



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 2, 2023 – 08:08 pm GMT

PDB ID : 1UUW
Title : NAPHTHALENE 1,2-DIOXYGENASE WITH NITRIC OXIDE BOUND IN THE ACTIVE SITE.
Authors : Karlsson, A.; Parales, J.V.; Parales, R.E.; Gibson, D.T.; Eklund, H.; Ramaswamy, S.
Deposited on : 2004-01-11
Resolution : 2.30 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

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>.

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
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

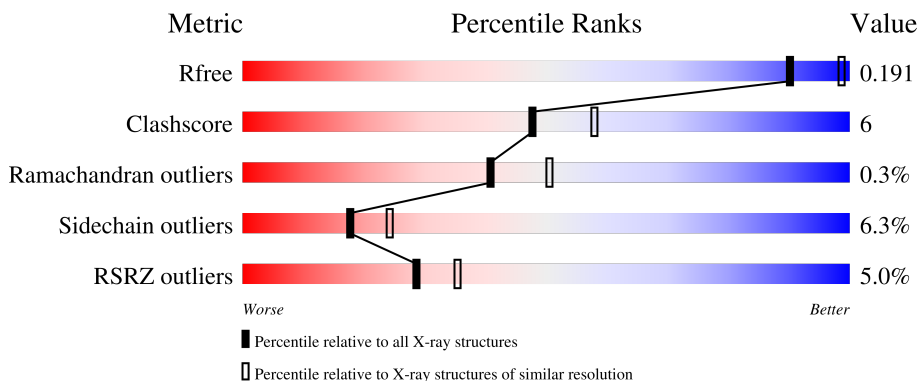
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


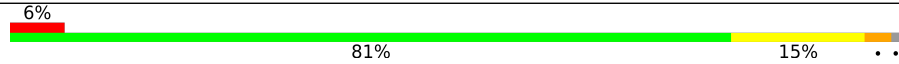
The reported resolution of this entry is 2.30 Å.

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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 ≥ 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	449	
2	B	194	

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	NO	A	1449	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 5453 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.

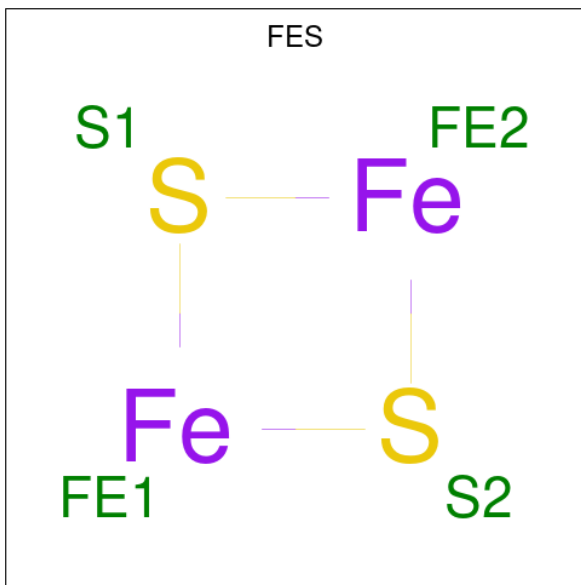
- Molecule 1 is a protein called NAPHTHALENE 1,2-DIOXYGENASE ALPHA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	447	3480	2202	597	665	16	0	0	0

- Molecule 2 is a protein called NAPHTHALENE 1,2-DIOXYGENASE BETA SUBUNIT.

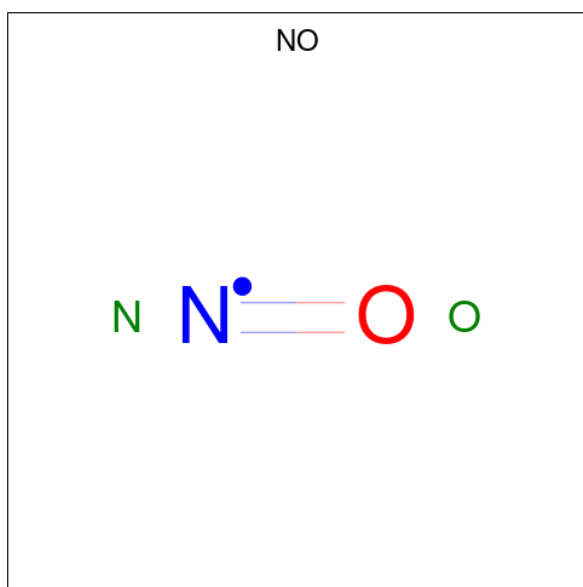
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	193	1608	1007	302	293	6	0	0	0

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
3	A	1	4	2	2	0	0

- Molecule 4 is NITRIC OXIDE (three-letter code: NO) (formula: NO).

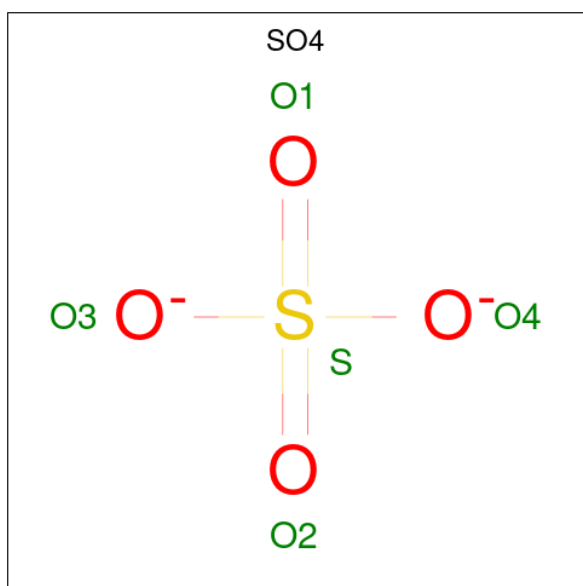


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	N	O		
4	A	1	2	1	1	0	0

- Molecule 5 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Fe		
5	A	1	1	1	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

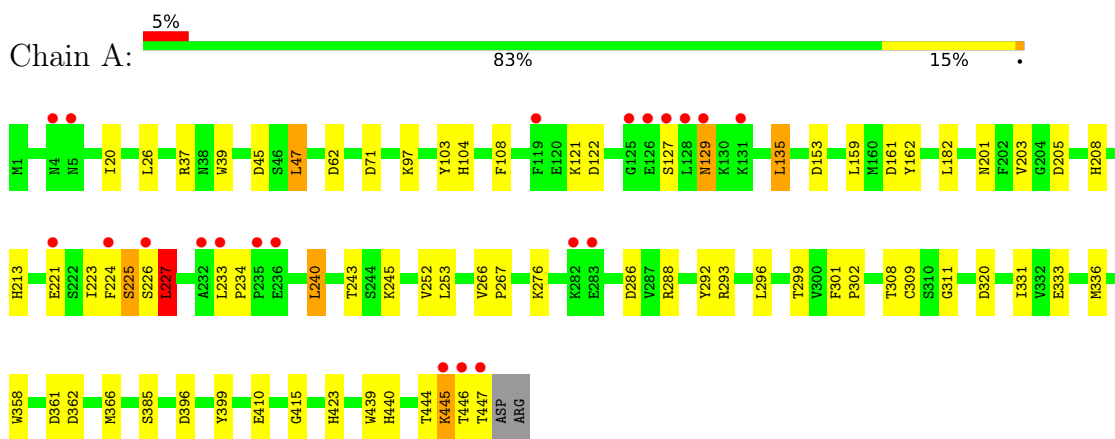
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	238	Total	O	0	0
			238	238		
7	B	110	Total	O	0	0
			110	110		

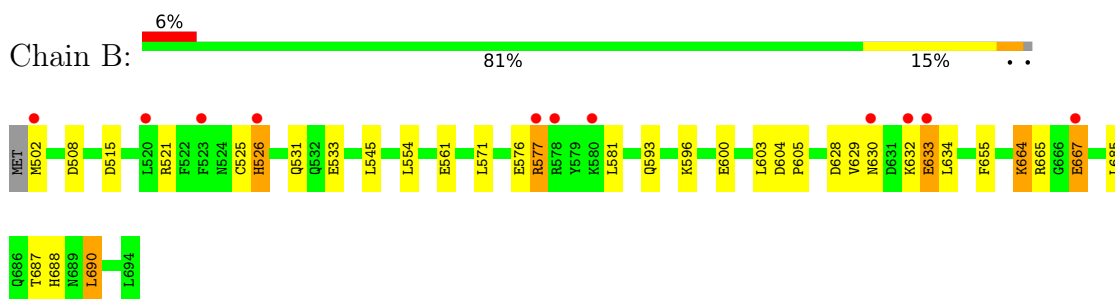
3 Residue-property plots [i](#)

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: NAPHTHALENE 1,2-DIOXYGENASE ALPHA SUBUNIT



- Molecule 2: NAPHTHALENE 1,2-DIOXYGENASE BETA SUBUNIT



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	140.56Å 140.56Å 210.29Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.30 29.23 – 2.30	Depositor EDS
% Data completeness (in resolution range)	91.9 (30.00-2.30) 91.9 (29.23-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.24 (at 2.31Å)	Xtrriage
Refinement program	REFMAC 5.0.36	Depositor
R, R_{free}	0.198 , 0.194 0.191 , 0.191	Depositor DCC
R_{free} test set	1041 reflections (3.17%)	wwPDB-VP
Wilson B-factor (Å ²)	28.1	Xtrriage
Anisotropy	0.015	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5453	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: SO4, NO, FES, FE

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	0.48	0/3572	0.78	11/4839 (0.2%)
2	B	0.49	0/1638	0.84	2/2209 (0.1%)
All	All	0.48	0/5210	0.80	13/7048 (0.2%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	320	ASP	CB-CG-OD2	7.21	124.79	118.30
1	A	153	ASP	CB-CG-OD2	7.00	124.60	118.30
1	A	286	ASP	CB-CG-OD2	6.92	124.52	118.30
1	A	362	ASP	CB-CG-OD2	6.28	123.95	118.30
1	A	71	ASP	CB-CG-OD2	6.00	123.70	118.30
1	A	62	ASP	CB-CG-OD2	5.97	123.67	118.30
1	A	161	ASP	CB-CG-OD2	5.76	123.48	118.30
1	A	361	ASP	CB-CG-OD2	5.68	123.41	118.30
1	A	45	ASP	CB-CG-OD2	5.66	123.39	118.30
2	B	515	ASP	CB-CG-OD2	5.47	123.22	118.30
1	A	205	ASP	CB-CG-OD2	5.43	123.18	118.30
1	A	122	ASP	CB-CG-OD2	5.17	122.96	118.30
2	B	628	ASP	CB-CG-OD2	5.13	122.92	118.30

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	3480	0	3316	42	0
2	B	1608	0	1583	19	0
3	A	4	0	0	1	0
4	A	2	0	0	0	0
5	A	1	0	0	0	0
6	B	10	0	0	1	0
7	A	238	0	0	2	0
7	B	110	0	0	1	0
All	All	5453	0	4899	61	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 (61) 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)
2:B:633:GLU:OE2	2:B:665:ARG:HB2	1.38	1.18
2:B:633:GLU:OE2	2:B:665:ARG:CB	2.24	0.83
2:B:664:LYS:O	2:B:664:LYS:HD3	1.79	0.81
1:A:129:ASN:H	1:A:129:ASN:ND2	1.84	0.76
2:B:526:HIS:CD2	2:B:526:HIS:H	2.05	0.74
1:A:226:SER:O	1:A:227:LEU:HB2	1.91	0.70
1:A:240:LEU:HD13	1:A:252:VAL:HB	1.75	0.69
2:B:633:GLU:CD	2:B:665:ARG:HB2	2.13	0.68
2:B:667:GLU:OE2	2:B:667:GLU:HA	1.94	0.67
1:A:226:SER:O	1:A:227:LEU:CB	2.44	0.66
1:A:47:LEU:HD22	1:A:182:LEU:HD23	1.79	0.65
1:A:311:GLY:HA2	1:A:331:ILE:HG13	1.84	0.59
2:B:664:LYS:NZ	6:B:1696:SO4:O4	2.35	0.59
1:A:446:THR:HG22	1:A:446:THR:O	2.05	0.57
1:A:129:ASN:H	1:A:129:ASN:HD22	1.50	0.56
1:A:224:PHE:O	1:A:226:SER:O	2.26	0.54
1:A:47:LEU:CD2	1:A:182:LEU:HD23	2.38	0.54
1:A:245:LYS:HB2	1:A:439:TRP:CE2	2.43	0.53
2:B:576:GLU:HA	2:B:577:ARG:NH1	2.25	0.52
2:B:664:LYS:HD3	2:B:664:LYS:C	2.32	0.50
1:A:252:VAL:HG22	1:A:296:LEU:CD2	2.43	0.48
1:A:129:ASN:HD22	1:A:129:ASN:N	2.12	0.48
2:B:533:GLU:OE1	7:B:2017:HOH:O	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:685:LEU:CD1	2:B:690:LEU:HB2	2.45	0.47
2:B:633:GLU:OE2	2:B:665:ARG:O	2.32	0.47
1:A:104:HIS:HB2	3:A:1448:FES:S1	2.55	0.47
1:A:108:PHE:CD2	1:A:135:LEU:HD13	2.50	0.46
1:A:288:ARG:HG3	7:A:2154:HOH:O	2.16	0.46
1:A:223:ILE:HG12	7:A:2143:HOH:O	2.16	0.46
1:A:252:VAL:HG22	1:A:296:LEU:HD22	1.97	0.45
2:B:687:THR:O	2:B:688:HIS:HB2	2.16	0.45
1:A:240:LEU:HD13	1:A:240:LEU:N	2.31	0.45
1:A:233:LEU:HD12	1:A:234:PRO:HD2	1.99	0.45
1:A:266:VAL:HB	1:A:267:PRO:HD3	1.99	0.44
2:B:604:ASP:HA	2:B:605:PRO:HD2	1.87	0.44
1:A:37:ARG:HD2	1:A:423:HIS:ND1	2.32	0.44
1:A:20:ILE:HA	1:A:26:LEU:HD23	2.01	0.43
1:A:444:THR:O	1:A:445:LYS:C	2.57	0.43
1:A:396:ASP:HB3	1:A:399:TYR:O	2.19	0.43
2:B:629:VAL:HG12	2:B:630:ASN:OD1	2.19	0.43
1:A:203:VAL:HG23	1:A:299:THR:HB	2.01	0.42
1:A:108:PHE:CE2	1:A:135:LEU:HD13	2.55	0.42
1:A:308:THR:O	1:A:309:CYS:HB2	2.19	0.42
1:A:301:PHE:HA	1:A:302:PRO:HA	1.73	0.42
1:A:39:TRP:HD1	1:A:162:TYR:CD1	2.37	0.42
2:B:526:HIS:CD2	2:B:526:HIS:N	2.79	0.41
2:B:596:LYS:NZ	2:B:600:GLU:OE1	2.52	0.41
1:A:446:THR:O	1:A:446:THR:CG2	2.66	0.41
2:B:664:LYS:C	2:B:664:LYS:CD	2.89	0.41
1:A:333:GLU:HB2	1:A:336:MET:HG3	2.02	0.41
1:A:129:ASN:ND2	1:A:129:ASN:N	2.55	0.41
1:A:213:HIS:HE1	1:A:358:TRP:O	2.04	0.41
1:A:240:LEU:N	1:A:240:LEU:CD1	2.84	0.41
1:A:243:THR:OG1	1:A:415:GLY:HA3	2.21	0.41
1:A:439:TRP:CG	1:A:440:HIS:N	2.88	0.41
2:B:655:PHE:CD2	2:B:690:LEU:HD13	2.56	0.41
1:A:385:SER:HA	1:A:410:GLU:OE1	2.21	0.41
1:A:201:ASN:HD21	1:A:208:HIS:CE1	2.39	0.40
1:A:159:LEU:O	1:A:162:TYR:HB3	2.22	0.40
1:A:276:LYS:HD2	1:A:292:TYR:CZ	2.56	0.40
1:A:221:GLU:HA	1:A:225:SER:OG	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	445/449 (99%)	429 (96%)	14 (3%)	2 (0%)	34	42
2	B	191/194 (98%)	184 (96%)	7 (4%)	0	100	100
All	All	636/643 (99%)	613 (96%)	21 (3%)	2 (0%)	41	50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	227	LEU
1	A	445	LYS

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	367/369 (100%)	353 (96%)	14 (4%)	33	47
2	B	172/173 (99%)	152 (88%)	20 (12%)	5	6
All	All	539/542 (99%)	505 (94%)	34 (6%)	18	24

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	LEU
1	A	97	LYS
1	A	103	TYR
1	A	121	LYS

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Mol	Chain	Res	Type
1	A	127	SER
1	A	129	ASN
1	A	135	LEU
1	A	225	SER
1	A	227	LEU
1	A	240	LEU
1	A	253	LEU
1	A	293	ARG
1	A	366	MET
1	A	447	THR
2	B	502	MET
2	B	508	ASP
2	B	521	ARG
2	B	525	CYS
2	B	526	HIS
2	B	531	GLN
2	B	545	LEU
2	B	554	LEU
2	B	561	GLU
2	B	571	LEU
2	B	577	ARG
2	B	581	LEU
2	B	593	GLN
2	B	603	LEU
2	B	632	LYS
2	B	633	GLU
2	B	634	LEU
2	B	664	LYS
2	B	667	GLU
2	B	690	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	GLN
1	A	129	ASN
1	A	201	ASN
2	B	514	HIS
2	B	526	HIS
2	B	531	GLN
2	B	532	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 5 ligands modelled in this entry, 1 is 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	FES	A	1448	1	0,4,4	-	-	-		
6	SO4	B	1695	-	4,4,4	0.16	0	6,6,6	0.07	0
4	NO	A	1449	-	0,1,1	-	-	-		
6	SO4	B	1696	-	4,4,4	0.13	0	6,6,6	0.14	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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FES	A	1448	1	-	-	0/1/1/1

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1448	FES	1	0
6	B	1696	SO4	1	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, 95th 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 ²)	Q<0.9
1	A	447/449 (99%)	-0.18	21 (4%) 31 38	17, 26, 56, 65	0
2	B	193/194 (99%)	-0.08	11 (5%) 23 30	17, 26, 53, 63	0
All	All	640/643 (99%)	-0.15	32 (5%) 28 35	17, 26, 55, 65	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	447	THR	10.6
1	A	236	GLU	5.3
2	B	502	MET	5.2
1	A	446	THR	4.6
2	B	577	ARG	4.3
2	B	523	PHE	4.2
1	A	129	ASN	4.1
1	A	119	PHE	4.1
1	A	226	SER	3.7
1	A	127	SER	3.4
2	B	633	GLU	3.3
1	A	125	GLY	3.3
1	A	232	ALA	3.3
1	A	282	LYS	3.2
1	A	128	LEU	3.0
2	B	630	ASN	3.0
1	A	221	GLU	2.8
2	B	526	HIS	2.8
1	A	445	LYS	2.7
1	A	4	ASN	2.7
1	A	233	LEU	2.6
2	B	667	GLU	2.6
2	B	578	ARG	2.5
1	A	5	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	224	PHE	2.4
1	A	126	GLU	2.3
2	B	632	LYS	2.3
1	A	283	GLU	2.2
2	B	520	LEU	2.2
1	A	235	PRO	2.2
2	B	580	LYS	2.0
1	A	131	LYS	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 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, 95th 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 ²)	Q<0.9
4	NO	A	1449	2/2	0.71	0.44	54,54,54,54	0
6	SO4	B	1695	5/5	0.93	0.23	62,64,64,64	0
6	SO4	B	1696	5/5	0.96	0.18	55,56,56,57	0
3	FES	A	1448	4/4	0.99	0.06	22,23,26,27	0
5	FE	A	1450	1/1	1.00	0.03	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.