



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 10:55 am GMT

PDB ID : 4JA3  
Title : Partially occluded inward open conformation of the xylose transporter XylE from E. coli  
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Deposited on : 2013-02-18  
Resolution : 3.80 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

<http://wwpdb.org/validation/2016/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  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

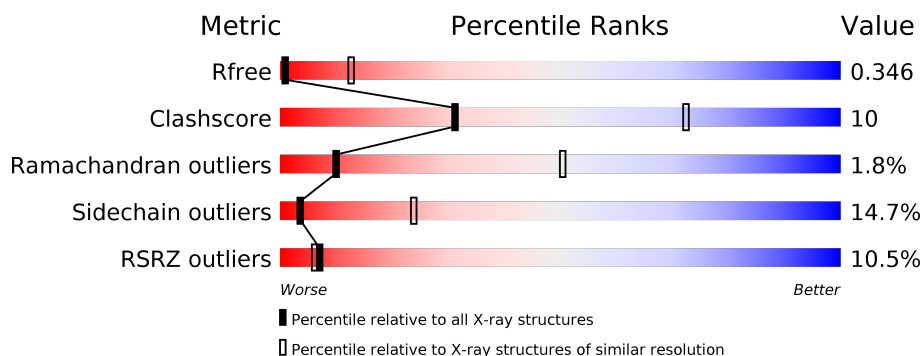
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.80 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))
$R_{free}$	100719	1019 (4.08-3.52)
Clashscore	112137	1030 (4.04-3.56)
Ramachandran outliers	110173	1011 (4.06-3.54)
Sidechain outliers	110143	1005 (4.06-3.54)
RSRZ outliers	101464	1032 (4.08-3.52)

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. 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	485	<div> <div>7%</div> <div>59%</div> <div>25%</div> <div>•</div> <div>12%</div> </div>
1	B	485	<div> <div>12%</div> <div>64%</div> <div>23%</div> <div>•</div> <div>9%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6626 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 D-xylose-proton symporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	426	Total	C	N	O	S	0	0	0
			3262	2156	517	566	23			
1	B	439	Total	C	N	O	S	0	0	0
			3359	2220	533	583	23			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	EXPRESSION TAG	UNP P0AGF4
B	1	GLY	-	EXPRESSION TAG	UNP P0AGF4

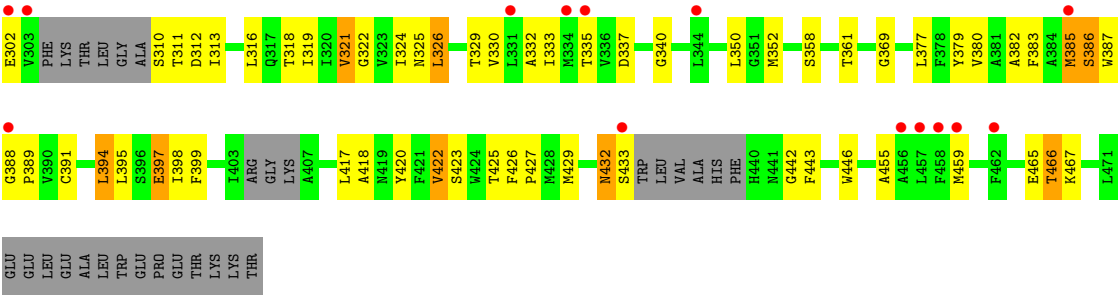
- Molecule 2 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cd	0	0
			1	1		

- Molecule 3 is LUTETIUM (III) ION (three-letter code: LU) (formula: Lu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Lu	0	0
			2	2		
3	A	2	Total	Lu	0	0
			2	2		





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	246.88Å 74.38Å 131.11Å 90.00° 117.71° 90.00°	Depositor
Resolution (Å)	25.26 – 3.80 48.49 – 3.80	Depositor EDS
% Data completeness (in resolution range)	82.3 (25.26-3.80) 82.4 (48.49-3.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.04 (at 3.77Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, $R_{free}$	0.285 , 0.315 0.311 , 0.346	Depositor DCC
$R_{free}$ test set	2604 reflections (7.81%)	DCC
Wilson B-factor (Å <sup>2</sup> )	154.0	Xtriage
Anisotropy	0.915	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 148.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.77	EDS
Total number of atoms	6626	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	232.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: LU, CD

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	0.43	0/3343	0.62	1/4547 (0.0%)
1	B	0.45	0/3442	0.67	1/4681 (0.0%)
All	All	0.44	0/6785	0.65	2/9228 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	432	ASN	C-N-CA	5.29	134.92	121.70
1	A	432	ASN	C-N-CA	5.07	134.38	121.70

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	3262	0	3303	77	0
1	B	3359	0	3411	61	0
2	A	1	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
All	All	6626	0	6714	138	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 (138) 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:B:332:ALA:HB1	1:B:389:PRO:HG3	1.32	1.10
1:A:332:ALA:HB1	1:A:389:PRO:HG3	1.33	1.08
1:A:249:ALA:O	1:A:253:VAL:HG23	1.71	0.90
1:A:58:GLY:HA2	1:A:427:PRO:HG2	1.51	0.89
1:A:183:TYR:HA	1:A:315:LEU:HD13	1.56	0.85
1:A:30:VAL:CG1	1:A:178:VAL:HG11	2.08	0.84
1:B:30:VAL:CG1	1:B:178:VAL:HG11	2.09	0.82
1:A:10:ILE:HB	1:A:243:ILE:HG12	1.62	0.81
1:B:10:ILE:HB	1:B:243:ILE:HG12	1.64	0.80
1:A:332:ALA:CB	1:A:389:PRO:HG3	2.12	0.79
1:A:58:GLY:CA	1:A:427:PRO:HG2	2.13	0.79
1:B:332:ALA:CB	1:B:389:PRO:HG3	2.13	0.74
1:A:30:VAL:HG12	1:A:178:VAL:HG11	1.68	0.74
1:B:30:VAL:HG12	1:B:178:VAL:HG11	1.67	0.73
1:A:284:LEU:O	1:A:288:GLN:HG3	1.88	0.73
1:B:284:LEU:O	1:B:288:GLN:HG3	1.89	0.71
1:A:179:TYR:HB3	1:A:319:ILE:HG12	1.73	0.71
1:A:176:LEU:HD21	1:A:322:GLY:O	1.93	0.68
1:A:30:VAL:HG13	1:A:178:VAL:HG11	1.75	0.67
1:A:321:VAL:HG13	1:A:380:VAL:HG21	1.76	0.67
1:B:394:LEU:HA	1:B:398:ILE:HD13	1.78	0.66
1:B:30:VAL:HG13	1:B:178:VAL:HG11	1.77	0.65
1:A:352:MET:HB2	1:A:379:TYR:CD2	2.32	0.64
1:B:288:GLN:HG2	1:B:387:TRP:HE1	1.63	0.64
1:A:324:ILE:HG13	1:A:377:LEU:HD22	1.79	0.63
1:A:288:GLN:HG2	1:A:387:TRP:HE1	1.63	0.63
1:B:352:MET:HB2	1:B:379:TYR:CD2	2.34	0.62
1:B:9:TYR:HB3	1:B:243:ILE:HD13	1.82	0.62
1:A:228:MET:CE	1:A:257:LYS:HG2	2.30	0.61
1:A:9:TYR:HB3	1:A:243:ILE:HD13	1.81	0.61
1:B:258:HIS:HA	1:B:261:ASP:HB3	1.83	0.61
1:A:172:ILE:HG22	1:A:326:LEU:HD12	1.83	0.60
1:A:24:PHE:HE1	1:A:144:SER:HB2	1.66	0.60
1:B:24:PHE:HE1	1:B:144:SER:HB2	1.66	0.59
1:A:176:LEU:HD21	1:A:322:GLY:C	2.23	0.59
1:B:172:ILE:HG22	1:B:326:LEU:HD12	1.84	0.59
1:B:324:ILE:HG13	1:B:377:LEU:HD22	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:285:SER:HA	1:B:288:GLN:CD	2.24	0.58
1:A:310:SER:HB3	1:A:313:ILE:HB	1.83	0.58
1:B:321:VAL:HG23	1:B:377:LEU:HD23	1.85	0.58
1:A:285:SER:HA	1:A:288:GLN:CD	2.23	0.58
1:A:18:THR:HG21	1:A:166:PHE:HD1	1.69	0.57
1:A:30:VAL:HG12	1:A:178:VAL:CG1	2.34	0.57
1:A:61:VAL:HG21	1:A:299:TYR:OH	2.04	0.57
1:A:345:GLN:HB2	1:A:459:MET:SD	2.44	0.57
1:B:18:THR:HG21	1:B:166:PHE:HD1	1.70	0.57
1:A:101:GLY:HA3	1:A:132:TYR:CD2	2.40	0.57
1:B:101:GLY:HA3	1:B:132:TYR:CD2	2.40	0.56
1:B:30:VAL:HG12	1:B:178:VAL:CG1	2.34	0.56
1:A:352:MET:HE3	1:A:383:PHE:HB2	1.88	0.56
1:A:303:VAL:HG11	1:A:445:TYR:OH	2.06	0.55
1:B:352:MET:HE3	1:B:383:PHE:HB2	1.89	0.54
1:B:58:GLY:HA2	1:B:427:PRO:HG2	1.89	0.54
1:B:394:LEU:O	1:B:398:ILE:HB	2.07	0.54
1:A:160:ARG:HH21	1:A:397:GLU:HB3	1.73	0.54
1:A:238:GLY:HA2	1:A:241:ARG:HE	1.74	0.53
1:B:61:VAL:HG21	1:B:299:TYR:OH	2.09	0.53
1:B:193:TRP:HA	1:B:196:THR:HG22	1.89	0.52
1:A:193:TRP:HA	1:A:196:THR:HG22	1.90	0.52
1:A:301:PRO:HG3	1:A:318:THR:HG21	1.90	0.52
1:B:221:PRO:HB2	1:B:239:ILE:HD13	1.92	0.51
1:B:466:THR:O	1:B:467:LYS:HB3	2.10	0.51
1:A:313:ILE:O	1:A:316:LEU:HB3	2.10	0.51
1:A:228:MET:HE1	1:A:257:LYS:CG	2.41	0.50
1:A:26:TYR:CZ	1:A:178:VAL:HG13	2.47	0.50
1:A:321:VAL:CG1	1:A:380:VAL:HG21	2.41	0.50
1:B:238:GLY:HA2	1:B:241:ARG:HE	1.77	0.50
1:B:160:ARG:HH21	1:B:397:GLU:HB3	1.76	0.50
1:B:455:ALA:O	1:B:459:MET:HG3	2.11	0.50
1:A:228:MET:HE1	1:A:257:LYS:HG2	1.92	0.50
1:A:221:PRO:HB2	1:A:239:ILE:HD13	1.92	0.50
1:B:176:LEU:HD21	1:B:322:GLY:O	2.12	0.50
1:B:382:ALA:O	1:B:386:SER:HB3	2.12	0.49
1:B:288:GLN:HG2	1:B:387:TRP:NE1	2.26	0.49
1:A:9:TYR:CE2	1:A:13:ILE:HD11	2.48	0.49
1:B:46:GLN:HG2	1:B:123:ALA:HB1	1.95	0.49
1:A:330:VAL:O	1:A:333:ILE:HG12	2.13	0.49
1:B:332:ALA:HB1	1:B:389:PRO:CG	2.23	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:ALA:HB1	1:A:389:PRO:CG	2.23	0.48
1:A:288:GLN:HG2	1:A:387:TRP:NE1	2.26	0.48
1:A:286:ILE:HG22	1:A:418:ALA:HB2	1.95	0.48
1:B:361:THR:HG23	1:B:446:TRP:HE1	1.78	0.48
1:B:9:TYR:CE2	1:B:13:ILE:HD11	2.48	0.48
1:B:286:ILE:HG22	1:B:418:ALA:HB2	1.95	0.48
1:A:179:TYR:HB3	1:A:319:ILE:CG1	2.43	0.48
1:B:26:TYR:CZ	1:B:178:VAL:HG13	2.48	0.48
1:A:382:ALA:O	1:A:386:SER:HB3	2.13	0.48
1:B:330:VAL:O	1:B:333:ILE:HG12	2.13	0.48
1:A:63:SER:HB2	1:A:130:VAL:HG13	1.96	0.48
1:B:133:ARG:HA	1:B:133:ARG:HD2	1.53	0.47
1:B:255:GLU:HA	1:B:258:HIS:CE1	2.50	0.47
1:A:46:GLN:HG2	1:A:123:ALA:HB1	1.96	0.47
1:A:75:GLY:O	1:A:79:SER:HB2	2.14	0.47
1:B:426:PHE:HB3	1:B:427:PRO:HD3	1.96	0.47
1:A:314:ALA:O	1:A:318:THR:HG23	2.15	0.46
1:A:310:SER:O	1:A:314:ALA:N	2.38	0.46
1:A:246:ASN:O	1:A:250:THR:OG1	2.31	0.46
1:A:183:TYR:HA	1:A:315:LEU:CD1	2.35	0.46
1:A:295:VAL:HG21	1:A:448:TYR:OH	2.16	0.46
1:B:63:SER:HB2	1:B:130:VAL:HG13	1.97	0.46
1:A:345:GLN:CB	1:A:459:MET:SD	3.03	0.46
1:A:299:TYR:CD2	1:A:426:PHE:CD2	3.05	0.45
1:A:422:VAL:HA	1:A:425:THR:HG22	1.99	0.44
1:B:301:PRO:HG3	1:B:318:THR:HG21	1.99	0.44
1:A:359:LEU:HD22	1:A:376:MET:HG2	1.99	0.44
1:A:357:PHE:O	1:A:361:THR:HG23	2.17	0.44
1:B:321:VAL:HG22	1:B:380:VAL:HG21	1.99	0.44
1:A:352:MET:HB2	1:A:379:TYR:CE2	2.53	0.44
1:A:172:ILE:HD13	1:A:329:THR:HG21	1.98	0.44
1:A:288:GLN:CG	1:A:387:TRP:HE1	2.30	0.43
1:B:255:GLU:HA	1:B:258:HIS:HE1	1.81	0.43
1:B:179:TYR:HB3	1:B:319:ILE:HG12	2.00	0.43
1:B:106:GLU:HB3	1:B:122:LEU:HD21	1.99	0.43
1:B:172:ILE:HD13	1:B:329:THR:HG21	2.01	0.43
1:B:422:VAL:HA	1:B:425:THR:HG22	2.01	0.43
1:A:104:TRP:O	1:A:107:LEU:HB2	2.19	0.43
1:A:36:GLU:O	1:A:40:THR:HG23	2.19	0.43
1:B:176:LEU:HD21	1:B:322:GLY:C	2.39	0.43
1:A:247:THR:OG1	1:A:248:LEU:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:ALA:HB2	1:A:385:MET:HA	2.01	0.43
1:B:186:ALA:HA	1:B:194:LEU:HD11	2.00	0.42
1:B:288:GLN:CG	1:B:387:TRP:HE1	2.31	0.42
1:A:186:ALA:HA	1:A:194:LEU:HD11	2.00	0.42
1:B:104:TRP:O	1:B:107:LEU:HB2	2.20	0.42
1:B:310:SER:HB2	1:B:313:ILE:HB	2.01	0.42
1:B:26:TYR:HE1	1:B:177:LEU:HD22	1.86	0.41
1:B:332:ALA:HB2	1:B:385:MET:HA	2.01	0.41
1:A:299:TYR:CE2	1:A:426:PHE:CD2	3.08	0.41
1:A:424:TRP:O	1:A:427:PRO:HD2	2.20	0.41
1:A:54:ASN:HB3	1:A:428:MET:HA	2.02	0.41
1:B:352:MET:HB2	1:B:379:TYR:CE2	2.56	0.41
1:A:133:ARG:HD2	1:A:133:ARG:HA	1.55	0.41
1:A:176:LEU:HD11	1:A:323:VAL:N	2.36	0.41
1:A:9:TYR:O	1:A:13:ILE:HG13	2.21	0.41
1:A:352:MET:HE1	1:A:383:PHE:HD2	1.85	0.41
1:B:59:PHE:HD1	1:B:420:TYR:HH	1.67	0.40
1:A:26:TYR:CE2	1:A:206:GLU:HB2	2.56	0.40
1:B:24:PHE:CE1	1:B:144:SER:HB2	2.52	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	416/485 (86%)	387 (93%)	22 (5%)	7 (2%)	11	51
1	B	429/485 (88%)	398 (93%)	23 (5%)	8 (2%)	9	50
All	All	845/970 (87%)	785 (93%)	45 (5%)	15 (2%)	10	50

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	107	LEU
1	B	107	LEU
1	A	116	ASN
1	B	116	ASN
1	A	247	THR
1	B	35	VAL
1	A	35	VAL
1	A	120	VAL
1	B	120	VAL
1	A	340	GLY
1	B	388	GLY
1	A	388	GLY
1	B	340	GLY
1	B	369	GLY
1	B	442	GLY

### 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	342/390 (88%)	292 (85%)	50 (15%)	3	24
1	B	353/390 (90%)	301 (85%)	52 (15%)	3	24
All	All	695/780 (89%)	593 (85%)	102 (15%)	3	24

All (102) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	SER
1	A	15	LEU
1	A	24	PHE
1	A	31	ILE
1	A	36	GLU
1	A	56	LEU
1	A	79	SER
1	A	81	ARG
1	A	133	ARG

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Mol	Chain	Res	Type
1	A	154	LEU
1	A	168	GLN
1	A	177	LEU
1	A	178	VAL
1	A	188	SER
1	A	194	LEU
1	A	196	THR
1	A	227	LEU
1	A	235	GLN
1	A	246	ASN
1	A	251	GLN
1	A	255	GLU
1	A	258	HIS
1	A	260	LEU
1	A	278	ILE
1	A	291	VAL
1	A	302	GLU
1	A	311	THR
1	A	312	ASP
1	A	316	LEU
1	A	318	THR
1	A	325	ASN
1	A	326	LEU
1	A	335	THR
1	A	337	ASP
1	A	350	LEU
1	A	385	MET
1	A	386	SER
1	A	391	CYS
1	A	394	LEU
1	A	395	LEU
1	A	397	GLU
1	A	417	LEU
1	A	429	MET
1	A	432	ASN
1	A	433	SER
1	A	441	ASN
1	A	444	SER
1	A	457	LEU
1	A	459	MET
1	A	465	GLU
1	B	12	SER

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Mol	Chain	Res	Type
1	B	15	LEU
1	B	24	PHE
1	B	31	ILE
1	B	36	GLU
1	B	56	LEU
1	B	74	LEU
1	B	79	SER
1	B	133	ARG
1	B	154	LEU
1	B	168	GLN
1	B	177	LEU
1	B	178	VAL
1	B	188	SER
1	B	194	LEU
1	B	196	THR
1	B	227	LEU
1	B	235	GLN
1	B	240	LEU
1	B	246	ASN
1	B	251	GLN
1	B	253	VAL
1	B	260	LEU
1	B	278	ILE
1	B	291	VAL
1	B	302	GLU
1	B	311	THR
1	B	312	ASP
1	B	316	LEU
1	B	321	VAL
1	B	325	ASN
1	B	326	LEU
1	B	335	THR
1	B	337	ASP
1	B	350	LEU
1	B	358	SER
1	B	385	MET
1	B	386	SER
1	B	391	CYS
1	B	394	LEU
1	B	395	LEU
1	B	397	GLU
1	B	399	PHE

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Mol	Chain	Res	Type
1	B	417	LEU
1	B	422	VAL
1	B	423	SER
1	B	429	MET
1	B	432	ASN
1	B	433	SER
1	B	443	PHE
1	B	465	GLU
1	B	466	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	233	GLN
1	A	262	HIS
1	A	325	ASN
1	B	233	GLN
1	B	325	ASN
1	B	366	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 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

## 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 ⓘ

### 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	426/485 (87%)	0.35	34 (7%) 13 10	166, 229, 268, 275	0
1	B	439/485 (90%)	0.48	57 (12%) 4 4	170, 235, 271, 284	0
All	All	865/970 (89%)	0.42	91 (10%) 7 6	166, 231, 270, 284	0

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	264	ARG	8.1
1	B	335	THR	8.0
1	B	197	ASP	6.5
1	B	201	TYR	5.9
1	B	331	LEU	5.4
1	A	187	ARG	5.2
1	B	158	HIS	5.0
1	B	115	ASP	4.7
1	A	127	PRO	4.4
1	B	48	LEU	4.3
1	A	263	GLY	4.3
1	A	396	SER	4.2
1	A	144	SER	4.1
1	A	312	ASP	4.1
1	B	159	ILE	4.1
1	A	228	MET	4.0
1	A	46	GLN	3.9
1	A	199	TRP	3.9
1	B	118	VAL	3.9
1	B	196	THR	3.8
1	B	153	GLU	3.7
1	B	458	PHE	3.6
1	B	247	THR	3.6
1	B	334	MET	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	294	ASN	3.6
1	A	261	ASP	3.5
1	A	128	GLU	3.5
1	B	116	ASN	3.5
1	A	397	GLU	3.4
1	B	459	MET	3.3
1	B	84	ARG	3.3
1	B	119	PRO	3.3
1	A	188	SER	3.3
1	A	200	ARG	3.2
1	B	29	ALA	3.2
1	B	150	TYR	3.2
1	B	46	GLN	3.2
1	B	385	MET	3.2
1	A	14	THR	2.9
1	A	260	LEU	2.9
1	B	131	ILE	2.9
1	B	120	VAL	2.8
1	A	395	LEU	2.8
1	B	344	LEU	2.8
1	B	457	LEU	2.8
1	A	294	ASN	2.8
1	B	433	SER	2.8
1	A	231	GLY	2.8
1	B	49	SER	2.7
1	B	198	GLY	2.7
1	B	25	GLY	2.7
1	B	157	ALA	2.7
1	A	126	VAL	2.6
1	A	344	LEU	2.6
1	B	113	ASN	2.6
1	A	386	SER	2.6
1	A	440	HIS	2.5
1	A	460	TRP	2.5
1	B	462	PHE	2.5
1	B	7	SER	2.5
1	B	127	PRO	2.5
1	B	129	PHE	2.5
1	B	303	VAL	2.4
1	B	107	LEU	2.4
1	A	334	MET	2.4
1	B	27	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	128	GLU	2.4
1	B	45	PRO	2.4
1	B	200	ARG	2.4
1	B	149	MET	2.4
1	A	43	VAL	2.4
1	A	262	HIS	2.4
1	B	248	LEU	2.4
1	A	109	PHE	2.3
1	B	52	ALA	2.3
1	A	347	ILE	2.3
1	B	130	VAL	2.2
1	B	246	ASN	2.2
1	B	50	GLU	2.2
1	A	369	GLY	2.2
1	B	135	ILE	2.2
1	B	168	GLN	2.2
1	B	302	GLU	2.1
1	B	388	GLY	2.1
1	A	392	TRP	2.1
1	B	100	VAL	2.1
1	B	199	TRP	2.1
1	A	28	THR	2.1
1	B	456	ALA	2.0
1	A	462	PHE	2.0
1	B	32	SER	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. 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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	LU	B	502	1/1	0.73	0.11	-	300,300,300,300	0
2	CD	A	501	1/1	0.95	0.10	-	300,300,300,300	0
3	LU	A	502	1/1	0.92	0.13	-	300,300,300,300	0
3	LU	A	503	1/1	0.98	0.25	-	295,295,295,295	0
3	LU	B	501	1/1	0.97	0.19	-	300,300,300,300	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.