Full wwPDB X-ray Structure Validation Report (i)

Dec 4, 2023 – 03:49 pm GMT

PDB ID	:	1O7M
Title	:	NAPHTHALENE 1,2-DIOXYGENASE, BINARY COMPLEX WITH DIOXYGEN
Authors	:	Karlsson, A.; Parales, J.V.; Parales, R.E.; Gibson, D.T.; Eklund, H.; Ramaswamy, S.
Deposited on	:	2002-11-11
Resolution	:	1.75 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 (i) 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 (i)) were used in the production of this report:

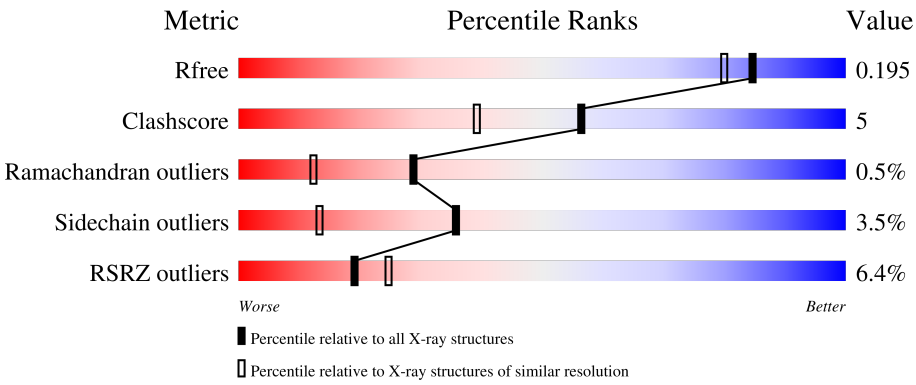
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 <=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	6% 87% 11% •
2	B	194	8% 89% 9% •••

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
3	EDO	B	1696	-	-	X	-

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 5694 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.

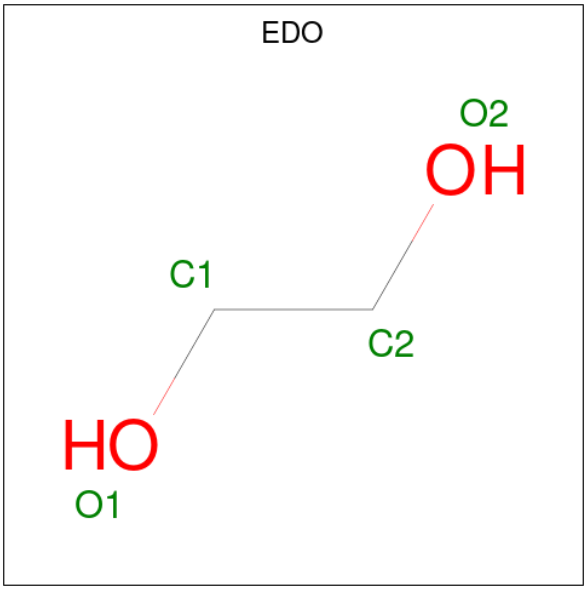
- Molecule 1 is a protein called NAPHTHALENE 1,2-DIOXYGENASE ALPHA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	448	3487	2205	599	666	17	0	2	1

- 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 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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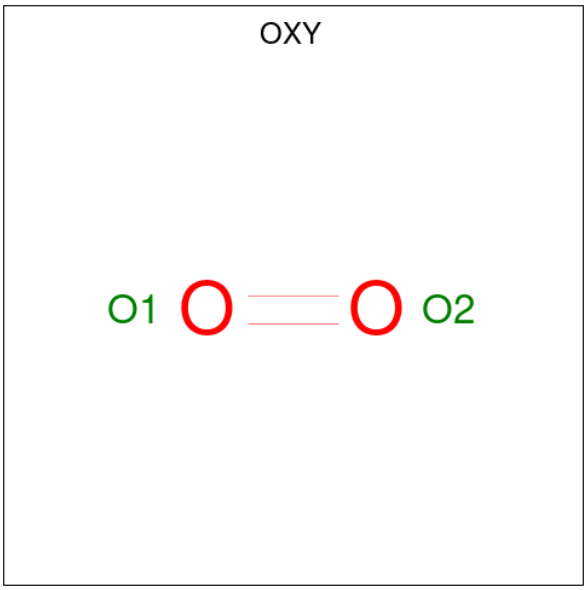
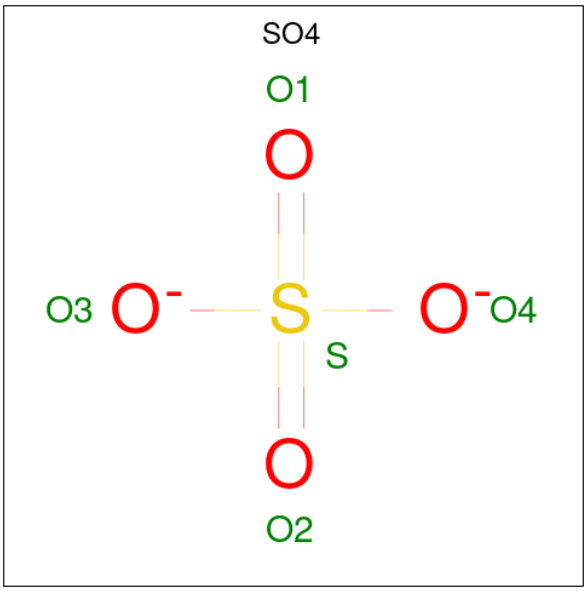
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	4	2	2	0	0
			Total	C	O		
3	B	1	4	2	2	0	0
			Total	C	O		
3	B	1	4	2	2	0	0
			Total	C	O		
3	B	1	4	2	2	0	0

- Molecule 4 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O_2).



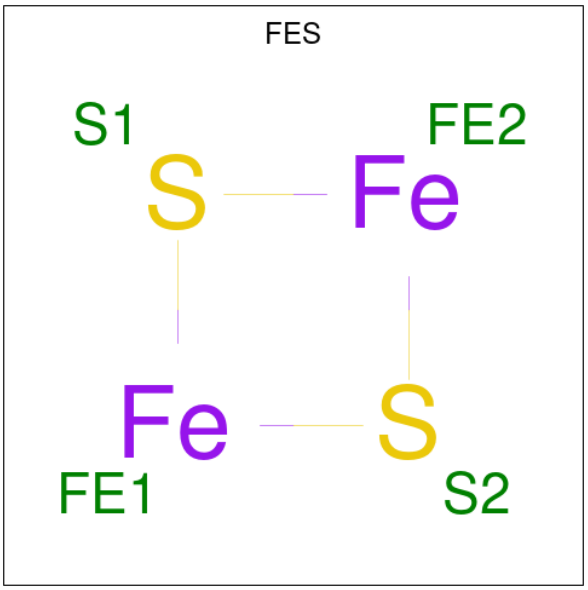
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	1	2	2	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 6 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



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

- Molecule 7 is FE (III) ION (three-letter code: FE) (formula: Fe).

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

- Molecule 8 is water.

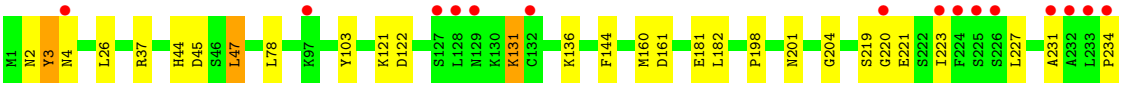
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	A	401	401	401	0	0
			Total	O		
8	B	152	152	152	0	0

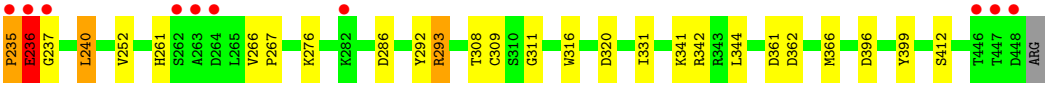
3 Residue-property plots (i)

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

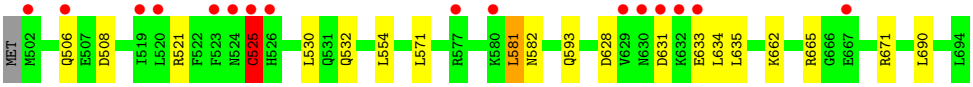
Chain A:





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

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	140.28Å 140.28Å 208.75Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.75 32.06 – 1.56	Depositor EDS
% Data completeness (in resolution range)	98.9 (30.00-1.75) 84.8 (32.06-1.56)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.53 (at 1.57Å)	Xtriage
Refinement program	REFMAC 5.0.36	Depositor
R, R_{free}	0.178 , 0.187 0.190 , 0.195	Depositor DCC
R_{free} test set	927 reflections (0.99%)	wwPDB-VP
Wilson B-factor (Å^2)	16.5	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 46.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5694	wwPDB-VP
Average B, all atoms (Å^2)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: FES, EDO, OXY, FE, 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	0.66	0/3589	0.86	10/4862 (0.2%)
2	B	0.61	0/1638	0.89	1/2209 (0.0%)
All	All	0.64	0/5227	0.87	11/7071 (0.2%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	286	ASP	CB-CG-OD2	7.18	124.76	118.30
1	A	320	ASP	CB-CG-OD2	6.65	124.28	118.30
1	A	293	ARG	NE-CZ-NH1	-6.50	117.05	120.30
1	A	37	ARG	NE-CZ-NH2	6.46	123.53	120.30
1	A	361	ASP	CB-CG-OD2	6.19	123.87	118.30
1	A	161	ASP	CB-CG-OD2	5.72	123.44	118.30
1	A	45	ASP	CB-CG-OD2	5.59	123.33	118.30
2	B	628	ASP	CB-CG-OD2	5.55	123.30	118.30
1	A	3	TYR	CB-CG-CD2	5.36	124.22	121.00
1	A	122	ASP	CB-CG-OD2	5.15	122.93	118.30
1	A	362	ASP	CB-CG-OD2	5.12	122.91	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	3487	0	3323	36	0
2	B	1608	0	1583	14	0
3	A	12	0	18	0	0
3	B	12	0	18	4	0
4	A	2	0	0	0	0
5	A	5	0	0	1	0
5	B	10	0	0	0	0
6	A	4	0	0	0	0
7	A	1	0	0	0	0
8	A	401	0	0	3	0
8	B	152	0	0	0	0
All	All	5694	0	4942	50	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 5.

All (50) 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:240:LEU:HD13	1:A:252:VAL:HB	1.40	1.04
1:A:131:LYS:HD3	5:A:1452:SO4:O2	1.68	0.93
1:A:342:ARG:HH11	1:A:342:ARG:HG2	1.34	0.89
1:A:227:LEU:CD2	1:A:234:PRO:HD3	2.14	0.77
1:A:342:ARG:HG2	1:A:342:ARG:NH1	1.99	0.77
2:B:581:LEU:HD13	3:B:1696:EDO:H21	1.66	0.75
1:A:47:LEU:HD22	1:A:182:LEU:HD23	1.80	0.62
1:A:240:LEU:CD1	1:A:252:VAL:HB	2.24	0.62
2:B:525:CYS:SG	2:B:525:CYS:O	2.59	0.61
2:B:581:LEU:HD13	3:B:1696:EDO:C2	2.31	0.60
1:A:227:LEU:HD21	1:A:234:PRO:HD3	1.84	0.59
1:A:235:PRO:HB2	1:A:236:GLU:OE1	2.03	0.59
1:A:227:LEU:HD22	1:A:234:PRO:HD3	1.84	0.59
1:A:220:GLY:HA3	8:A:2228:HOH:O	2.03	0.59
2:B:581:LEU:CD1	3:B:1696:EDO:H21	2.33	0.58
2:B:634:LEU:HD11	2:B:662:LYS:HB3	1.87	0.56
2:B:631:ASP:OD1	2:B:633:GLU:HB2	2.07	0.55
1:A:366[B]:MET:HE1	8:A:2219:HOH:O	2.06	0.55
1:A:240:LEU:HD13	1:A:252:VAL:CB	2.28	0.54
1:A:220:GLY:O	1:A:221:GLU:HB2	2.09	0.53
1:A:266:VAL:HB	1:A:267:PRO:HD3	1.91	0.52
1:A:3:TYR:CE2	1:A:26:LEU:HD13	2.45	0.52
1:A:144:PHE:HD1	1:A:160:MET:HE1	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:665:ARG:HG2	2:B:671:ARG:HG2	1.92	0.50
1:A:231:ALA:HB2	8:A:2230:HOH:O	2.12	0.50
1:A:144:PHE:CD1	1:A:160:MET:HE1	2.48	0.49
1:A:204:GLY:HA3	1:A:412:SER:HB2	1.96	0.48
1:A:2:ASN:OD1	1:A:4:ASN:HB2	2.12	0.48
2:B:665:ARG:HA	2:B:671:ARG:HA	1.96	0.47
1:A:236:GLU:HB2	1:A:237:GLY:H	1.36	0.47
1:A:44:HIS:HB2	1:A:182:LEU:HD22	1.97	0.47
2:B:581:LEU:HD13	3:B:1696:EDO:C1	2.45	0.46
2:B:634:LEU:HD21	2:B:662:LYS:HD3	1.96	0.46
1:A:198:PRO:HB2	1:A:316:TRP:CE2	2.52	0.45
1:A:234:PRO:HA	1:A:235:PRO:HD2	1.79	0.45
1:A:160:MET:HE3	1:A:160:MET:HB2	1.65	0.45
1:A:261:HIS:NE2	1:A:344:LEU:HD11	2.32	0.45
1:A:181:GLU:OE1	1:A:341:LYS:NZ	2.40	0.44
2:B:581:LEU:O	2:B:582:ASN:C	2.56	0.44
2:B:530:LEU:HD21	2:B:635:LEU:HD13	2.01	0.43
1:A:311:GLY:HA2	1:A:331:ILE:HG13	2.00	0.43
1:A:236:GLU:H	1:A:236:GLU:HG3	1.46	0.43
1:A:78:LEU:HD22	1:A:136:LYS:HD3	2.02	0.42
1:A:276:LYS:HD2	1:A:292:TYR:CZ	2.55	0.41
1:A:261:HIS:NE2	1:A:344:LEU:CD1	2.84	0.41
1:A:396:ASP:HB3	1:A:399:TYR:O	2.21	0.40
1:A:308:THR:O	1:A:309:CYS:HB2	2.20	0.40
2:B:631:ASP:C	2:B:633:GLU:H	2.23	0.40
1:A:223:ILE:HD12	1:A:223:ILE:HA	1.89	0.40
2:B:631:ASP:C	2:B:633:GLU:N	2.75	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	448/449 (100%)	431 (96%)	15 (3%)	2 (0%)	34	17
2	B	191/194 (98%)	184 (96%)	6 (3%)	1 (0%)	29	12
All	All	639/643 (99%)	615 (96%)	21 (3%)	3 (0%)	29	12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	236	GLU
2	B	525	CYS
1	A	235	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	369/369 (100%)	360 (98%)	9 (2%)	49	26
2	B	172/173 (99%)	162 (94%)	10 (6%)	20	4
All	All	541/542 (100%)	522 (96%)	19 (4%)	36	13

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	LEU
1	A	103	TYR
1	A	121	LYS
1	A	131	LYS
1	A	201	ASN
1	A	219	SER
1	A	236	GLU
1	A	240	LEU
1	A	293	ARG
2	B	506	GLN
2	B	508	ASP
2	B	521	ARG
2	B	525	CYS

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Mol	Chain	Res	Type
2	B	532	GLN
2	B	554	LEU
2	B	571	LEU
2	B	581	LEU
2	B	593	GLN
2	B	690	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	GLN
1	A	201	ASN
2	B	506	GLN
2	B	514	HIS
2	B	526	HIS

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 12 ligands modelled in this entry, 1 is monoatomic - leaving 11 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	EDO	A	1449	-	3,3,3	0.49	0	2,2,2	0.70	0
3	EDO	B	1695	-	3,3,3	0.34	0	2,2,2	0.40	0
3	EDO	A	1450	-	3,3,3	0.40	0	2,2,2	0.45	0
5	SO4	A	1452	-	4,4,4	0.11	0	6,6,6	0.39	0
3	EDO	B	1696	-	3,3,3	0.40	0	2,2,2	0.36	0
5	SO4	B	1698	-	4,4,4	0.14	0	6,6,6	0.29	0
4	OXY	A	1451	7	1,1,1	1.19	0	-		
3	EDO	B	1699	-	3,3,3	0.50	0	2,2,2	0.39	0
5	SO4	B	1697	-	4,4,4	0.18	0	6,6,6	0.10	0
3	EDO	A	1448	-	3,3,3	0.48	0	2,2,2	0.24	0
6	FES	A	1453	1	0,4,4	-	-	-		

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	EDO	A	1449	-	-	0/1/1/1	-
3	EDO	B	1695	-	-	0/1/1/1	-
3	EDO	A	1450	-	-	0/1/1/1	-
3	EDO	B	1696	-	-	1/1/1/1	-
3	EDO	B	1699	-	-	0/1/1/1	-
3	EDO	A	1448	-	-	0/1/1/1	-
6	FES	A	1453	1	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1696	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1452	SO4	1	0
3	B	1696	EDO	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 (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, 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	448/449 (99%)	0.03	25 (5%)	24	30	7, 13, 30, 44	0
2	B	193/194 (99%)	0.28	16 (8%)	11	14	8, 14, 38, 46	0
All	All	641/643 (99%)	0.11	41 (6%)	19	25	7, 13, 33, 46	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	502	MET	10.6
2	B	525	CYS	10.5
1	A	448	ASP	9.9
1	A	447	THR	9.8
1	A	446	THR	7.7
2	B	667	GLU	6.5
1	A	224	PHE	6.1
2	B	577	ARG	5.9
1	A	232	ALA	5.8
2	B	523	PHE	5.5
1	A	234	PRO	5.5
1	A	235	PRO	5.5
2	B	629	VAL	5.4
1	A	233	LEU	5.2
1	A	236	GLU	5.1
2	B	630	ASN	4.7
2	B	633	GLU	4.4
1	A	264	ASP	4.0
1	A	226	SER	3.9
2	B	519	ILE	3.8
2	B	524	ASN	3.6
1	A	127	SER	3.3
1	A	282	LYS	3.2
1	A	129	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	132	CYS	3.1
1	A	262	SER	3.0
2	B	520	LEU	3.0
2	B	631	ASP	3.0
2	B	526	HIS	2.9
1	A	128	LEU	2.9
1	A	231	ALA	2.8
1	A	263	ALA	2.7
1	A	223	ILE	2.7
2	B	580	LYS	2.6
1	A	4	ASN	2.5
1	A	237	GLY	2.2
2	B	632	LYS	2.2
1	A	225	SER	2.2
2	B	506	GLN	2.1
1	A	97	LYS	2.1
1	A	220	GLY	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
3	EDO	A	1450	4/4	0.43	0.22	41,41,41,43	0
5	SO4	B	1697	5/5	0.50	0.33	45,47,49,50	0
5	SO4	A	1452	5/5	0.78	0.30	51,52,53,53	0
4	OXY	A	1451	2/2	0.83	0.10	36,36,36,38	0
3	EDO	A	1449	4/4	0.92	0.13	15,21,22,22	0
3	EDO	B	1699	4/4	0.95	0.15	12,22,23,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	EDO	B	1696	4/4	0.95	0.16	24,26,27,28	0
5	SO4	B	1698	5/5	0.96	0.14	36,36,37,37	0
3	EDO	A	1448	4/4	0.98	0.08	8,10,11,11	0
3	EDO	B	1695	4/4	0.98	0.09	11,12,13,13	0
6	FES	A	1453	4/4	0.99	0.05	11,12,13,14	0
7	FE	A	1454	1/1	0.99	0.07	22,22,22,22	0

6.5 Other polymers (i)

There are no such residues in this entry.