



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 04:25 AM GMT

PDB ID : 2DV2  
Title : Crystal structure of D141E mutant of BpKatG at pH 8.0  
Authors : Deemagarn, T.; Wiseman, B.; Carpena, X.; Ivancich, A.; Fita, I.; Loewen, P.C.  
Deposited on : 2006-07-28  
Resolution : 2.15 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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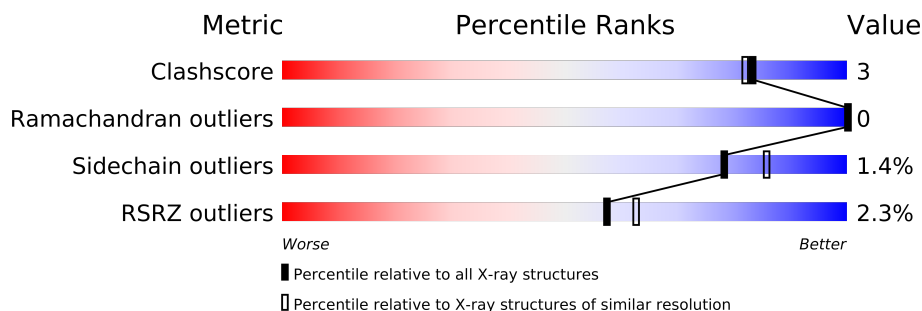
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.15 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))
Clashscore	79885	1299 (2.18-2.14)
Ramachandran outliers	78287	1272 (2.18-2.14)
Sidechain outliers	78261	1272 (2.18-2.14)
RSRZ outliers	66119	1094 (2.18-2.14)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	748	
1	B	748	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	TRS	A	1001	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12477 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Peroxidase/catalase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	714	Total	C	N	O	S	0	1	0
			5513	3481	981	1037	14			
1	B	714	Total	C	N	O	S	0	2	0
			5520	3485	984	1037	14			

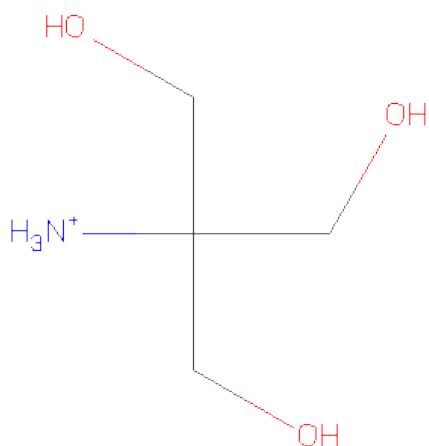
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	111	TOX	TRP	MODIFIED RESIDUE	UNP Q939D2
A	141	GLU	ASP	ENGINEERED	UNP Q939D2
B	111	TOX	TRP	MODIFIED RESIDUE	UNP Q939D2
B	141	GLU	ASP	ENGINEERED	UNP Q939D2

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

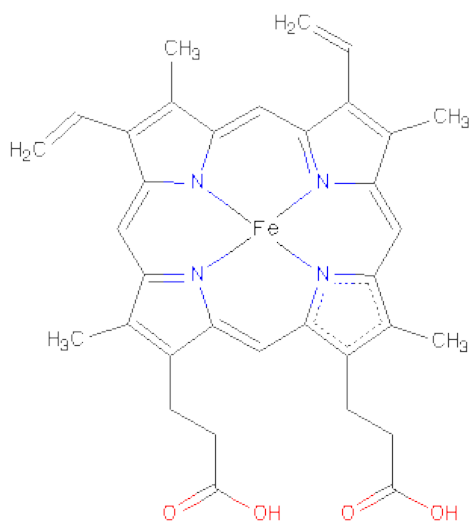
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Na	0	0
			1	1		
2	A	1	Total	Na	0	0
			1	1		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	4	1	3		
3	B	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 5 is water.

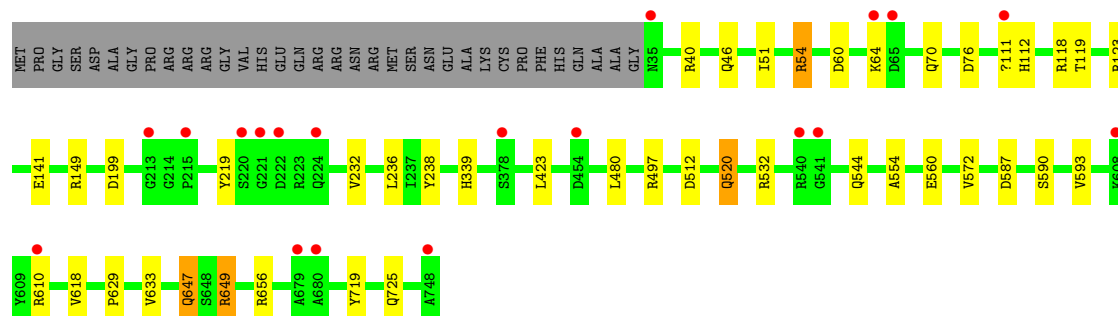
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	640	Total	O	0	0
			640	640		
5	B	700	Total	O	0	0
			700	700		

### 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.

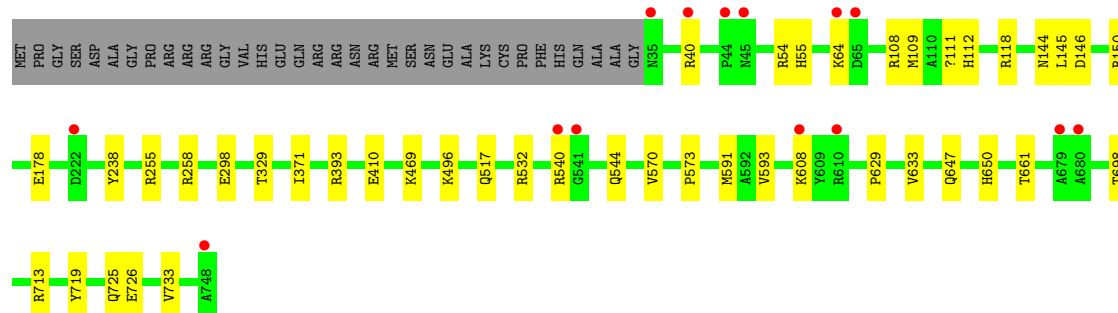
- Molecule 1: Peroxidase/catalase

Chain A: 



- Molecule 1: Peroxidase/catalase

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.33Å 114.82Å 174.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.96 – 2.15 29.05 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.1 (29.96-2.15) 99.1 (29.05-2.15)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.14 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.148 , 0.185 0.160 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	21.6	Xtriage
Anisotropy	0.496	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 39.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 108879 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	12477	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, TOX, TRS, NA

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	0.82	1/5641 (0.0%)	0.80	9/7668 (0.1%)
1	B	0.83	1/5652 (0.0%)	0.82	9/7682 (0.1%)
All	All	0.82	2/11293 (0.0%)	0.81	18/15350 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	726	GLU	CG-CD	5.90	1.60	1.51
1	A	520	GLN	CB-CG	5.41	1.67	1.52

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	532	ARG	NE-CZ-NH2	-10.69	114.96	120.30
1	B	108	ARG	NE-CZ-NH2	-7.83	116.38	120.30
1	B	532	ARG	NE-CZ-NH2	-7.53	116.53	120.30
1	A	532	ARG	NE-CZ-NH1	6.70	123.65	120.30
1	B	591	MET	CG-SD-CE	6.40	110.44	100.20
1	B	54	ARG	CG-CD-NE	-6.18	98.82	111.80
1	B	258	ARG	NE-CZ-NH1	6.14	123.37	120.30
1	B	393	ARG	NE-CZ-NH2	-6.03	117.29	120.30
1	B	150	ARG	NE-CZ-NH2	-5.99	117.31	120.30
1	A	60	ASP	CB-CG-OD1	5.95	123.66	118.30
1	B	108	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	B	713	ARG	NE-CZ-NH1	5.57	123.08	120.30
1	A	54	ARG	NE-CZ-NH2	-5.44	117.58	120.30
1	A	649	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	A	149	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	A	76	ASP	CB-CG-OD2	-5.18	113.64	118.30
1	A	123	ARG	NE-CZ-NH1	5.12	122.86	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	497	ARG	NE-CZ-NH1	5.10	122.85	120.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Close contacts ⓘ

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5513	0	5322	34	0
1	B	5520	0	5331	30	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	8	0	12	0	0
3	B	8	0	12	0	0
4	A	43	0	30	0	0
4	B	43	0	30	0	0
5	A	640	0	0	7	0
5	B	700	0	0	9	0
All	All	12477	0	10737	63	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (63) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:111:TOX:H10	1:A:238:TYR:CE1	1.12	1.61
1:A:111:TOX:CH2	1:A:238:TYR:HE1	1.11	1.58
1:B:111:TOX:H10	1:B:238:TYR:CE1	1.04	1.56
1:B:111:TOX:CH2	1:B:238:TYR:HE1	1.25	1.46
1:B:111:TOX:H10	1:B:238:TYR:CD1	1.90	1.05
1:A:111:TOX:H10	1:A:238:TYR:CD1	1.99	0.96
1:B:111:TOX:H13	1:B:112:HIS:HE2	1.29	0.81
1:B:410:GLU:OE1	5:B:2246:HOH:O	2.01	0.77
1:A:141:GLU:HG3	1:A:236:LEU:HD23	1.67	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:725:GLN:OE1	5:A:1908:HOH:O	2.01	0.77
1:B:725:GLN:NE2	5:B:2454:HOH:O	2.20	0.74
1:B:647:GLN:HG2	5:B:2404:HOH:O	1.89	0.73
1:A:544:GLN:OE1	5:A:1806:HOH:O	2.08	0.71
1:B:255[B]:ARG:HD3	5:B:2507:HOH:O	1.91	0.70
1:A:111:TOX:H13	1:A:112:HIS:HE2	1.34	0.70
1:A:629:PRO:O	1:A:633:VAL:HG23	1.97	0.65
1:B:55:HIS:HD2	5:B:2105:HOH:O	1.80	0.64
1:B:633:VAL:HG22	1:B:719:TYR:CZ	2.33	0.63
1:A:141:GLU:HG3	1:A:236:LEU:CD2	2.29	0.62
1:B:650:HIS:HD2	1:B:698:THR:OG1	1.85	0.59
1:B:111:TOX:CZ3	1:B:238:TYR:HE1	2.06	0.59
1:B:111:TOX:NE1	1:B:111:TOX:O1	2.36	0.58
1:A:111:TOX:O2	1:A:112:HIS:NE2	2.27	0.57
1:B:178:GLU:OE1	5:B:2093:HOH:O	2.18	0.56
1:A:520:GLN:HG3	5:A:1776:HOH:O	2.04	0.56
1:B:540:ARG:HA	1:B:540:ARG:NE	2.20	0.56
1:A:725:GLN:CD	5:A:1908:HOH:O	2.42	0.56
1:A:141:GLU:HG3	1:A:236:LEU:HA	1.89	0.55
1:A:339:HIS:HB2	5:A:1980:HOH:O	2.09	0.52
1:B:661:THR:HA	1:B:725:GLN:HE22	1.76	0.50
1:A:480:LEU:HD22	1:A:554:ALA:HB1	1.93	0.50
1:A:111:TOX:O1	1:A:112:HIS:NE2	2.43	0.48
1:A:647:GLN:HA	1:A:647:GLN:NE2	2.29	0.48
1:A:633:VAL:HG22	1:A:719:TYR:CZ	2.49	0.47
1:A:219:TYR:OH	1:A:232:VAL:HG12	2.15	0.47
1:A:560:GLU:HG3	1:A:572:VAL:HG23	1.95	0.47
1:B:111:TOX:H11	5:B:2006:HOH:O	2.14	0.47
1:A:647:GLN:HE21	1:A:647:GLN:HA	1.80	0.47
1:A:112:HIS:CE1	1:A:141:GLU:O	2.68	0.46
1:A:111:TOX:CH2	1:A:238:TYR:CD1	2.77	0.46
1:A:54:ARG:NE	1:A:199:ASP:OD2	2.42	0.45
1:A:46:GLN:NE2	1:B:298:GLU:O	2.49	0.45
1:B:144:ASN:HA	1:B:146:ASP:OD1	2.16	0.45
1:A:587:ASP:HB3	1:A:590[A]:SER:HB3	1.99	0.45
1:B:661:THR:HA	1:B:725:GLN:NE2	2.33	0.45
1:B:633:VAL:HG22	1:B:719:TYR:CE1	2.52	0.44
1:A:112:HIS:HE1	1:A:141:GLU:O	2.01	0.44
1:B:629:PRO:O	1:B:633:VAL:HG23	2.17	0.44
1:B:469:LYS:HD3	5:B:2334:HOH:O	2.17	0.44
1:B:329:THR:HB	1:B:371:ILE:HG21	2.00	0.43
1:A:587:ASP:HB3	1:A:590[B]:SER:HB3	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:111:TOX:CZ3	1:B:238:TYR:CE1	2.87	0.42
1:B:410:GLU:CD	1:B:410:GLU:H	2.23	0.42
1:A:725:GLN:CG	5:A:1908:HOH:O	2.68	0.42
1:B:517:GLN:NE2	5:B:2326:HOH:O	2.52	0.42
1:A:119:THR:HG23	1:A:593:VAL:HG11	2.02	0.41
1:A:111:TOX:H8	1:A:423:LEU:HD21	2.01	0.41
1:A:512:ASP:OD2	5:A:1795:HOH:O	2.22	0.41
1:A:51:ILE:HD11	1:A:618:VAL:HG12	2.02	0.41
1:A:633:VAL:HG22	1:A:719:TYR:CE1	2.55	0.41
1:B:109:MET:HB2	1:B:145:LEU:HD22	2.03	0.41
1:B:570:VAL:HG11	1:B:733:VAL:HG21	2.02	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	712/748 (95%)	700 (98%)	12 (2%)	0	100	100
1	B	713/748 (95%)	701 (98%)	12 (2%)	0	100	100
All	All	1425/1496 (95%)	1401 (98%)	24 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	550/576 (96%)	542 (98%)	8 (2%)	76	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	551/576 (96%)	544 (99%)	7 (1%)	80	87
All	All	1101/1152 (96%)	1086 (99%)	15 (1%)	78	86

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	64	LYS
1	A	70	GLN
1	A	118	ARG
1	A	610	ARG
1	A	647	GLN
1	A	649	ARG
1	A	656	ARG
1	B	40	ARG
1	B	64	LYS
1	B	118	ARG
1	B	496	LYS
1	B	544	GLN
1	B	573	PRO
1	B	608	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	85	HIS
1	A	247	ASN
1	A	520	GLN
1	A	544	GLN
1	A	647	GLN
1	B	55	HIS
1	B	339	HIS
1	B	647	GLN
1	B	650	HIS
1	B	725	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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	$\# Z  > 2$
1	TOX	A	111	1	16,17,18	14.66	4 (25%)	18,23,25	1.96	4 (22%)
1	TOX	B	111	1	16,17,18	12.28	4 (25%)	18,23,25	2.05	4 (22%)

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
1	TOX	A	111	1	-	0/4/8/10	0/0/2/2
1	TOX	B	111	1	-	0/4/8/10	0/0/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	111	TOX	O1-NE1	55.96	2.64	1.38
1	B	111	TOX	O1-NE1	43.91	2.36	1.38
1	B	111	TOX	O-C	21.11	1.26	1.11
1	A	111	TOX	O-C	16.24	1.22	1.11
1	A	111	TOX	CA-C	4.86	1.57	1.48
1	B	111	TOX	CA-C	4.55	1.57	1.48
1	B	111	TOX	CZ2-CE2	-2.88	1.34	1.41
1	A	111	TOX	CB-CG	-2.14	1.48	1.51

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	111	TOX	CG-CD1-NE1	-6.98	110.21	112.88
1	A	111	TOX	CG-CD1-NE1	-6.57	110.37	112.88
1	B	111	TOX	C-CA-N	-2.98	110.85	113.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	111	TOX	C-CA-N	-2.64	111.19	113.83
1	A	111	TOX	CD2-CE2-NE1	-2.29	107.85	111.27
1	A	111	TOX	CD1-NE1-CE2	2.27	107.81	103.79
1	B	111	TOX	CD2-CE2-NE1	-2.04	108.23	111.27
1	B	111	TOX	CD1-NE1-CE2	2.02	107.36	103.79

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	TRS	A	1001	-	7,7,7	0.71	0	9,9,9	0.95	1 (11%)
4	HEM	A	1500	1	49,50,50	2.55	16 (32%)	46,82,82	1.90	13 (28%)
4	HEM	B	1500	1	49,50,50	2.53	15 (30%)	46,82,82	1.89	6 (13%)
3	TRS	B	2001	-	7,7,7	0.70	0	9,9,9	1.06	1 (11%)

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
3	TRS	A	1001	-	-	0/9/9/9	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	HEM	A	1500	1	-	0/14/114/114	0/0/8/8
4	HEM	B	1500	1	-	0/14/114/114	0/0/8/8
3	TRS	B	2001	-	-	0/9/9/9	0/0/0/0

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1500	HEM	C3D-C4D	-8.37	1.42	1.44
4	A	1500	HEM	C2D-C1D	-6.97	1.42	1.44
4	A	1500	HEM	C3D-C4D	6.27	1.46	1.44
4	A	1500	HEM	C2B-C1B	5.60	1.46	1.44
4	B	1500	HEM	C3B-C2B	-5.42	1.34	1.43
4	A	1500	HEM	C3B-C2B	-4.93	1.35	1.43
4	B	1500	HEM	C3B-CAB	4.93	1.55	1.40
4	B	1500	HEM	C2D-C1D	4.88	1.45	1.44
4	A	1500	HEM	C3B-CAB	4.81	1.55	1.40
4	B	1500	HEM	C3C-C2C	-4.76	1.35	1.43
4	A	1500	HEM	C3C-CAC	4.75	1.55	1.40
4	A	1500	HEM	C3D-C2D	4.68	1.51	1.43
4	B	1500	HEM	C3D-C2D	4.58	1.51	1.43
4	A	1500	HEM	FE-ND	4.18	2.13	1.97
4	B	1500	HEM	C3C-CAC	4.08	1.53	1.40
4	B	1500	HEM	C4A-C3A	3.98	1.45	1.40
4	A	1500	HEM	C3C-C2C	-3.82	1.37	1.43
4	B	1500	HEM	FE-ND	3.65	2.11	1.97
4	A	1500	HEM	FE-NA	3.43	2.07	1.92
4	B	1500	HEM	CMB-C2B	3.11	1.57	1.47
4	B	1500	HEM	FE-NB	2.95	2.08	1.97
4	B	1500	HEM	FE-NC	2.91	2.08	1.97
4	A	1500	HEM	CMB-C2B	2.86	1.56	1.47
4	A	1500	HEM	C4A-C3A	2.71	1.43	1.40
4	A	1500	HEM	FE-NC	2.55	2.07	1.97
4	A	1500	HEM	CMD-C2D	2.42	1.54	1.47
4	B	1500	HEM	CMC-C2C	2.41	1.54	1.47
4	B	1500	HEM	CMD-C2D	2.35	1.54	1.47
4	A	1500	HEM	CMC-C2C	2.12	1.54	1.47
4	B	1500	HEM	CHA-C4D	2.08	1.38	1.35
4	A	1500	HEM	CHA-C4D	2.03	1.38	1.35

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1500	HEM	C3B-C4B-NB	-7.61	108.56	114.00
4	B	1500	HEM	C4D-ND-C1D	6.27	111.58	105.16
4	A	1500	HEM	C3B-C4B-NB	-6.24	109.54	114.00
4	A	1500	HEM	C4D-ND-C1D	5.36	110.65	105.16
4	B	1500	HEM	C2D-C1D-ND	-3.75	108.50	112.93
4	A	1500	HEM	CMA-C3A-C4A	-2.95	124.09	128.62
4	A	1500	HEM	C4C-NC-C1C	2.88	108.53	105.53
4	A	1500	HEM	O1A-CGA-CBA	-2.70	113.75	123.03
4	A	1500	HEM	CAA-CBA-CGA	-2.51	105.40	113.47
4	B	1500	HEM	CMA-C3A-C4A	-2.46	124.84	128.62
4	B	1500	HEM	CHA-C4D-ND	2.41	127.62	124.31
4	A	1500	HEM	C2D-C1D-ND	-2.40	110.10	112.93
4	A	1500	HEM	C1A-C2A-C3A	2.36	109.36	106.92
4	B	1500	HEM	CAA-CBA-CGA	-2.31	106.04	113.47
4	A	1500	HEM	CHD-C4C-NC	2.23	126.67	124.73
3	B	2001	TRS	O1-C1-C	2.22	116.42	111.55
4	A	1500	HEM	CMA-C3A-C2A	2.15	128.99	124.94
4	A	1500	HEM	CAD-C3D-C4D	2.14	128.38	124.53
4	A	1500	HEM	CMC-C2C-C3C	2.13	131.17	126.16
4	A	1500	HEM	O2A-CGA-CBA	2.06	121.49	114.22
3	A	1001	TRS	O3-C3-C	2.01	115.96	111.55

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	714/748 (95%)	-0.39	19 (2%)	52	56	14, 20, 38, 51	0
1	B	714/748 (95%)	-0.53	14 (1%)	62	67	13, 19, 34, 52	1 (0%)
All	All	1428/1496 (95%)	-0.46	33 (2%)	57	63	13, 20, 36, 52	1 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	679	ALA	3.8
1	A	748	ALA	3.6
1	A	541	GLY	3.5
1	A	220	SER	3.4
1	B	35	ASN	3.3
1	A	680	ALA	3.1
1	A	540	ARG	3.1
1	B	680	ALA	3.1
1	A	64	LYS	3.0
1	B	65	ASP	3.0
1	A	222	ASP	3.0
1	B	540	ARG	2.9
1	B	608	LYS	2.8
1	B	610	ARG	2.7
1	A	35	ASN	2.7
1	A	65	ASP	2.7
1	A	215	PRO	2.6
1	B	64	LYS	2.6
1	A	111	TOX	2.4
1	A	221	GLY	2.4
1	A	224	GLN	2.4
1	A	679	ALA	2.4
1	B	40	ARG	2.4
1	B	748	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	44	PRO	2.3
1	A	454	ASP	2.3
1	A	610	ARG	2.2
1	A	608	LYS	2.2
1	B	541	GLY	2.2
1	A	213	GLY	2.2
1	B	45	ASN	2.1
1	A	378	SER	2.1
1	B	222	ASP	2.0

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

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	TOX	A	111	16/17	0.18	2.34	15,17,46,48	0
1	TOX	B	111	16/17	0.14	1.12	15,17,44,44	0

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	TRS	A	1001	8/8	0.13	3.51	29,32,32,33	0
4	HEM	A	1500	43/43	0.14	1.11	11,16,19,21	0
4	HEM	B	1500	43/43	0.12	0.45	11,14,16,18	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	TRS	B	2001	8/8	0.08	-0.29	22,24,24,25	0
2	NA	A	1000	1/1	0.04	-1.60	21,21,21,21	0
2	NA	B	2000	1/1	0.03	-3.80	16,16,16,16	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.