



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:15 PM GMT

PDB ID : 4BZ9  
Title : Crystal structure of Schistosoma mansoni HDAC8 complexed with J1075  
Authors : Marek, M.; Romier, C.  
Deposited on : 2013-07-24  
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

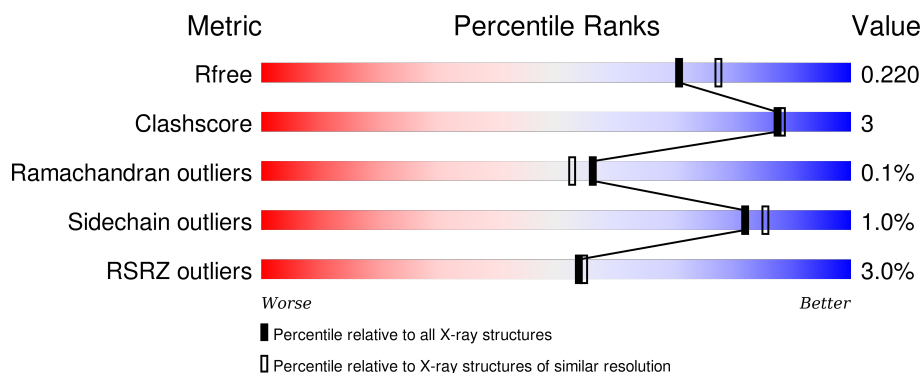
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	446	<div> <div>4%</div> <div>84%</div> <div>11%</div> </div>
1	B	446	<div> <div>%</div> <div>86%</div> <div>6%</div> <div>7%</div> </div>
1	C	446	<div> <div>2%</div> <div>86%</div> <div>6%</div> <div>7%</div> </div>
1	D	446	<div> <div>4%</div> <div>85%</div> <div>11%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	KMY	A	700	-	-	-	X
4	KMY	A	701	-	-	-	X
4	KMY	B	700	-	-	-	X
4	KMY	B	701	-	-	-	X
4	KMY	C	700	-	-	-	X
4	KMY	C	701	-	-	-	X
4	KMY	D	700	-	-	-	X
4	KMY	D	701	-	-	-	X
5	DMF	C	900	-	-	X	X
5	DMF	C	901	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 13756 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 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	396	Total	C	N	O	S	0	2	0
			3174	2047	528	584	15			
1	B	414	Total	C	N	O	S	0	0	0
			3301	2123	553	609	16			
1	C	413	Total	C	N	O	S	0	1	0
			3299	2128	552	603	16			
1	D	398	Total	C	N	O	S	0	0	0
			3184	2054	530	586	14			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	441	GLY	-	EXPRESSION TAG	UNP A5H660
A	442	SER	-	EXPRESSION TAG	UNP A5H660
A	443	LEU	-	EXPRESSION TAG	UNP A5H660
A	444	VAL	-	EXPRESSION TAG	UNP A5H660
A	445	PRO	-	EXPRESSION TAG	UNP A5H660
A	446	ARG	-	EXPRESSION TAG	UNP A5H660
B	441	GLY	-	EXPRESSION TAG	UNP A5H660
B	442	SER	-	EXPRESSION TAG	UNP A5H660
B	443	LEU	-	EXPRESSION TAG	UNP A5H660
B	444	VAL	-	EXPRESSION TAG	UNP A5H660
B	445	PRO	-	EXPRESSION TAG	UNP A5H660
B	446	ARG	-	EXPRESSION TAG	UNP A5H660
C	441	GLY	-	EXPRESSION TAG	UNP A5H660
C	442	SER	-	EXPRESSION TAG	UNP A5H660
C	443	LEU	-	EXPRESSION TAG	UNP A5H660
C	444	VAL	-	EXPRESSION TAG	UNP A5H660
C	445	PRO	-	EXPRESSION TAG	UNP A5H660
C	446	ARG	-	EXPRESSION TAG	UNP A5H660
D	441	GLY	-	EXPRESSION TAG	UNP A5H660
D	442	SER	-	EXPRESSION TAG	UNP A5H660
D	443	LEU	-	EXPRESSION TAG	UNP A5H660

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
D	444	VAL	-	EXPRESSION TAG	UNP A5H660
D	445	PRO	-	EXPRESSION TAG	UNP A5H660
D	446	ARG	-	EXPRESSION TAG	UNP A5H660

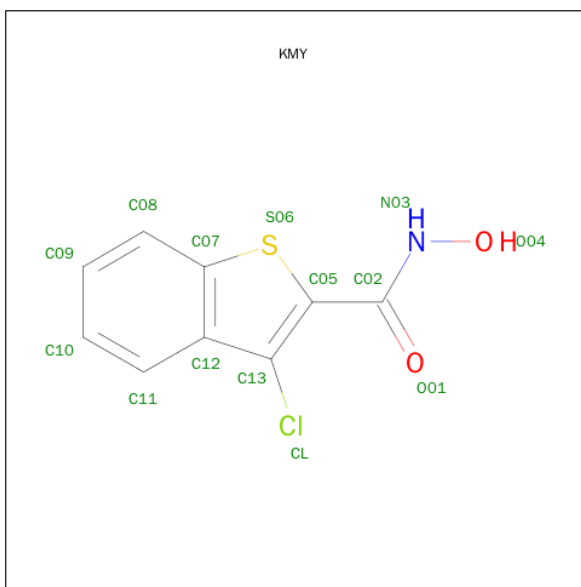
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0

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

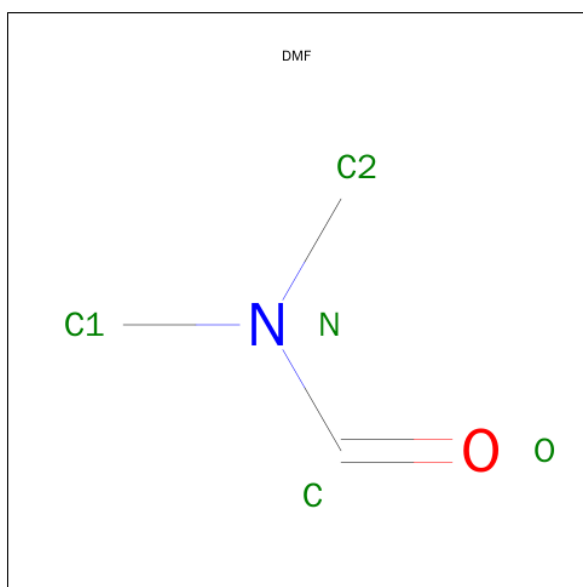
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total K 2 2	0	0
3	A	2	Total K 2 2	0	0
3	D	2	Total K 2 2	0	0
3	C	2	Total K 2 2	0	0

- Molecule 4 is 3-CHLOROBENZOTHIOPHENE-2-CARBOHYDROXAMIC ACID (three-letter code: KMY) (formula: C<sub>9</sub>H<sub>6</sub>ClNO<sub>2</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total 14	C 9	Cl 1	N 1	O 2	S 1	0	0
4	A	1	Total 14	C 9	Cl 1	N 1	O 2	S 1	0	0
4	B	1	Total 14	C 9	Cl 1	N 1	O 2	S 1	0	0
4	B	1	Total 14	C 9	Cl 1	N 1	O 2	S 1	0	0
4	C	1	Total 14	C 9	Cl 1	N 1	O 2	S 1	0	0
4	C	1	Total 14	C 9	Cl 1	N 1	O 2	S 1	0	0
4	D	1	Total 14	C 9	Cl 1	N 1	O 2	S 1	0	0
4	D	1	Total 14	C 9	Cl 1	N 1	O 2	S 1	0	0

- Molecule 5 is DIMETHYLFORMAMIDE (three-letter code: DMF) (formula: C<sub>3</sub>H<sub>7</sub>NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			5	3	1	1		
5	C	1	Total	C	N	O	0	0
			5	3	1	1		
5	C	1	Total	C	N	O	0	0
			5	3	1	1		
5	C	1	Total	C	N	O	0	0
			5	3	1	1		
5	D	1	Total	C	N	O	0	0
			5	3	1	1		
5	D	1	Total	C	N	O	0	0
			5	3	1	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is water.

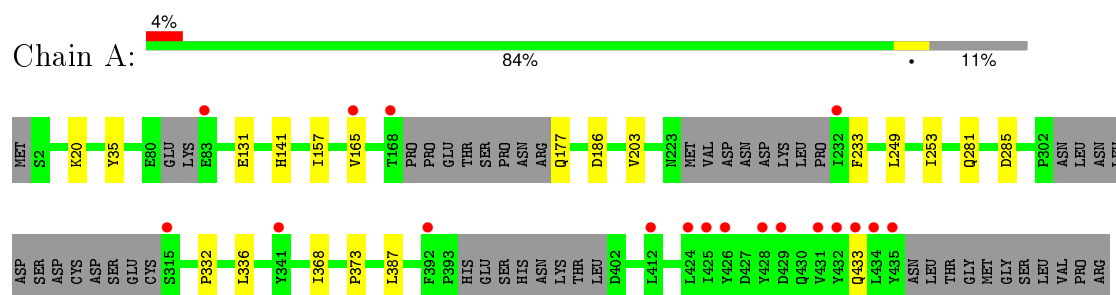
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	138	Total	O	0	0
			138	138		
7	B	178	Total	O	0	0
			178	178		
7	C	186	Total	O	0	0
			186	186		
7	D	130	Total	O	0	0
			130	130		



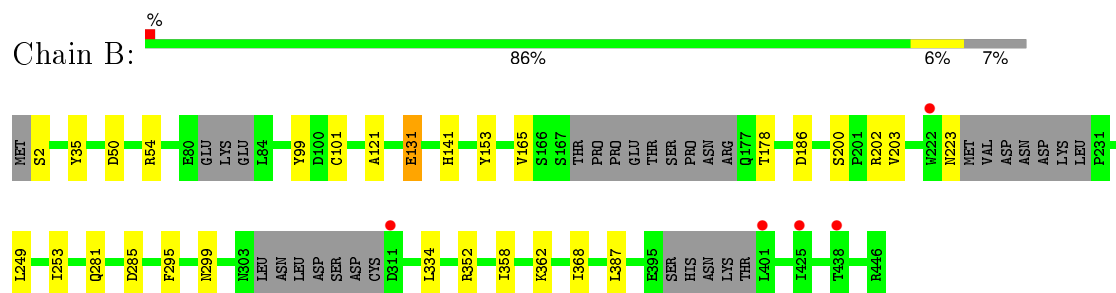
### 3 Residue-property plots

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

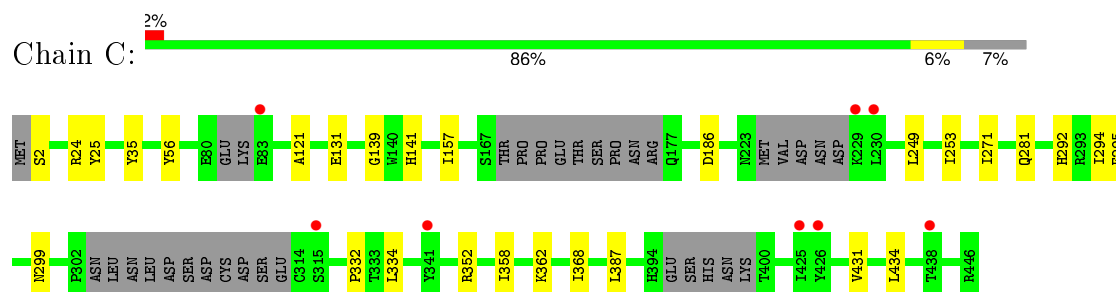
#### • Molecule 1: HISTONE DEACETYLASE 8



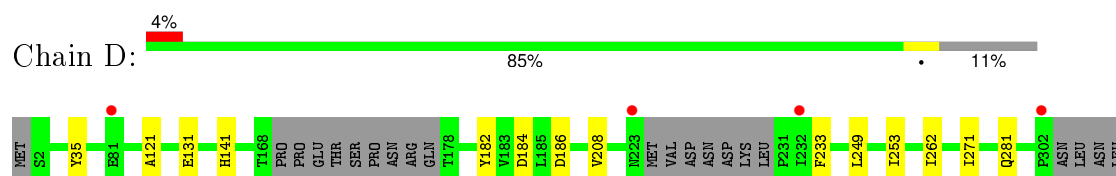
#### • Molecule 1: HISTONE DEACETYLASE 8

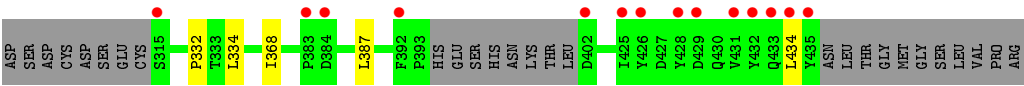


#### • Molecule 1: HISTONE DEACETYLASE 8



#### • Molecule 1: HISTONE DEACETYLASE 8





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.28Å 70.32Å 98.13Å 77.93° 75.59° 85.54°	Depositor
Resolution (Å)	20.16 – 2.00 49.61 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.1 (20.16-2.00) 91.4 (49.61-2.00)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.08 (at 2.00Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, $R_{free}$	0.191 , 0.221 0.188 , 0.220	Depositor DCC
$R_{free}$ test set	5916 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	19.3	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 48.9	EDS
Estimated twinning fraction	0.074 for -k,-h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 116716 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	13756	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, KMY, K, DMF

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	0.50	0/3268	0.60	0/4445
1	B	0.52	0/3392	0.60	0/4612
1	C	0.52	0/3393	0.61	0/4614
1	D	0.50	0/3274	0.59	0/4453
All	All	0.51	0/13327	0.60	0/18124

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	3174	0	3065	14	0
1	B	3301	0	3184	18	0
1	C	3299	0	3204	23	0
1	D	3184	0	3075	12	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	2	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	28	0	11	2	0
4	B	28	0	12	0	0
4	C	28	0	11	0	0
4	D	28	0	11	0	0
5	A	5	0	7	0	0
5	C	15	0	21	6	0
5	D	10	0	14	0	0
6	B	6	0	8	0	0
6	D	6	0	8	0	0
7	A	138	0	0	0	0
7	B	178	0	0	0	0
7	C	186	0	0	1	0
7	D	130	0	0	0	0
All	All	13756	0	12631	68	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 3.

All (68) 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:C:25:TYR:H	5:C:900:DMF:HC	1.23	0.98
1:B:368:ILE:HG21	1:B:387:LEU:CD2	1.98	0.93
1:C:25:TYR:N	5:C:900:DMF:HC	1.86	0.89
1:C:24:ARG:HH21	5:C:900:DMF:H23	1.41	0.86
1:C:368:ILE:HG21	1:C:387:LEU:CD2	2.07	0.85
1:C:368:ILE:CG2	1:C:387:LEU:HD22	2.15	0.76
1:B:368:ILE:CG2	1:B:387:LEU:CD2	2.64	0.75
1:C:25:TYR:H	5:C:900:DMF:C	2.01	0.73
1:B:368:ILE:HG21	1:B:387:LEU:HD22	1.71	0.73
1:B:368:ILE:CG2	1:B:387:LEU:HD22	2.20	0.72
1:D:368:ILE:HG21	1:D:387:LEU:CD2	2.19	0.71
1:C:368:ILE:HG21	1:C:387:LEU:HD22	1.71	0.70
1:C:368:ILE:CG2	1:C:387:LEU:CD2	2.68	0.70
1:C:35:TYR:CE1	1:C:368:ILE:HG23	2.28	0.67
1:A:368:ILE:HG21	1:A:387:LEU:CD2	2.27	0.64
1:D:368:ILE:HG21	1:D:387:LEU:HD22	1.80	0.64
1:A:20:LYS:NZ	4:A:700:KMY:H11	2.13	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:TYR:CE1	1:B:368:ILE:HG23	2.32	0.63
1:D:35:TYR:CE1	1:D:368:ILE:HG23	2.35	0.62
1:B:50:ASP:H	1:B:54:ARG:HH11	1.48	0.62
1:C:2:SER:N	1:C:131:GLU:OE1	2.34	0.60
1:D:368:ILE:CG2	1:D:387:LEU:HD22	2.32	0.59
1:A:20:LYS:HZ2	4:A:700:KMY:H11	1.68	0.59
1:C:368:ILE:HG21	1:C:387:LEU:HD21	1.86	0.58
1:B:368:ILE:HG21	1:B:387:LEU:HD21	1.83	0.58
1:A:186:ASP:HB2	1:A:281:GLN:OE1	2.04	0.57
1:C:24:ARG:NH2	5:C:900:DMF:H23	2.16	0.56
1:C:271:ILE:HD12	1:C:434:LEU:HD12	1.88	0.55
1:A:368:ILE:CG2	1:A:387:LEU:HD22	2.37	0.54
1:B:2:SER:N	1:B:131:GLU:OE1	2.41	0.54
1:D:271:ILE:HD12	1:D:434:LEU:HD11	1.90	0.53
1:A:368:ILE:HG21	1:A:387:LEU:HD22	1.91	0.52
1:D:186:ASP:HB2	1:D:281:GLN:OE1	2.08	0.52
1:D:249:LEU:HD13	1:D:253:ILE:HD13	1.92	0.52
1:C:249:LEU:HD13	1:C:253:ILE:HD13	1.92	0.52
1:C:186:ASP:HB2	1:C:281:GLN:OE1	2.10	0.52
1:B:186:ASP:HB2	1:B:281:GLN:OE1	2.11	0.51
1:B:299:ASN:O	1:B:352:ARG:HD2	2.12	0.50
1:C:299:ASN:O	1:C:352:ARG:HD2	2.12	0.49
1:A:165:VAL:HG11	1:A:203:VAL:CG2	2.43	0.49
1:C:358:ILE:HG23	1:C:362:LYS:HD3	1.95	0.48
1:B:165:VAL:HG11	1:B:203:VAL:HG22	1.94	0.48
1:C:431:VAL:O	1:C:434:LEU:HB3	2.14	0.47
1:B:50:ASP:HB2	1:B:54:ARG:HD3	1.97	0.47
1:A:249:LEU:HD13	1:A:253:ILE:HD13	1.97	0.46
1:C:139:GLY:HA2	1:C:157:ILE:HD11	1.97	0.46
1:B:249:LEU:HD13	1:B:253:ILE:HD13	1.99	0.45
1:C:253:ILE:HG22	1:C:295:PHE:CD1	2.51	0.45
1:B:358:ILE:HG23	1:B:362:LYS:HD3	1.97	0.45
1:A:165:VAL:HG11	1:A:203:VAL:HG22	1.97	0.45
5:C:900:DMF:H13	7:C:2069:HOH:O	2.17	0.44
1:C:292:HIS:HB3	1:C:294:ILE:HD12	1.98	0.44
1:A:368:ILE:CG2	1:A:387:LEU:CD2	2.94	0.44
1:A:131:GLU:O	1:A:332:PRO:HA	2.18	0.44
1:D:368:ILE:CG2	1:D:387:LEU:CD2	2.91	0.44
1:C:131:GLU:O	1:C:332:PRO:HA	2.19	0.43
1:B:178:THR:HB	1:B:202:ARG:HH21	1.83	0.43
1:A:35:TYR:CE1	1:A:368:ILE:HG23	2.53	0.42

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:121:ALA:HB1	1:C:334:LEU:HD13	2.01	0.42
1:A:35:TYR:CZ	1:A:373:PRO:HD3	2.55	0.42
1:A:157:ILE:HG12	1:A:336:LEU:HD13	2.01	0.42
1:D:208:VAL:HG11	1:D:262:ILE:HD12	2.02	0.42
1:B:101:CYS:HB3	1:B:153:TYR:CE2	2.55	0.42
1:B:253:ILE:HG22	1:B:295:PHE:CD1	2.55	0.42
1:D:121:ALA:HB1	1:D:334:LEU:HD13	2.02	0.41
1:B:121:ALA:HB1	1:B:334:LEU:HD13	2.03	0.41
1:D:182:TYR:CE2	1:D:184:ASP:HB2	2.57	0.40
1:D:131:GLU:O	1:D:332:PRO:HA	2.21	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	386/446 (86%)	377 (98%)	9 (2%)	0	100	100
1	B	402/446 (90%)	394 (98%)	7 (2%)	1 (0%)	52	48
1	C	402/446 (90%)	394 (98%)	8 (2%)	0	100	100
1	D	388/446 (87%)	380 (98%)	8 (2%)	0	100	100
All	All	1578/1784 (88%)	1545 (98%)	32 (2%)	1 (0%)	56	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	99	TYR

### 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	345/391 (88%)	340 (99%)	5 (1%)	74	77
1	B	359/391 (92%)	354 (99%)	5 (1%)	74	77
1	C	359/391 (92%)	357 (99%)	2 (1%)	90	93
1	D	345/391 (88%)	343 (99%)	2 (1%)	90	93
All	All	1408/1564 (90%)	1394 (99%)	14 (1%)	82	85

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	141	HIS
1	A	177	GLN
1	A	233	PHE
1	A	285	ASP
1	A	433	GLN
1	B	131	GLU
1	B	141	HIS
1	B	200	SER
1	B	223	ASN
1	B	285	ASP
1	C	56	TYR
1	C	141	HIS
1	D	141	HIS
1	D	233	PHE

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

Mol	Chain	Res	Type
1	C	408	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.



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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 28 ligands modelled in this entry, 12 are monoatomic - leaving 16 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	KMY	A	700	2	9,15,15	3.41	2 (22%)	8,21,21	1.52	1 (12%)
4	KMY	A	701	-	9,15,15	3.39	3 (33%)	8,21,21	1.67	1 (12%)
5	DMF	A	901	-	4,4,4	0.73	0	4,4,4	0.22	0
4	KMY	B	700	2	9,15,15	3.53	2 (22%)	8,21,21	1.59	1 (12%)
4	KMY	B	701	-	9,15,15	3.39	2 (22%)	8,21,21	1.72	1 (12%)
6	GOL	B	800	-	5,5,5	0.76	0	5,5,5	1.05	0
4	KMY	C	700	2	9,15,15	3.57	2 (22%)	8,21,21	1.60	1 (12%)
4	KMY	C	701	-	9,15,15	3.20	2 (22%)	8,21,21	1.77	1 (12%)
5	DMF	C	900	-	4,4,4	0.73	0	4,4,4	0.74	0
5	DMF	C	901	-	4,4,4	0.61	0	4,4,4	0.43	0
5	DMF	C	902	-	4,4,4	0.71	0	4,4,4	0.25	0
4	KMY	D	700	2	9,15,15	3.45	2 (22%)	8,21,21	1.61	1 (12%)
4	KMY	D	701	-	9,15,15	3.38	2 (22%)	8,21,21	1.68	1 (12%)
6	GOL	D	800	-	5,5,5	0.72	0	5,5,5	1.07	0
5	DMF	D	900	-	4,4,4	0.62	0	4,4,4	0.31	0
5	DMF	D	901	-	4,4,4	0.70	0	4,4,4	0.36	0

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
4	KMY	A	700	2	-	0/2/6/6	0/2/2/2
4	KMY	A	701	-	-	0/2/6/6	0/2/2/2
5	DMF	A	901	-	-	0/2/2/2	0/0/0/0
4	KMY	B	700	2	-	0/2/6/6	0/2/2/2
4	KMY	B	701	-	-	0/2/6/6	0/2/2/2
6	GOL	B	800	-	-	0/4/4/4	0/0/0/0
4	KMY	C	700	2	-	0/2/6/6	0/2/2/2
4	KMY	C	701	-	-	0/2/6/6	0/2/2/2
5	DMF	C	900	-	-	0/2/2/2	0/0/0/0
5	DMF	C	901	-	-	0/2/2/2	0/0/0/0
5	DMF	C	902	-	-	0/2/2/2	0/0/0/0
4	KMY	D	700	2	-	0/2/6/6	0/2/2/2
4	KMY	D	701	-	-	0/2/6/6	0/2/2/2
6	GOL	D	800	-	-	0/4/4/4	0/0/0/0
5	DMF	D	900	-	-	0/2/2/2	0/0/0/0
5	DMF	D	901	-	-	0/2/2/2	0/0/0/0

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	700	KMY	O04-N03	-5.95	1.29	1.39
4	B	700	KMY	O04-N03	-5.86	1.29	1.39
4	C	700	KMY	O04-N03	-5.84	1.29	1.39
4	A	700	KMY	O04-N03	-5.81	1.29	1.39
4	A	701	KMY	O04-N03	-5.16	1.30	1.39
4	D	701	KMY	O04-N03	-5.07	1.30	1.39
4	B	701	KMY	O04-N03	-4.84	1.31	1.39
4	C	701	KMY	O04-N03	-4.82	1.31	1.39
4	A	701	KMY	C09-C08	2.05	1.41	1.36
4	C	701	KMY	C02-N03	7.75	1.43	1.32
4	D	700	KMY	C02-N03	7.81	1.43	1.32
4	A	700	KMY	C02-N03	8.05	1.43	1.32
4	A	701	KMY	C02-N03	8.22	1.43	1.32
4	D	701	KMY	C02-N03	8.33	1.44	1.32
4	B	700	KMY	C02-N03	8.41	1.44	1.32
4	B	701	KMY	C02-N03	8.45	1.44	1.32
4	C	700	KMY	C02-N03	8.65	1.44	1.32

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
4	D	701	KMY	C11-C12-C13	-4.55	125.35	135.20
4	A	701	KMY	C11-C12-C13	-4.55	125.36	135.20
4	B	701	KMY	C11-C12-C13	-4.53	125.40	135.20
4	C	701	KMY	C11-C12-C13	-4.41	125.66	135.20
4	D	700	KMY	C11-C12-C13	-4.29	125.91	135.20
4	C	700	KMY	C11-C12-C13	-4.24	126.03	135.20
4	B	700	KMY	C11-C12-C13	-4.21	126.09	135.20
4	A	700	KMY	C11-C12-C13	-4.10	126.32	135.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	700	KMY	2	0
5	C	900	DMF	6	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	396/446 (88%)	0.19	18 (4%) 37 38	12, 22, 54, 86	0
1	B	414/446 (92%)	-0.04	5 (1%) 81 81	10, 18, 41, 74	0
1	C	413/446 (92%)	0.02	8 (1%) 70 70	10, 19, 40, 79	0
1	D	398/446 (89%)	0.16	18 (4%) 37 38	12, 21, 54, 76	0
All	All	1621/1784 (90%)	0.08	49 (3%) 54 55	10, 20, 46, 86	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	425	ILE	7.1
1	A	432	TYR	6.9
1	D	432	TYR	6.4
1	A	426	TYR	6.3
1	C	230	LEU	6.0
1	A	429	ASP	6.0
1	A	434	LEU	5.7
1	D	426	TYR	5.4
1	D	435	TYR	5.4
1	D	434	LEU	4.8
1	D	81	GLU	4.5
1	A	435	TYR	4.5
1	A	428	TYR	4.4
1	D	428	TYR	4.3
1	D	315	SER	4.2
1	D	425	ILE	4.1
1	D	429	ASP	3.9
1	A	433	GLN	3.5
1	A	168	THR	3.5
1	A	232	ILE	3.4
1	C	426	TYR	3.3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	392	PHE	3.2
1	A	315	SER	3.2
1	D	383	PRO	3.1
1	A	165	VAL	3.0
1	C	83	GLU	3.0
1	D	223	ASN	3.0
1	D	433	GLN	2.9
1	C	341	TYR	2.8
1	B	311	ASP	2.8
1	C	438	THR	2.6
1	C	425	ILE	2.5
1	A	412	LEU	2.5
1	A	431	VAL	2.5
1	A	341	TYR	2.4
1	D	392	PHE	2.4
1	D	402	ASP	2.3
1	B	401	LEU	2.3
1	D	431	VAL	2.3
1	A	424	LEU	2.2
1	A	83	GLU	2.2
1	C	229	LYS	2.2
1	B	425	ILE	2.1
1	B	438	THR	2.1
1	D	384	ASP	2.1
1	D	232	ILE	2.1
1	D	302	PRO	2.1
1	C	315	SER	2.1
1	B	222	TRP	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	KMY	C	701	14/14	0.60	0.32	14.81	47,57,71,75	0
4	KMY	D	701	14/14	0.66	0.32	14.48	47,58,68,71	0
4	KMY	B	701	14/14	0.72	0.26	13.40	33,49,63,66	0
5	DMF	C	900	5/5	0.76	0.23	12.22	22,30,33,33	0
4	KMY	A	701	14/14	0.73	0.32	7.57	51,58,65,67	0
4	KMY	D	700	14/14	0.76	0.39	7.44	41,43,45,46	0
4	KMY	A	700	14/14	0.92	0.28	4.04	31,39,41,46	0
4	KMY	B	700	14/14	0.67	0.24	3.91	38,40,45,48	0
5	DMF	C	901	5/5	0.92	0.19	3.05	29,33,35,38	0
4	KMY	C	700	14/14	0.78	0.21	2.11	35,40,46,53	0
5	DMF	D	901	5/5	0.85	0.15	1.48	28,32,34,36	0
5	DMF	C	902	5/5	0.92	0.14	0.46	35,35,37,37	0
6	GOL	D	800	6/6	0.91	0.17	0.41	25,26,27,27	0
5	DMF	A	901	5/5	0.88	0.15	0.18	34,35,37,37	0
5	DMF	D	900	5/5	0.95	0.13	0.06	28,29,30,32	0
6	GOL	B	800	6/6	0.91	0.12	-0.22	26,29,31,31	0
3	K	B	601	1/1	0.97	0.07	-1.55	27,27,27,27	0
2	ZN	B	500	1/1	0.99	0.06	-2.40	26,26,26,26	0
3	K	D	600	1/1	0.99	0.06	-2.78	13,13,13,13	0
3	K	C	600	1/1	0.99	0.07	-2.78	13,13,13,13	0
3	K	A	600	1/1	1.00	0.06	-3.12	14,14,14,14	0
3	K	C	601	1/1	0.98	0.05	-3.17	28,28,28,28	0
3	K	D	601	1/1	0.98	0.04	-3.32	25,25,25,25	0
3	K	A	601	1/1	0.99	0.07	-3.33	25,25,25,25	0
2	ZN	D	500	1/1	1.00	0.05	-3.61	27,27,27,27	0
3	K	B	600	1/1	1.00	0.06	-4.20	12,12,12,12	0
2	ZN	C	500	1/1	0.99	0.06	-4.89	27,27,27,27	0
2	ZN	A	500	1/1	1.00	0.04	-4.95	27,27,27,27	0

## 6.5 Other polymers

There are no such residues in this entry.