



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 03:32 am BST

PDB ID : 3Q02  
Title : Crystal structure of plasminogen activator inhibitor-1 in a metastable active conformation.  
Authors : Jensen, J.K.; Morth, J.P.  
Deposited on : 2010-12-15  
Resolution : 2.30 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](mailto: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 ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) 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 : 2.11  
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) : 2.11

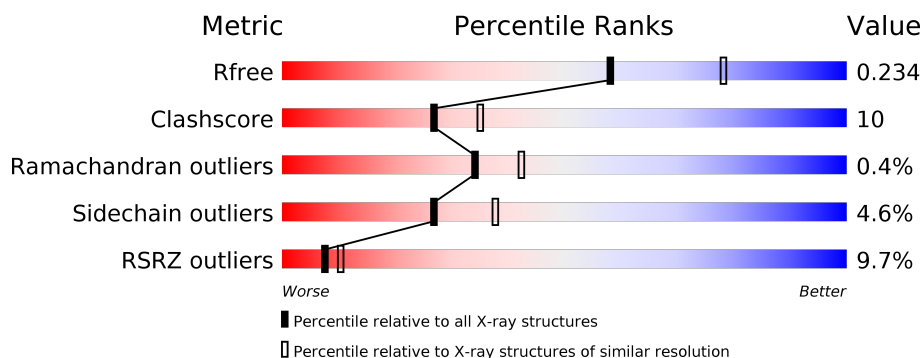
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 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  $\leq 5\%$ . 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	379	<div> <div>11%</div> <div> <div></div> <div>73%</div> <div>20%</div> <div>• 6%</div> </div> </div>
1	B	379	<div> <div>7%</div> <div> <div></div> <div>72%</div> <div>22%</div> <div>• •</div> </div> </div>

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	B	383	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5907 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 Plasminogen activator inhibitor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	358	Total	C	N	O	S	0	1	0
			2869	1841	487	526	15			
1	B	362	Total	C	N	O	S	0	0	0
			2900	1862	495	528	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	175	PHE	TRP	ENGINEERED MUTATION	UNP P05121
B	175	PHE	TRP	ENGINEERED MUTATION	UNP P05121

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		
2	A	1	Total	Cl	0	0
			1	1		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Zn	0	0
			2	2		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		

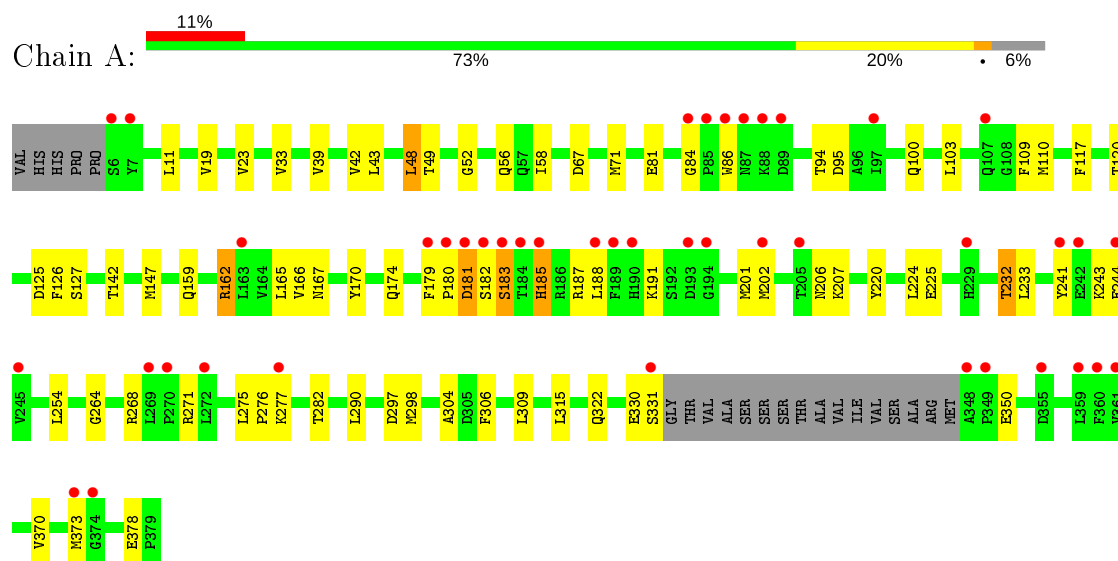
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	65	Total	O	0	0
			65	65		
5	B	65	Total	O	0	0
			65	65		

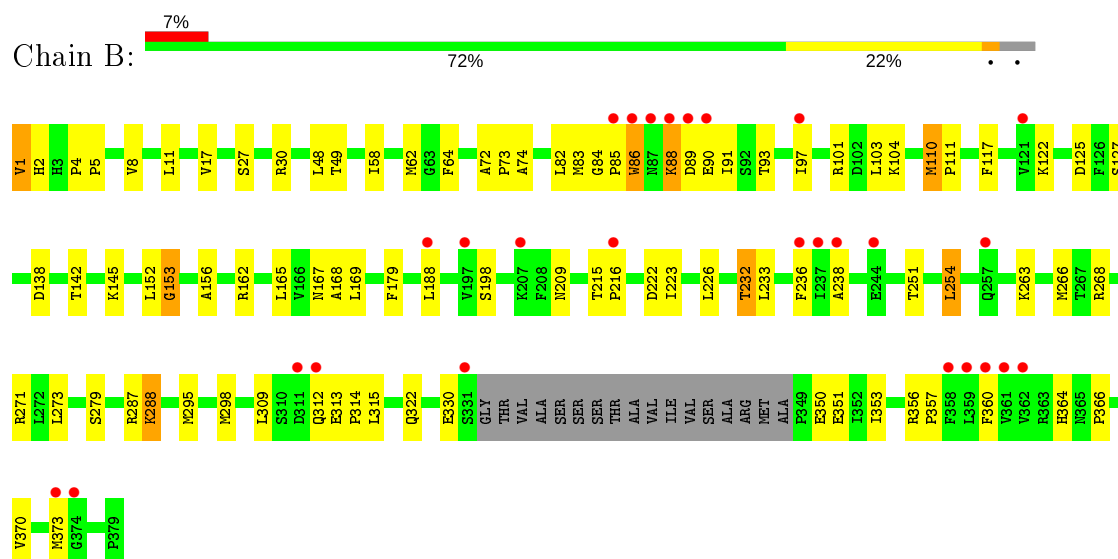
### 3 Residue-property plots [i](#)

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: Plasminogen activator inhibitor 1



#### • Molecule 1: Plasminogen activator inhibitor 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.44Å 67.17Å 90.36Å 90.00° 98.50° 90.00°	Depositor
Resolution (Å)	24.94 – 2.30 29.95 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.7 (24.94-2.30) 98.8 (29.95-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.47 (at 2.31Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, $R_{free}$	0.193 , 0.238 0.189 , 0.234	Depositor DCC
$R_{free}$ test set	2027 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.6	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 48.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5907	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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: ZN, EDO, CL

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	0.37	0/2940	0.51	0/3980
1	B	0.36	0/2972	0.52	0/4025
All	All	0.37	0/5912	0.51	0/8005

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

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	2869	0	2857	51	0
1	B	2900	0	2888	68	0
2	A	1	0	0	0	0
2	B	1	0	0	1	0
3	B	2	0	0	0	0
4	B	4	0	6	4	0
5	A	65	0	0	4	0
5	B	65	0	0	2	0
All	All	5907	0	5751	117	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.



All (117) 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:202:MET:HA	5:A:420:HOH:O	1.78	0.83
1:B:27:SER:HA	1:B:30:ARG:HH21	1.43	0.82
1:B:88:LYS:HB3	1:B:145:LYS:NZ	2.00	0.77
1:B:153:GLY:H	1:B:156:ALA:HB3	1.54	0.72
1:A:162:ARG:HH11	1:A:162:ARG:HG3	1.55	0.71
1:B:263:LYS:HA	1:B:266:MET:HG2	1.73	0.71
1:B:88:LYS:HG3	1:B:91:ILE:O	1.91	0.70
1:A:264:GLY:O	1:B:85:PRO:HB3	1.92	0.69
1:A:100:GLN:HE22	1:A:126:PHE:H	1.40	0.68
1:B:88:LYS:HB3	1:B:145:LYS:HZ2	1.59	0.68
1:B:370:VAL:HG11	1:B:373:MET:HE3	1.76	0.68
1:A:162:ARG:HH11	1:A:162:ARG:CG	2.08	0.67
1:A:275:LEU:HD12	1:A:276:PRO:HD2	1.77	0.67
1:B:138:ASP:O	1:B:142:THR:HG23	1.95	0.66
1:A:243:LYS:HG3	5:A:409:HOH:O	1.96	0.65
1:A:271:ARG:NH1	1:A:350:GLU:HB2	2.11	0.65
1:B:251:THR:HA	1:B:254:LEU:HD22	1.78	0.65
1:B:125:ASP:OD1	1:B:127:SER:HB3	2.00	0.62
1:B:27:SER:HA	1:B:30:ARG:NH2	2.14	0.61
1:B:153:GLY:HA2	1:B:156:ALA:H	1.66	0.61
1:A:181:ASP:C	1:A:183:SER:H	2.04	0.60
1:A:58:ILE:HD11	1:A:298:MET:CE	2.31	0.59
1:A:43:LEU:HD11	1:A:290:LEU:HD21	1.85	0.58
1:B:232:THR:HG21	4:B:383:EDO:O1	2.04	0.57
1:B:17:VAL:HG22	1:B:373:MET:HE3	1.87	0.56
1:B:232:THR:HG23	1:B:364:HIS:CD2	2.40	0.56
1:A:42:VAL:HB	1:A:165:LEU:HD11	1.88	0.56
1:B:72:ALA:HB3	1:B:73:PRO:HD3	1.87	0.55
1:B:295:MET:HB3	1:B:298:MET:HE3	1.88	0.55
1:B:48:LEU:HD22	1:B:117:PHE:HE2	1.73	0.54
1:B:88:LYS:O	1:B:90:GLU:HA	2.08	0.54
1:A:185:HIS:CD2	1:A:187:ARG:HE	2.25	0.54
1:B:288:LYS:N	1:B:288:LYS:HD2	2.23	0.53
1:A:271:ARG:HH11	1:A:350:GLU:HB2	1.73	0.53
1:B:84:GLY:HA2	1:B:86:TRP:H	1.74	0.53
1:B:188:LEU:HD12	1:B:188:LEU:N	2.25	0.52
1:A:180:PRO:HG2	1:A:183:SER:OG	2.10	0.52
1:A:49:THR:HG22	1:A:109:PHE:CZ	2.45	0.51
1:B:62:MET:HE2	1:B:64:PHE:CZ	2.44	0.51
1:B:168:ALA:C	1:B:169:LEU:HD12	2.31	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:LEU:HD12	1:A:166:VAL:N	2.26	0.51
1:A:33:VAL:HG12	1:A:282:THR:OG1	2.11	0.50
1:B:84:GLY:O	4:B:383:EDO:H12	2.11	0.50
1:A:52:GLY:O	1:A:56:GLN:HG2	2.12	0.50
1:B:357:PRO:HG2	2:B:382:CL:CL	2.49	0.50
1:B:88:LYS:HB3	1:B:145:LYS:HZ1	1.74	0.50
1:B:83:MET:HE3	1:B:88:LYS:HE2	1.93	0.50
1:A:84:GLY:C	1:A:86:TRP:N	2.66	0.50
1:A:181:ASP:O	1:A:183:SER:N	2.45	0.49
1:B:232:THR:HG22	1:B:233:LEU:HG	1.94	0.49
1:A:206:ASN:CG	1:A:207:LYS:H	2.16	0.48
1:B:82:LEU:O	4:B:383:EDO:H21	2.13	0.48
1:B:72:ALA:N	1:B:73:PRO:CD	2.76	0.48
1:B:83:MET:HB3	1:B:88:LYS:NZ	2.27	0.48
1:B:223:ILE:N	1:B:223:ILE:HD12	2.29	0.48
1:B:1:VAL:HG13	1:B:366:PRO:O	2.14	0.47
1:A:220:TYR:CZ	1:B:1:VAL:HG22	2.49	0.47
1:B:222:ASP:O	1:B:238:ALA:HA	2.15	0.47
1:A:19:VAL:O	1:A:23:VAL:HG23	2.15	0.47
1:B:209:ASN:OD1	1:B:268:ARG:HG2	2.14	0.47
1:A:84:GLY:C	1:A:86:TRP:H	2.19	0.47
1:B:271:ARG:HH11	1:B:350:GLU:HB2	1.78	0.47
1:B:8:VAL:HG11	1:B:74:ALA:HB1	1.97	0.47
1:A:42:VAL:HG12	1:A:95:ASP:HB3	1.97	0.46
1:A:110:MET:HE1	1:A:120:THR:HB	1.97	0.46
1:B:104:LYS:HD3	1:B:312:GLN:OE1	2.16	0.46
1:A:162:ARG:HD2	5:A:443:HOH:O	2.15	0.45
1:A:181:ASP:C	1:A:183:SER:N	2.70	0.45
1:B:103:LEU:CD1	1:B:315:LEU:HD21	2.47	0.45
1:B:4:PRO:HB2	1:B:5:PRO:HD3	1.97	0.45
1:A:224:LEU:HD23	1:A:225:GLU:N	2.32	0.45
1:B:287:ARG:HD2	5:B:413:HOH:O	2.15	0.45
1:A:232:THR:HG22	1:A:233:LEU:HG	1.98	0.45
1:B:236:PHE:O	1:B:360:PHE:HA	2.16	0.45
1:B:167:ASN:O	1:B:322:GLN:HA	2.16	0.45
1:B:313:GLU:HA	1:B:314:PRO:HD3	1.75	0.45
1:B:88:LYS:HG2	1:B:145:LYS:HE3	1.97	0.44
1:A:241:TYR:HA	5:A:412:HOH:O	2.17	0.44
1:B:89:ASP:HA	1:B:90:GLU:HA	1.65	0.43
1:A:48:LEU:CD2	1:A:117:PHE:HE2	2.31	0.43
1:A:147:MET:HG3	1:A:170:TYR:CD1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:ARG:NH1	1:A:162:ARG:CG	2.72	0.43
1:B:232:THR:HG21	4:B:383:EDO:C1	2.49	0.43
1:B:271:ARG:HD3	1:B:350:GLU:CB	2.48	0.43
1:B:58:ILE:HG12	1:B:298:MET:HE1	2.00	0.43
1:A:201:MET:HA	1:A:276:PRO:HA	2.01	0.43
1:B:295:MET:HB3	1:B:298:MET:CE	2.49	0.43
1:A:191:LYS:HD3	1:A:378:GLU:CD	2.39	0.42
1:A:174:GLN:HG3	1:A:331:SER:HA	2.00	0.42
1:B:97:ILE:HG12	1:B:165:LEU:HD13	2.00	0.42
1:B:271:ARG:HD3	1:B:350:GLU:HB3	2.01	0.42
1:B:58:ILE:HD11	1:B:298:MET:HE2	2.01	0.42
1:A:179:PHE:O	1:A:330:GLU:HB3	2.20	0.42
1:A:159:GLN:H	1:A:159:GLN:HG2	1.58	0.42
1:A:297:ASP:O	1:A:304:ALA:HB2	2.20	0.42
1:A:167:ASN:O	1:A:322:GLN:HA	2.20	0.42
1:A:39:VAL:HG22	1:A:43:LEU:HD12	2.02	0.42
1:B:153:GLY:H	1:B:156:ALA:CB	2.28	0.42
1:B:169:LEU:N	1:B:169:LEU:HD12	2.34	0.42
1:A:49:THR:HG1	1:A:306:PHE:HD2	1.67	0.42
1:B:370:VAL:HG11	1:B:373:MET:CE	2.49	0.41
1:A:49:THR:HB	1:A:309:LEU:HB2	2.02	0.41
1:B:351:GLU:HG2	1:B:353:ILE:HD11	2.03	0.41
1:A:125:ASP:OD1	1:A:127:SER:HB2	2.21	0.41
1:A:370:VAL:HG11	1:A:373:MET:CE	2.51	0.41
1:A:100:GLN:HE22	1:A:126:PHE:N	2.15	0.41
1:B:179:PHE:O	1:B:330:GLU:HB3	2.20	0.41
1:B:356:ARG:HB2	1:B:357:PRO:HD2	2.02	0.41
1:B:110:MET:N	1:B:111:PRO:HD2	2.36	0.41
1:A:103:LEU:CD1	1:A:315:LEU:HD21	2.51	0.40
1:B:152:LEU:O	1:B:153:GLY:O	2.39	0.40
1:B:215:THR:HB	1:B:216:PRO:HD2	2.02	0.40
1:A:43:LEU:CD1	1:A:290:LEU:HD21	2.50	0.40
1:B:226:LEU:HD21	1:B:273:LEU:CD2	2.51	0.40
1:B:49:THR:HB	1:B:309:LEU:HB2	2.03	0.40
1:B:122:LYS:NZ	5:B:399:HOH:O	2.55	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	355/379 (94%)	341 (96%)	13 (4%)	1 (0%)	41	50
1	B	358/379 (94%)	343 (96%)	13 (4%)	2 (1%)	25	31
All	All	713/758 (94%)	684 (96%)	26 (4%)	3 (0%)	34	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	182	SER
1	B	153	GLY
1	B	86	TRP

### 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	317/333 (95%)	301 (95%)	16 (5%)	24	34
1	B	321/333 (96%)	308 (96%)	13 (4%)	31	44
All	All	638/666 (96%)	609 (96%)	29 (4%)	27	39

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LEU
1	A	48	LEU
1	A	67	ASP

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Mol	Chain	Res	Type
1	A	71	MET
1	A	81	GLU
1	A	94	THR
1	A	162	ARG
1	A	181	ASP
1	A	183	SER
1	A	185	HIS
1	A	188	LEU
1	A	232	THR
1	A	244	GLU
1	A	254	LEU
1	A	268	ARG
1	A	277	LYS
1	B	1	VAL
1	B	2	HIS
1	B	11	LEU
1	B	88	LYS
1	B	93	THR
1	B	101	ARG
1	B	110	MET
1	B	162	ARG
1	B	198	SER
1	B	232	THR
1	B	254	LEU
1	B	279	SER
1	B	288	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	100	GLN
1	A	190	HIS
1	A	204	GLN
1	A	265	ASN
1	B	3	HIS
1	B	204	GLN
1	B	219	HIS

### 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 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	$\# Z  > 2$
4	EDO	B	383	-	3,3,3	0.53	0	2,2,2	0.30	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
4	EDO	B	383	-	-	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.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	383	EDO	4	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

### 6.1 Protein, DNA and RNA chains

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	358/379 (94%)	0.54	43 (12%) <b>4</b> <b>6</b>	36, 60, 152, 192	0
1	B	362/379 (95%)	0.22	27 (7%) <b>14</b> <b>19</b>	34, 56, 100, 172	0
All	All	720/758 (94%)	0.38	70 (9%) <b>7</b> <b>10</b>	34, 58, 127, 192	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	86	TRP	12.6
1	A	194	GLY	8.0
1	B	86	TRP	8.0
1	B	89	ASP	7.6
1	A	87	ASN	7.3
1	A	88	LYS	7.0
1	A	348	ALA	6.2
1	A	180	PRO	5.6
1	B	87	ASN	4.8
1	A	179	PHE	4.5
1	A	182	SER	4.5
1	A	190	HIS	4.1
1	A	181	ASP	4.0
1	A	241	TYR	3.7
1	A	188	LEU	3.6
1	A	349	PRO	3.3
1	B	359	LEU	3.3
1	A	89	ASP	3.2
1	A	331	SER	3.2
1	A	361	VAL	3.2
1	A	355	ASP	3.2
1	A	107	GLN	3.1
1	A	205	THR	3.1
1	B	312	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	360	PHE	3.0
1	B	361	VAL	3.0
1	A	185	HIS	2.9
1	A	193	ASP	2.9
1	A	85	PRO	2.8
1	B	216	PRO	2.8
1	B	237	ILE	2.8
1	A	244	GLU	2.8
1	A	7	TYR	2.8
1	A	359	LEU	2.7
1	B	121	VAL	2.7
1	B	197	VAL	2.7
1	B	360	PHE	2.7
1	B	244	GLU	2.6
1	A	189	PHE	2.6
1	A	373	MET	2.6
1	B	311	ASP	2.6
1	A	245	VAL	2.5
1	A	229	HIS	2.5
1	A	270	PRO	2.5
1	A	183	SER	2.4
1	A	184	THR	2.4
1	B	207	LYS	2.4
1	A	272	LEU	2.4
1	B	257	GLN	2.4
1	A	242	GLU	2.4
1	A	277	LYS	2.4
1	B	331	SER	2.4
1	B	88	LYS	2.3
1	A	97	ILE	2.3
1	B	188	LEU	2.3
1	A	6	SER	2.3
1	B	374	GLY	2.2
1	B	85	PRO	2.2
1	A	374	GLY	2.2
1	A	163	LEU	2.2
1	B	373	MET	2.2
1	B	236	PHE	2.2
1	A	269	LEU	2.1
1	B	90	GLU	2.1
1	A	84	GLY	2.1
1	B	358	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	362	VAL	2.1
1	A	202	MET	2.0
1	B	238	ALA	2.0
1	B	97	ILE	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<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	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	B	383	4/4	0.66	0.36	68,76,76,77	0
2	CL	B	382	1/1	0.91	0.11	81,81,81,81	0
2	CL	A	380	1/1	0.93	0.08	81,81,81,81	0
3	ZN	B	381	1/1	0.95	0.04	76,76,76,76	0
3	ZN	B	380	1/1	0.96	0.04	86,86,86,86	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.