



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2018 – 08:05 pm GMT

PDB ID : 2VQJ  
Title : Structure of HDAC4 catalytic domain bound to a trifluoromethylketone inhibitor  
Authors : Bottomley, M.J.; Lo Surdo, P.; Di Giovine, P.; Cirillo, A.; Scarpelli, R.; Ferrigno, F.; Jones, P.; Neddermann, P.; De Francesco, R.; Steinkuhler, C.; Gallinari, P.; Carfi, A.  
Deposited on : 2008-03-17  
Resolution : 2.10 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  
Mogul : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk31020  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk31020

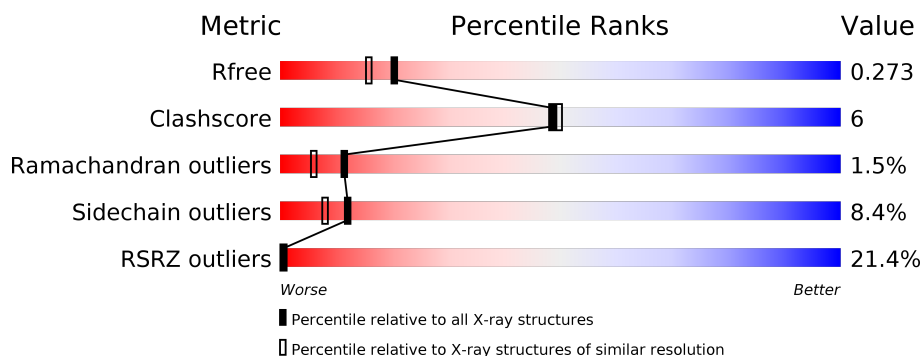
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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))
$R_{free}$	111664	4608 (2.10-2.10)
Clashscore	122126	5109 (2.10-2.10)
Ramachandran outliers	120053	5059 (2.10-2.10)
Sidechain outliers	120020	5060 (2.10-2.10)
RSRZ outliers	108989	4497 (2.10-2.10)

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	413	<div> <div>21%</div> <div>80%</div> <div>14%</div> <div>• •</div> </div>

## 2 Entry composition [i](#)

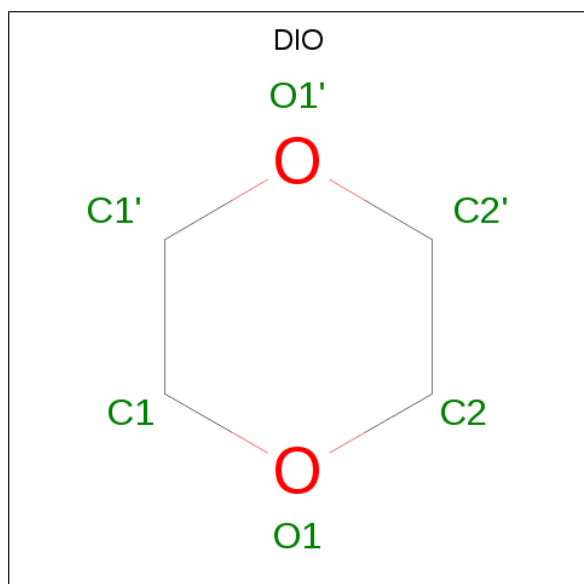
There are 7 unique types of molecules in this entry. The entry contains 3297 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HISTONE DEACETYLASE 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	402	3021	1895	532	573	21	0	0	0

- Molecule 2 is 1,4-DIETHYLENE DIOXIDE (three-letter code: DIO) (formula: C<sub>4</sub>H<sub>8</sub>O<sub>2</sub>).



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

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

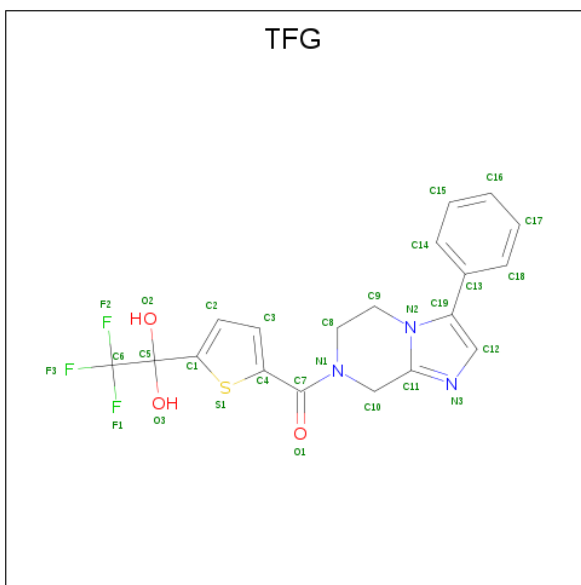
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	K		
3	A	2	2	2	0	0

- 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	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is 2,2,2-TRIFLUORO-1-{5-[(3-PHENYL-5,6-DIHYDROIMIDAZO[1,2-A]PYR AZIN-7(8H)-YL)CARBONYL]THIOPHEN-2-YL}ETHANE-1,1-DIOL (three-letter code: TFG) (formula: C<sub>19</sub>H<sub>16</sub>F<sub>3</sub>N<sub>3</sub>O<sub>3</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	F	N	O	S	0	0
			29	19	3	3	3	1		

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Zn	0	0
			2	2		

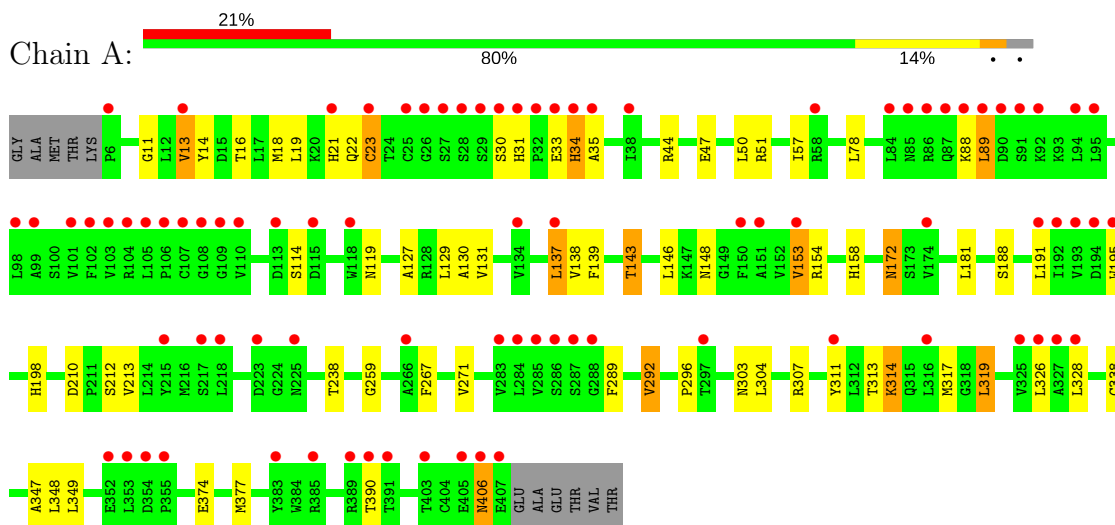
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	222	Total	O	0	0
			222	222		

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

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: HISTONE DEACETYLASE 4



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	106.77Å 137.56Å 68.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.00 – 2.10 28.97 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (84.00-2.10) 99.7 (28.97-2.10)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.62 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.225 , 0.276 0.223 , 0.273	Depositor DCC
$R_{free}$ test set	1526 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.7	Xtriage
Anisotropy	0.516	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 52.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3297	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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: TFG, ZN, DIO, K, SO4

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	0.45	0/3086	0.62	1/4189 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	319	LEU	CA-CB-CG	5.80	128.65	115.30

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	3021	0	2952	36	0
2	A	6	0	8	0	0
3	A	2	0	0	0	0
4	A	15	0	0	0	0
5	A	29	0	15	4	0
6	A	2	0	0	0	0
7	A	222	0	0	0	0
All	All	3297	0	2975	39	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 6.

All (39) 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:313:THR:HG22	1:A:317:MET:HE2	1.48	0.93
1:A:13:VAL:HG22	1:A:137:LEU:HG	1.65	0.79
1:A:313:THR:HG22	1:A:317:MET:CE	2.14	0.76
1:A:317:MET:HE3	1:A:347:ALA:HB1	1.81	0.63
5:A:1414:TFG:C9	5:A:1414:TFG:H18	2.30	0.61
1:A:21:HIS:CE1	1:A:23:CYS:HG	2.13	0.61
1:A:21:HIS:HE2	1:A:23:CYS:HG	0.66	0.61
1:A:21:HIS:NE2	1:A:23:CYS:SG	2.46	0.60
1:A:314:LYS:HE3	1:A:317:MET:HE3	1.84	0.60
1:A:44:ARG:HD2	1:A:338:CYS:HB3	1.83	0.60
1:A:11:GLY:HA3	1:A:146:LEU:HD13	1.82	0.59
1:A:130:ALA:HB1	1:A:153:VAL:HG22	1.84	0.59
1:A:317:MET:CE	1:A:347:ALA:HB1	2.34	0.58
1:A:114:SER:HA	1:A:119:ASN:HD22	1.66	0.57
1:A:148:ASN:ND2	1:A:348:LEU:O	2.38	0.57
1:A:130:ALA:CB	1:A:153:VAL:HG22	2.36	0.56
1:A:34:HIS:O	1:A:35:ALA:HB3	2.06	0.55
1:A:289:PHE:O	1:A:292:VAL:HG13	2.08	0.54
1:A:139:PHE:O	1:A:143:THR:HB	2.08	0.53
5:A:1414:TFG:C9	5:A:1414:TFG:C18	2.85	0.53
1:A:57:ILE:HD11	1:A:146:LEU:HD11	1.91	0.53
1:A:13:VAL:CG2	1:A:137:LEU:HG	2.38	0.52
1:A:374:GLU:HA	1:A:377:MET:HE2	1.92	0.52
5:A:1414:TFG:H9C2	5:A:1414:TFG:H18	1.91	0.51
1:A:138:VAL:CG1	1:A:181:LEU:HD11	2.41	0.51
1:A:18:MET:HG3	1:A:129:LEU:HD23	1.94	0.50
1:A:172:ASN:C	1:A:172:ASN:HD22	2.15	0.49
1:A:313:THR:C	1:A:317:MET:HE2	2.32	0.49
1:A:198:HIS:CE1	5:A:1414:TFG:S1	3.06	0.49
1:A:267:PHE:HA	1:A:271:VAL:HB	1.96	0.48
1:A:259:GLY:C	1:A:304:LEU:HD22	2.35	0.47
1:A:16:THR:HG21	1:A:22:GLN:HE22	1.79	0.47
1:A:127:ALA:O	1:A:131:VAL:HG23	2.16	0.45
1:A:374:GLU:HA	1:A:377:MET:CE	2.47	0.44
1:A:210:ASP:OD1	1:A:212:SER:OG	2.29	0.43
1:A:50:LEU:HD22	1:A:349:LEU:HD12	2.00	0.43
1:A:314:LYS:HA	1:A:317:MET:CE	2.48	0.43
1:A:14:TYR:OH	1:A:19:LEU:HD11	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:ARG:O	1:A:311:TYR:HD1	2.03	0.42

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	400/413 (97%)	371 (93%)	23 (6%)	6 (2%)	<b>11</b> <b>6</b>

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	88	LYS
1	A	406	ASN
1	A	31	HIS
1	A	30	SER
1	A	89	LEU
1	A	296	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	323/335 (96%)	296 (92%)	27 (8%)	<b>12</b> <b>8</b>

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	VAL
1	A	23	CYS
1	A	33	GLU
1	A	34	HIS
1	A	47	GLU
1	A	51	ARG
1	A	78	LEU
1	A	89	LEU
1	A	137	LEU
1	A	143	THR
1	A	153	VAL
1	A	154	ARG
1	A	158	HIS
1	A	172	ASN
1	A	188	SER
1	A	191	LEU
1	A	195	TRP
1	A	213	VAL
1	A	238	THR
1	A	292	VAL
1	A	303	ASN
1	A	314	LYS
1	A	319	LEU
1	A	326	LEU
1	A	328	LEU
1	A	390	THR
1	A	406	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	119	ASN
1	A	122	HIS
1	A	172	ASN
1	A	204	GLN
1	A	245	ASN
1	A	247	ASN
1	A	315	GLN
1	A	368	ASN
1	A	406	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](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 4 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$
2	DIO	A	1408	-	6,6,6	0.55	0	6,6,6	0.61	0
4	SO4	A	1411	-	4,4,4	0.15	0	6,6,6	0.34	0
4	SO4	A	1412	-	4,4,4	0.08	0	6,6,6	0.16	0
4	SO4	A	1413	-	4,4,4	0.17	0	6,6,6	0.12	0
5	TFG	A	1414	6	25,32,32	2.06	5 (20%)	25,49,49	1.83	6 (24%)

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	DIO	A	1408	-	-	0/0/6/6	0/1/1/1
4	SO4	A	1411	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1412	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1413	-	-	0/0/0/0	0/0/0/0
5	TFG	A	1414	6	-	0/17/36/36	0/3/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1414	TFG	C13-C19	-4.58	1.40	1.48
5	A	1414	TFG	C1-S1	-2.81	1.68	1.74
5	A	1414	TFG	C12-C19	-2.66	1.33	1.38
5	A	1414	TFG	O3-C5	4.39	1.44	1.40
5	A	1414	TFG	O2-C5	6.30	1.46	1.40

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1414	TFG	O1-C7-N1	-4.64	114.45	122.35
5	A	1414	TFG	C11-C10-N1	-2.76	106.03	111.24
5	A	1414	TFG	C8-N1-C7	-2.22	115.61	122.78
5	A	1414	TFG	C12-C19-C13	2.85	131.78	128.32
5	A	1414	TFG	C4-C7-N1	3.55	128.95	119.84
5	A	1414	TFG	C6-C5-C1	3.97	114.91	109.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1414	TFG	4	0

## 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	402/413 (97%)	1.16	86 (21%) <b>1</b> <b>0</b>	27, 41, 84, 90	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	30	SER	9.2
1	A	89	LEU	8.3
1	A	31	HIS	8.2
1	A	103	VAL	7.4
1	A	29	SER	6.8
1	A	88	LYS	6.4
1	A	107	CYS	6.1
1	A	32	PRO	6.0
1	A	90	ASP	5.7
1	A	94	LEU	5.7
1	A	28	SER	5.6
1	A	106	PRO	5.6
1	A	285	VAL	5.5
1	A	390	THR	5.3
1	A	105	LEU	5.3
1	A	406	ASN	5.1
1	A	27	SER	5.1
1	A	104	ARG	5.0
1	A	193	VAL	5.0
1	A	87	GLN	4.6
1	A	327	ALA	4.6
1	A	355	PRO	4.6
1	A	311	TYR	4.5
1	A	102	PHE	4.5
1	A	385	ARG	4.4
1	A	297	THR	4.2
1	A	326	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	109	GLY	4.0
1	A	34	HIS	4.0
1	A	353	LEU	4.0
1	A	192	ILE	3.9
1	A	35	ALA	3.9
1	A	354	ASP	3.9
1	A	284	LEU	3.7
1	A	407	GLU	3.7
1	A	218	LEU	3.7
1	A	84	LEU	3.6
1	A	328	LEU	3.6
1	A	26	GLY	3.6
1	A	118	TRP	3.5
1	A	108	GLY	3.4
1	A	92	LYS	3.4
1	A	98	LEU	3.4
1	A	405	GLU	3.3
1	A	153	VAL	3.2
1	A	195	TRP	3.2
1	A	99	ALA	3.2
1	A	110	VAL	3.2
1	A	91	SER	3.0
1	A	151	ALA	3.0
1	A	283	VAL	3.0
1	A	86	ARG	3.0
1	A	115	ASP	3.0
1	A	174	VAL	2.9
1	A	58	ARG	2.9
1	A	287	SER	2.9
1	A	325	VAL	2.9
1	A	352	GLU	2.8
1	A	85	ASN	2.8
1	A	33	GLU	2.8
1	A	38	ILE	2.8
1	A	134	VAL	2.7
1	A	6	PRO	2.7
1	A	21	HIS	2.7
1	A	101	VAL	2.5
1	A	286	SER	2.5
1	A	191	LEU	2.5
1	A	150	PHE	2.5
1	A	391	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	389	ARG	2.5
1	A	316	LEU	2.4
1	A	217	SER	2.4
1	A	225	ASN	2.3
1	A	223	ASP	2.3
1	A	95	LEU	2.3
1	A	13	VAL	2.3
1	A	113	ASP	2.2
1	A	266	ALA	2.2
1	A	215	TYR	2.2
1	A	383	TYR	2.2
1	A	23	CYS	2.1
1	A	194	ASP	2.1
1	A	288	GLY	2.1
1	A	25	CYS	2.1
1	A	137	LEU	2.0
1	A	403	THR	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	DIO	A	1408	6/6	0.83	0.27	72,72,72,72	0
4	SO4	A	1413	5/5	0.90	0.24	93,94,94,94	0
6	ZN	A	1416	1/1	0.94	0.05	76,76,76,76	0
5	TFG	A	1414	29/29	0.94	0.13	31,42,44,45	0
3	K	A	1410	1/1	0.95	0.24	54,54,54,54	0
4	SO4	A	1411	5/5	0.95	0.10	59,60,61,61	0

*Continued on next page...*



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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	SO4	A	1412	5/5	0.97	0.15	57,57,58,59	0
3	K	A	1409	1/1	0.98	0.05	39,39,39,39	0
6	ZN	A	1415	1/1	1.00	0.13	30,30,30,30	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.