



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 19, 2023 – 06:08 AM EDT

PDB ID : 4ZYN  
Title : Crystal Structure of Parkin E3 ubiquitin ligase (linker deletion; delta 86-130)  
Authors : Lilov, A.; Sauve, V.; Trempe, J.F.; Rodionov, D.; Wang, J.; Gehring, K.  
Deposited on : 2015-05-21  
Resolution : 2.54 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.35.1  
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) : 2.35.1

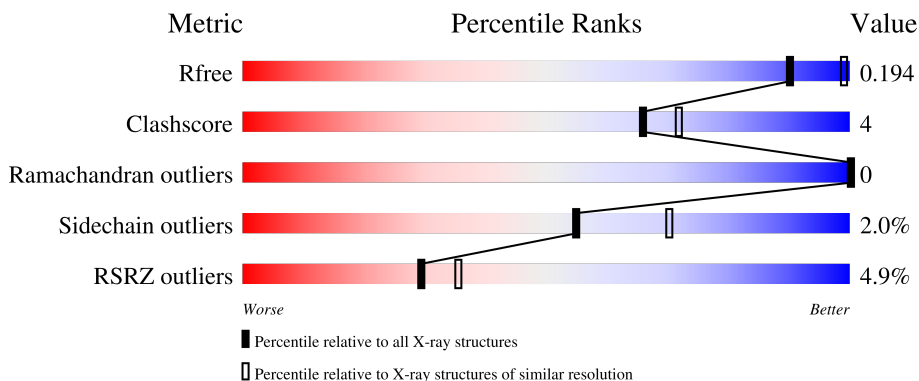
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.54 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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 of 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	425	 6% 78% 8% 14%
1	B	425	 3% 80% 10% 9%

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 5824 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 E3 ubiquitin-protein ligase parkin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	367	2762	1720	501	502	39	0	2	0
1	B	385	2952	1840	537	535	40	0	3	0

There are 104 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP Q9JK66
A	-3	PRO	-	expression tag	UNP Q9JK66
A	-2	LEU	-	expression tag	UNP Q9JK66
A	-1	GLY	-	expression tag	UNP Q9JK66
A	0	SER	-	expression tag	UNP Q9JK66
A	?	-	ASP	deletion	UNP Q9JK66
A	?	-	LYS	deletion	UNP Q9JK66
A	?	-	PRO	deletion	UNP Q9JK66
A	?	-	GLN	deletion	UNP Q9JK66
A	?	-	SER	deletion	UNP Q9JK66
A	?	-	THR	deletion	UNP Q9JK66
A	?	-	PRO	deletion	UNP Q9JK66
A	?	-	GLU	deletion	UNP Q9JK66
A	?	-	GLY	deletion	UNP Q9JK66
A	?	-	SER	deletion	UNP Q9JK66
A	?	-	ILE	deletion	UNP Q9JK66
A	?	-	TRP	deletion	UNP Q9JK66
A	?	-	GLU	deletion	UNP Q9JK66
A	?	-	PRO	deletion	UNP Q9JK66
A	?	-	ARG	deletion	UNP Q9JK66
A	?	-	SER	deletion	UNP Q9JK66
A	?	-	LEU	deletion	UNP Q9JK66
A	?	-	THR	deletion	UNP Q9JK66
A	?	-	ARG	deletion	UNP Q9JK66
A	?	-	VAL	deletion	UNP Q9JK66

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASP	deletion	UNP Q9JK66
A	?	-	LEU	deletion	UNP Q9JK66
A	?	-	SER	deletion	UNP Q9JK66
A	?	-	SER	deletion	UNP Q9JK66
A	?	-	HIS	deletion	UNP Q9JK66
A	?	-	ILE	deletion	UNP Q9JK66
A	?	-	LEU	deletion	UNP Q9JK66
A	?	-	PRO	deletion	UNP Q9JK66
A	?	-	ALA	deletion	UNP Q9JK66
A	?	-	ASP	deletion	UNP Q9JK66
A	?	-	SER	deletion	UNP Q9JK66
A	?	-	VAL	deletion	UNP Q9JK66
A	?	-	GLY	deletion	UNP Q9JK66
A	?	-	LEU	deletion	UNP Q9JK66
A	?	-	ALA	deletion	UNP Q9JK66
A	?	-	VAL	deletion	UNP Q9JK66
A	?	-	ILE	deletion	UNP Q9JK66
A	?	-	LEU	deletion	UNP Q9JK66
A	?	-	ASP	deletion	UNP Q9JK66
A	?	-	THR	deletion	UNP Q9JK66
A	?	-	ASP	deletion	UNP Q9JK66
A	?	-	SER	deletion	UNP Q9JK66
A	?	-	LYS	deletion	UNP Q9JK66
A	?	-	SER	deletion	UNP Q9JK66
A	?	-	ASP	deletion	UNP Q9JK66
A	138	ALA	GLU	conflict	UNP Q9JK66
A	348	ARG	LYS	conflict	UNP Q9JK66
B	-4	GLY	-	expression tag	UNP Q9JK66
B	-3	PRO	-	expression tag	UNP Q9JK66
B	-2	LEU	-	expression tag	UNP Q9JK66
B	-1	GLY	-	expression tag	UNP Q9JK66
B	0	SER	-	expression tag	UNP Q9JK66
B	?	-	ASP	deletion	UNP Q9JK66
B	?	-	LYS	deletion	UNP Q9JK66
B	?	-	PRO	deletion	UNP Q9JK66
B	?	-	GLN	deletion	UNP Q9JK66
B	?	-	SER	deletion	UNP Q9JK66
B	?	-	THR	deletion	UNP Q9JK66
B	?	-	PRO	deletion	UNP Q9JK66
B	?	-	GLU	deletion	UNP Q9JK66
B	?	-	GLY	deletion	UNP Q9JK66
B	?	-	SER	deletion	UNP Q9JK66

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	ILE	deletion	UNP Q9JK66
B	?	-	TRP	deletion	UNP Q9JK66
B	?	-	GLU	deletion	UNP Q9JK66
B	?	-	PRO	deletion	UNP Q9JK66
B	?	-	ARG	deletion	UNP Q9JK66
B	?	-	SER	deletion	UNP Q9JK66
B	?	-	LEU	deletion	UNP Q9JK66
B	?	-	THR	deletion	UNP Q9JK66
B	?	-	ARG	deletion	UNP Q9JK66
B	?	-	VAL	deletion	UNP Q9JK66
B	?	-	ASP	deletion	UNP Q9JK66
B	?	-	LEU	deletion	UNP Q9JK66
B	?	-	SER	deletion	UNP Q9JK66
B	?	-	SER	deletion	UNP Q9JK66
B	?	-	HIS	deletion	UNP Q9JK66
B	?	-	ILE	deletion	UNP Q9JK66
B	?	-	LEU	deletion	UNP Q9JK66
B	?	-	PRO	deletion	UNP Q9JK66
B	?	-	ALA	deletion	UNP Q9JK66
B	?	-	ASP	deletion	UNP Q9JK66
B	?	-	SER	deletion	UNP Q9JK66
B	?	-	VAL	deletion	UNP Q9JK66
B	?	-	GLY	deletion	UNP Q9JK66
B	?	-	LEU	deletion	UNP Q9JK66
B	?	-	ALA	deletion	UNP Q9JK66
B	?	-	VAL	deletion	UNP Q9JK66
B	?	-	ILE	deletion	UNP Q9JK66
B	?	-	LEU	deletion	UNP Q9JK66
B	?	-	ASP	deletion	UNP Q9JK66
B	?	-	THR	deletion	UNP Q9JK66
B	?	-	ASP	deletion	UNP Q9JK66
B	?	-	SER	deletion	UNP Q9JK66
B	?	-	LYS	deletion	UNP Q9JK66
B	?	-	SER	deletion	UNP Q9JK66
B	?	-	ASP	deletion	UNP Q9JK66
B	138	ALA	GLU	conflict	UNP Q9JK66
B	348	ARG	LYS	conflict	UNP Q9JK66

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

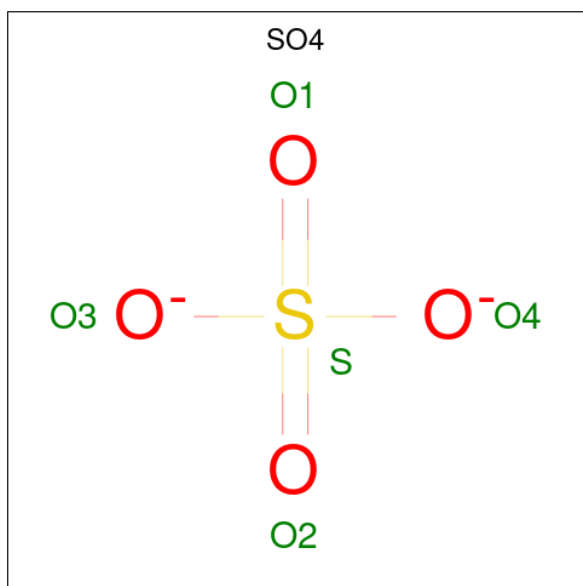
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	8	Total Zn 8 8	0	0
2	B	8	Total Zn 8 8	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



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

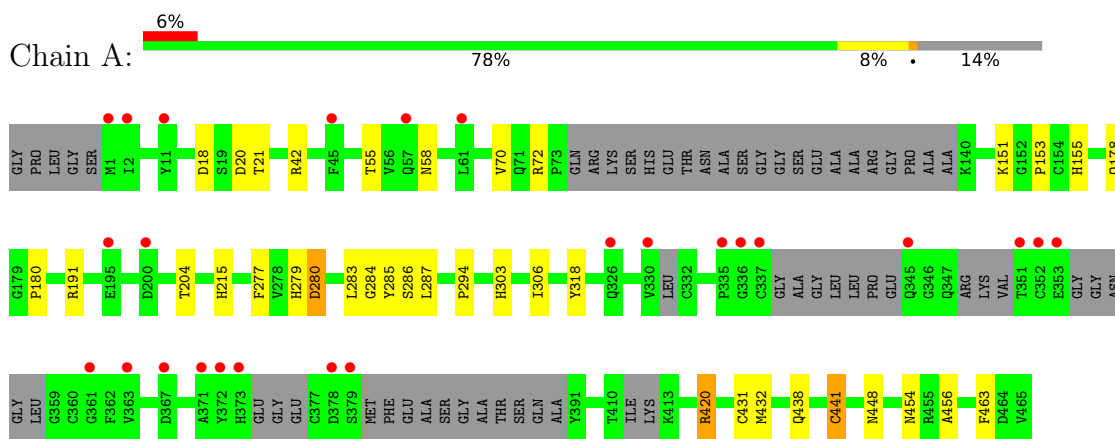
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	33	Total 33	O 33	0	0
4	B	31	Total 31	O 31	0	0

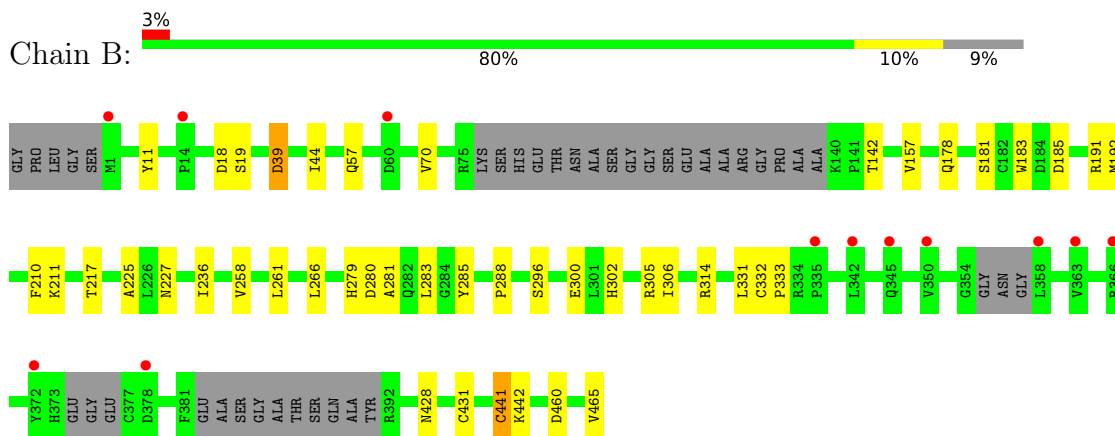
### 3 Residue-property plots [i](#)

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: E3 ubiquitin-protein ligase parkin



- Molecule 1: E3 ubiquitin-protein ligase parkin





## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.11Å 114.11Å 186.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.62 – 2.54 36.62 – 2.54	Depositor EDS
% Data completeness (in resolution range)	99.0 (36.62-2.54) 99.0 (36.62-2.54)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.38 (at 2.54Å)	Xtrriage
Refinement program	REFMAC 5.8.0107	Depositor
R, $R_{free}$	0.193 , 0.235 0.164 , 0.194	Depositor DCC
$R_{free}$ test set	1485 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.0	Xtrriage
Anisotropy	0.147	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 65.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.045 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5824	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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: SO4, ZN

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	0.46	0/2832	0.68	4/3841 (0.1%)
1	B	0.48	0/3026	0.70	0/4104
All	All	0.47	0/5858	0.69	4/7945 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	191	ARG	NE-CZ-NH2	6.07	123.34	120.30
1	A	191	ARG	NE-CZ-NH1	-5.89	117.36	120.30
1	A	280	ASP	N-CA-C	-5.40	96.43	111.00
1	A	420	ARG	NE-CZ-NH1	5.15	122.88	120.30

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	2762	0	2489	19	0
1	B	2952	0	2722	27	0
2	A	8	0	0	0	0
2	B	8	0	0	1	0
3	A	20	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	0	0	0	0
4	A	33	0	0	0	0
4	B	31	0	0	0	0
All	All	5824	0	5211	44	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 4.

All (44) 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:CYS:HG	2:B:505:ZN:ZN	0.67	0.94
1:B:11[A]:TYR:OH	1:B:333:PRO:HA	1.73	0.88
1:B:280:ASP:HB3	1:B:283:LEU:HB3	1.72	0.72
1:B:279:HIS:HB2	1:B:285:TYR:CE1	2.26	0.70
1:B:39:ASP:N	1:B:39:ASP:OD1	2.27	0.68
1:A:294:PRO:CG	1:B:281:ALA:HB3	2.29	0.62
1:B:178:GLN:NE2	1:B:431:CYS:SG	2.73	0.61
1:A:294:PRO:HG3	1:B:281:ALA:HB3	1.83	0.59
1:B:185:ASP:HA	1:B:191:ARG:HG2	1.85	0.58
1:A:280:ASP:N	1:A:284:GLY:O	2.36	0.57
1:B:157:VAL:HG21	1:B:306:ILE:HD12	1.88	0.55
1:B:261:LEU:HD13	1:B:306:ILE:HD11	1.89	0.54
1:A:55:THR:OG1	1:A:58:ASN:OD1	2.25	0.54
1:B:280:ASP:CB	1:B:283:LEU:HB3	2.38	0.54
1:B:11[B]:TYR:OH	1:B:331:LEU:HB2	2.09	0.52
1:A:279:HIS:HB2	1:A:285:TYR:CE1	2.45	0.51
1:B:236:ILE:HG21	1:B:258:VAL:HG21	1.94	0.49
1:B:211:LYS:HE3	1:B:217:THR:OG1	2.13	0.49
1:B:428:ASN:OD1	1:B:428:ASN:N	2.46	0.48
1:A:303:HIS:O	1:A:306:ILE:HG13	2.12	0.48
1:A:178:GLN:NE2	1:A:431:CYS:SG	2.86	0.48
1:A:280:ASP:HB3	1:A:283:LEU:HB3	1.96	0.48
1:B:44:ILE:HD11	1:B:266:LEU:HG	1.98	0.46
1:B:142:THR:CG2	1:B:460:ASP:OD2	2.63	0.46
1:A:151:LYS:O	1:A:155:HIS:CD2	2.69	0.46
1:A:153:PRO:HD2	1:A:215:HIS:NE2	2.32	0.44
1:A:286:SER:OG	1:A:287:LEU:N	2.51	0.43
1:B:288:PRO:HA	1:B:296:SER:O	2.19	0.43
1:A:454:ASN:OD1	1:A:456:ALA:N	2.52	0.43
1:A:20:ASP:O	1:A:55:THR:HG22	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:261:LEU:HD13	1:B:306:ILE:CD1	2.48	0.43
1:B:183:TRP:CZ2	1:B:227:ASN:HA	2.54	0.43
1:B:302[B]:HIS:CD2	1:B:305:ARG:HE	2.37	0.42
1:A:42:ARG:HD2	1:A:72:ARG:HG3	2.01	0.42
1:A:432:MET:CE	1:A:448:ASN:HB2	2.49	0.42
1:B:300:GLU:HB3	1:B:302[A]:HIS:CE1	2.54	0.42
1:A:420:ARG:NH1	1:A:441:CYS:O	2.52	0.42
1:B:210:PHE:CD2	1:B:225:ALA:HB2	2.55	0.42
1:B:19:SER:HB3	1:B:57:GLN:HG2	2.01	0.41
1:A:18:ASP:N	1:A:21:THR:OG1	2.53	0.41
1:A:277:PHE:HB2	1:A:318:TYR:CZ	2.54	0.41
1:A:180:PRO:O	1:A:463:PHE:HB3	2.20	0.41
1:B:441:CYS:SG	1:B:442:LYS:N	2.93	0.40
1:B:279:HIS:HB2	1:B:285:TYR:CD1	2.56	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	351/425 (83%)	338 (96%)	13 (4%)	0	100	100
1	B	378/425 (89%)	359 (95%)	19 (5%)	0	100	100
All	All	729/850 (86%)	697 (96%)	32 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	286/362 (79%)	282 (99%)	4 (1%)	67	79
1	B	312/362 (86%)	304 (97%)	8 (3%)	46	61
All	All	598/724 (83%)	586 (98%)	12 (2%)	55	70

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	VAL
1	A	204	THR
1	A	438	GLN
1	A	441	CYS
1	B	18	ASP
1	B	39	ASP
1	B	70	VAL
1	B	181	SER
1	B	192	MET
1	B	314	ARG
1	B	441	CYS
1	B	465	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	155	HIS
1	A	178	GLN
1	A	279	HIS
1	B	178	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](#)

Of 22 ligands modelled in this entry, 16 are monoatomic - leaving 6 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
3	SO4	B	510	-	4,4,4	0.28	0	6,6,6	0.10	0
3	SO4	A	509	-	4,4,4	0.44	0	6,6,6	0.34	0
3	SO4	A	512	-	4,4,4	0.33	0	6,6,6	0.05	0
3	SO4	A	511	-	4,4,4	0.34	0	6,6,6	0.06	0
3	SO4	B	509	-	4,4,4	0.42	0	6,6,6	0.20	0
3	SO4	A	510	-	4,4,4	0.32	0	6,6,6	0.08	0

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 [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	367/425 (86%)	0.13	25 (6%) 17 20	36, 69, 156, 206	0
1	B	385/425 (90%)	-0.00	12 (3%) 49 56	32, 59, 127, 180	0
All	All	752/850 (88%)	0.06	37 (4%) 29 35	32, 63, 144, 206	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	353	GLU	6.4
1	A	335	PRO	6.3
1	B	1	MET	5.9
1	A	337	CYS	4.6
1	A	200	ASP	4.3
1	B	345	GLN	4.3
1	A	372	TYR	3.7
1	B	350	VAL	3.6
1	A	336	GLY	3.4
1	A	351	THR	3.4
1	A	45	PHE	3.3
1	A	326	GLN	3.2
1	B	363	VAL	3.1
1	A	1	MET	3.1
1	B	342	LEU	3.1
1	A	11[A]	TYR	3.1
1	A	361	GLY	3.1
1	A	61	LEU	3.1
1	A	57	GLN	3.0
1	A	345	GLN	2.9
1	B	372	TYR	2.9
1	A	371	ALA	2.8
1	B	358	LEU	2.8
1	B	378	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	352	CYS	2.6
1	B	366	ARG	2.5
1	A	379	SER	2.5
1	A	330	VAL	2.4
1	A	195	GLU	2.4
1	B	335	PRO	2.4
1	A	373	HIS	2.4
1	A	363	VAL	2.3
1	B	14	PRO	2.2
1	A	367	ASP	2.2
1	A	2	ILE	2.2
1	B	60	ASP	2.0
1	A	378	ASP	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](#)

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(Å <sup>2</sup> )	Q<0.9
2	ZN	B	506	1/1	0.75	0.16	235,235,235,235	0
3	SO4	A	511	5/5	0.87	0.22	146,147,149,149	0
3	SO4	A	510	5/5	0.90	0.19	142,142,142,144	0
3	SO4	A	512	5/5	0.90	0.16	122,123,126,127	0
2	ZN	A	506	1/1	0.92	0.12	210,210,210,210	0
2	ZN	A	505	1/1	0.95	0.03	136,136,136,136	0
3	SO4	B	510	5/5	0.96	0.11	75,76,80,82	0
2	ZN	A	507	1/1	0.97	0.12	61,61,61,61	0
2	ZN	B	507	1/1	0.98	0.11	46,46,46,46	0
3	SO4	A	509	5/5	0.98	0.09	36,42,45,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	A	508	1/1	0.99	0.10	37,37,37,37	0
2	ZN	B	501	1/1	0.99	0.14	42,42,42,42	0
2	ZN	B	503	1/1	0.99	0.12	46,46,46,46	0
2	ZN	B	504	1/1	0.99	0.10	49,49,49,49	0
2	ZN	B	505	1/1	0.99	0.06	113,113,113,113	0
3	SO4	B	509	5/5	0.99	0.08	36,37,39,40	0
2	ZN	A	502	1/1	0.99	0.09	81,81,81,81	0
2	ZN	A	503	1/1	1.00	0.13	55,55,55,55	0
2	ZN	B	502	1/1	1.00	0.06	65,65,65,65	0
2	ZN	A	504	1/1	1.00	0.06	68,68,68,68	0
2	ZN	B	508	1/1	1.00	0.13	43,43,43,43	0
2	ZN	A	501	1/1	1.00	0.11	47,47,47,47	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.