,2	0.27	0
4	EDO	А	3011[B]	-	3,3,3	0.47	0	2,2,2	0.29	0
4	EDO	В	3010	-	3,3,3	0.41	0	2,2,2	0.48	0
4	EDO	А	3011[A]	-	3,3,3	0.46	0	2,2,2	0.16	0
4	EDO	В	3015	-	3,3,3	0.49	0	2,2,2	0.03	0
4	EDO	А	3017	-	3,3,3	0.51	0	2,2,2	0.08	0
4	EDO	В	3001	-	3,3,3	0.51	0	2,2,2	0.31	0
3	PO4	А	2003	-	4,4,4	1.11	0	6,6,6	0.44	0
4	EDO	А	3019	-	3,3,3	0.43	0	2,2,2	0.30	0
4	EDO	А	3012	-	3,3,3	0.48	0	2,2,2	0.34	0
4	EDO	А	3006	-	3,3,3	0.44	0	2,2,2	0.36	0
4	EDO	А	3020	-	3,3,3	0.45	0	2,2,2	0.33	0
4	EDO	А	3007	-	3,3,3	0.39	0	2,2,2	0.22	0
4	EDO	В	3014	-	3,3,3	0.45	0	2,2,2	0.29	0
4	EDO	В	3022	-	3,3,3	0.46	0	2,2,2	0.41	0

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).

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
4	EDO	А	3016[A]	-	-	0/1/1/1	-
4	EDO	В	3003	-	-	0/1/1/1	-
4	EDO	В	3008	-	-	0/1/1/1	-
4	EDO	А	3023	-	-	0/1/1/1	-



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	А	3016[B]	-	-	1/1/1/1	-
4	EDO	В	3018	-	-	0/1/1/1	-
4	EDO	В	3005	-	-	1/1/1/1	-
4	EDO	А	3025	-	-	0/1/1/1	-
4	EDO	В	3004	-	-	0/1/1/1	-
4	EDO	В	3009	-	-	1/1/1/1	-
4	EDO	А	3021	-	-	0/1/1/1	-
4	EDO	А	3002	-	-	0/1/1/1	-
4	EDO	А	3024	-	-	0/1/1/1	-
4	EDO	В	3013	-	-	1/1/1/1	-
4	EDO	А	3011[B]	-	-	1/1/1/1	-
4	EDO	В	3010	-	-	0/1/1/1	-
4	EDO	А	3011[A]	-	-	0/1/1/1	-
4	EDO	В	3015	-	-	1/1/1/1	-
4	EDO	А	3017	-	-	0/1/1/1	-
4	EDO	В	3001	-	-	0/1/1/1	-
4	EDO	А	3019	-	-	1/1/1/1	-
4	EDO	А	3012	-	-	0/1/1/1	-
4	EDO	А	3006	-	-	0/1/1/1	-
4	EDO	A	3020	-	-	1/1/1/1	-
4	EDO	A	3007	-	-	0/1/1/1	-
4	EDO	В	3014	-	-	1/1/1/1	-
4	EDO	В	3022	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	В	3005	EDO	O1-C1-C2-O2
4	А	3016[B]	EDO	O1-C1-C2-O2
4	А	3020	EDO	O1-C1-C2-O2
4	В	3014	EDO	O1-C1-C2-O2
4	В	3015	EDO	O1-C1-C2-O2
4	В	3009	EDO	O1-C1-C2-O2
4	А	3019	EDO	O1-C1-C2-O2
4	А	3011[B]	EDO	O1-C1-C2-O2
4	В	3013	EDO	O1-C1-C2-O2

There are no ring outliers.



Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	В	3008	EDO	3	0
4	А	3016[B]	EDO	2	0
4	В	3018	EDO	1	0
4	В	3005	EDO	1	0
4	В	3009	EDO	2	0
4	А	3021	EDO	1	0
4	А	3011[A]	EDO	2	0
4	В	3001	EDO	1	0
4	А	3007	EDO	3	0
4	В	3014	EDO	6	0

10 monomers are involved in 22 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, 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	А	342/353~(96%)	-0.56	4 (1%) 79 82	5, 9, 16, 26	0
1	В	341/353~(96%)	-0.58	2 (0%) 89 91	5, 9, 16, 25	0
All	All	683/706~(96%)	-0.57	6 (0%) 84 87	5, 9, 16, 26	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	4[A]	THR	4.0
1	В	4	THR	3.3
1	А	3	ALA	2.5
1	А	180[A]	LYS	2.3
1	В	182[A]	SER	2.0
1	А	89[A]	ASP	2.0

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. 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	\mathbf{Res}	Atoms	RSCC	RSR	${f B} ext{-factors}({ m \AA}^2)$	$Q{<}0.9$
4	EDO	А	3020	4/4	0.78	0.14	$45,\!45,\!45,\!45$	0
4	EDO	А	3012	4/4	0.79	0.14	$25,\!25,\!25,\!25$	0
4	EDO	А	3021	4/4	0.80	0.13	$29,\!30,\!30,\!31$	0
4	EDO	В	3022	4/4	0.80	0.14	$22,\!23,\!23,\!23$	0
4	EDO	В	3018	4/4	0.82	0.19	$15,\!15,\!16,\!17$	4
4	EDO	В	3009	4/4	0.82	0.14	34,34,35,35	0
4	EDO	А	3019	4/4	0.86	0.25	24,24,24,24	4
4	EDO	В	3014	4/4	0.87	0.21	23,23,24,24	4
4	EDO	В	3015	4/4	0.90	0.11	$22,\!23,\!23,\!23$	0
4	EDO	В	3010	4/4	0.90	0.13	31,31,32,32	0
4	EDO	А	3025	4/4	0.91	0.09	$28,\!28,\!28,\!29$	0
4	EDO	В	3013	4/4	0.91	0.11	$25,\!25,\!26,\!26$	0
4	EDO	В	3005	4/4	0.91	0.12	22,22,23,25	4
4	EDO	А	3016[A]	4/4	0.92	0.15	$21,\!22,\!23,\!23$	4
4	EDO	В	3008	4/4	0.92	0.15	$14,\!15,\!16,\!16$	4
4	EDO	А	3023	4/4	0.92	0.09	$29,\!30,\!30,\!31$	0
4	EDO	А	3016[B]	4/4	0.92	0.15	$18,\!18,\!18,\!18$	4
4	EDO	А	3017	4/4	0.92	0.13	21,22,22,23	0
4	EDO	А	3011[A]	4/4	0.94	0.11	$17,\!19,\!19,\!20$	4
4	EDO	В	3001	4/4	0.94	0.08	20,22,23,24	0
4	EDO	А	3007	4/4	0.94	0.11	$17,\!18,\!18,\!18$	0
3	PO4	А	2003	5/5	0.94	0.12	22,22,22,23	5
4	EDO	А	3011[B]	4/4	0.94	0.11	$23,\!23,\!23,\!23$	4
4	EDO	А	3006	4/4	0.95	0.10	$15,\!15,\!15,\!16$	0
4	EDO	А	3024	4/4	0.96	0.08	$17,\!19,\!20,\!21$	0
4	EDO	В	3004	4/4	0.96	0.09	$13,\!14,\!15,\!15$	0
4	EDO	В	3003	4/4	0.97	0.08	$7,\!9,\!9,\!10$	0
4	EDO	А	3002	4/4	0.97	0.09	$7,\!9,\!10,\!10$	0
2	CA	В	2001	1/1	1.00	0.03	5, 5, 5, 5	0
2	CA	А	2002	1/1	1.00	0.03	5, 5, 5, 5	0

6.5 Other polymers (i)

There are no such residues in this entry.

