



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 12, 2024 – 08:46 am BST

PDB ID : 5CAW  
Title : Structure of Pediculus humanus Parkin bound to phospho-ubiquitin  
Authors : Wauer, T.; Komander, D.  
Deposited on : 2015-06-30  
Resolution : 2.62 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

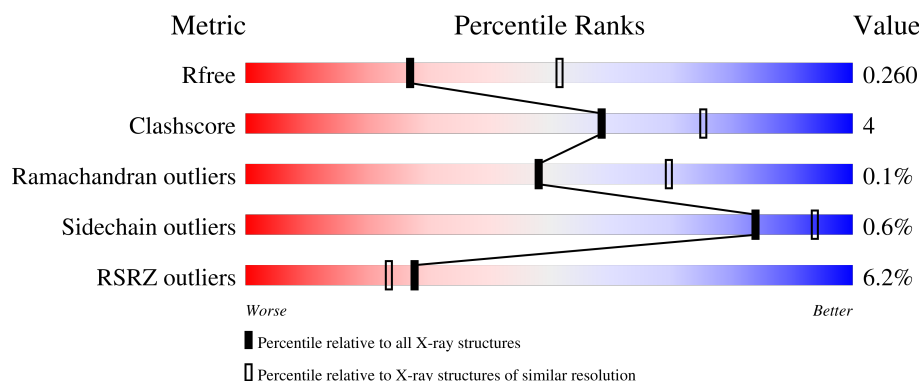
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.62 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))
$R_{free}$	164625	4623 (2.64-2.60)
Clashscore	180529	5071 (2.64-2.60)
Ramachandran outliers	177936	5006 (2.64-2.60)
Sidechain outliers	177891	5006 (2.64-2.60)
RSRZ outliers	164620	4622 (2.64-2.60)

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	321	<div> <div>7%</div> <div>82%</div> <div>11%</div> <div>7%</div> </div>
1	C	321	<div> <div>7%</div> <div>89%</div> <div>9%</div> <div>.</div> </div>
2	B	76	<div> <div>%</div> <div>84%</div> <div>16%</div> </div>
2	D	76	<div> <div>4%</div> <div>83%</div> <div>16%</div> <div>.</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5627 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
1	A	298	Total	C	N	O	S	0	0	0
			2145	1359	376	374	36			
1	C	315	Total	C	N	O	S	0	0	0
			2275	1438	399	402	36			

- Molecule 2 is a protein called Polyubiquitin-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	76	Total	C	N	O	P S	0	0	0
			572	361	98	111	1 1			
2	D	76	Total	C	N	O	P S	0	0	0
			561	352	98	109	1 1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	76	3CN	GLY	engineered mutation	UNP P0CG47
D	76	3CN	GLY	engineered mutation	UNP P0CG47

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	8	Total	Zn	0	0
			8	8		
3	C	8	Total	Zn	0	0
			8	8		

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



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

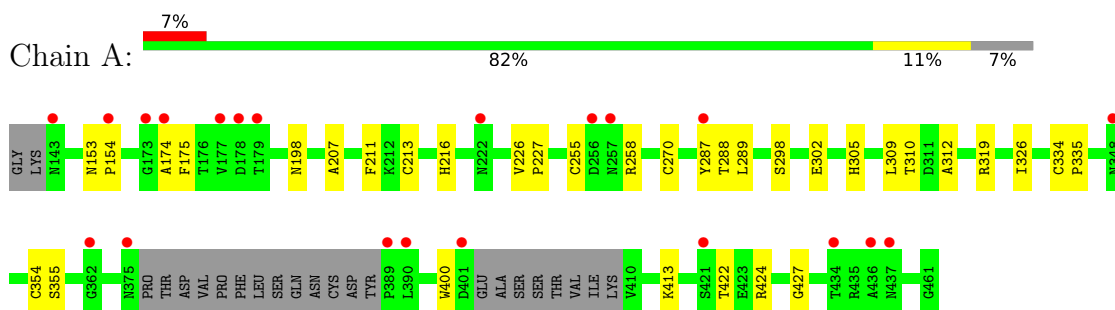
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	10	Total	O	0	0
			10	10		
5	B	1	Total	O	0	0
			1	1		
5	C	17	Total	O	0	0
			17	17		
5	D	5	Total	O	0	0
			5	5		

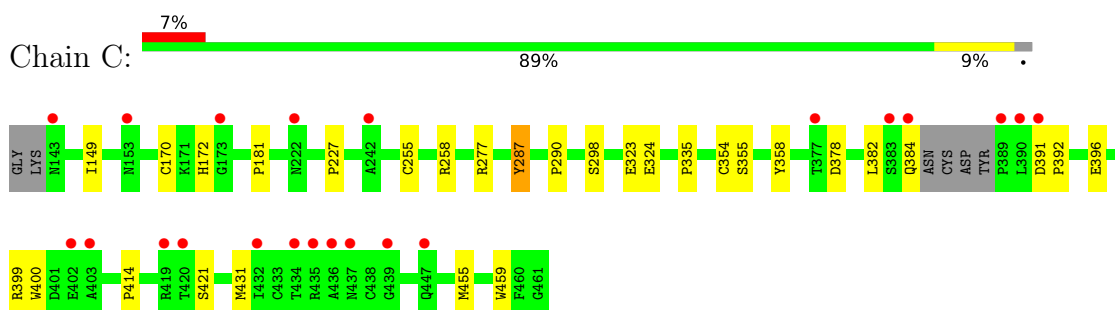
### 3 Residue-property plots

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.

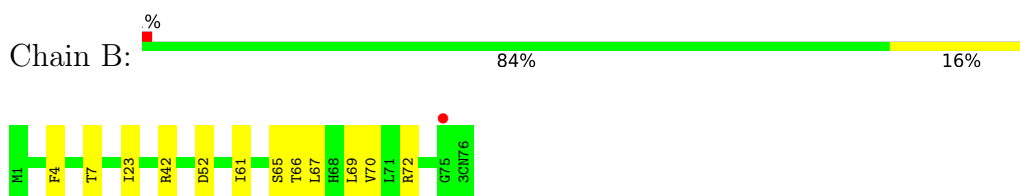
- Molecule 1: E3 ubiquitin-protein ligase parkin



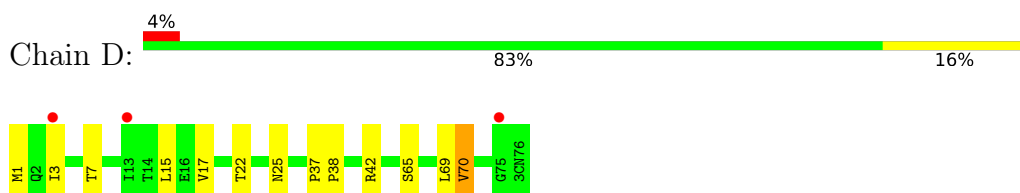
- Molecule 1: E3 ubiquitin-protein ligase parkin



- Molecule 2: Polyubiquitin-B



- Molecule 2: Polyubiquitin-B



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.17Å 44.12Å 204.53Å 90.00° 92.55° 90.00°	Depositor
Resolution (Å)	34.05 – 2.62 34.05 – 2.62	Depositor EDS
% Data completeness (in resolution range)	98.6 (34.05-2.62) 98.6 (34.05-2.62)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.79 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.228 , 0.260 0.231 , 0.260	Depositor DCC
$R_{free}$ test set	1351 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	60.6	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 56.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.026 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5627	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.38% 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: 3CN, SO4, ZN, SEP

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	0.23	0/2208	0.39	0/3011
1	C	0.22	0/2341	0.39	0/3193
2	B	0.21	0/563	0.39	0/762
2	D	0.21	0/552	0.41	0/750
All	All	0.22	0/5664	0.39	0/7716

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 [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	2145	0	1816	18	0
1	C	2275	0	1943	16	0
2	B	572	0	569	6	0
2	D	561	0	537	6	0
3	A	8	0	0	0	0
3	C	8	0	0	0	0
4	A	5	0	0	0	0
4	C	15	0	0	0	0
4	D	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	10	0	0	0	0
5	B	1	0	0	0	0
5	C	17	0	0	0	0
5	D	5	0	0	0	0
All	All	5627	0	4865	45	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 (45) 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:354:CYS:SG	1:A:355:SER:N	2.69	0.66
2:B:4:PHE:HB2	2:B:66:THR:HG22	1.76	0.66
1:C:354:CYS:SG	1:C:355:SER:N	2.69	0.65
1:A:424:ARG:HH21	1:A:427:GLY:HA2	1.63	0.64
2:D:42:ARG:HB2	2:D:70:VAL:HG12	1.81	0.62
2:D:1:MET:N	2:D:17:VAL:O	2.26	0.60
1:C:277:ARG:NH2	1:C:323:GLU:OE1	2.35	0.59
1:A:326:ILE:HD11	2:B:70:VAL:HG21	1.86	0.58
2:D:3:ILE:HG22	2:D:15:LEU:HB2	1.86	0.56
1:A:270:CYS:HB2	1:A:309:LEU:HD21	1.87	0.56
1:A:258:ARG:HB3	1:A:400:TRP:HB3	1.88	0.56
2:B:23:ILE:HB	2:B:52:ASP:HA	1.89	0.54
1:C:170:CYS:SG	1:C:172:HIS:ND1	2.76	0.53
1:C:335:PRO:HG2	1:C:358:TYR:HE2	1.77	0.50
1:C:258:ARG:HB3	1:C:400:TRP:HB3	1.94	0.50
2:B:42:ARG:HH12	2:B:72:ARG:HH11	1.58	0.49
1:A:255:CYS:HB3	1:A:298:SER:HB3	1.95	0.49
1:A:413:LYS:O	1:A:422:THR:OG1	2.25	0.49
1:A:211:PHE:CD1	1:A:227:PRO:HG3	2.48	0.48
1:C:391:ASP:HA	1:C:392:PRO:HD3	1.79	0.46
2:D:22:THR:HG23	2:D:25:ASN:H	1.80	0.46
1:A:174:ALA:HB1	1:A:198:ASN:HB3	1.98	0.45
1:C:149:ILE:HG22	1:C:227:PRO:HA	1.99	0.45
1:A:310:THR:HG22	1:A:312:ALA:H	1.80	0.45
2:D:7:THR:HG22	2:D:69:LEU:HB3	1.99	0.45
1:C:455:MET:O	1:C:459:TRP:HB2	2.17	0.45
1:C:396:GLU:OE2	1:C:399:ARG:NH1	2.47	0.44
1:C:181:PRO:HD2	1:C:459:TRP:CE2	2.52	0.44
1:C:414:PRO:HA	1:C:421:SER:HA	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:CYS:HA	1:A:335:PRO:HD3	1.78	0.44
1:C:382:LEU:HG	1:C:384:GLN:H	1.82	0.43
2:B:61:ILE:HD13	2:B:67:LEU:HD21	2.00	0.43
2:B:7:THR:HG22	2:B:69:LEU:HB3	2.01	0.42
1:A:288:THR:OG1	1:A:289:LEU:N	2.52	0.42
1:A:302:GLU:HB3	1:A:305:HIS:CE1	2.55	0.42
1:C:378:ASP:N	1:C:378:ASP:OD1	2.49	0.42
1:C:287:TYR:OH	1:C:324:GLU:HG3	2.20	0.41
1:C:431:MET:HE3	1:C:431:MET:HB2	2.01	0.41
2:D:37:PRO:HA	2:D:38:PRO:HD3	1.91	0.41
1:A:213:CYS:HB3	1:A:216:HIS:CE1	2.56	0.41
1:C:255:CYS:HB3	1:C:298:SER:HB2	2.03	0.41
1:A:226:VAL:HA	1:A:227:PRO:HD3	1.89	0.41
1:A:319:ARG:HH11	1:A:319:ARG:HG2	1.86	0.41
1:A:153:ASN:HA	1:A:154:PRO:HA	1.78	0.40
1:A:175:PHE:CE1	1:A:207:ALA:HB2	2.57	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	292/321 (91%)	280 (96%)	12 (4%)	0	100	100
1	C	311/321 (97%)	298 (96%)	12 (4%)	1 (0%)	37	57
2	B	72/76 (95%)	72 (100%)	0	0	100	100
2	D	72/76 (95%)	72 (100%)	0	0	100	100
All	All	747/794 (94%)	722 (97%)	24 (3%)	1 (0%)	48	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	290	PRO

### 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	199/280 (71%)	198 (100%)	1 (0%)	86	95
1	C	213/280 (76%)	212 (100%)	1 (0%)	86	95
2	B	58/67 (87%)	58 (100%)	0	100	100
2	D	54/67 (81%)	53 (98%)	1 (2%)	52	75
All	All	524/694 (76%)	521 (99%)	3 (1%)	84	94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	287	TYR
1	C	287	TYR
2	D	70	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	257	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	SEP	D	65	2	8,9,10	1.54	1 (12%)	8,12,14	1.50	2 (25%)
2	SEP	B	65	2	8,9,10	1.57	1 (12%)	8,12,14	1.66	2 (25%)

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	SEP	D	65	2	-	2/5/8/10	-
2	SEP	B	65	2	-	1/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	65	SEP	P-O1P	3.40	1.61	1.50
2	D	65	SEP	P-O1P	3.31	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	65	SEP	OG-CB-CA	3.05	111.11	108.14
2	B	65	SEP	P-OG-CB	-2.97	110.10	118.30
2	D	65	SEP	P-OG-CB	-2.72	110.79	118.30
2	D	65	SEP	OG-CB-CA	2.64	110.71	108.14

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	65	SEP	CB-OG-P-O1P
2	B	65	SEP	CB-OG-P-O2P
2	D	65	SEP	CB-OG-P-O2P

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 16 are monoatomic - leaving 5 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	$\# Z  > 2$
4	SO4	C	1011	-	4,4,4	0.14	0	6,6,6	0.05	0
4	SO4	D	101	-	4,4,4	0.14	0	6,6,6	0.04	0
4	SO4	C	1009	-	4,4,4	0.13	0	6,6,6	0.04	0
4	SO4	C	1010	-	4,4,4	0.13	0	6,6,6	0.06	0
4	SO4	A	1009	-	4,4,4	0.15	0	6,6,6	0.04	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	298/321 (92%)	0.55	21 (7%) 24 20	44, 68, 110, 126	0
1	C	315/321 (98%)	0.49	22 (6%) 24 20	39, 67, 106, 154	0
2	B	74/76 (97%)	0.22	1 (1%) 73 69	50, 68, 92, 101	0
2	D	74/76 (97%)	0.42	3 (4%) 42 37	46, 72, 93, 110	0
All	All	761/794 (95%)	0.48	47 (6%) 28 23	39, 68, 106, 154	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	402	GLU	4.0
1	A	437	ASN	3.9
2	D	75	GLY	3.9
1	C	437	ASN	3.8
1	A	421	SER	3.7
1	C	143	ASN	3.6
1	C	390	LEU	3.5
1	A	173	GLY	3.4
1	C	439	GLY	3.1
1	A	256	ASP	3.0
1	A	174	ALA	2.9
1	C	389	PRO	2.9
1	C	447	GLN	2.9
2	D	3	ILE	2.8
1	A	401	ASP	2.8
1	C	222	ASN	2.8
1	C	384	GLN	2.7
1	C	391	ASP	2.7
1	C	383	SER	2.7
1	C	153	ASN	2.6
1	C	436	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	434	THR	2.6
1	C	173	GLY	2.6
1	A	179	THR	2.6
1	C	242	ALA	2.5
2	D	13	ILE	2.5
1	A	154	PRO	2.5
1	A	287	TYR	2.4
1	A	436	ALA	2.4
1	A	222	ASN	2.4
1	A	348	ASN	2.4
1	C	403	ALA	2.4
1	A	257	ASN	2.3
1	C	419	ARG	2.2
1	C	377	THR	2.2
1	A	390	LEU	2.2
1	A	375	ASN	2.2
1	A	389	PRO	2.2
1	A	143	ASN	2.1
1	C	432	ILE	2.1
1	A	362	GLY	2.1
2	B	75	GLY	2.1
1	C	420	THR	2.1
1	A	177	VAL	2.1
1	C	435	ARG	2.0
1	C	434	THR	2.0
1	A	178	ASP	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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	SEP	B	65	10/11	0.97	0.07	51,58,61,66	0
2	SEP	D	65	10/11	0.97	0.07	47,57,61,74	0

## 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
4	SO4	D	101	5/5	0.60	0.13	140,140,140,140	0
4	SO4	C	1011	5/5	0.75	0.12	125,126,126,126	0
4	SO4	C	1010	5/5	0.78	0.21	125,125,125,125	0
4	SO4	C	1009	5/5	0.82	0.20	97,98,98,98	0
4	SO4	A	1009	5/5	0.87	0.14	84,84,85,86	0
3	ZN	C	1006	1/1	0.97	0.05	65,65,65,65	0
3	ZN	A	1005	1/1	0.98	0.05	59,59,59,59	0
3	ZN	C	1002	1/1	0.99	0.03	59,59,59,59	0
3	ZN	C	1003	1/1	0.99	0.05	74,74,74,74	0
3	ZN	C	1005	1/1	0.99	0.03	60,60,60,60	0
3	ZN	A	1002	1/1	0.99	0.03	65,65,65,65	0
3	ZN	C	1007	1/1	0.99	0.03	97,97,97,97	0
3	ZN	C	1008	1/1	0.99	0.03	66,66,66,66	0
3	ZN	A	1003	1/1	0.99	0.02	79,79,79,79	0
3	ZN	A	1004	1/1	0.99	0.02	65,65,65,65	0
3	ZN	A	1001	1/1	0.99	0.02	62,62,62,62	0
3	ZN	A	1007	1/1	0.99	0.03	96,96,96,96	0
3	ZN	A	1008	1/1	0.99	0.04	55,55,55,55	0
3	ZN	A	1006	1/1	1.00	0.05	67,67,67,67	0
3	ZN	C	1001	1/1	1.00	0.02	65,65,65,65	0
3	ZN	C	1004	1/1	1.00	0.04	65,65,65,65	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.