



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:32 PM GMT

PDB ID : 4LUQ  
Title : Crystal structure of virulence effector Tse3 in complex with neutralizer Tsi3  
Authors : Wang, T.; Li, L.; Zhang, W.  
Deposited on : 2013-07-25  
Resolution : 1.77 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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

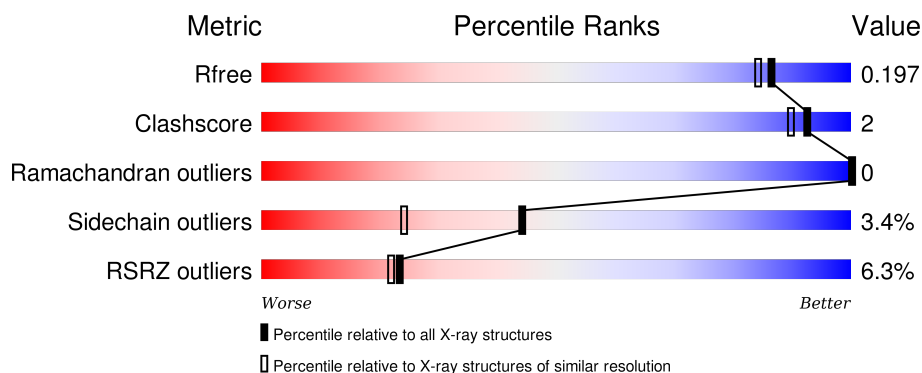
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.77 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	6655 (1.80-1.76)
Clashscore	102246	7658 (1.80-1.76)
Ramachandran outliers	100387	7570 (1.80-1.76)
Sidechain outliers	100360	7569 (1.80-1.76)
RSRZ outliers	91569	6671 (1.80-1.76)

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	428	<div> <div>3%</div> <div>87%</div> <div>8%</div> <div>• •</div> </div>
1	B	428	<div> <div>5%</div> <div>84%</div> <div>9%</div> <div>• •</div> </div>
2	C	144	<div> <div>4%</div> <div>78%</div> <div>7%</div> <div>• 15%</div> </div>
2	D	144	<div> <div>20%</div> <div>76%</div> <div>9%</div> <div>• • 13%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8997 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	0	0
			3137	1982	552	597	6			
1	B	409	Total	C	N	O	S	0	0	0
			3137	1982	552	597	6			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q9HYC5
A	-18	GLY	-	EXPRESSION TAG	UNP Q9HYC5
A	-17	SER	-	EXPRESSION TAG	UNP Q9HYC5
A	-16	SER	-	EXPRESSION TAG	UNP Q9HYC5
A	-15	HIS	-	EXPRESSION TAG	UNP Q9HYC5
A	-14	HIS	-	EXPRESSION TAG	UNP Q9HYC5
A	-13	HIS	-	EXPRESSION TAG	UNP Q9HYC5
A	-12	HIS	-	EXPRESSION TAG	UNP Q9HYC5
A	-11	HIS	-	EXPRESSION TAG	UNP Q9HYC5
A	-10	HIS	-	EXPRESSION TAG	UNP Q9HYC5
A	-9	SER	-	EXPRESSION TAG	UNP Q9HYC5
A	-8	SER	-	EXPRESSION TAG	UNP Q9HYC5
A	-7	GLY	-	EXPRESSION TAG	UNP Q9HYC5
A	-6	LEU	-	EXPRESSION TAG	UNP Q9HYC5
A	-5	VAL	-	EXPRESSION TAG	UNP Q9HYC5
A	-4	PRO	-	EXPRESSION TAG	UNP Q9HYC5
A	-3	ARG	-	EXPRESSION TAG	UNP Q9HYC5
A	-2	GLY	-	EXPRESSION TAG	UNP Q9HYC5
A	-1	SER	-	EXPRESSION TAG	UNP Q9HYC5
A	0	HIS	-	EXPRESSION TAG	UNP Q9HYC5
B	-19	MET	-	EXPRESSION TAG	UNP Q9HYC5
B	-18	GLY	-	EXPRESSION TAG	UNP Q9HYC5
B	-17	SER	-	EXPRESSION TAG	UNP Q9HYC5
B	-16	SER	-	EXPRESSION TAG	UNP Q9HYC5
B	-15	HIS	-	EXPRESSION TAG	UNP Q9HYC5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	EXPRESSION TAG	UNP Q9HYC5
B	-13	HIS	-	EXPRESSION TAG	UNP Q9HYC5
B	-12	HIS	-	EXPRESSION TAG	UNP Q9HYC5
B	-11	HIS	-	EXPRESSION TAG	UNP Q9HYC5
B	-10	HIS	-	EXPRESSION TAG	UNP Q9HYC5
B	-9	SER	-	EXPRESSION TAG	UNP Q9HYC5
B	-8	SER	-	EXPRESSION TAG	UNP Q9HYC5
B	-7	GLY	-	EXPRESSION TAG	UNP Q9HYC5
B	-6	LEU	-	EXPRESSION TAG	UNP Q9HYC5
B	-5	VAL	-	EXPRESSION TAG	UNP Q9HYC5
B	-4	PRO	-	EXPRESSION TAG	UNP Q9HYC5
B	-3	ARG	-	EXPRESSION TAG	UNP Q9HYC5
B	-2	GLY	-	EXPRESSION TAG	UNP Q9HYC5
B	-1	SER	-	EXPRESSION TAG	UNP Q9HYC5
B	0	HIS	-	EXPRESSION TAG	UNP Q9HYC5

- Molecule 2 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	123	Total	C	N	O		0	0	0
			964	597	181	186				
2	D	126	Total	C	N	O	S	0	0	0
			988	611	186	190	1			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	2	MET	-	EXPRESSION TAG	UNP Q9HYC4
C	3	GLY	-	EXPRESSION TAG	UNP Q9HYC4
C	4	SER	-	EXPRESSION TAG	UNP Q9HYC4
C	5	SER	-	EXPRESSION TAG	UNP Q9HYC4
C	6	HIS	-	EXPRESSION TAG	UNP Q9HYC4
C	7	HIS	-	EXPRESSION TAG	UNP Q9HYC4
C	8	HIS	-	EXPRESSION TAG	UNP Q9HYC4
C	9	HIS	-	EXPRESSION TAG	UNP Q9HYC4
C	10	HIS	-	EXPRESSION TAG	UNP Q9HYC4
C	11	HIS	-	EXPRESSION TAG	UNP Q9HYC4
C	12	SER	-	EXPRESSION TAG	UNP Q9HYC4
C	13	SER	-	EXPRESSION TAG	UNP Q9HYC4
C	14	GLY	-	EXPRESSION TAG	UNP Q9HYC4
C	15	LEU	-	EXPRESSION TAG	UNP Q9HYC4
C	16	VAL	-	EXPRESSION TAG	UNP Q9HYC4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	17	PRO	-	EXPRESSION TAG	UNP Q9HYC4
C	18	ARG	-	EXPRESSION TAG	UNP Q9HYC4
C	19	GLY	-	EXPRESSION TAG	UNP Q9HYC4
C	20	SER	-	EXPRESSION TAG	UNP Q9HYC4
C	21	HIS	-	EXPRESSION TAG	UNP Q9HYC4
C	22	MET	-	EXPRESSION TAG	UNP Q9HYC4
D	2	MET	-	EXPRESSION TAG	UNP Q9HYC4
D	3	GLY	-	EXPRESSION TAG	UNP Q9HYC4
D	4	SER	-	EXPRESSION TAG	UNP Q9HYC4
D	5	SER	-	EXPRESSION TAG	UNP Q9HYC4
D	6	HIS	-	EXPRESSION TAG	UNP Q9HYC4
D	7	HIS	-	EXPRESSION TAG	UNP Q9HYC4
D	8	HIS	-	EXPRESSION TAG	UNP Q9HYC4
D	9	HIS	-	EXPRESSION TAG	UNP Q9HYC4
D	10	HIS	-	EXPRESSION TAG	UNP Q9HYC4
D	11	HIS	-	EXPRESSION TAG	UNP Q9HYC4
D	12	SER	-	EXPRESSION TAG	UNP Q9HYC4
D	13	SER	-	EXPRESSION TAG	UNP Q9HYC4
D	14	GLY	-	EXPRESSION TAG	UNP Q9HYC4
D	15	LEU	-	EXPRESSION TAG	UNP Q9HYC4
D	16	VAL	-	EXPRESSION TAG	UNP Q9HYC4
D	17	PRO	-	EXPRESSION TAG	UNP Q9HYC4
D	18	ARG	-	EXPRESSION TAG	UNP Q9HYC4
D	19	GLY	-	EXPRESSION TAG	UNP Q9HYC4
D	20	SER	-	EXPRESSION TAG	UNP Q9HYC4
D	21	HIS	-	EXPRESSION TAG	UNP Q9HYC4
D	22	MET	-	EXPRESSION TAG	UNP Q9HYC4

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	3	Total Ca 3 3	0	0
3	A	3	Total Ca 3 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	348	Total O 348 348	0	0

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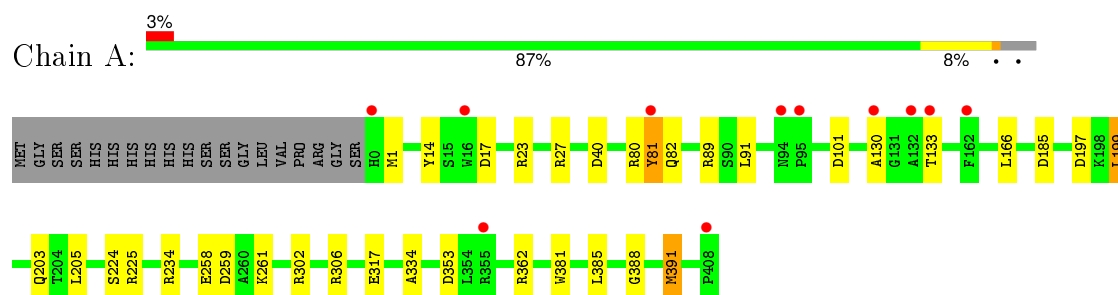
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	292	Total 292	O 292	0	0
4	C	81	Total 81	O 81	0	0
4	D	44	Total 44	O 44	0	0

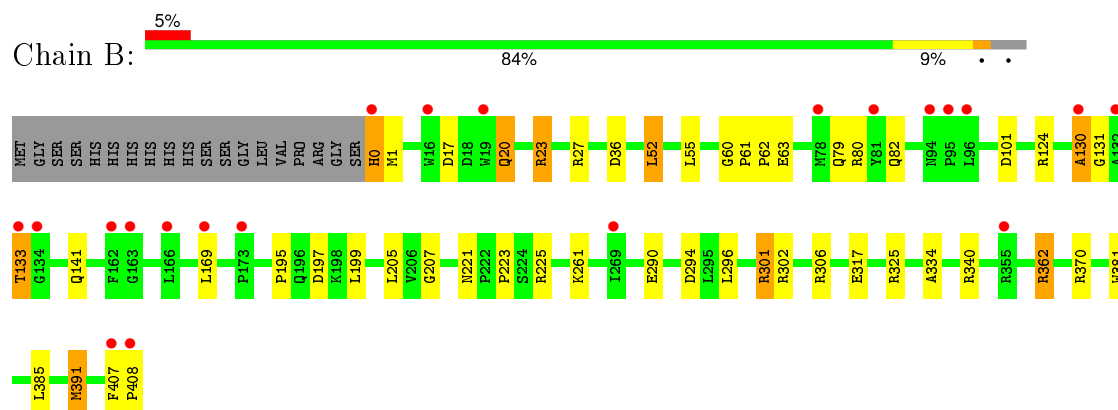
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

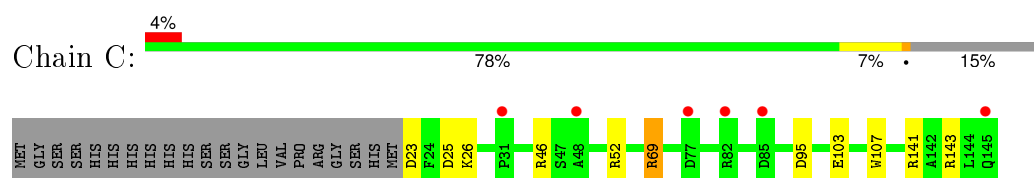
- Molecule 1: Uncharacterized protein



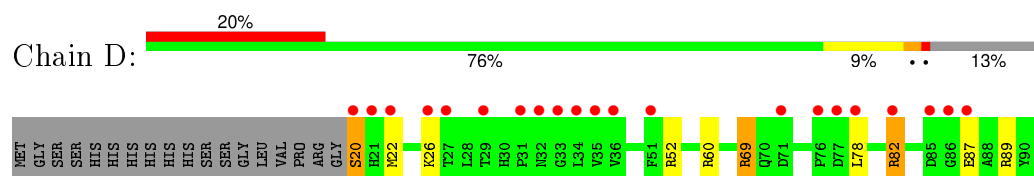
- Molecule 1: Uncharacterized protein

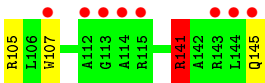


- Molecule 2: Uncharacterized protein



- Molecule 2: Uncharacterized protein







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.33Å 81.29Å 111.41Å 90.00° 93.64° 90.00°	Depositor
Resolution (Å)	40.52 – 1.77 40.49 – 1.77	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.52-1.77) 99.2 (40.49-1.77)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.88 (at 1.77Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.139 , 0.188 0.152 , 0.197	Depositor DCC
$R_{free}$ test set	5496 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	18.5	Xtriage
Anisotropy	0.208	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 49.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 109525 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8997	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

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

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

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	1.00	3/3205 (0.1%)	1.04	23/4370 (0.5%)
1	B	0.95	1/3205 (0.0%)	1.12	24/4370 (0.5%)
2	C	1.01	2/986 (0.2%)	1.15	9/1334 (0.7%)
2	D	0.92	2/1011 (0.2%)	1.08	8/1367 (0.6%)
All	All	0.97	8/8407 (0.1%)	1.09	64/11441 (0.6%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	103	GLU	CD-OE2	6.75	1.33	1.25
2	D	107	TRP	CB-CG	-5.95	1.39	1.50
1	A	81	TYR	CG-CD1	5.79	1.46	1.39
2	C	107	TRP	CB-CG	-5.48	1.40	1.50
2	D	103	GLU	CD-OE1	5.36	1.31	1.25
1	A	258	GLU	CD-OE2	5.33	1.31	1.25
1	A	81	TYR	CE1-CZ	5.02	1.45	1.38
1	B	301	ARG	CD-NE	-5.02	1.38	1.46

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	301	ARG	NE-CZ-NH2	-17.29	111.66	120.30
2	C	69	ARG	NE-CZ-NH1	16.88	128.74	120.30
2	D	69	ARG	NE-CZ-NH1	13.65	127.12	120.30
1	A	362	ARG	NE-CZ-NH2	-13.02	113.79	120.30
1	B	301	ARG	NE-CZ-NH1	12.84	126.72	120.30
1	B	27	ARG	NE-CZ-NH1	11.80	126.20	120.30
1	B	27	ARG	NE-CZ-NH2	-11.19	114.71	120.30
2	C	69	ARG	NE-CZ-NH2	-11.16	114.72	120.30
1	B	302	ARG	NE-CZ-NH2	-10.33	115.14	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	101	ASP	CB-CG-OD2	9.07	126.46	118.30
1	B	131	GLY	N-CA-C	9.03	135.68	113.10
1	B	52	LEU	CB-CG-CD2	9.00	126.30	111.00
1	B	340	ARG	NE-CZ-NH1	8.05	124.33	120.30
1	B	80	ARG	NE-CZ-NH1	-7.91	116.34	120.30
2	D	105	ARG	NE-CZ-NH1	7.31	123.96	120.30
1	A	89	ARG	NE-CZ-NH1	7.22	123.91	120.30
2	C	141	ARG	NE-CZ-NH2	-7.03	116.78	120.30
2	C	46	ARG	NE-CZ-NH1	6.91	123.75	120.30
1	A	353	ASP	CB-CG-OD1	6.90	124.51	118.30
1	B	340	ARG	NE-CZ-NH2	-6.65	116.97	120.30
2	D	141	ARG	NE-CZ-NH1	6.64	123.62	120.30
2	D	69	ARG	NE-CZ-NH2	-6.61	116.99	120.30
1	B	130	ALA	N-CA-C	6.52	128.61	111.00
2	C	141	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	A	197	ASP	CB-CG-OD1	6.48	124.13	118.30
1	B	306	ARG	NE-CZ-NH1	6.47	123.53	120.30
1	A	185	ASP	CB-CG-OD1	6.46	124.11	118.30
1	A	199	LEU	CA-CB-CG	6.38	129.98	115.30
1	B	325	ARG	NE-CZ-NH1	6.35	123.47	120.30
1	B	23	ARG	NE-CZ-NH2	-6.35	117.13	120.30
1	A	80	ARG	NE-CZ-NH1	-6.34	117.13	120.30
1	B	36	ASP	CB-CG-OD1	6.28	123.95	118.30
1	A	302	ARG	NE-CZ-NH2	-6.22	117.19	120.30
2	D	82	ARG	NE-CZ-NH1	6.21	123.41	120.30
1	A	353	ASP	CB-CG-OD2	-6.03	112.87	118.30
2	C	69	ARG	CD-NE-CZ	5.96	131.95	123.60
2	D	105	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	A	259	ASP	CB-CG-OD1	5.92	123.63	118.30
1	A	362	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	B	325	ARG	NE-CZ-NH2	-5.74	117.43	120.30
1	A	17	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	A	23	ARG	CG-CD-NE	-5.68	99.88	111.80
2	C	52	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	A	362	ARG	CG-CD-NE	-5.55	100.14	111.80
1	A	234	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	A	101	ASP	CB-CG-OD1	-5.48	113.36	118.30
1	B	294	ASP	CB-CG-OD1	5.40	123.16	118.30
1	B	362	ARG	NE-CZ-NH1	-5.39	117.61	120.30
1	A	306	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	B	385	LEU	CB-CG-CD1	-5.38	101.85	111.00
1	A	385	LEU	CB-CG-CD1	-5.33	101.93	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	197	ASP	CB-CG-OD1	5.29	123.06	118.30
1	A	27	ARG	NE-CZ-NH1	5.21	122.90	120.30
1	B	370	ARG	NE-CZ-NH2	-5.18	117.71	120.30
2	C	25	ASP	N-CA-C	5.17	124.95	111.00
1	B	101	ASP	CB-CG-OD2	5.14	122.93	118.30
1	B	391	MET	CB-CG-SD	5.12	127.77	112.40
1	B	17	ASP	CB-CG-OD1	5.12	122.91	118.30
2	D	52	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	A	199	LEU	CB-CG-CD1	5.03	119.54	111.00
2	C	95	ASP	CB-CG-OD2	5.01	122.81	118.30
2	D	60	ARG	NE-CZ-NH1	-5.01	117.80	120.30
1	A	40	ASP	CB-CG-OD1	5.00	122.80	118.30
1	A	91	LEU	CA-CB-CG	-5.00	103.80	115.30

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	3137	0	3122	8	0
1	B	3137	0	3121	20	0
2	C	964	0	922	0	0
2	D	988	0	943	6	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	A	348	0	0	1	0
4	B	292	0	0	2	0
4	C	81	0	0	0	0
4	D	44	0	0	0	0
All	All	8997	0	8108	33	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 2.

All (33) 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:203:GLN:HG2	4:A:916:HOH:O	1.61	0.98
1:B:362:ARG:HD3	4:B:836:HOH:O	1.70	0.90
1:B:195:PRO:O	1:B:199:LEU:HD23	1.95	0.66
1:B:290:GLU:OE1	1:B:301:ARG:NH2	2.33	0.59
1:B:124:ARG:HA	2:D:20:SER:HB2	1.89	0.54
1:B:133:THR:HG22	1:B:207:GLY:HA2	1.89	0.53
1:B:133:THR:O	1:B:133:THR:HG23	2.10	0.51
1:B:20:GLN:OE1	1:B:60:GLY:N	2.44	0.51
2:D:141:ARG:CG	2:D:141:ARG:HH11	2.24	0.50
1:A:130:ALA:HB3	1:A:224:SER:H	1.77	0.49
1:B:205:LEU:O	1:B:225:ARG:HD3	2.15	0.47
1:B:130:ALA:HB2	1:B:221:ASN:O	2.14	0.47
1:B:20:GLN:OE1	1:B:60:GLY:HA3	2.15	0.47
1:B:130:ALA:HA	1:B:223:PRO:HA	1.96	0.47
1:B:79:GLN:OE1	1:B:82:GLN:HG3	2.16	0.46
1:B:61:PRO:HA	1:B:62:PRO:HD3	1.88	0.45
1:B:362:ARG:CD	4:B:836:HOH:O	2.45	0.44
1:B:23:ARG:NH2	1:B:63:GLU:OE2	2.51	0.44
2:D:141:ARG:HH11	2:D:141:ARG:HG3	1.82	0.43
1:A:334:ALA:HB2	1:A:381:TRP:CE2	2.53	0.43
2:D:78:LEU:O	2:D:89:ARG:NH1	2.50	0.43
1:A:205:LEU:O	1:A:225:ARG:HD3	2.18	0.43
1:B:0:HIS:CG	1:B:1:MET:H	2.37	0.43
1:B:407:PHE:HA	1:B:408:PRO:HD2	1.56	0.41
1:A:166:LEU:HD12	1:A:166:LEU:HA	1.80	0.41
1:B:20:GLN:OE1	1:B:60:GLY:CA	2.68	0.41
1:B:334:ALA:HB2	1:B:381:TRP:CE2	2.56	0.41
2:D:91:LYS:HG3	2:D:92:VAL:N	2.35	0.41
2:D:20:SER:C	2:D:22:MET:H	2.25	0.41
1:B:296:LEU:O	1:B:301:ARG:HD3	2.21	0.40
1:A:388:GLY:O	1:A:391:MET:HE3	2.21	0.40
1:A:14:TYR:C	1:A:14:TYR:CD2	2.95	0.40
1:A:14:TYR:O	1:A:14:TYR:CD2	2.75	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	407/428 (95%)	398 (98%)	9 (2%)	0	100	100
1	B	407/428 (95%)	400 (98%)	7 (2%)	0	100	100
2	C	121/144 (84%)	117 (97%)	4 (3%)	0	100	100
2	D	124/144 (86%)	117 (94%)	7 (6%)	0	100	100
All	All	1059/1144 (93%)	1032 (98%)	27 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	329/346 (95%)	321 (98%)	8 (2%)	57	38
1	B	329/346 (95%)	319 (97%)	10 (3%)	48	29
2	C	96/114 (84%)	92 (96%)	4 (4%)	36	16
2	D	99/114 (87%)	92 (93%)	7 (7%)	18	5
All	All	853/920 (93%)	824 (97%)	29 (3%)	44	24

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

Mol	Chain	Res	Type
1	A	1	MET
1	A	81	TYR
1	A	82	GLN
1	A	133	THR
1	A	199	LEU
1	A	261	LYS
1	A	317	GLU
1	A	391	MET

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Mol	Chain	Res	Type
1	B	0	HIS
1	B	20	GLN
1	B	52	LEU
1	B	55	LEU
1	B	133	THR
1	B	141	GLN
1	B	169	LEU
1	B	261	LYS
1	B	317	GLU
1	B	391	MET
2	C	23	ASP
2	C	26	LYS
2	C	69	ARG
2	C	143	ARG
2	D	20	SER
2	D	26	LYS
2	D	69	ARG
2	D	82	ARG
2	D	87	GLU
2	D	141	ARG
2	D	145	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	165	GLN
1	B	0	HIS
2	D	64	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 6 ligands modelled in this entry, 6 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	409/428 (95%)	0.01	11 (2%) 58 56	10, 19, 37, 46	0
1	B	409/428 (95%)	0.02	21 (5%) 32 30	11, 21, 39, 51	0
2	C	123/144 (85%)	0.12	6 (4%) 33 31	12, 31, 45, 52	0
2	D	126/144 (87%)	1.04	29 (23%) 1 1	14, 42, 60, 68	0
All	All	1067/1144 (93%)	0.15	67 (6%) 23 22	10, 22, 46, 68	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	144	LEU	6.4
1	B	162	PHE	6.1
1	B	166	LEU	6.1
1	B	408	PRO	5.5
1	A	162	PHE	5.2
2	D	85	ASP	5.1
1	A	81	TYR	4.9
2	D	77	ASP	4.6
2	D	145	GLN	4.5
1	B	81	TYR	4.2
2	D	22	MET	4.1
2	D	31	PRO	4.0
2	D	34	LEU	3.8
2	C	77	ASP	3.8
2	C	145	GLN	3.8
2	D	114	ALA	3.7
1	A	408	PRO	3.7
1	B	95	PRO	3.6
1	B	133	THR	3.6
2	D	115	ARG	3.6
2	C	48	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	133	THR	3.5
2	D	35	VAL	3.5
1	A	95	PRO	3.5
2	D	27	THR	3.5
2	D	21	HIS	3.4
2	D	107	TRP	3.4
1	B	0	HIS	3.4
2	D	78	LEU	3.1
1	B	94	ASN	3.1
2	D	143	ARG	3.0
1	A	0	HIS	2.9
2	D	20	SER	2.9
2	D	29	THR	2.9
1	A	94	ASN	2.9
1	B	169	LEU	2.8
2	D	113	GLY	2.8
2	C	82	ARG	2.8
1	B	16	TRP	2.7
2	D	51	PHE	2.7
1	B	132	ALA	2.6
1	B	78	MET	2.5
1	A	132	ALA	2.5
1	B	269	ILE	2.4
2	D	71	ASP	2.4
2	D	86	GLY	2.4
2	D	112	ALA	2.4
1	A	355	ARG	2.4
2	D	87	GLU	2.3
2	D	36	VAL	2.3
2	D	33	GLY	2.3
1	B	163	GLY	2.3
2	C	85	ASP	2.3
1	B	355	ARG	2.2
1	A	16	TRP	2.2
1	A	130	ALA	2.2
2	D	32	ASN	2.2
1	B	130	ALA	2.2
1	B	19	TRP	2.1
2	D	82	ARG	2.1
1	B	173	PRO	2.1
2	C	31	PRO	2.1
2	D	76	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
2	D	26	LYS	2.1
1	B	134	GLY	2.1
1	B	96	LEU	2.1
1	B	407	PHE	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(Å <sup>2</sup> )	Q<0.9
3	CA	A	503	1/1	1.00	0.10	0.46	12,12,12,12	0
3	CA	B	502	1/1	1.00	0.09	0.37	14,14,14,14	0
3	CA	A	501	1/1	1.00	0.08	-0.41	13,13,13,13	0
3	CA	B	501	1/1	1.00	0.07	-0.80	16,16,16,16	0
3	CA	A	502	1/1	1.00	0.08	-1.03	13,13,13,13	0
3	CA	B	503	1/1	1.00	0.06	-1.27	16,16,16,16	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.