



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2024 – 03:33 am BST

PDB ID : 5NHB  
Title : Crystal structure of xylose isomerase from *Piromyces* E2 in complex with two Fe<sup>2+</sup> ions  
Authors : Rozeboom, H.J.; Janssen, D.B.  
Deposited on : 2017-03-21  
Resolution : 2.40 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 : 2.36.2  
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) : 2.36.2

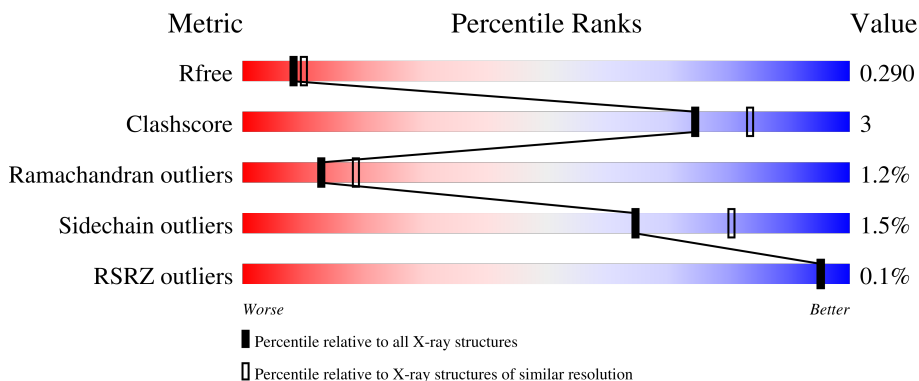
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	437	92% 6% .
1	B	437	92% 6% .
1	C	437	93% 6% .
1	D	437	92% 7% .

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 14366 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 Xylose isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	436	3469	2201	582	667	19	0	0	0
1	B	436	3469	2201	582	667	19	0	0	0
1	C	435	3464	2198	581	666	19	0	0	0
1	D	435	3464	2198	581	666	19	0	0	0

- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

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

- Molecule 3 is SULFATE ION (three-letter code: SO4) (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	C	1	Total O S 5 4 1	0	0

- Molecule 4 is water.

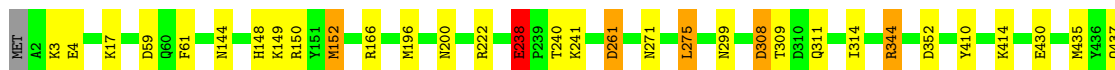
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	122	Total O 122 122	0	0
4	B	131	Total O 131 131	0	0
4	C	117	Total O 117 117	0	0
4	D	107	Total O 107 107	0	0

### 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.

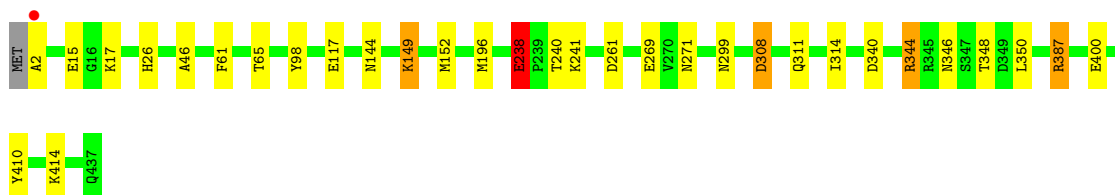
- Molecule 1: Xylose isomerase

Chain A:  92% 6%



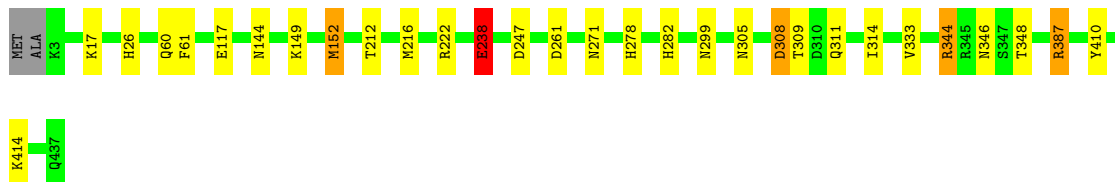
- Molecule 1: Xylose isomerase

Chain B:  92% 6%



- Molecule 1: Xylose isomerase

Chain C:  93% 6%



- Molecule 1: Xylose isomerase

Chain D:  92% 7%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.54Å 79.51Å 92.23Å 115.57° 89.96° 116.69°	Depositor
Resolution (Å)	45.30 – 2.40 45.30 – 2.40	Depositor EDS
% Data completeness (in resolution range)	85.7 (45.30-2.40) 85.7 (45.30-2.40)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.8.0073	Depositor
R, $R_{free}$	0.245 , 0.282 0.254 , 0.290	Depositor DCC
$R_{free}$ test set	2908 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.3	Xtrriage
Anisotropy	0.318	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 6.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.032 for k,h,-h-k-l	Xtrriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	14366	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, FE2

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	0.60	0/3547	0.74	5/4775 (0.1%)
1	B	0.61	0/3547	0.75	6/4775 (0.1%)
1	C	0.60	0/3542	0.72	6/4768 (0.1%)
1	D	0.63	0/3542	0.73	3/4768 (0.1%)
All	All	0.61	0/14178	0.73	20/19086 (0.1%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	275	LEU	CB-CG-CD2	7.01	122.91	111.00
1	A	308	ASP	CB-CG-OD2	6.56	124.20	118.30
1	D	308	ASP	CB-CG-OD2	6.49	124.14	118.30
1	B	149	LYS	N-CA-CB	-6.44	99.01	110.60
1	B	350	LEU	CB-CG-CD2	6.35	121.79	111.00
1	C	308	ASP	CB-CG-OD2	6.22	123.89	118.30
1	B	308	ASP	CB-CG-OD2	5.76	123.48	118.30
1	A	344	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	222	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	C	387	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	C	308	ASP	CB-CG-OD1	-5.46	113.39	118.30
1	B	350	LEU	CA-CB-CG	5.36	127.63	115.30
1	B	344	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	D	308	ASP	CB-CG-OD1	-5.21	113.61	118.30
1	D	222	ARG	NE-CZ-NH1	5.14	122.87	120.30
1	B	387	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	C	222	ARG	NE-CZ-NH1	5.07	122.84	120.30
1	C	344	ARG	NE-CZ-NH1	5.06	122.83	120.30
1	C	387	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	A	222	ARG	NE-CZ-NH2	-5.03	117.78	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	3469	0	3351	35	0
1	B	3469	0	3351	27	0
1	C	3464	0	3346	23	0
1	D	3464	0	3346	28	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	10	0	0	0	0
3	C	5	0	0	0	0
4	A	122	0	0	3	0
4	B	131	0	0	5	0
4	C	117	0	0	4	0
4	D	107	0	0	3	0
All	All	14366	0	13394	87	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 (87) 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:352:ASP:OD1	1:D:425:LYS:NZ	1.99	0.95
1:A:196:MET:CE	1:A:240:THR:HA	2.12	0.79
1:B:196:MET:CE	1:B:240:THR:HA	2.15	0.76
1:A:196:MET:HE3	1:A:240:THR:HA	1.72	0.70
1:B:311:GLN:NE2	4:B:604:HOH:O	2.25	0.69
1:A:430:GLU:OE2	4:A:601:HOH:O	2.09	0.68
1:A:149:LYS:O	1:A:152:MET:HB2	1.96	0.66
1:A:150:ARG:NH1	1:A:166:ARG:NE	2.42	0.66
1:B:15:GLU:OE1	4:B:601:HOH:O	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:311:GLN:NE2	4:C:604:HOH:O	2.29	0.65
1:C:149:LYS:O	1:C:152:MET:HB2	1.96	0.65
1:A:150:ARG:NH1	1:A:166:ARG:CZ	2.60	0.64
1:D:149:LYS:O	1:D:152:MET:HB2	1.96	0.64
1:A:150:ARG:HH12	1:A:166:ARG:NE	1.95	0.63
1:A:150:ARG:HH12	1:A:166:ARG:CZ	2.12	0.62
1:B:348:THR:HG23	1:D:152:MET:HE1	1.82	0.62
1:C:26:HIS:O	4:C:601:HOH:O	2.16	0.60
1:A:241:LYS:HA	1:C:305:ASN:HD21	1.67	0.58
1:A:148:HIS:CD2	1:A:150:ARG:HE	2.21	0.57
1:B:348:THR:CG2	1:D:152:MET:HE1	2.35	0.57
1:B:196:MET:HE1	1:B:240:THR:HA	1.87	0.56
1:A:152:MET:HE1	1:C:348:THR:HG23	1.88	0.56
1:B:241:LYS:HA	1:D:305:ASN:HD21	1.70	0.55
1:D:410:TYR:CZ	1:D:414:LYS:HD2	2.42	0.55
1:C:247:ASP:OD2	1:C:278:HIS:HE1	1.89	0.55
1:B:196:MET:HE3	1:B:240:THR:HA	1.89	0.55
1:A:410:TYR:OH	1:B:117:GLU:OE2	2.12	0.54
1:B:346:ASN:HA	1:D:152:MET:CE	2.37	0.54
1:B:400:GLU:HB2	4:B:670:HOH:O	2.07	0.54
1:A:238:GLU:OE2	1:C:61:PHE:HE1	1.90	0.54
1:A:3:LYS:HG2	1:A:4:GLU:H	1.73	0.53
1:B:410:TYR:CE2	1:B:414:LYS:HE2	2.42	0.53
1:D:247:ASP:OD2	1:D:278:HIS:HE1	1.91	0.53
1:A:152:MET:HE1	1:C:348:THR:CG2	2.39	0.53
1:C:410:TYR:CZ	1:C:414:LYS:HD2	2.44	0.53
1:D:212:THR:O	1:D:216:MET:HG3	2.09	0.52
1:A:410:TYR:CZ	1:A:414:LYS:HD2	2.45	0.52
1:A:59:ASP:HA	1:C:60:GLN:HE22	1.75	0.51
1:A:152:MET:CE	1:C:346:ASN:HA	2.41	0.51
1:D:271:ASN:HD21	1:D:309:THR:H	1.59	0.50
1:B:2:ALA:CB	4:B:729:HOH:O	2.60	0.50
1:D:387:ARG:NH1	4:D:606:HOH:O	2.44	0.49
1:C:271:ASN:HD21	1:C:309:THR:H	1.60	0.49
1:C:387:ARG:NH1	1:D:200:ASN:O	2.45	0.48
1:D:4:GLU:OE1	4:D:601:HOH:O	2.19	0.48
1:B:346:ASN:HA	1:D:152:MET:HE1	1.96	0.47
1:B:65:THR:HB	1:D:152:MET:HE3	1.96	0.47
1:B:348:THR:HG21	1:D:152:MET:CE	2.44	0.47
1:A:150:ARG:HH11	1:A:166:ARG:CG	2.27	0.47
1:A:148:HIS:HD2	1:A:150:ARG:NE	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:238:GLU:OE2	1:D:61:PHE:HE1	1.98	0.46
1:A:144:ASN:OD1	1:A:144:ASN:C	2.53	0.46
1:C:212:THR:HG22	1:C:216:MET:CE	2.45	0.46
1:A:3:LYS:CG	1:A:4:GLU:N	2.78	0.46
1:A:150:ARG:HH11	1:A:166:ARG:HG2	1.79	0.46
1:B:348:THR:HG21	1:D:152:MET:HE3	1.97	0.46
1:D:299:ASN:HB2	1:D:311:GLN:O	2.16	0.46
1:A:299:ASN:HB2	1:A:311:GLN:O	2.16	0.46
1:A:200:ASN:O	1:B:387:ARG:NH1	2.49	0.45
1:A:3:LYS:CG	1:A:4:GLU:H	2.29	0.45
1:A:196:MET:HE1	1:A:240:THR:HA	1.96	0.45
1:C:144:ASN:OD1	1:C:144:ASN:C	2.55	0.45
1:D:421:GLN:NE2	4:D:602:HOH:O	2.37	0.45
1:C:282:HIS:HE1	4:C:603:HOH:O	1.99	0.45
1:D:144:ASN:OD1	1:D:144:ASN:C	2.54	0.45
1:C:299:ASN:HB2	1:C:311:GLN:O	2.16	0.45
1:A:152:MET:CE	1:C:348:THR:HG21	2.47	0.44
1:A:148:HIS:CD2	1:A:150:ARG:NE	2.85	0.44
1:A:61:PHE:HE1	1:C:238:GLU:OE2	2.00	0.44
1:C:333:VAL:N	4:C:610:HOH:O	2.47	0.44
1:A:311:GLN:NE2	4:A:610:HOH:O	2.50	0.44
1:D:99:TYR:OH	1:D:131:GLN:NE2	2.51	0.44
1:B:26:HIS:CE1	4:B:678:HOH:O	2.71	0.43
1:B:299:ASN:HB2	1:B:311:GLN:O	2.17	0.43
1:A:309:THR:CB	1:A:311:GLN:HE21	2.31	0.43
1:B:61:PHE:HE1	1:D:238:GLU:OE2	2.01	0.43
1:B:348:THR:CG2	1:D:152:MET:CE	2.96	0.43
1:B:144:ASN:C	1:B:144:ASN:OD1	2.57	0.43
1:B:269:GLU:OE1	1:B:340:ASP:OD2	2.37	0.43
1:B:346:ASN:HD22	1:D:153:ASN:ND2	2.16	0.43
1:D:238:GLU:HA	1:D:239:PRO:HA	1.85	0.43
1:B:46:ALA:HA	1:B:98:TYR:O	2.18	0.43
1:C:309:THR:CB	1:C:311:GLN:HE21	2.33	0.42
1:D:309:THR:CB	1:D:311:GLN:HE21	2.33	0.41
1:C:117:GLU:OE2	1:D:410:TYR:OH	2.27	0.41
1:A:261:ASP:HB3	4:A:679:HOH:O	2.21	0.41
1:A:152:MET:HE3	1:C:348:THR:HG21	2.03	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	434/437 (99%)	416 (96%)	13 (3%)	5 (1%)	13	19
1	B	434/437 (99%)	418 (96%)	10 (2%)	6 (1%)	11	15
1	C	433/437 (99%)	417 (96%)	11 (2%)	5 (1%)	13	19
1	D	433/437 (99%)	416 (96%)	13 (3%)	4 (1%)	17	25
All	All	1734/1748 (99%)	1667 (96%)	47 (3%)	20 (1%)	13	19

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	MET
1	C	152	MET
1	D	152	MET
1	B	149	LYS
1	B	152	MET
1	A	238	GLU
1	A	261	ASP
1	A	314	ILE
1	B	17	LYS
1	B	238	GLU
1	C	238	GLU
1	C	314	ILE
1	D	238	GLU
1	D	261	ASP
1	B	261	ASP
1	B	314	ILE
1	C	17	LYS
1	C	261	ASP
1	D	314	ILE
1	A	17	LYS

### 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	357/358 (100%)	350 (98%)	7 (2%)	55	74
1	B	357/358 (100%)	353 (99%)	4 (1%)	73	87
1	C	357/358 (100%)	354 (99%)	3 (1%)	81	91
1	D	357/358 (100%)	349 (98%)	8 (2%)	52	71
All	All	1428/1432 (100%)	1406 (98%)	22 (2%)	65	80

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	238	GLU
1	A	271	ASN
1	A	275	LEU
1	A	308	ASP
1	A	344	ARG
1	A	435	MET
1	A	437	GLN
1	B	238	GLU
1	B	271	ASN
1	B	308	ASP
1	B	344	ARG
1	C	238	GLU
1	C	308	ASP
1	C	344	ARG
1	D	109	GLU
1	D	223	SER
1	D	238	GLU
1	D	262	LYS
1	D	308	ASP
1	D	344	ARG
1	D	425	LYS
1	D	435	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	HIS
1	A	311	GLN
1	A	437	GLN
1	B	311	GLN
1	B	421	GLN
1	C	60	GLN
1	C	242	HIS
1	C	258	HIS
1	C	271	ASN
1	C	278	HIS
1	C	282	HIS
1	C	305	ASN
1	C	311	GLN
1	C	321	GLN
1	C	357	HIS
1	D	131	GLN
1	D	153	ASN
1	D	170	GLN
1	D	271	ASN
1	D	278	HIS
1	D	282	HIS
1	D	305	ASN
1	D	311	GLN
1	D	321	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 11 ligands modelled in this entry, 8 are monoatomic - leaving 3 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	A	503	-	4,4,4	0.61	0	6,6,6	0.53	0
3	SO4	A	504	-	4,4,4	0.94	0	6,6,6	1.01	0
3	SO4	C	503	-	4,4,4	0.86	0	6,6,6	0.82	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	436/437 (99%)	-0.62	0 100   100	19, 30, 45, 50	0
1	B	436/437 (99%)	-0.64	1 (0%) 95   94	19, 27, 39, 48	0
1	C	435/437 (99%)	-0.61	0 100   100	19, 31, 45, 50	0
1	D	435/437 (99%)	-0.68	0 100   100	17, 26, 40, 52	0
All	All	1742/1748 (99%)	-0.64	1 (0%) 95   95	17, 28, 43, 52	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	ALA	4.3

### 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
3	SO4	C	503	5/5	0.91	0.28	32,35,41,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SO4	A	504	5/5	0.95	0.22	22,24,26,27	0
3	SO4	A	503	5/5	0.96	0.18	27,30,33,34	0
2	FE2	A	502	1/1	0.98	0.05	21,21,21,21	0
2	FE2	C	501	1/1	0.98	0.04	25,25,25,25	0
2	FE2	D	502	1/1	0.98	0.05	18,18,18,18	0
2	FE2	D	501	1/1	0.99	0.03	19,19,19,19	0
2	FE2	B	501	1/1	0.99	0.02	22,22,22,22	0
2	FE2	B	502	1/1	0.99	0.04	17,17,17,17	0
2	FE2	A	501	1/1	0.99	0.04	27,27,27,27	0
2	FE2	C	502	1/1	0.99	0.03	23,23,23,23	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.