



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 01:11 PM BST

PDB ID : 3VON  
Title : Crystalstructure of the ubiquitin protease  
Authors : Sato, Y.; Fukai, S.  
Deposited on : 2012-01-30  
Resolution : 3.15 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
Xtriage (Phenix)	:	1.13
EDS	:	2.13
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)	:	2.13

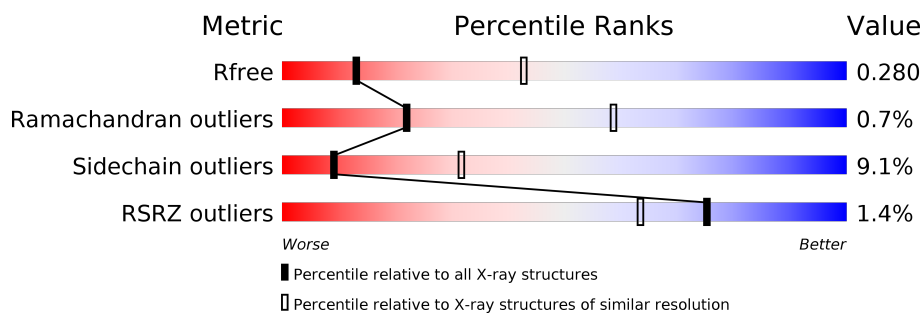
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.15 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.






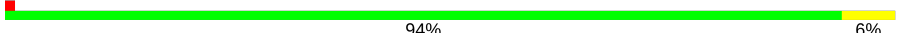










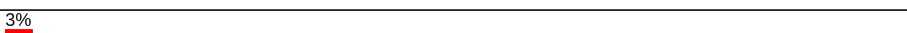

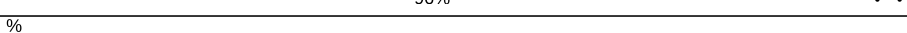


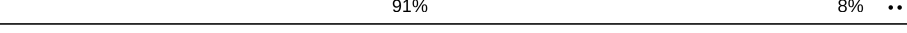





Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1665 (3.20-3.12)
Ramachandran outliers	138981	1770 (3.20-3.12)
Sidechain outliers	138945	1769 (3.20-3.12)
RSRZ outliers	127900	1616 (3.20-3.12)

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	228	<div> <div>0%</div> <div>85% 7% 8%</div> </div>
1	H	228	<div> <div>7%</div> <div>84% 10% 6%</div> </div>
1	O	228	<div> <div></div> <div>88% 7% 5%</div> </div>
1	V	228	<div> <div>2%</div> <div>90% 6%</div> </div>
1	c	228	<div> <div>4%</div> <div>87% 8% 5%</div> </div>
1	j	228	<div> <div>13%</div> <div>83% 9% 8%</div> </div>
2	B	138	<div> <div></div> <div>95% 5%</div> </div>

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Mol	Chain	Length	Quality of chain
2	D	138	 93% 7% .
2	F	138	 92% 7% .
2	I	138	 85% 14% .
2	K	138	 94% 6% .
2	M	138	 91% 9% .
2	P	138	 91% 9% .
2	R	138	 98% ..
2	T	138	 89% 10% .
2	W	138	 89% 10% .
2	Y	138	 94% 5% .
2	a	138	 93% 6% .
2	d	138	 93% 7% .
2	f	138	 90% 9% .
2	h	138	 93% 7% .
2	k	138	 91% 9% .
2	m	138	 96% ..
2	o	138	 93% 7% .
3	C	148	 84% 14% ..
3	E	148	 91% 8% ..
3	G	148	 89% 10% ..
3	J	148	 91% 9% .
3	L	148	 91% 9% .
3	N	148	 89% 9% ..
3	Q	148	 90% 8% ..
3	S	148	 90% 9% .

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Mol	Chain	Length	Quality of chain
3	U	148	<div><div></div><div>91%</div><div>7% ..</div></div>
3	X	148	<div><div></div><div>89%</div><div>11% .</div></div>
3	Z	148	<div><div></div><div>91%</div><div>9%</div></div>
3	b	148	<div><div></div><div>91%</div><div>8% .</div></div>
3	e	148	<div><div></div><div>88%</div><div>9% ..</div></div>
3	g	148	<div><div></div><div>91%</div><div>9%</div></div>
3	i	148	<div><div></div><div>91%</div><div>9%</div></div>
3	l	148	<div><div>%</div><div></div><div>89%</div><div>9% ..</div></div>
3	n	148	<div><div>%</div><div></div><div>91%</div><div>9% .</div></div>
3	p	148	<div><div>%</div><div></div><div>90%</div><div>9% .</div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 51450 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 Ubiquitin thioesterase OTUB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	0	0
			1731	1111	284	330	6			
1	H	214	Total	C	N	O	S	0	0	0
			1767	1133	290	339	5			
1	O	216	Total	C	N	O	S	0	0	0
			1786	1148	292	340	6			
1	V	215	Total	C	N	O	S	0	0	0
			1777	1140	292	339	6			
1	c	217	Total	C	N	O	S	0	0	0
			1785	1144	293	342	6			
1	j	210	Total	C	N	O	S	0	0	0
			1730	1112	284	329	5			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	44	SER	-	EXPRESSION TAG	UNP Q96FW1
H	44	SER	-	EXPRESSION TAG	UNP Q96FW1
O	44	SER	-	EXPRESSION TAG	UNP Q96FW1
V	44	SER	-	EXPRESSION TAG	UNP Q96FW1
c	44	SER	-	EXPRESSION TAG	UNP Q96FW1
j	44	SER	-	EXPRESSION TAG	UNP Q96FW1

- Molecule 2 is a protein called Ubiquitin-conjugating enzyme E2 variant 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			
2	D	137	Total	C	N	O	S	0	0	0
			1092	687	190	207	8			
2	F	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			
2	K	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			
2	M	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			
2	P	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			
2	R	137	Total	C	N	O	S	0	0	0
			1092	687	190	207	8			
2	T	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			
2	W	137	Total	C	N	O	S	0	0	0
			1092	687	190	207	8			
2	Y	137	Total	C	N	O	S	0	0	0
			1092	687	190	207	8			
2	a	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			
2	d	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			
2	f	137	Total	C	N	O	S	0	0	0
			1092	687	190	207	8			
2	h	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			
2	k	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			
2	m	137	Total	C	N	O	S	0	0	0
			1092	687	190	207	8			
2	o	138	Total	C	N	O	S	0	0	0
			1096	689	191	208	8			

- Molecule 3 is a protein called Ubiquitin-conjugating enzyme E2 N.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	E	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	G	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	J	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			

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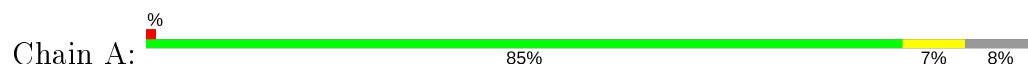
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	N	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	Q	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	S	148	Total	C	N	O	S	0	0	0
			1179	757	203	215	4			
3	U	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	X	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	Z	148	Total	C	N	O	S	0	0	0
			1179	757	203	215	4			
3	b	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	e	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	g	148	Total	C	N	O	S	0	0	0
			1179	757	203	215	4			
3	i	148	Total	C	N	O	S	0	0	0
			1179	757	203	215	4			
3	l	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	n	147	Total	C	N	O	S	0	0	0
			1175	755	202	214	4			
3	p	148	Total	C	N	O	S	0	0	0
			1179	757	203	215	4			

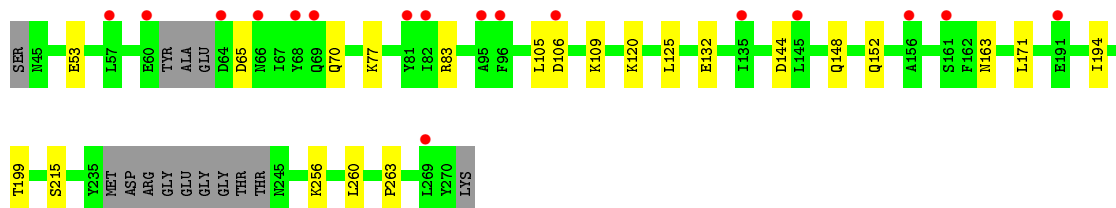
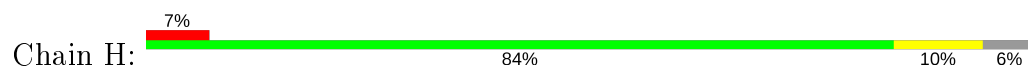
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

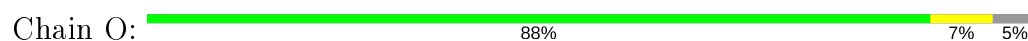
- Molecule 1: Ubiquitin thioesterase OTUB1



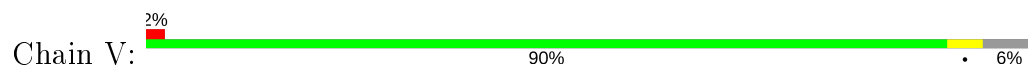
- Molecule 1: Ubiquitin thioesterase OTUB1



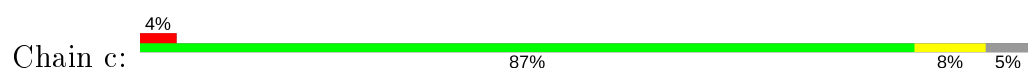
- Molecule 1: Ubiquitin thioesterase OTUB1



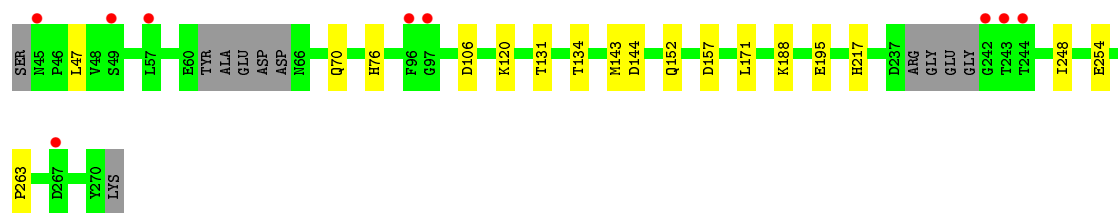
- Molecule 1: Ubiquitin thioesterase OTUB1



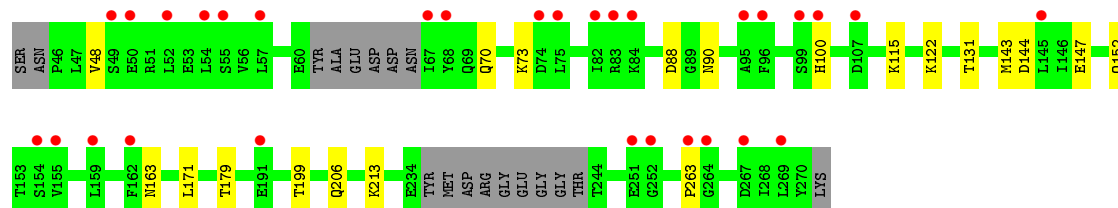
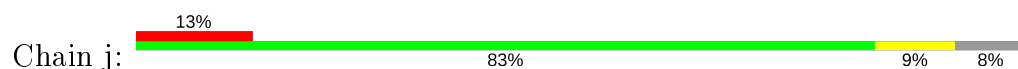
- Molecule 1: Ubiquitin thioesterase OTUB1







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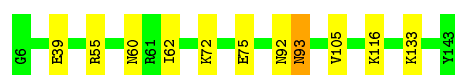
- Molecule 2: Ubiquitin-conjugating enzyme E2 variant 2



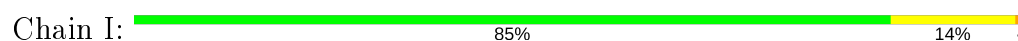
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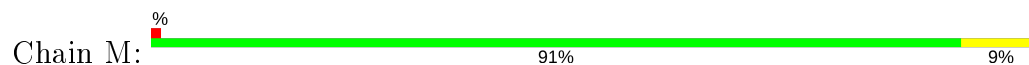


- Molecule 2: Ubiquitin-conjugating enzyme E2 variant 2

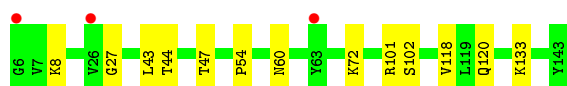
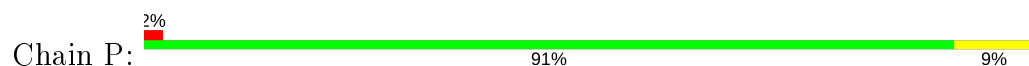




- Molecule 2: Ubiquitin-conjugating enzyme E2 variant 2



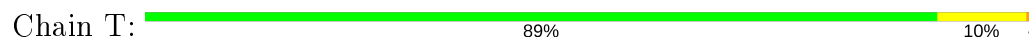
- Molecule 2: Ubiquitin-conjugating enzyme E2 variant 2



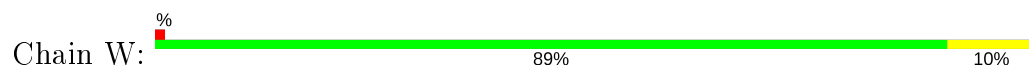
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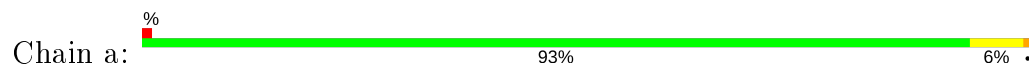
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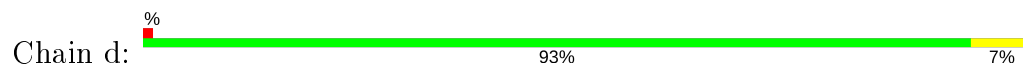


- Molecule 2: Ubiquitin-conjugating enzyme E2 variant 2

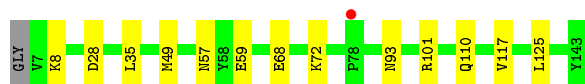
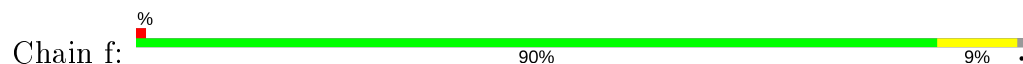




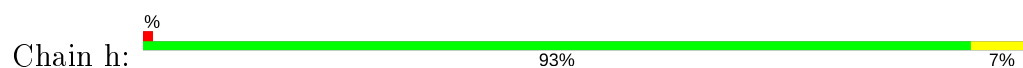
- Molecule 2: Ubiquitin-conjugating enzyme E2 variant 2



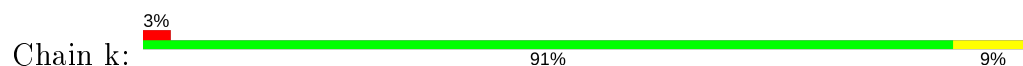
- Molecule 2: Ubiquitin-conjugating enzyme E2 variant 2



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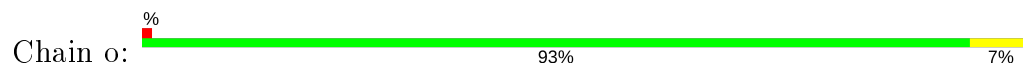
- Molecule 2: Ubiquitin-conjugating enzyme E2 variant 2




- Molecule 2: Ubiquitin-conjugating enzyme E2 variant 2



- Molecule 2: Ubiquitin-conjugating enzyme E2 variant 2




- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain C:  84% 14% ..




- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain E:  91% 8% ..




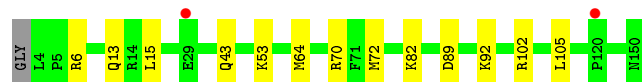
- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain G:  89% 10% ..




- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain J:  91% 9% .




- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain L:  91% 9% .




- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain N:  89% 9% ..




- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain Q:  90% 8% ..



- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain S:  90% 9% .




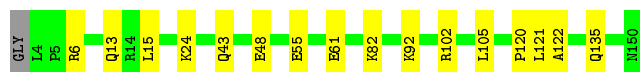
- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain U:  91% 7% ..



- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain X:  89% 11% .



- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain Z:  91% 9%




- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain b:  91% 8% .



- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain e:  88% 9% ..




- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain g:  91% 9%




- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain i:  91% 9%




- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain l:  89% 9% ..




- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain n:  91% 9% .



- Molecule 3: Ubiquitin-conjugating enzyme E2 N

Chain p:  90% 9% .



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.06Å 137.28Å 257.11Å 90.00° 90.03° 90.00°	Depositor
Resolution (Å)	50.00 – 3.15 46.92 – 3.15	Depositor EDS
% Data completeness (in resolution range)	96.8 (50.00-3.15) 96.6 (46.92-3.15)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.22 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.223 , 0.281 0.223 , 0.280	Depositor DCC
$R_{free}$ test set	5967 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.3	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 5.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.427 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	51450	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 51.65 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.4409e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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](#)

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	0.36	0/1769	0.48	0/2381
1	H	0.35	0/1806	0.49	0/2434
1	O	0.36	0/1826	0.47	0/2457
1	V	0.36	0/1816	0.48	0/2444
1	c	0.36	0/1824	0.49	0/2458
1	j	0.35	0/1768	0.47	0/2381
2	B	0.34	0/1119	0.50	0/1512
2	D	0.32	0/1115	0.51	0/1507
2	F	0.37	0/1119	0.54	0/1512
2	I	0.35	0/1119	0.54	0/1512
2	K	0.34	0/1119	0.53	0/1512
2	M	0.34	0/1119	0.52	0/1512
2	P	0.35	0/1119	0.53	0/1512
2	R	0.34	0/1115	0.52	0/1507
2	T	0.34	0/1119	0.51	0/1512
2	W	0.36	0/1115	0.52	0/1507
2	Y	0.33	0/1115	0.52	0/1507
2	a	0.34	0/1119	0.53	0/1512
2	d	0.34	0/1119	0.51	0/1512
2	f	0.32	0/1115	0.53	0/1507
2	h	0.38	0/1119	0.52	0/1512
2	k	0.35	0/1119	0.54	0/1512
2	m	0.34	0/1115	0.52	0/1507
2	o	0.34	0/1119	0.50	0/1512
3	C	0.35	0/1205	0.57	1/1640 (0.1%)
3	E	0.33	0/1205	0.55	1/1640 (0.1%)
3	G	0.36	0/1205	0.59	1/1640 (0.1%)
3	J	0.34	0/1205	0.54	0/1640
3	L	0.34	0/1205	0.53	0/1640
3	N	0.36	0/1205	0.55	0/1640
3	Q	0.34	0/1205	0.59	1/1640 (0.1%)
3	S	0.34	0/1209	0.50	0/1645
3	U	0.35	0/1205	0.55	1/1640 (0.1%)
3	X	0.34	0/1205	0.55	0/1640



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
3	Z	0.35	0/1209	0.54	0/1645
3	b	0.35	0/1205	0.52	0/1640
3	e	0.34	0/1205	0.58	2/1640 (0.1%)
3	g	0.34	0/1209	0.50	0/1645
3	i	0.36	0/1209	0.54	0/1645
3	l	0.33	0/1205	0.55	1/1640 (0.1%)
3	n	0.32	0/1205	0.51	0/1640
3	p	0.35	0/1209	0.55	1/1645 (0.1%)
All	All	0.35	0/52637	0.52	9/71286 (0.0%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	121	LEU	CA-CB-CG	7.25	131.98	115.30
3	C	106	LEU	CA-CB-CG	6.32	129.83	115.30
3	l	106	LEU	CA-CB-CG	6.17	129.50	115.30
3	e	106	LEU	CA-CB-CG	6.05	129.21	115.30
3	e	146	LEU	CA-CB-CG	5.66	128.33	115.30
3	E	54	LEU	CA-CB-CG	5.48	127.91	115.30
3	p	4	LEU	CA-CB-CG	5.39	127.70	115.30
3	U	4	LEU	CA-CB-CG	5.13	127.09	115.30
3	Q	106	LEU	CA-CB-CG	5.10	127.02	115.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	204/228 (90%)	195 (96%)	8 (4%)	1 (0%)	29	65
1	H	208/228 (91%)	199 (96%)	7 (3%)	2 (1%)	15	51
1	O	210/228 (92%)	202 (96%)	7 (3%)	1 (0%)	29	65
1	V	209/228 (92%)	201 (96%)	7 (3%)	1 (0%)	29	65
1	c	211/228 (92%)	200 (95%)	9 (4%)	2 (1%)	17	53
1	j	204/228 (90%)	190 (93%)	11 (5%)	3 (2%)	10	41
2	B	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
2	D	135/138 (98%)	129 (96%)	5 (4%)	1 (1%)	22	59
2	F	136/138 (99%)	130 (96%)	4 (3%)	2 (2%)	10	41
2	I	136/138 (99%)	122 (90%)	11 (8%)	3 (2%)	6	32
2	K	136/138 (99%)	132 (97%)	4 (3%)	0	100	100
2	M	136/138 (99%)	133 (98%)	2 (2%)	1 (1%)	22	59
2	P	136/138 (99%)	128 (94%)	6 (4%)	2 (2%)	10	41
2	R	135/138 (98%)	129 (96%)	6 (4%)	0	100	100
2	T	136/138 (99%)	128 (94%)	5 (4%)	3 (2%)	6	32
2	W	135/138 (98%)	129 (96%)	5 (4%)	1 (1%)	22	59
2	Y	135/138 (98%)	130 (96%)	4 (3%)	1 (1%)	22	59
2	a	136/138 (99%)	128 (94%)	5 (4%)	3 (2%)	6	32
2	d	136/138 (99%)	133 (98%)	2 (2%)	1 (1%)	22	59
2	f	135/138 (98%)	129 (96%)	5 (4%)	1 (1%)	22	59
2	h	136/138 (99%)	132 (97%)	3 (2%)	1 (1%)	22	59
2	k	136/138 (99%)	127 (93%)	9 (7%)	0	100	100
2	m	135/138 (98%)	130 (96%)	5 (4%)	0	100	100
2	o	136/138 (99%)	131 (96%)	3 (2%)	2 (2%)	10	41
3	C	145/148 (98%)	135 (93%)	7 (5%)	3 (2%)	7	33
3	E	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
3	G	145/148 (98%)	134 (92%)	9 (6%)	2 (1%)	11	43
3	J	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
3	L	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
3	N	145/148 (98%)	136 (94%)	7 (5%)	2 (1%)	11	43
3	Q	145/148 (98%)	135 (93%)	8 (6%)	2 (1%)	11	43
3	S	146/148 (99%)	142 (97%)	3 (2%)	1 (1%)	22	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	U	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
3	X	145/148 (98%)	135 (93%)	8 (6%)	2 (1%)	11	43
3	Z	146/148 (99%)	142 (97%)	4 (3%)	0	100	100
3	b	145/148 (98%)	135 (93%)	10 (7%)	0	100	100
3	e	145/148 (98%)	136 (94%)	7 (5%)	2 (1%)	11	43
3	g	146/148 (99%)	140 (96%)	6 (4%)	0	100	100
3	i	146/148 (99%)	135 (92%)	11 (8%)	0	100	100
3	l	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
3	n	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
3	p	146/148 (99%)	136 (93%)	10 (7%)	0	100	100
All	All	6303/6516 (97%)	5983 (95%)	274 (4%)	46 (1%)	22	59

All (46) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	93	ASN
1	H	152	GLN
2	I	107	ALA
2	T	93	ASN
1	V	152	GLN
1	j	152	GLN
2	I	26	VAL
2	a	27	GLY
2	a	93	ASN
1	c	152	GLN
1	j	263	PRO
2	o	27	GLY
3	G	119	ASP
3	N	120	PRO
2	P	27	GLY
3	Q	121	LEU
2	T	92	ASN
3	X	120	PRO
3	X	122	ALA
2	f	57	ASN
2	o	40	ASP
3	C	119	ASP
1	H	263	PRO

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Mol	Chain	Res	Type
2	M	27	GLY
3	N	44	ASP
1	O	152	GLN
2	Y	40	ASP
1	c	263	PRO
3	e	123	ASN
2	h	27	GLY
1	A	263	PRO
3	C	116	ASN
2	D	57	ASN
3	G	122	ALA
3	S	123	ASN
2	F	92	ASN
2	I	105	VAL
2	P	54	PRO
3	Q	123	ASN
2	T	27	GLY
2	a	92	ASN
3	e	120	PRO
1	j	88	ASP
3	C	117	PRO
2	W	29	GLY
2	d	29	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	193/207 (93%)	178 (92%)	15 (8%)	12	40
1	H	197/207 (95%)	177 (90%)	20 (10%)	7	27
1	O	198/207 (96%)	182 (92%)	16 (8%)	11	39
1	V	198/207 (96%)	190 (96%)	8 (4%)	31	64
1	c	199/207 (96%)	183 (92%)	16 (8%)	12	39
1	j	193/207 (93%)	176 (91%)	17 (9%)	10	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	123/123 (100%)	116 (94%)	7 (6%)	20	53
2	D	123/123 (100%)	115 (94%)	8 (6%)	17	48
2	F	123/123 (100%)	113 (92%)	10 (8%)	11	39
2	I	123/123 (100%)	104 (85%)	19 (15%)	2	12
2	K	123/123 (100%)	115 (94%)	8 (6%)	17	48
2	M	123/123 (100%)	112 (91%)	11 (9%)	9	33
2	P	123/123 (100%)	112 (91%)	11 (9%)	9	33
2	R	123/123 (100%)	121 (98%)	2 (2%)	62	83
2	T	123/123 (100%)	110 (89%)	13 (11%)	6	25
2	W	123/123 (100%)	110 (89%)	13 (11%)	6	25
2	Y	123/123 (100%)	117 (95%)	6 (5%)	25	59
2	a	123/123 (100%)	116 (94%)	7 (6%)	20	53
2	d	123/123 (100%)	115 (94%)	8 (6%)	17	48
2	f	123/123 (100%)	111 (90%)	12 (10%)	8	28
2	h	123/123 (100%)	115 (94%)	8 (6%)	17	48
2	k	123/123 (100%)	110 (89%)	13 (11%)	6	25
2	m	123/123 (100%)	118 (96%)	5 (4%)	30	63
2	o	123/123 (100%)	115 (94%)	8 (6%)	17	48
3	C	126/126 (100%)	105 (83%)	21 (17%)	2	9
3	E	126/126 (100%)	113 (90%)	13 (10%)	7	26
3	G	126/126 (100%)	112 (89%)	14 (11%)	6	24
3	J	126/126 (100%)	113 (90%)	13 (10%)	7	26
3	L	126/126 (100%)	113 (90%)	13 (10%)	7	26
3	N	126/126 (100%)	112 (89%)	14 (11%)	6	24
3	Q	126/126 (100%)	113 (90%)	13 (10%)	7	26
3	S	126/126 (100%)	111 (88%)	15 (12%)	5	21
3	U	126/126 (100%)	114 (90%)	12 (10%)	8	30
3	X	126/126 (100%)	112 (89%)	14 (11%)	6	24
3	Z	126/126 (100%)	113 (90%)	13 (10%)	7	26
3	b	126/126 (100%)	114 (90%)	12 (10%)	8	30
3	e	126/126 (100%)	110 (87%)	16 (13%)	4	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	g	126/126 (100%)	113 (90%)	13 (10%)	7	26
3	i	126/126 (100%)	112 (89%)	14 (11%)	6	24
3	l	126/126 (100%)	111 (88%)	15 (12%)	5	21
3	n	126/126 (100%)	113 (90%)	13 (10%)	7	26
3	p	126/126 (100%)	111 (88%)	15 (12%)	5	21
All	All	5660/5724 (99%)	5146 (91%)	514 (9%)	9	32

All (514) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	91	CYS
1	A	113	ARG
1	A	124	ASP
1	A	131	THR
1	A	133	PHE
1	A	135	ILE
1	A	144	ASP
1	A	171	LEU
1	A	188	LYS
1	A	195	GLU
1	A	198	ARG
1	A	217	HIS
1	A	248	ILE
1	A	256	LYS
2	B	32	SER
2	B	49	MET
2	B	50	ILE
2	B	93	ASN
2	B	101	ARG
2	B	129	LYS
2	B	133	LYS
3	C	10	LYS
3	C	13	GLN
3	C	14	ARG
3	C	18	GLU
3	C	24	LYS
3	C	26	GLU
3	C	29	GLU
3	C	43	GLN

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Mol	Chain	Res	Type
3	C	44	ASP
3	C	70	ARG
3	C	92	LYS
3	C	102	ARG
3	C	106	LEU
3	C	107	SER
3	C	108	ILE
3	C	116	ASN
3	C	121	LEU
3	C	127	GLU
3	C	128	GLN
3	C	129	TRP
3	C	146	LEU
2	D	21	GLU
2	D	31	VAL
2	D	35	LEU
2	D	49	MET
2	D	81	ARG
2	D	108	LYS
2	D	110	GLN
2	D	133	LYS
3	E	6	ARG
3	E	14	ARG
3	E	54	LEU
3	E	73	THR
3	E	87	CYS
3	E	92	LYS
3	E	93	ASP
3	E	96	SER
3	E	106	LEU
3	E	107	SER
3	E	111	LEU
3	E	124	ASP
3	E	138	GLU
2	F	39	GLU
2	F	55	ARG
2	F	60	ASN
2	F	62	ILE
2	F	72	LYS
2	F	75	GLU
2	F	93	ASN
2	F	105	VAL

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Mol	Chain	Res	Type
2	F	116	LYS
2	F	133	LYS
3	G	4	LEU
3	G	6	ARG
3	G	24	LYS
3	G	64	MET
3	G	103	THR
3	G	105	LEU
3	G	107	SER
3	G	116	ASN
3	G	121	LEU
3	G	123	ASN
3	G	124	ASP
3	G	128	GLN
3	G	141	ARG
3	G	150	ASN
1	H	53	GLU
1	H	65	ASP
1	H	70	GLN
1	H	77	LYS
1	H	83	ARG
1	H	105	LEU
1	H	106	ASP
1	H	109	LYS
1	H	120	LYS
1	H	125	LEU
1	H	132	GLU
1	H	144	ASP
1	H	148	GLN
1	H	163	ASN
1	H	171	LEU
1	H	194	ILE
1	H	199	THR
1	H	215	SER
1	H	256	LYS
1	H	260	LEU
2	I	8	LYS
2	I	14	ARG
2	I	30	THR
2	I	35	LEU
2	I	49	MET
2	I	56	THR

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Mol	Chain	Res	Type
2	I	57	ASN
2	I	61	ARG
2	I	72	LYS
2	I	75	GLU
2	I	82	PHE
2	I	91	ILE
2	I	101	ARG
2	I	105	VAL
2	I	109	TRP
2	I	110	GLN
2	I	111	ASN
2	I	120	GLN
2	I	125	LEU
3	J	6	ARG
3	J	13	GLN
3	J	15	LEU
3	J	43	GLN
3	J	53	LYS
3	J	64	MET
3	J	70	ARG
3	J	72	MET
3	J	82	LYS
3	J	89	ASP
3	J	92	LYS
3	J	102	ARG
3	J	105	LEU
2	K	8	LYS
2	K	16	LEU
2	K	35	LEU
2	K	64	SER
2	K	68	GLU
2	K	97	MET
2	K	101	ARG
2	K	110	GLN
3	L	10	LYS
3	L	14	ARG
3	L	18	GLU
3	L	34	TYR
3	L	73	THR
3	L	74	LYS
3	L	89	ASP
3	L	92	LYS

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Mol	Chain	Res	Type
3	L	105	LEU
3	L	106	LEU
3	L	118	ASP
3	L	121	LEU
3	L	124	ASP
2	M	39	GLU
2	M	49	MET
2	M	55	ARG
2	M	59	GLU
2	M	62	ILE
2	M	64	SER
2	M	81	ARG
2	M	84	THR
2	M	93	ASN
2	M	101	ARG
2	M	105	VAL
3	N	30	SER
3	N	44	ASP
3	N	45	SER
3	N	51	THR
3	N	53	LYS
3	N	105	LEU
3	N	109	GLN
3	N	113	SER
3	N	124	ASP
3	N	127	GLU
3	N	128	GLN
3	N	141	ARG
3	N	145	ARG
3	N	146	LEU
1	O	51	ARG
1	O	69	GLN
1	O	70	GLN
1	O	73	LYS
1	O	109	LYS
1	O	134	THR
1	O	144	ASP
1	O	152	GLN
1	O	166	SER
1	O	171	LEU
1	O	186	GLU
1	O	192	HIS

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Mol	Chain	Res	Type
1	O	195	GLU
1	O	217	HIS
1	O	248	ILE
1	O	254	GLU
2	P	8	LYS
2	P	43	LEU
2	P	44	THR
2	P	47	THR
2	P	60	ASN
2	P	72	LYS
2	P	101	ARG
2	P	102	SER
2	P	118	VAL
2	P	120	GLN
2	P	133	LYS
3	Q	16	LEU
3	Q	24	LYS
3	Q	43	GLN
3	Q	64	MET
3	Q	70	ARG
3	Q	89	ASP
3	Q	92	LYS
3	Q	102	ARG
3	Q	106	LEU
3	Q	123	ASN
3	Q	129	TRP
3	Q	135	GLN
3	Q	145	ARG
2	R	66	LYS
2	R	133	LYS
3	S	4	LEU
3	S	18	GLU
3	S	29	GLU
3	S	61	GLU
3	S	73	THR
3	S	89	ASP
3	S	92	LYS
3	S	93	ASP
3	S	105	LEU
3	S	116	ASN
3	S	123	ASN
3	S	124	ASP

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Mol	Chain	Res	Type
3	S	128	GLN
3	S	146	LEU
3	S	150	ASN
2	T	20	GLU
2	T	23	GLN
2	T	26	VAL
2	T	35	LEU
2	T	39	GLU
2	T	49	MET
2	T	55	ARG
2	T	62	ILE
2	T	93	ASN
2	T	97	MET
2	T	105	VAL
2	T	129	LYS
2	T	133	LYS
3	U	4	LEU
3	U	14	ARG
3	U	16	LEU
3	U	20	VAL
3	U	43	GLN
3	U	93	ASP
3	U	105	LEU
3	U	123	ASN
3	U	125	VAL
3	U	129	TRP
3	U	135	GLN
3	U	137	ILE
1	V	59	LYS
1	V	70	GLN
1	V	71	LYS
1	V	90	ASN
1	V	147	GLU
1	V	151	LYS
1	V	171	LEU
1	V	248	ILE
2	W	23	GLN
2	W	58	TYR
2	W	80	VAL
2	W	86	ILE
2	W	99	ASP
2	W	108	LYS

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Mol	Chain	Res	Type
2	W	110	GLN
2	W	118	VAL
2	W	120	GLN
2	W	123	ARG
2	W	124	ARG
2	W	133	LYS
2	W	142	THR
3	X	6	ARG
3	X	13	GLN
3	X	15	LEU
3	X	24	LYS
3	X	43	GLN
3	X	48	GLU
3	X	55	GLU
3	X	61	GLU
3	X	82	LYS
3	X	92	LYS
3	X	102	ARG
3	X	105	LEU
3	X	121	LEU
3	X	135	GLN
2	Y	35	LEU
2	Y	61	ARG
2	Y	68	GLU
2	Y	101	ARG
2	Y	112	SER
2	Y	133	LYS
3	Z	20	VAL
3	Z	29	GLU
3	Z	61	GLU
3	Z	73	THR
3	Z	74	LYS
3	Z	89	ASP
3	Z	93	ASP
3	Z	105	LEU
3	Z	121	LEU
3	Z	128	GLN
3	Z	135	GLN
3	Z	137	ILE
3	Z	145	ARG
2	a	8	LYS
2	a	14	ARG

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Mol	Chain	Res	Type
2	a	35	LEU
2	a	45	ARG
2	a	93	ASN
2	a	105	VAL
2	a	127	MET
3	b	20	VAL
3	b	81	ASP
3	b	89	ASP
3	b	93	ASP
3	b	105	LEU
3	b	106	LEU
3	b	123	ASN
3	b	128	GLN
3	b	129	TRP
3	b	137	ILE
3	b	141	ARG
3	b	149	MET
1	c	47	LEU
1	c	70	GLN
1	c	76	HIS
1	c	106	ASP
1	c	120	LYS
1	c	131	THR
1	c	134	THR
1	c	143	MET
1	c	144	ASP
1	c	157	ASP
1	c	171	LEU
1	c	188	LYS
1	c	195	GLU
1	c	217	HIS
1	c	248	ILE
1	c	254	GLU
2	d	31	VAL
2	d	44	THR
2	d	64	SER
2	d	75	GLU
2	d	79	SER
2	d	101	ARG
2	d	123	ARG
2	d	133	LYS
3	e	9	ILE

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Mol	Chain	Res	Type
3	e	10	LYS
3	e	11	GLU
3	e	14	ARG
3	e	26	GLU
3	e	64	MET
3	e	70	ARG
3	e	72	MET
3	e	106	LEU
3	e	111	LEU
3	e	118	ASP
3	e	119	ASP
3	e	123	ASN
3	e	128	GLN
3	e	129	TRP
3	e	146	LEU
2	f	8	LYS
2	f	28	ASP
2	f	35	LEU
2	f	49	MET
2	f	59	GLU
2	f	68	GLU
2	f	72	LYS
2	f	93	ASN
2	f	101	ARG
2	f	110	GLN
2	f	117	VAL
2	f	125	LEU
3	g	4	LEU
3	g	6	ARG
3	g	72	MET
3	g	73	THR
3	g	87	CYS
3	g	89	ASP
3	g	92	LYS
3	g	94	LYS
3	g	106	LEU
3	g	107	SER
3	g	113	SER
3	g	121	LEU
3	g	128	GLN
2	h	24	LYS
2	h	47	THR

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Mol	Chain	Res	Type
2	h	49	MET
2	h	55	ARG
2	h	62	ILE
2	h	101	ARG
2	h	105	VAL
2	h	130	GLU
3	i	4	LEU
3	i	6	ARG
3	i	14	ARG
3	i	18	GLU
3	i	23	ILE
3	i	26	GLU
3	i	103	THR
3	i	105	LEU
3	i	106	LEU
3	i	118	ASP
3	i	121	LEU
3	i	128	GLN
3	i	129	TRP
3	i	135	GLN
1	j	48	VAL
1	j	70	GLN
1	j	73	LYS
1	j	90	ASN
1	j	100	HIS
1	j	115	LYS
1	j	122	LYS
1	j	131	THR
1	j	143	MET
1	j	144	ASP
1	j	147	GLU
1	j	163	ASN
1	j	171	LEU
1	j	179	THR
1	j	199	THR
1	j	206	GLN
1	j	213	LYS
2	k	14	ARG
2	k	24	LYS
2	k	38	ASP
2	k	49	MET
2	k	57	ASN

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Mol	Chain	Res	Type
2	k	82	PHE
2	k	89	ASN
2	k	101	ARG
2	k	102	SER
2	k	109	TRP
2	k	111	ASN
2	k	125	LEU
2	k	127	MET
3	l	6	ARG
3	l	15	LEU
3	l	18	GLU
3	l	24	LYS
3	l	26	GLU
3	l	72	MET
3	l	82	LYS
3	l	89	ASP
3	l	105	LEU
3	l	106	LEU
3	l	107	SER
3	l	116	ASN
3	l	132	ASN
3	l	141	ARG
3	l	149	MET
2	m	12	ASN
2	m	30	THR
2	m	31	VAL
2	m	35	LEU
2	m	68	GLU
3	n	13	GLN
3	n	14	ARG
3	n	73	THR
3	n	87	CYS
3	n	89	ASP
3	n	92	LYS
3	n	94	LYS
3	n	102	ARG
3	n	105	LEU
3	n	106	LEU
3	n	121	LEU
3	n	128	GLN
3	n	150	ASN
2	o	55	ARG

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Mol	Chain	Res	Type
2	o	60	ASN
2	o	93	ASN
2	o	101	ARG
2	o	105	VAL
2	o	106	LEU
2	o	130	GLU
2	o	133	LYS
3	p	4	LEU
3	p	9	ILE
3	p	14	ARG
3	p	51	THR
3	p	72	MET
3	p	89	ASP
3	p	90	ILE
3	p	105	LEU
3	p	111	LEU
3	p	116	ASN
3	p	127	GLU
3	p	130	LYS
3	p	139	THR
3	p	141	ARG
3	p	146	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (98) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	76	HIS
1	A	219	HIS
2	B	60	ASN
2	B	89	ASN
2	B	93	ASN
2	B	120	GLN
3	C	43	GLN
3	C	109	GLN
3	C	135	GLN
2	D	12	ASN
2	D	23	GLN
2	D	110	GLN
2	D	120	GLN
2	F	12	ASN
2	F	60	ASN

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Mol	Chain	Res	Type
2	F	89	ASN
3	G	79	ASN
3	G	116	ASN
3	G	123	ASN
3	G	135	GLN
1	H	70	GLN
1	H	112	GLN
1	H	148	GLN
2	I	60	ASN
2	I	110	GLN
2	I	111	ASN
3	J	109	GLN
3	J	116	ASN
2	K	23	GLN
2	K	92	ASN
3	L	13	GLN
3	L	116	ASN
2	M	60	ASN
2	M	110	GLN
2	M	120	GLN
3	N	100	GLN
1	O	45	ASN
1	O	70	GLN
2	P	60	ASN
2	P	87	ASN
3	Q	100	GLN
3	Q	123	ASN
3	Q	128	GLN
2	R	120	GLN
3	S	13	GLN
3	S	116	ASN
2	T	12	ASN
2	T	60	ASN
2	T	120	GLN
3	U	13	GLN
3	U	43	GLN
3	U	123	ASN
3	U	135	GLN
1	V	70	GLN
1	V	90	ASN
1	V	219	HIS
1	V	225	GLN

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Mol	Chain	Res	Type
2	W	87	ASN
2	W	93	ASN
2	W	110	GLN
2	W	120	GLN
3	X	109	GLN
3	X	123	ASN
3	X	128	GLN
2	Y	110	GLN
2	Y	120	GLN
3	Z	116	ASN
2	a	120	GLN
3	b	123	ASN
1	c	66	ASN
1	c	219	HIS
1	c	245	ASN
2	d	89	ASN
2	d	93	ASN
2	d	120	GLN
3	e	79	ASN
3	e	123	ASN
2	f	23	GLN
3	g	43	GLN
3	g	116	ASN
2	h	12	ASN
2	h	23	GLN
2	h	110	GLN
3	i	109	GLN
1	j	219	HIS
2	k	60	ASN
2	k	92	ASN
2	k	111	ASN
2	k	120	GLN
3	l	109	GLN
3	l	116	ASN
3	l	123	ASN
2	m	23	GLN
3	n	13	GLN
2	o	60	ASN
2	o	120	GLN
3	p	43	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 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	210/228 (92%)	0.12	3 (1%) 75 63	58, 87, 128, 158	0
1	H	214/228 (93%)	0.64	17 (7%) 12 6	95, 129, 181, 205	0
1	O	216/228 (94%)	-0.01	1 (0%) 91 86	59, 78, 110, 142	0
1	V	215/228 (94%)	0.10	5 (2%) 60 46	57, 78, 113, 153	0
1	c	217/228 (95%)	0.19	9 (4%) 37 22	58, 87, 133, 174	0
1	j	210/228 (92%)	0.85	30 (14%) 2 1	97, 131, 177, 194	0
2	B	138/138 (100%)	-0.29	0 100 100	47, 62, 80, 106	0
2	D	137/138 (99%)	-0.15	0 100 100	59, 84, 113, 138	0
2	F	138/138 (100%)	-0.26	0 100 100	42, 57, 83, 102	0
2	I	138/138 (100%)	-0.01	0 100 100	61, 88, 118, 152	0
2	K	138/138 (100%)	-0.21	1 (0%) 87 81	53, 67, 82, 99	0
2	M	138/138 (100%)	-0.23	1 (0%) 87 81	51, 66, 86, 113	0
2	P	138/138 (100%)	0.07	3 (2%) 62 47	71, 98, 131, 153	0
2	R	137/138 (99%)	-0.28	0 100 100	53, 67, 84, 94	0
2	T	138/138 (100%)	-0.17	0 100 100	56, 73, 103, 132	0
2	W	137/138 (99%)	0.01	1 (0%) 87 81	69, 94, 122, 138	0
2	Y	137/138 (99%)	-0.18	0 100 100	54, 70, 87, 97	0
2	a	138/138 (100%)	-0.19	1 (0%) 87 81	53, 71, 103, 127	0
2	d	138/138 (100%)	-0.26	1 (0%) 87 81	48, 62, 81, 105	0
2	f	137/138 (99%)	-0.02	1 (0%) 87 81	61, 83, 109, 131	0
2	h	138/138 (100%)	-0.24	1 (0%) 87 81	42, 57, 81, 100	0
2	k	138/138 (100%)	0.08	4 (2%) 51 35	64, 89, 117, 155	0
2	m	137/138 (99%)	-0.17	0 100 100	54, 69, 84, 98	0
2	o	138/138 (100%)	-0.25	1 (0%) 87 81	50, 65, 87, 107	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
3	C	147/148 (99%)	-0.14	0 100 100	40, 63, 95, 119	0
3	E	147/148 (99%)	-0.15	0 100 100	51, 81, 135, 155	0
3	G	147/148 (99%)	-0.21	0 100 100	39, 56, 92, 104	0
3	J	147/148 (99%)	-0.01	2 (1%) 75 63	57, 78, 116, 136	0
3	L	147/148 (99%)	-0.13	1 (0%) 87 81	54, 83, 138, 167	0
3	N	147/148 (99%)	-0.17	0 100 100	54, 68, 97, 106	0
3	Q	147/148 (99%)	-0.21	0 100 100	49, 65, 95, 109	0
3	S	148/148 (100%)	-0.18	0 100 100	49, 75, 103, 115	0
3	U	147/148 (99%)	-0.15	0 100 100	50, 66, 98, 114	0
3	X	147/148 (99%)	-0.24	0 100 100	50, 67, 98, 110	0
3	Z	148/148 (100%)	-0.21	0 100 100	49, 75, 105, 116	0
3	b	147/148 (99%)	-0.23	0 100 100	49, 66, 96, 113	0
3	e	147/148 (99%)	-0.23	0 100 100	40, 63, 96, 108	0
3	g	148/148 (100%)	-0.13	0 100 100	48, 81, 137, 158	0
3	i	148/148 (100%)	-0.21	0 100 100	39, 57, 93, 111	0
3	l	147/148 (99%)	-0.05	2 (1%) 75 63	57, 82, 121, 145	0
3	n	147/148 (99%)	-0.12	1 (0%) 87 81	58, 86, 140, 166	0
3	p	148/148 (100%)	-0.13	1 (0%) 87 81	55, 70, 101, 115	0
All	All	6411/6516 (98%)	-0.06	87 (1%) 75 63	39, 74, 129, 205	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	j	96	PHE	5.6
1	H	68	TYR	5.5
1	c	45	ASN	5.0
1	j	82	ILE	4.8
1	H	81	TYR	4.4
1	j	95	ALA	4.3
2	K	6	GLY	4.2
1	j	269	LEU	4.2
1	j	145	LEU	4.0
1	H	57	LEU	3.9
1	j	57	LEU	3.8
1	j	83	ARG	3.8
1	j	264	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
1	c	242	GLY	3.5
1	H	156	ALA	3.4
1	H	106	ASP	3.4
1	j	155	VAL	3.4
1	H	60	GLU	3.3
1	j	159	LEU	3.3
2	W	26	VAL	3.3
1	H	82	ILE	3.2
1	j	67	ILE	3.2
1	j	252	GLY	3.2
1	H	96	PHE	3.2
1	H	95	ALA	3.2
1	j	154	SER	3.1
1	c	57	LEU	2.9
1	c	97	GLY	2.9
1	j	267	ASP	2.9
2	P	6	GLY	2.9
1	H	145	LEU	2.8
1	j	55	SER	2.8
1	j	191	GLU	2.8
1	c	49	SER	2.8
2	P	63	TYR	2.8
1	c	267	ASP	2.7
1	j	50	GLU	2.7
1	j	107	ASP	2.7
2	k	139	GLU	2.7
1	V	107	ASP	2.7
2	a	6	GLY	2.6
2	h	38	ASP	2.6
1	j	49	SER	2.6
1	j	84	LYS	2.6
3	p	117	PRO	2.6
2	d	6	GLY	2.6
1	H	161	SER	2.5
1	O	68	TYR	2.5
1	V	74	ASP	2.5
2	o	38	ASP	2.5
3	L	150	ASN	2.5
1	j	52	LEU	2.4
1	j	75	LEU	2.4
1	c	243	THR	2.4
1	j	251	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
3	l	116	ASN	2.4
1	j	99	SER	2.4
1	H	191	GLU	2.4
1	H	64	ASP	2.3
2	M	27	GLY	2.3
3	l	150	ASN	2.3
2	k	6	GLY	2.3
3	J	120	PRO	2.3
1	j	100	HIS	2.3
1	j	74	ASP	2.3
3	n	150	ASN	2.3
1	H	66	ASN	2.2
2	k	28	ASP	2.2
2	f	78	PRO	2.2
1	j	263	PRO	2.2
1	H	269	LEU	2.2
1	H	69	GLN	2.2
1	A	132	GLU	2.2
1	j	162	PHE	2.2
1	V	263	PRO	2.1
1	H	135	ILE	2.1
2	P	26	VAL	2.1
2	k	27	GLY	2.1
1	A	85	THR	2.1
1	V	264	GLY	2.1
1	V	45	ASN	2.1
3	J	29	GLU	2.1
1	c	96	PHE	2.1
1	j	68	TYR	2.1
1	A	60	GLU	2.0
1	c	244	THR	2.0
1	j	54	LEU	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.