



# Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 09:17 am BST

PDB ID : 3MSU  
Title : Crystal Structure of Citrate Synthase from *Francisella tularensis*  
Authors : Maltseva, N.; Kim, Y.; Hasseman, J.; Anderson, W.F.; Joachimiak, A.; Center  
for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2010-04-29  
Resolution : 1.84 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.

---

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

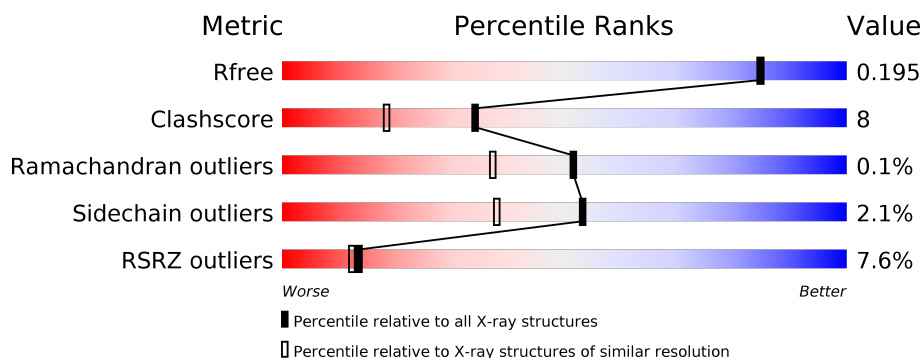
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.84 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	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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	427	<div> <div>13%</div> <div>79%</div> <div>18%</div> <div>• •</div> </div>
1	B	427	<div> <div>2%</div> <div>86%</div> <div>13%</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
2	OAA	A	430[B]	-	-	X	-
6	ACY	B	431	-	-	X	-

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7528 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.

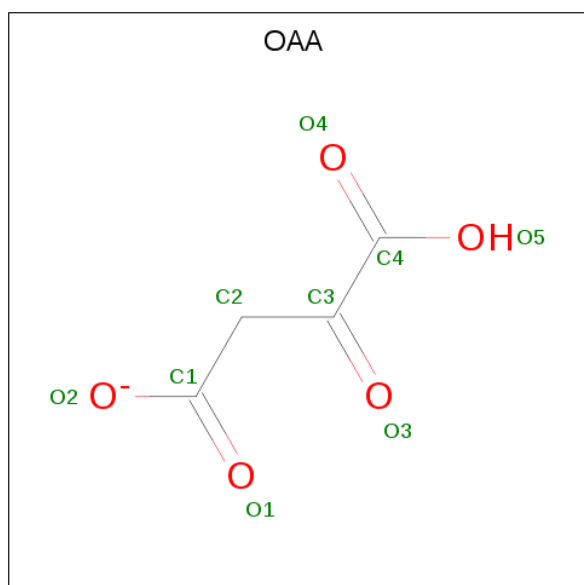
- Molecule 1 is a protein called Citrate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	415	Total	C	N	O	S	0	19	0
			3379	2149	566	637	27			
1	B	426	Total	C	N	O	S	0	21	0
			3503	2224	589	663	27			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	EXPRESSION TAG	UNP Q5NIJ6
A	-1	ASN	-	EXPRESSION TAG	UNP Q5NIJ6
A	0	ALA	-	EXPRESSION TAG	UNP Q5NIJ6
B	-2	SER	-	EXPRESSION TAG	UNP Q5NIJ6
B	-1	ASN	-	EXPRESSION TAG	UNP Q5NIJ6
B	0	ALA	-	EXPRESSION TAG	UNP Q5NIJ6

- Molecule 2 is OXALOACETATE ION (three-letter code: OAA) (formula:  $C_4H_3O_5$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	1
			18	8	10		
2	B	1	Total	C	O	0	1
			18	8	10		

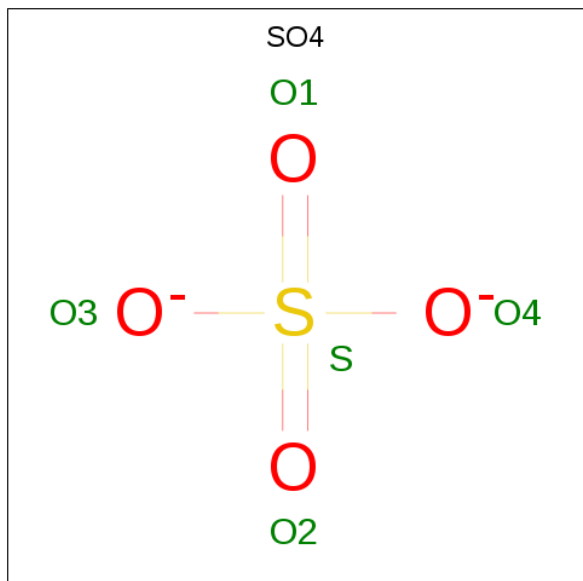
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		
3	A	1	Total	Zn	0	0
			1	1		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



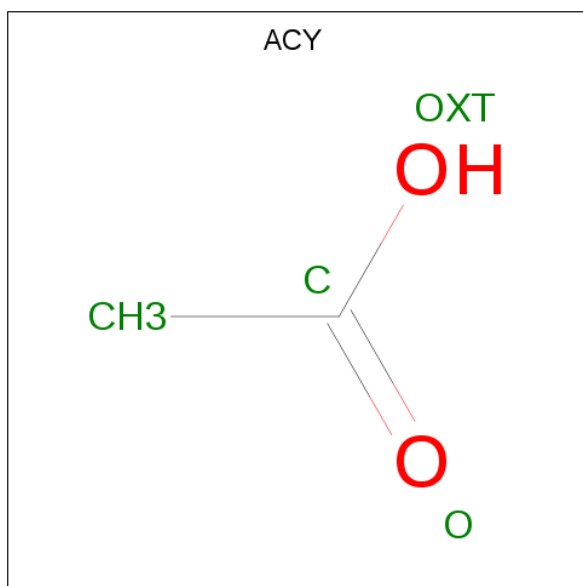
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

*Continued on next page...*

*Continued from previous page...*

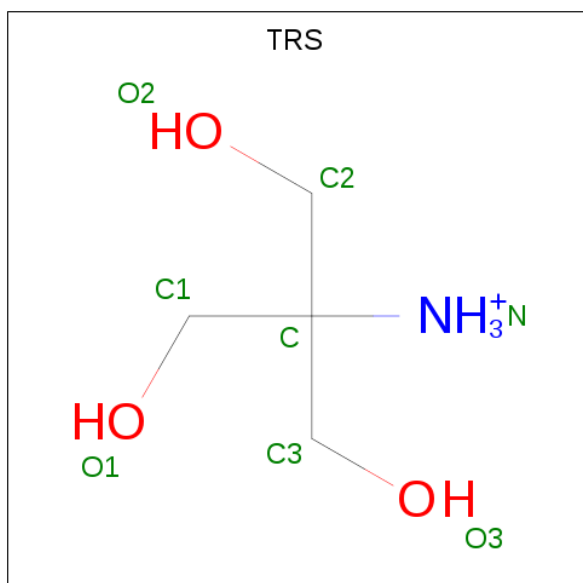
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is ACETIC ACID (three-letter code: ACY) (formula:  $C_2H_4O_2$ ).



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

- Molecule 7 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula:  $C_4H_{12}NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			8	4	1	3		

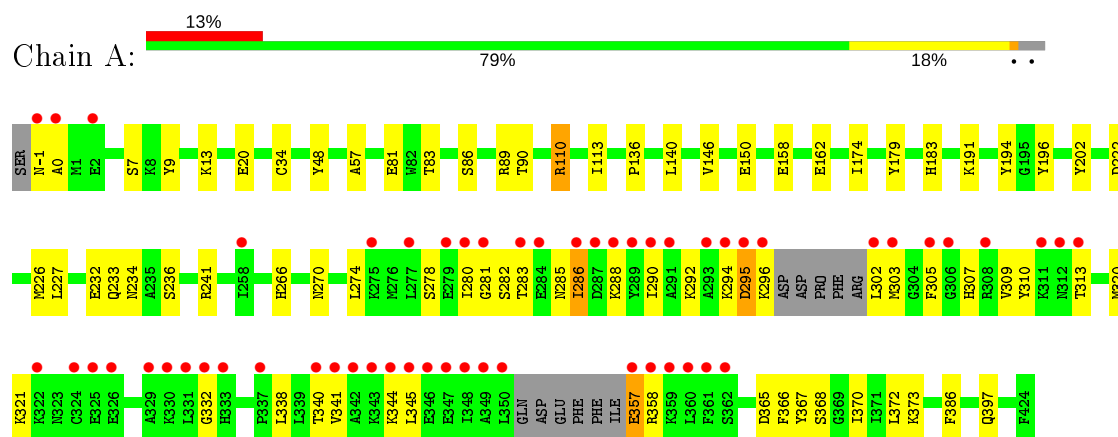
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	229	Total	O	0	0
			229	229		
8	B	351	Total	O	0	0
			351	351		

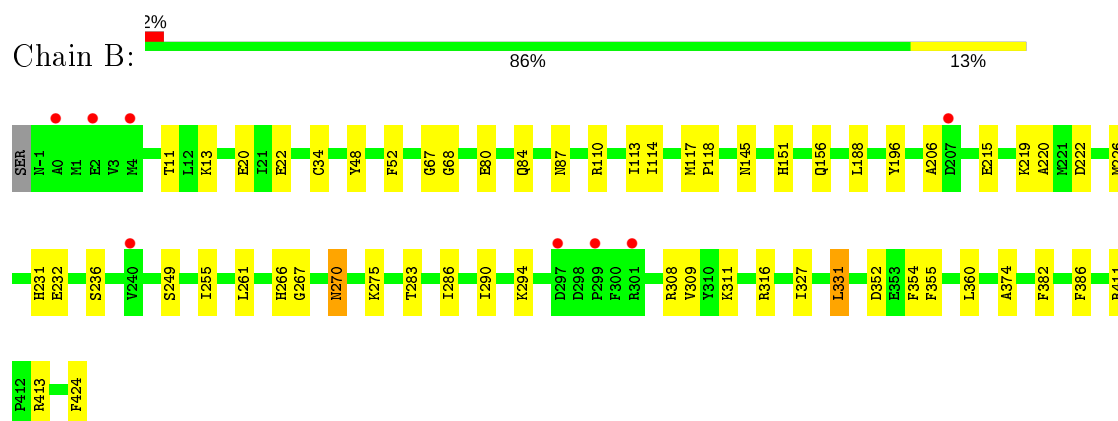
### 3 Residue-property plots [i](#)

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: Citrate synthase



#### • Molecule 1: Citrate synthase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.40Å 76.38Å 154.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.63 – 1.84 42.63 – 1.84	Depositor EDS
% Data completeness (in resolution range)	99.4 (42.63-1.84) 99.4 (42.63-1.84)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.62 (at 1.84Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6 _289)	Depositor
R, $R_{free}$	0.160 , 0.200 0.156 , 0.195	Depositor DCC
$R_{free}$ test set	3886 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.0	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 53.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7528	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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, OAA, CL, SO4, TRS, ACY

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	0.47	0/3461	0.57	0/4673
1	B	0.54	0/3587	0.60	0/4845
All	All	0.51	0/7048	0.59	0/9518

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	3379	0	3362	74	0
1	B	3503	0	3461	47	0
2	A	18	0	4	5	0
2	B	18	0	4	3	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	1	0
5	A	10	0	0	0	0
5	B	5	0	0	0	0
6	B	4	0	3	3	0
7	B	8	0	12	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	229	0	0	3	0
8	B	351	0	0	6	0
All	All	7528	0	6846	116	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 8.

All (116) 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:286:ILE:HB	8:A:502:HOH:O	1.75	0.86
1:A:57:ALA:HB3	8:A:440:HOH:O	1.74	0.86
1:A:307:HIS:HD2	1:A:309:VAL:H	1.28	0.82
1:A:307:HIS:CD2	1:A:309:VAL:H	2.01	0.78
1:B:87:ASN:HD22	6:B:431:ACY:H3	1.49	0.76
1:A:283:THR:O	1:A:286:ILE:HG12	1.89	0.72
1:A:227:LEU:CD1	1:A:320:MET:HG2	2.21	0.70
1:A:7[B]:SER:HG	1:A:9:TYR:HD1	1.41	0.69
1:A:288:LYS:O	1:A:292:LYS:HG3	1.92	0.68
1:B:331[A]:LEU:HD11	1:B:374:ALA:HB2	1.76	0.68
1:A:280:ILE:HD11	1:A:341:VAL:CG1	2.24	0.67
1:A:191[B]:LYS:HE3	1:A:202:TYR:CZ	2.30	0.66
1:B:87:ASN:HD22	6:B:431:ACY:CH3	2.08	0.66
1:B:283:THR:HA	1:B:286:ILE:HD13	1.81	0.63
1:A:81:GLU:HG3	1:B:424:PHE:CD1	2.33	0.63
1:B:84:GLN:HG3	8:B:570:HOH:O	1.98	0.62
1:A:280:ILE:HD11	1:A:341:VAL:HG11	1.80	0.62
1:A:89:ARG:HD3	1:A:110:ARG:HD3	1.82	0.60
1:A:234:ASN:HA	1:B:411[B]:ARG:HD3	1.83	0.59
1:B:236:SER:OG	1:B:266:HIS:HE1	1.87	0.58
1:B:331[A]:LEU:HD11	1:B:374:ALA:CB	2.34	0.57
1:A:290:ILE:HG22	1:A:294:LYS:HE2	1.87	0.56
1:A:140[B]:LEU:HD13	1:A:174:ILE:HG22	1.88	0.56
1:A:13[A]:LYS:HE2	1:A:20:GLU:OE2	2.06	0.56
1:A:191[B]:LYS:HD2	1:A:194:TYR:CE2	2.41	0.56
1:B:352:ASP:HB3	1:B:355:PHE:HD2	1.70	0.56
1:B:316[B]:ARG:NH2	8:B:735:HOH:O	2.21	0.56
1:A:110:ARG:HH11	2:A:430[B]:OAA:C1	2.19	0.55
1:B:294:LYS:HG2	1:B:354:PHE:CE2	2.41	0.55
1:B:11[B]:THR:HG22	1:B:22:GLU:HG2	1.88	0.55
1:B:68:GLY:HA2	1:B:311:LYS:HD2	1.88	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:283:THR:HA	1:B:286:ILE:CD1	2.37	0.55
1:A:89:ARG:HD2	1:A:110:ARG:HB2	1.89	0.54
1:B:266:HIS:HD2	8:B:471:HOH:O	1.90	0.54
1:A:307:HIS:HD2	1:A:309:VAL:N	2.02	0.53
1:B:196:TYR:HB2	2:B:436[B]:OAA:H21	1.91	0.52
1:A:280:ILE:HD11	1:A:341:VAL:HG13	1.92	0.52
1:A:310:TYR:HB3	1:A:313:THR:O	2.10	0.52
1:B:215[B]:GLU:OE2	1:B:219:LYS:HG3	2.09	0.52
1:A:295:ASP:O	1:A:296:LYS:C	2.48	0.52
1:A:236:SER:OG	1:A:266:HIS:HE1	1.94	0.51
1:A:86:SER:OG	1:A:90[B]:THR:OG1	2.28	0.51
1:A:146:VAL:O	1:A:150[B]:GLU:HG3	2.11	0.51
1:A:136:PRO:O	1:A:140[B]:LEU:HD23	2.10	0.51
1:A:113[B]:ILE:HD12	2:A:430[B]:OAA:O4	2.11	0.51
1:A:89:ARG:CD	1:A:110:ARG:HD3	2.40	0.51
1:A:307:HIS:CD2	1:A:310:TYR:H	2.29	0.51
2:B:436[A]:OAA:O3	2:B:436[A]:OAA:O1	2.26	0.51
1:B:270[A]:ASN:HB3	1:B:382:PHE:CD1	2.46	0.51
1:B:222[B]:ASP:O	1:B:226[B]:MET:HG3	2.12	0.51
1:A:283:THR:HB	1:A:344:LYS:NZ	2.26	0.50
1:B:308:ARG:HG2	8:B:581:HOH:O	2.12	0.50
1:B:275:LYS:HD2	8:B:474:HOH:O	2.12	0.50
1:A:233:GLN:HE22	1:A:397:GLN:HE22	1.59	0.50
1:B:13:LYS:HG2	1:B:20:GLU:HG3	1.94	0.50
1:B:236:SER:H	1:B:266:HIS:CE1	2.30	0.50
1:A:321:LYS:HG2	1:A:367:TYR:CZ	2.48	0.49
1:A:305:PHE:CZ	1:A:345:LEU:HD22	2.48	0.48
1:A:150[A]:GLU:OE1	4:A:432:CL:CL	2.68	0.48
1:A:241:ARG:HH11	1:A:397:GLN:NE2	2.10	0.48
1:B:113:ILE:HD12	2:B:436[B]:OAA:O1	2.14	0.48
1:A:270[B]:ASN:HD21	1:A:365:ASP:HA	1.78	0.47
1:B:151:HIS:HD2	1:B:249:SER:OG	1.97	0.47
1:A:158[B]:GLU:HG2	1:A:162:GLU:HB3	1.96	0.47
1:A:34[A]:CYS:HB3	1:B:48:TYR:HB2	1.96	0.47
1:A:283:THR:HB	1:A:344:LYS:HZ2	1.80	0.47
1:A:292:LYS:HE2	1:A:292:LYS:HB3	1.73	0.47
1:B:352:ASP:HB3	1:B:355:PHE:CD2	2.49	0.47
1:A:236:SER:H	1:A:266:HIS:CE1	2.32	0.47
1:A:270[B]:ASN:ND2	1:A:365:ASP:HA	2.30	0.46
1:A:7[B]:SER:OG	1:A:9:TYR:HD1	1.99	0.46
1:B:13:LYS:HE2	1:B:20:GLU:OE1	2.16	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:331[B]:LEU:HD21	1:B:374:ALA:HB2	1.97	0.45
1:B:87:ASN:HB3	6:B:431:ACY:H1	1.98	0.45
1:A:179:TYR:CE2	1:A:183:HIS:CE1	3.05	0.45
1:B:331[A]:LEU:HA	1:B:331[A]:LEU:HD12	1.56	0.45
1:A:89:ARG:HB3	2:A:430[B]:OAA:C3	2.47	0.44
1:A:233:GLN:O	1:B:411[B]:ARG:CZ	2.66	0.44
1:A:274:LEU:HD11	1:A:373:LYS:HD2	1.99	0.44
1:A:344:LYS:HE2	1:A:344:LYS:HB3	1.86	0.44
1:A:-1:ASN:ND2	1:A:0:ALA:H	2.14	0.44
1:A:136:PRO:O	1:A:140[B]:LEU:CD2	2.65	0.43
1:A:285:ASN:O	1:A:288:LYS:HB3	2.18	0.43
1:A:340:THR:O	1:A:344:LYS:HE3	2.19	0.43
1:A:321:LYS:HD2	1:A:367:TYR:OH	2.18	0.43
1:A:357:GLU:CD	1:A:357:GLU:N	2.73	0.42
1:A:222:ASP:OD1	2:A:430[A]:OAA:O4	2.37	0.42
1:B:117:MET:N	1:B:118:PRO:CD	2.82	0.42
1:B:188:LEU:CD1	1:B:206:ALA:HB3	2.49	0.42
1:A:332:GLY:O	1:A:340:THR:HG22	2.19	0.42
1:A:57:ALA:HB2	1:B:52:PHE:CE1	2.54	0.42
1:A:282:SER:HA	1:A:341:VAL:CG2	2.50	0.42
1:A:227:LEU:HD12	1:A:320:MET:HG2	2.00	0.42
1:A:366:PHE:O	1:A:370:ILE:HG12	2.19	0.42
1:B:411[B]:ARG:HG3	8:B:742:HOH:O	2.20	0.42
1:A:280:ILE:HG13	1:A:281:GLY:N	2.33	0.42
1:B:145:ASN:HA	1:B:255[A]:ILE:HD11	2.01	0.42
1:B:411[A]:ARG:HG3	1:B:411[A]:ARG:O	2.20	0.42
1:A:266:HIS:HD2	8:A:497:HOH:O	2.02	0.41
1:B:151:HIS:CD2	1:B:156:GLN:HG2	2.55	0.41
1:A:357:GLU:HB2	1:A:358:ARG:H	1.47	0.41
1:B:261:LEU:O	1:B:267:GLY:HA3	2.20	0.41
1:A:196:TYR:HB3	2:A:430[B]:OAA:H21	2.01	0.41
1:A:236:SER:CB	1:A:266:HIS:HE1	2.33	0.41
1:A:320:MET:HE1	1:A:368:SER:HB3	2.01	0.41
1:A:83:THR:HG22	1:A:226:MET:HE3	2.01	0.41
1:B:290:ILE:HA	1:B:290:ILE:HD13	1.85	0.41
1:A:227:LEU:CD1	1:A:320:MET:CG	2.96	0.41
1:B:110:ARG:O	1:B:114[A]:ILE:HG12	2.20	0.41
1:B:67:GLY:HA3	1:B:309:VAL:O	2.20	0.41
1:B:220:ALA:HB2	1:B:327:ILE:HD12	2.03	0.41
1:B:236:SER:CB	1:B:266:HIS:HE1	2.33	0.41
1:A:278:SER:HA	1:A:338:LEU:HD11	2.03	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:TYR:HB2	1:B:34:CYS:HB3	2.03	0.40
1:A:372:LEU:HA	1:A:372:LEU:HD23	1.93	0.40
1:A:274:LEU:CD1	1:A:373:LYS:HD2	2.52	0.40

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	428/427 (100%)	417 (97%)	10 (2%)	1 (0%)	47	33
1	B	445/427 (104%)	441 (99%)	4 (1%)	0	100	100
All	All	873/854 (102%)	858 (98%)	14 (2%)	1 (0%)	51	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	286	ILE

### 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	A	363/356 (102%)	356 (98%)	7 (2%)	57	42
1	B	376/356 (106%)	365 (97%)	11 (3%)	42	25

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	739/712 (104%)	721 (98%)	18 (2%)	53 32

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	110	ARG
1	A	232	GLU
1	A	295	ASP
1	A	302	LEU
1	A	303	MET
1	A	357	GLU
1	A	386	PHE
1	B	80[A]	GLU
1	B	80[B]	GLU
1	B	231	HIS
1	B	232	GLU
1	B	270[A]	ASN
1	B	270[B]	ASN
1	B	331[A]	LEU
1	B	331[B]	LEU
1	B	360	LEU
1	B	386	PHE
1	B	413	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-1	ASN
1	A	133	HIS
1	A	266	HIS
1	A	307	HIS
1	A	397	GLN
1	B	111	GLN
1	B	151	HIS
1	B	153	HIS
1	B	160	GLN
1	B	266	HIS
1	B	403	ASN

### 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 12 ligands modelled in this entry, 3 are monoatomic - leaving 9 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
2	OAA	A	430[A]	-	2,8,8	4.14	1 (50%)	2,10,10	1.62	0
2	OAA	A	430[B]	-	2,8,8	3.83	1 (50%)	2,10,10	1.54	0
5	SO4	A	425	-	4,4,4	0.23	0	6,6,6	0.26	0
5	SO4	A	435	-	4,4,4	0.10	0	6,6,6	0.15	0
7	TRS	B	433	-	7,7,7	0.34	0	9,9,9	0.48	0
2	OAA	B	436[A]	-	2,8,8	4.41	1 (50%)	2,10,10	2.32	1 (50%)
5	SO4	B	432	-	4,4,4	0.12	0	6,6,6	0.29	0
6	ACY	B	431	-	1,3,3	2.03	1 (100%)	0,3,3	0.00	-
2	OAA	B	436[B]	-	2,8,8	3.97	1 (50%)	2,10,10	1.40	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
2	OAA	A	430[B]	-	-	0/2/8/8	-
2	OAA	A	430[A]	-	-	0/2/8/8	-
2	OAA	B	436[A]	-	-	0/2/8/8	-
2	OAA	B	436[B]	-	-	0/2/8/8	-
7	TRS	B	433	-	-	5/9/9/9	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	436[A]	OAA	O3-C3	6.20	1.32	1.22
2	A	430[A]	OAA	O3-C3	5.85	1.31	1.22
2	B	436[B]	OAA	O3-C3	5.59	1.31	1.22
2	A	430[B]	OAA	O3-C3	5.35	1.30	1.22
6	B	431	ACY	CH3-C	2.03	1.51	1.48

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	436[A]	OAA	C1-C2-C3	-3.25	109.71	115.51

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	433	TRS	N-C-C2-O2
7	B	433	TRS	C3-C-C1-O1
7	B	433	TRS	C3-C-C2-O2
7	B	433	TRS	N-C-C1-O1
7	B	433	TRS	C2-C-C1-O1

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	430[A]	OAA	1	0
2	A	430[B]	OAA	4	0
2	B	436[A]	OAA	1	0
6	B	431	ACY	3	0
2	B	436[B]	OAA	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 ⓘ

### 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	415/427 (97%)	0.44	56 (13%) 3 2	14, 30, 91, 151	0
1	B	426/427 (99%)	-0.11	8 (1%) 66 65	13, 22, 43, 80	0
All	All	841/854 (98%)	0.16	64 (7%) 13 12	13, 25, 68, 151	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	350	LEU	9.2
1	A	295	ASP	6.3
1	A	344	LYS	6.1
1	A	349	ALA	6.1
1	A	348	ILE	5.8
1	A	332	GLY	5.4
1	A	286	ILE	5.2
1	A	333	HIS	5.2
1	A	347	GLU	5.1
1	A	302	LEU	5.0
1	A	331	LEU	4.7
1	A	283	THR	4.2
1	A	329	ALA	4.2
1	A	345	LEU	4.2
1	A	291	ALA	4.1
1	A	296	LYS	4.1
1	A	343	LYS	4.0
1	A	359	LYS	4.0
1	A	358	ARG	4.0
1	A	361	PHE	4.0
1	A	308	ARG	3.8
1	B	301	ARG	3.7
1	A	312	ASN	3.4
1	A	360	LEU	3.4

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	293	ALA	3.3
1	A	290	ILE	3.2
1	A	330	LYS	3.1
1	A	340	THR	3.1
1	B	299	PRO	3.0
1	A	294	LYS	3.0
1	A	326	GLU	2.9
1	A	280	ILE	2.9
1	A	311	LYS	2.8
1	A	289	TYR	2.8
1	A	325	GLU	2.7
1	A	357	GLU	2.7
1	B	207[A]	ASP	2.7
1	A	279	GLU	2.7
1	B	0	ALA	2.6
1	A	342	ALA	2.6
1	B	2	GLU	2.6
1	A	341	VAL	2.6
1	A	313	THR	2.5
1	A	288	LYS	2.5
1	B	4	MET	2.5
1	A	287	ASP	2.5
1	A	0	ALA	2.4
1	A	281	GLY	2.4
1	B	240	VAL	2.4
1	A	306	GLY	2.3
1	A	346	GLU	2.3
1	A	284	GLU	2.3
1	A	305	PHE	2.3
1	A	277	LEU	2.2
1	A	2	GLU	2.2
1	A	324	CYS	2.1
1	B	297	ASP	2.1
1	A	303	MET	2.1
1	A	362	SER	2.0
1	A	275	LYS	2.0
1	A	322	LYS	2.0
1	A	258	ILE	2.0
1	A	337	PRO	2.0
1	A	-1	ASN	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
7	TRS	B	433	8/8	0.79	0.30	38,53,59,59	0
6	ACY	B	431	4/4	0.83	0.17	31,48,51,62	0
2	OAA	A	430[A]	9/9	0.87	0.20	28,39,44,53	9
2	OAA	A	430[B]	9/9	0.87	0.20	33,39,41,42	9
5	SO4	B	432	5/5	0.95	0.11	39,51,55,64	0
3	ZN	A	431	1/1	0.96	0.09	82,82,82,82	0
5	SO4	A	435	5/5	0.96	0.18	48,63,64,70	0
3	ZN	B	434	1/1	0.96	0.05	43,43,43,43	1
5	SO4	A	425	5/5	0.97	0.25	33,43,57,60	0
2	OAA	B	436[A]	9/9	0.97	0.18	19,21,31,44	9
2	OAA	B	436[B]	9/9	0.97	0.18	20,22,33,36	9
4	CL	A	432	1/1	0.99	0.15	43,43,43,43	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.