



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 07:54 pm GMT

PDB ID : 1O7P
Title : NAPHTHALENE 1,2-DIOXYGENASE, PRODUCT COMPLEX
Authors : Karlsson, A.; Parales, J.V.; Parales, R.E.; Gibson, D.T.; Eklund, H.; Ramaswamy, S.
Deposited on : 2002-11-11
Resolution : 1.95 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

<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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

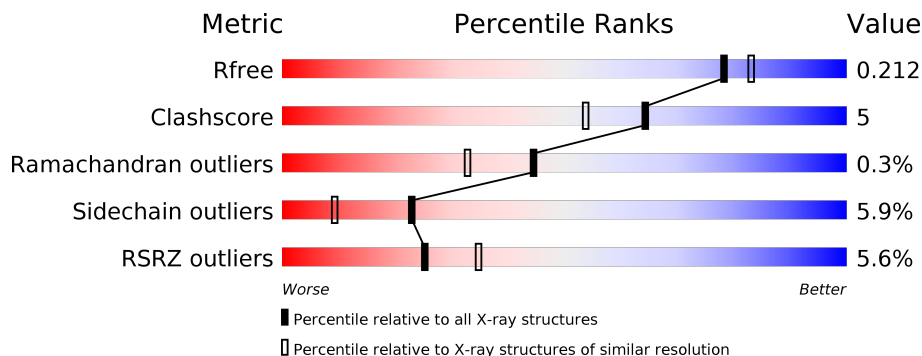
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	100719	2004 (1.96-1.96)
Clashscore	112137	2136 (1.96-1.96)
Ramachandran outliers	110173	2117 (1.96-1.96)
Sidechain outliers	110143	2117 (1.96-1.96)
RSRZ outliers	101464	2018 (1.96-1.96)

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 ≥ 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	449	<div> <div>6%</div> <div> <div></div> <div>88%</div> <div>10%</div> <div>.</div> </div> </div>
2	B	194	<div> <div>4%</div> <div> <div></div> <div>81%</div> <div>14%</div> <div>..</div> </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
3	EDO	B	1697	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 5568 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
1	A	447	Total	C	N	O	S	0	0	0
			3480	2202	597	665	16			

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

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

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



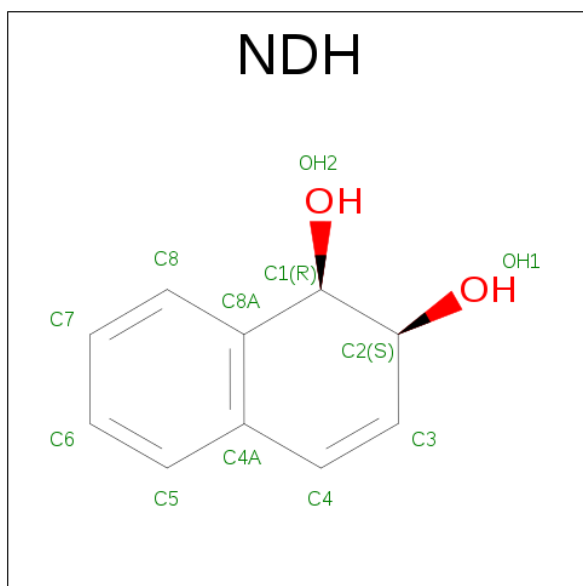
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 4 is (1R, 2S)-CIS 1,2 DIHYDROXY-1,2-DIHYDRONAPHTHALENE (three-letter code: NDH) (formula: C₁₀H₁₀O₂).



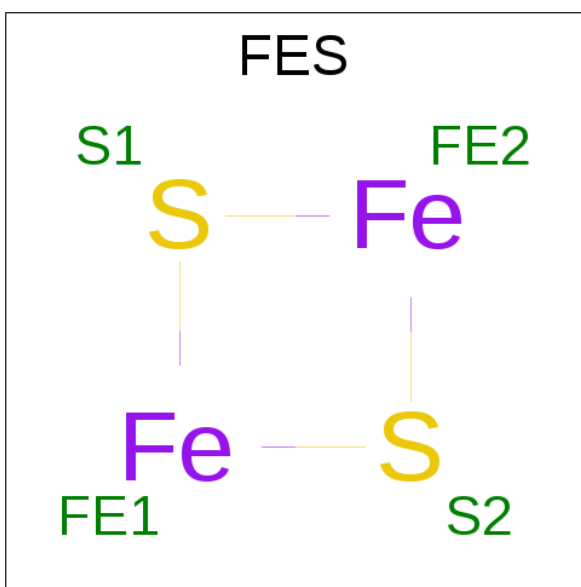
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	10	2		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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



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

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

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

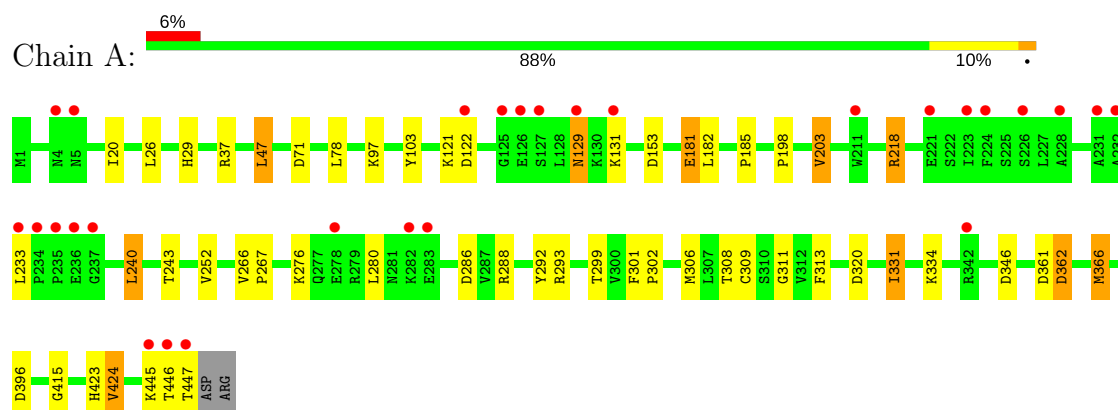
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	291	Total 291	O 291	0	0
8	B	133	Total 133	O 133	0	0

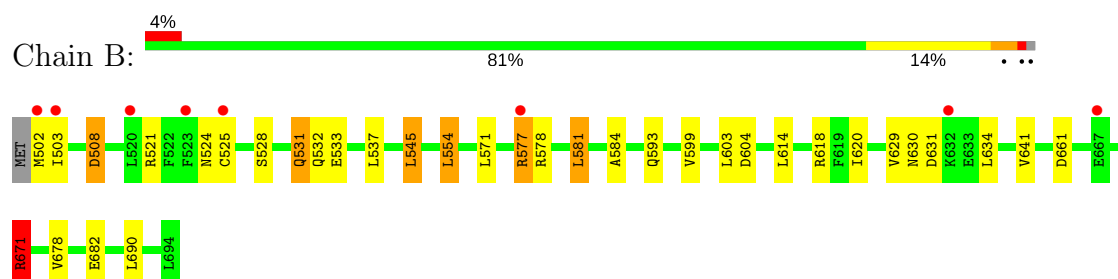
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 ($\text{RSRZ} > 2$). 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	139.67Å 139.67Å 208.44Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.95 14.96 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.5 (30.00-1.95) 99.8 (14.96-1.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.95 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.0.36	Depositor
R, R_{free}	0.184 , 0.219 0.187 , 0.212	Depositor DCC
R_{free} test set	2882 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5568	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% 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: NDH, SO4, FE, FES, EDO

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	0.80	0/3572	0.92	13/4839 (0.3%)
2	B	0.77	1/1638 (0.1%)	0.99	7/2209 (0.3%)
All	All	0.79	1/5210 (0.0%)	0.94	20/7048 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	682	GLU	CD-OE2	-5.14	1.20	1.25

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	671	ARG	NE-CZ-NH2	-7.45	116.58	120.30
1	A	153	ASP	CB-CG-OD2	6.85	124.47	118.30
1	A	361	ASP	CB-CG-OD2	6.85	124.47	118.30
2	B	508	ASP	CB-CG-OD2	5.88	123.59	118.30
1	A	346	ASP	CB-CG-OD1	5.72	123.45	118.30
2	B	631	ASP	CB-CG-OD2	5.63	123.37	118.30
1	A	362	ASP	CB-CG-OD2	5.58	123.32	118.30
1	A	320	ASP	CB-CG-OD2	5.55	123.29	118.30
1	A	286	ASP	CB-CG-OD2	5.50	123.25	118.30
1	A	71	ASP	CB-CG-OD2	5.47	123.22	118.30
1	A	122	ASP	CB-CG-OD2	5.30	123.07	118.30
2	B	614	LEU	CB-CG-CD1	5.23	119.89	111.00
1	A	218	ARG	NE-CZ-NH2	5.20	122.90	120.30
1	A	47	LEU	CB-CG-CD1	5.19	119.83	111.00
1	A	424	VAL	CG1-CB-CG2	-5.19	102.60	110.90
2	B	661	ASP	CB-CG-OD1	5.15	122.94	118.30
2	B	671	ARG	NE-CZ-NH1	5.08	122.84	120.30
2	B	503	ILE	CB-CA-C	-5.04	101.52	111.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	396	ASP	CB-CG-OD2	5.03	122.83	118.30
1	A	182	LEU	CA-CB-CG	5.02	126.85	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	34	0
2	B	1608	0	1583	15	0
3	A	8	0	12	0	0
3	B	16	0	24	3	0
4	A	12	0	9	0	0
5	A	5	0	0	0	0
5	B	10	0	0	0	0
6	A	4	0	0	0	0
7	A	1	0	0	0	0
8	A	291	0	0	1	0
8	B	133	0	0	1	0
All	All	5568	0	4944	48	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 (48) 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	1.48	0.93
1:A:306:MET:HE2	1:A:313:PHE:CE1	2.16	0.80
1:A:129:ASN:ND2	1:A:129:ASN:H	1.87	0.72
3:B:1696:EDO:H22	8:B:2131:HOH:O	1.94	0.66
1:A:306:MET:HE2	1:A:313:PHE:HE1	1.63	0.64
1:A:198:PRO:HB3	1:A:366:MET:HE3	1.80	0.62
2:B:533:GLU:OE2	2:B:671:ARG:HD2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:LEU:CD1	1:A:252:VAL:HB	2.26	0.62
1:A:362:ASP:O	1:A:366:MET:HG2	2.00	0.62
1:A:198:PRO:HA	1:A:366:MET:HE1	1.81	0.62
1:A:203:VAL:HG23	1:A:299:THR:HB	1.82	0.61
2:B:577:ARG:NH2	2:B:578:ARG:HH21	1.99	0.61
2:B:629:VAL:HG12	2:B:630:ASN:OD1	2.00	0.61
1:A:308:THR:O	1:A:309:CYS:HB2	2.02	0.59
1:A:306:MET:CE	1:A:313:PHE:CE1	2.85	0.59
1:A:306:MET:CE	1:A:313:PHE:HE1	2.16	0.58
1:A:311:GLY:HA2	1:A:331:ILE:HG13	1.88	0.55
1:A:266:VAL:HB	1:A:267:PRO:HD3	1.88	0.55
1:A:29:HIS:HD2	1:A:424:VAL:HG13	1.72	0.54
2:B:554:LEU:HD22	2:B:599:VAL:HG21	1.88	0.54
2:B:577:ARG:NH2	2:B:578:ARG:NH2	2.56	0.54
1:A:181:GLU:HG2	1:A:334:LYS:HG2	1.91	0.53
2:B:678:VAL:HA	3:B:1697:EDO:H21	1.90	0.52
2:B:581:LEU:HD13	3:B:1698:EDO:H21	1.93	0.51
1:A:306:MET:HE2	1:A:313:PHE:CD1	2.47	0.50
2:B:531:GLN:NE2	2:B:532:GLN:OE1	2.45	0.49
1:A:198:PRO:HA	1:A:366:MET:CE	2.42	0.49
1:A:446:THR:HG22	1:A:446:THR:O	2.13	0.49
1:A:240:LEU:N	1:A:240:LEU:HD13	2.27	0.48
1:A:218:ARG:HD2	2:B:604:ASP:OD1	2.15	0.47
1:A:20:ILE:HA	1:A:26:LEU:HD23	1.97	0.46
2:B:577:ARG:HH21	2:B:578:ARG:NE	2.15	0.45
1:A:203:VAL:CG2	1:A:299:THR:HB	2.48	0.43
1:A:243:THR:OG1	1:A:415:GLY:HA3	2.18	0.43
1:A:240:LEU:N	1:A:240:LEU:CD1	2.81	0.43
1:A:331:ILE:HD13	1:A:331:ILE:HG21	1.78	0.43
1:A:37:ARG:HD2	1:A:423:HIS:ND1	2.34	0.42
2:B:545:LEU:HA	2:B:545:LEU:HD12	1.90	0.42
1:A:29:HIS:CD2	1:A:424:VAL:HG13	2.52	0.41
2:B:620:ILE:HD13	2:B:641:VAL:HG23	2.02	0.41
1:A:280:LEU:HA	1:A:280:LEU:HD23	1.88	0.41
1:A:276:LYS:HD2	1:A:292:TYR:OH	2.20	0.41
1:A:185:PRO:HD2	2:B:584:ALA:O	2.21	0.41
2:B:545:LEU:HB3	2:B:618:ARG:CZ	2.51	0.41
2:B:641:VAL:HG13	2:B:641:VAL:O	2.20	0.41
1:A:301:PHE:HA	1:A:302:PRO:HA	1.78	0.41
1:A:129:ASN:HD22	1:A:129:ASN:H	1.63	0.40
1:A:288:ARG:HG3	8:A:2189:HOH:O	2.22	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%)	15 (3%)	1 (0%)	51	41
2	B	191/194 (98%)	185 (97%)	5 (3%)	1 (0%)	32	19
All	All	636/643 (99%)	614 (96%)	20 (3%)	2 (0%)	44	33

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	445	LYS
2	B	524	ASN

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%)	352 (96%)	15 (4%)	35	21
2	B	172/173 (99%)	155 (90%)	17 (10%)	9	2
All	All	539/542 (99%)	507 (94%)	32 (6%)	23	9

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	LEU

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Mol	Chain	Res	Type
1	A	78	LEU
1	A	97	LYS
1	A	103	TYR
1	A	121	LYS
1	A	129	ASN
1	A	131	LYS
1	A	181	GLU
1	A	203	VAL
1	A	233	LEU
1	A	240	LEU
1	A	293	ARG
1	A	331	ILE
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	528	SER
2	B	531	GLN
2	B	537	LEU
2	B	545	LEU
2	B	554	LEU
2	B	571	LEU
2	B	577	ARG
2	B	581	LEU
2	B	593	GLN
2	B	603	LEU
2	B	634	LEU
2	B	671	ARG
2	B	690	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	GLN
1	A	129	ASN
2	B	514	HIS
2	B	531	GLN

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 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	1448	-	3,3,3	0.43	0	2,2,2	0.26	0
3	EDO	A	1449	-	3,3,3	0.48	0	2,2,2	0.11	0
4	NDH	A	1450	7	13,13,13	1.96	4 (30%)	18,18,18	3.19	6 (33%)
5	SO4	A	1451	-	4,4,4	0.20	0	6,6,6	0.47	0
6	FES	A	1452	1	0,4,4	0.00	-	0,4,4	0.00	-
3	EDO	B	1695	-	3,3,3	0.44	0	2,2,2	0.33	0
3	EDO	B	1696	-	3,3,3	0.45	0	2,2,2	0.53	0
3	EDO	B	1697	-	3,3,3	0.28	0	2,2,2	0.67	0
3	EDO	B	1698	-	3,3,3	0.27	0	2,2,2	0.35	0
5	SO4	B	1699	-	4,4,4	0.25	0	6,6,6	0.15	0
5	SO4	B	1700	-	4,4,4	0.12	0	6,6,6	0.66	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
3	EDO	A	1448	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1449	-	-	0/1/1/1	0/0/0/0
4	NDH	A	1450	7	-	0/0/13/13	0/2/2/2
5	SO4	A	1451	-	-	0/0/0/0	0/0/0/0
6	FES	A	1452	1	-	0/0/4/4	0/1/1/1
3	EDO	B	1695	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1696	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1697	-	-	0/1/1/1	0/0/0/0
3	EDO	B	1698	-	-	0/1/1/1	0/0/0/0
5	SO4	B	1699	-	-	0/0/0/0	0/0/0/0
5	SO4	B	1700	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1450	NDH	OH2-C1	2.32	1.47	1.42
4	A	1450	NDH	C4-C3	2.48	1.37	1.33
4	A	1450	NDH	C1-C2	2.65	1.56	1.51
4	A	1450	NDH	C4A-C4	4.60	1.54	1.44

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1450	NDH	OH2-C1-C2	-3.99	103.28	110.94
4	A	1450	NDH	OH1-C2-C1	-3.36	105.24	111.07
4	A	1450	NDH	C4A-C8A-C1	-2.06	116.05	118.31
4	A	1450	NDH	C8-C8A-C4A	2.45	121.70	119.43
4	A	1450	NDH	C8A-C1-C2	6.33	119.90	111.27
4	A	1450	NDH	OH2-C1-C8A	9.88	130.40	110.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1696	EDO	1	0
3	B	1697	EDO	1	0
3	B	1698	EDO	1	0

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, 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%)	0.07	28 (6%) 21 30	21, 30, 52, 70	0
2	B	193/194 (99%)	0.18	8 (4%) 38 48	21, 29, 55, 65	0
All	All	640/643 (99%)	0.11	36 (5%) 25 35	21, 30, 54, 70	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	447	THR	15.4
1	A	236	GLU	8.5
1	A	233	LEU	7.8
2	B	523	PHE	7.5
1	A	446	THR	6.9
2	B	525	CYS	6.4
2	B	577	ARG	6.4
2	B	502	MET	5.2
1	A	235	PRO	4.9
2	B	667	GLU	4.8
1	A	232	ALA	4.2
1	A	282	LYS	3.7
1	A	237	GLY	3.7
1	A	226	SER	3.5
1	A	125	GLY	3.1
1	A	223	ILE	3.0
1	A	224	PHE	3.0
1	A	445	LYS	2.9
1	A	228	ALA	2.8
1	A	127	SER	2.8
1	A	129	ASN	2.7
1	A	283	GLU	2.6
1	A	131	LYS	2.5
1	A	221	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	5	ASN	2.5
1	A	122	ASP	2.4
1	A	234	PRO	2.4
1	A	342	ARG	2.4
1	A	4	ASN	2.3
2	B	632	LYS	2.3
1	A	231	ALA	2.3
1	A	126	GLU	2.3
2	B	503	ILE	2.2
1	A	278	GLU	2.1
1	A	211	TRP	2.1
2	B	520	LEU	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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	EDO	B	1697	4/4	0.96	0.13	2.05	28,37,39,44	0
3	EDO	A	1449	4/4	0.96	0.11	1.45	27,34,36,36	0
3	EDO	A	1448	4/4	0.98	0.09	1.33	23,24,29,30	0
4	NDH	A	1450	12/12	0.82	0.17	1.24	45,46,52,53	0
3	EDO	B	1695	4/4	0.94	0.11	1.07	33,34,35,37	0
3	EDO	B	1698	4/4	0.98	0.17	0.58	42,42,43,44	0
5	SO4	B	1700	5/5	0.97	0.09	-0.78	55,57,57,59	0
6	FES	A	1452	4/4	1.00	0.04	-2.94	24,26,26,28	0
3	EDO	B	1696	4/4	0.80	0.12	-	49,52,53,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	SO4	A	1451	5/5	0.93	0.28	-	71,73,74,74	0
7	FE	A	1453	1/1	0.99	0.06	-	37,37,37,37	0
5	SO4	B	1699	5/5	0.88	0.27	-	62,64,65,65	0

6.5 Other polymers [i](#)

There are no such residues in this entry.