



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 10:25 am GMT

PDB ID : 3O5A
Title : Crystal Structure of partially reduced Periplasmic Nitrate Reductase from Cupriavidus necator using Ionic Liquids
Authors : Coelho, C.; Trincao, J.; Romao, M.J.
Deposited on : 2010-07-28
Resolution : 1.72 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

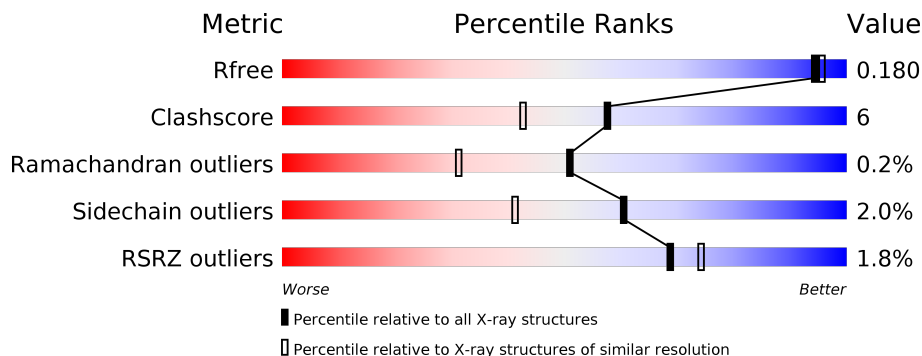
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.72 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	4385 (1.74-1.70)
Clashscore	112137	4841 (1.74-1.70)
Ramachandran outliers	110173	4771 (1.74-1.70)
Sidechain outliers	110143	4771 (1.74-1.70)
RSRZ outliers	101464	4426 (1.74-1.70)

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	802	<div> <div>85%</div> <div>14% ..</div> </div>
2	B	135	<div> <div>10%</div> <div>64%</div> <div>16% •</div> <div>20%</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
6	FMT	A	803	-	-	-	X
6	FMT	A	805	-	-	-	X
6	FMT	A	806	-	-	X	X
6	FMT	A	807	-	-	X	X
6	FMT	A	814	-	-	-	X
6	FMT	B	136	-	-	-	X
6	FMT	B	137	-	-	-	X
6	FMT	B	138	-	-	-	X
6	FMT	B	139	-	-	X	X

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 8171 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.

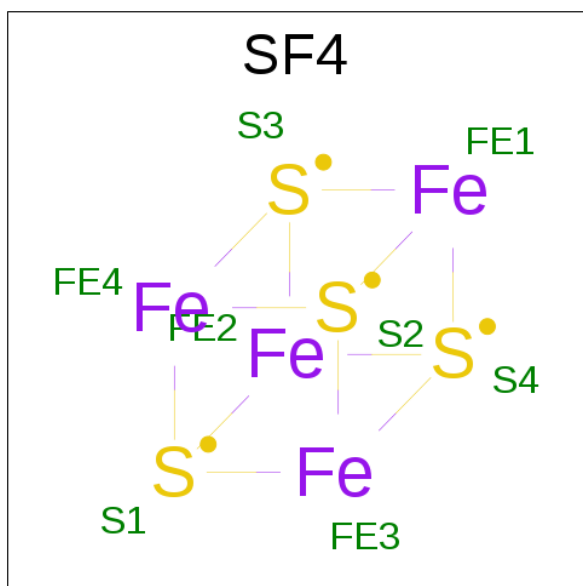
- Molecule 1 is a protein called Periplasmic nitrate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	792	6302	4027	1106	1135	34	0	3	0

- Molecule 2 is a protein called Diheme cytochrome c napB.

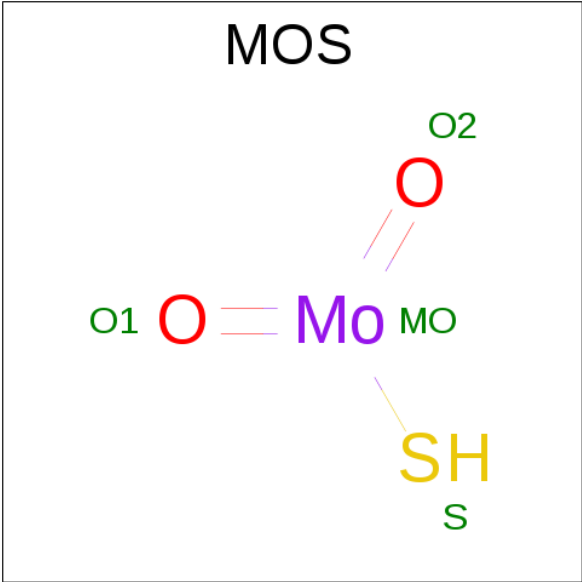
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	108	834	524	150	152	8	0	0	0

- Molecule 3 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



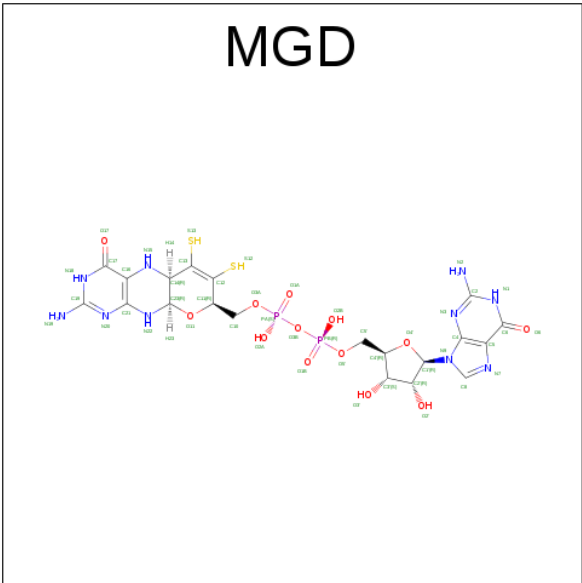
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
3	A	1	8	4	4	0	0

- Molecule 4 is DIOXOTHIO MOLYBDENUM(VI) ION (three-letter code: MOS) (formula: HMoO₂S).



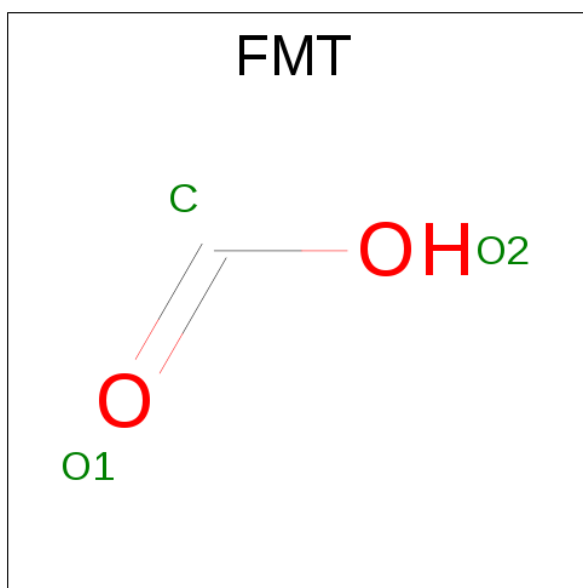
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Mo	S	0	0
			2	1	1		

- Molecule 5 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (three-letter code: MGD) (formula: C₂₀H₂₆N₁₀O₁₃P₂S₂).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
5	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		

- Molecule 6 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



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

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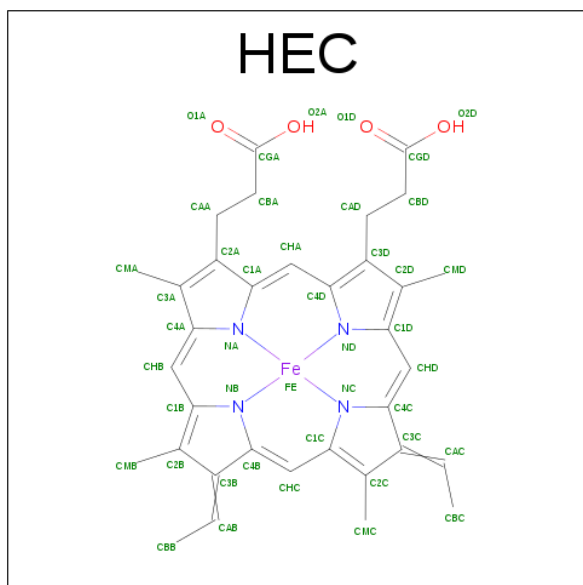
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			3	1	2		
6	B	1	Total	C	O	0	0
			3	1	2		
6	B	1	Total	C	O	0	0
			3	1	2		
6	B	1	Total	C	O	0	0
			3	1	2		
6	B	1	Total	C	O	0	0
			3	1	2		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 8 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



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

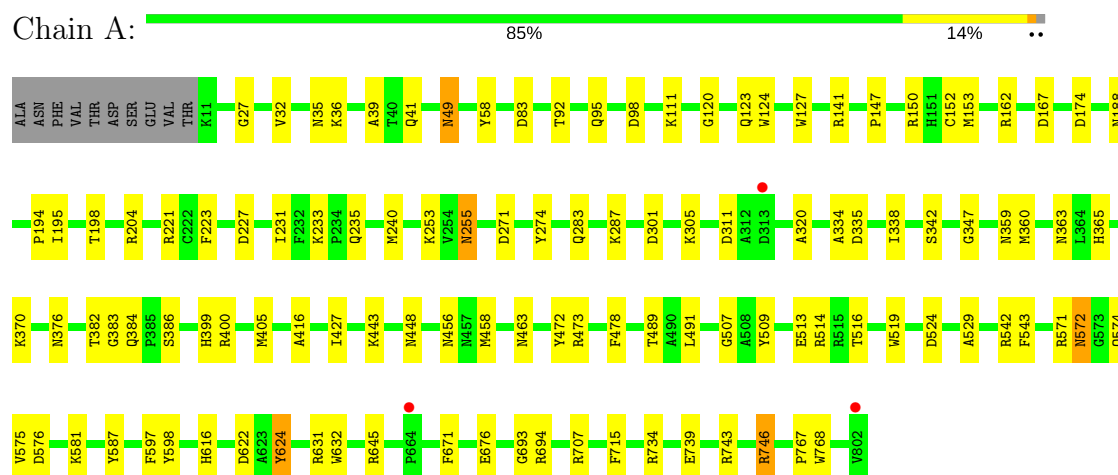
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	701	Total 701	O 701	0	0
9	B	86	Total 86	O 86	0	0

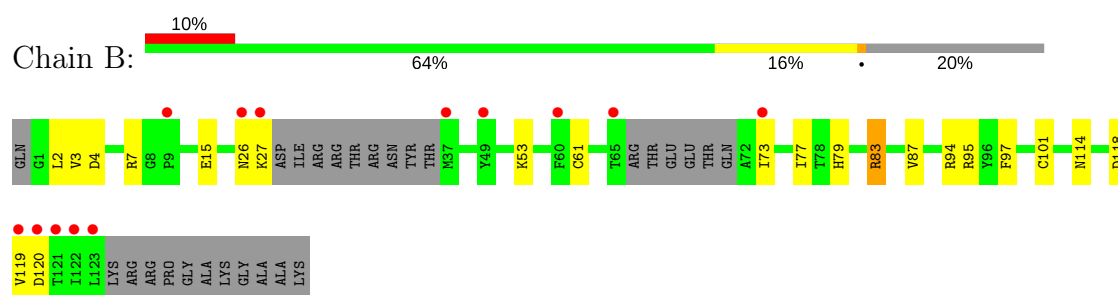
3 Residue-property plots [i](#)

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 ($RSRZ > 2$). 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: Periplasmic nitrate reductase



• Molecule 2: Diheme cytochrome c napB



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	119.40Å 71.41Å 128.41Å 90.00° 121.04° 90.00°	Depositor
Resolution (Å)	27.63 – 1.72 27.63 – 1.72	Depositor EDS
% Data completeness (in resolution range)	99.6 (27.63-1.72) 99.6 (27.63-1.72)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.90 (at 1.72Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.143 , 0.181 0.142 , 0.180	Depositor DCC
R_{free} test set	4889 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	10.1	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 51.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8171	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MGD, MOS, SF4, CL, HEC, OCS, FMT

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	1.29	9/6474 (0.1%)	1.13	26/8780 (0.3%)
2	B	1.19	4/854 (0.5%)	1.11	4/1165 (0.3%)
All	All	1.28	13/7328 (0.2%)	1.12	30/9945 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	83	ARG	CZ-NH1	8.05	1.43	1.33
1	A	472	TYR	CD2-CE2	5.98	1.48	1.39
2	B	15	GLU	CB-CG	-5.83	1.41	1.52
2	B	83	ARG	CZ-NH2	5.78	1.40	1.33
2	B	97	PHE	CE1-CZ	5.62	1.48	1.37

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	240	MET	CG-SD-CE	-11.04	82.54	100.20
1	A	301	ASP	CB-CG-OD1	-9.30	109.93	118.30
1	A	141	ARG	NE-CZ-NH2	-9.20	115.70	120.30
1	A	311	ASP	CB-CG-OD2	8.74	126.17	118.30
1	A	571	ARG	NE-CZ-NH1	-8.69	115.95	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	376	ASN	Peptide
1	A	632	TRP	Peptide

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	6302	0	6168	60	0
2	B	834	0	795	21	0
3	A	8	0	0	0	0
4	A	2	0	0	0	0
5	A	94	0	44	4	0
6	A	39	0	13	8	0
6	B	18	0	6	7	0
7	A	1	0	0	0	0
8	B	86	0	62	8	0
9	A	701	0	0	2	0
9	B	86	0	0	5	0
All	All	8171	0	7088	79	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.

The worst 5 of 79 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:73:ILE:HG22	8:B:1128:HEC:O2D	1.49	1.11
2:B:61:CYS:SG	8:B:1128:HEC:HAC	1.95	1.05
1:A:35:ASN:HD21	1:A:524:ASP:H	1.07	1.02
2:B:101:CYS:SG	8:B:1129:HEC:HAC	2.04	0.94
1:A:162:ARG:HE	1:A:359:ASN:HD21	1.15	0.91

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	792/802 (99%)	766 (97%)	25 (3%)	1 (0%)	55	35
2	B	102/135 (76%)	98 (96%)	3 (3%)	1 (1%)	18	4
All	All	894/937 (95%)	864 (97%)	28 (3%)	2 (0%)	51	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	120	ASP
1	A	147	PRO

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	654/664 (98%)	639 (98%)	15 (2%)	56	35
2	B	90/118 (76%)	90 (100%)	0	100	100
All	All	744/782 (95%)	729 (98%)	15 (2%)	60	41

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	235	GLN
1	A	255	ASN
1	A	581	LYS
1	A	194	PRO

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Mol	Chain	Res	Type
1	A	572	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	363	ASN
1	A	365	HIS
1	A	535	GLN
1	A	350	GLN
1	A	359	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	OCS	A	784	1	8,8,9	1.59	2 (25%)	7,11,13	1.38	1 (14%)

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	OCS	A	784	1	-	1/4/7/9	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	784	OCS	OD3-SG	-2.82	1.36	1.45
1	A	784	OCS	OD1-SG	-2.05	1.39	1.45

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	784	OCS	OD2-SG-CB	-2.52	102.93	106.01

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	784	OCS	SG-CB-CA-N

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 1 is monoatomic - leaving 25 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	SF4	A	1801	1	0,12,12	0.00	-	0,24,24	0.00	-
4	MOS	A	1802	1,5	0,1,3	0.00	-	0,0,3	0.00	-
5	MGD	A	1803	4	41,52,52	1.49	6 (14%)	37,81,81	2.61	13 (35%)
5	MGD	A	1804	4	41,52,52	1.26	4 (9%)	37,81,81	2.57	15 (40%)
6	FMT	A	803	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	804	-	0,2,2	0.00	-	0,1,1	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	FMT	A	805	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	806	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	807	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	808	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	809	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	810	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	811	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	812	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	813	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	814	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	815	-	0,2,2	0.00	-	0,1,1	0.00	-
8	HEC	B	1128	2	28,50,50	2.10	8 (28%)	16,82,82	2.61	5 (31%)
8	HEC	B	1129	2	28,50,50	2.23	8 (28%)	16,82,82	1.95	5 (31%)
6	FMT	B	135	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	B	136	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	B	137	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	B	138	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	B	139	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	B	140	-	0,2,2	0.00	-	0,1,1	0.00	-

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	SF4	A	1801	1	-	0/0/48/48	0/6/5/5
4	MOS	A	1802	1,5	-	0/0/0/0	0/0/0/0
5	MGD	A	1803	4	-	0/18/66/66	0/6/6/6
5	MGD	A	1804	4	-	0/18/66/66	0/6/6/6
6	FMT	A	803	-	-	0/0/0/0	0/0/0/0
6	FMT	A	804	-	-	0/0/0/0	0/0/0/0
6	FMT	A	805	-	-	0/0/0/0	0/0/0/0
6	FMT	A	806	-	-	0/0/0/0	0/0/0/0
6	FMT	A	807	-	-	0/0/0/0	0/0/0/0
6	FMT	A	808	-	-	0/0/0/0	0/0/0/0
6	FMT	A	809	-	-	0/0/0/0	0/0/0/0
6	FMT	A	810	-	-	0/0/0/0	0/0/0/0
6	FMT	A	811	-	-	0/0/0/0	0/0/0/0
6	FMT	A	812	-	-	0/0/0/0	0/0/0/0
6	FMT	A	813	-	-	0/0/0/0	0/0/0/0
6	FMT	A	814	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	FMT	A	815	-	-	0/0/0/0	0/0/0/0
8	HEC	B	1128	2	-	0/6/54/54	0/0/8/8
8	HEC	B	1129	2	-	0/6/54/54	0/0/8/8
6	FMT	B	135	-	-	0/0/0/0	0/0/0/0
6	FMT	B	136	-	-	0/0/0/0	0/0/0/0
6	FMT	B	137	-	-	0/0/0/0	0/0/0/0
6	FMT	B	138	-	-	0/0/0/0	0/0/0/0
6	FMT	B	139	-	-	0/0/0/0	0/0/0/0
6	FMT	B	140	-	-	0/0/0/0	0/0/0/0

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	1129	HEC	C3C-C2C	-6.62	1.33	1.40
8	B	1128	HEC	C3C-C2C	-5.84	1.34	1.40
8	B	1129	HEC	C3B-C2B	-5.40	1.35	1.40
8	B	1128	HEC	C3B-C2B	-3.45	1.37	1.40
8	B	1129	HEC	C1A-NA	-2.93	1.33	1.36

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1804	MGD	C6-C5-C4	-7.46	113.42	120.84
8	B	1128	HEC	CAD-CBD-CGD	-6.23	102.01	112.66
5	A	1803	MGD	C5-C6-N1	-6.20	114.65	123.48
5	A	1803	MGD	C4'-O4'-C1'	-6.12	103.26	109.77
8	B	1128	HEC	CMC-C2C-C1C	-5.83	119.51	128.46

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

13 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1803	MGD	2	0
5	A	1804	MGD	2	0
6	A	804	FMT	1	0
6	A	806	FMT	2	0
6	A	807	FMT	2	0
6	A	809	FMT	1	0
6	A	811	FMT	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	814	FMT	1	0
8	B	1128	HEC	4	0
8	B	1129	HEC	4	0
6	B	137	FMT	1	0
6	B	138	FMT	1	0
6	B	139	FMT	5	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	791/802 (98%)	-0.51	3 (0%) 92 94	4, 9, 19, 31	0
2	B	108/135 (80%)	0.23	13 (12%) 5 6	7, 17, 36, 48	0
All	All	899/937 (95%)	-0.42	16 (1%) 69 74	4, 10, 22, 48	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	121	THR	5.4
2	B	120	ASP	4.1
2	B	122	ILE	4.0
2	B	123	LEU	3.9
2	B	119	VAL	3.7

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	OCS	A	784	9/10	0.98	0.06	-	4,6,14,21	0

6.3 Carbohydrates [i](#)

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, 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
6	FMT	A	807	3/3	0.87	0.23	20.95	35,35,38,40	0
6	FMT	A	806	3/3	0.94	0.21	15.40	27,27,29,30	0
6	FMT	B	137	3/3	0.91	0.26	10.02	32,32,32,34	0
6	FMT	B	136	3/3	0.92	0.17	8.91	32,32,33,36	0
6	FMT	A	814	3/3	0.92	0.20	7.09	23,23,24,26	0
6	FMT	A	805	3/3	0.92	0.12	5.85	20,20,20,21	0
6	FMT	A	803	3/3	0.94	0.08	3.90	17,17,20,22	0
6	FMT	B	139	3/3	0.96	0.24	2.58	29,29,30,31	0
6	FMT	B	138	3/3	0.92	0.20	2.50	28,28,29,32	0
6	FMT	A	804	3/3	0.97	0.10	0.14	23,23,24,29	0
8	HEC	B	1128	43/43	0.97	0.10	0.05	9,16,30,41	0
7	CL	A	816	1/1	0.99	0.07	-0.10	13,13,13,13	0
8	HEC	B	1129	43/43	0.99	0.07	-0.26	3,9,20,26	0
3	SF4	A	1801	8/8	1.00	0.06	-0.39	5,6,7,7	0
5	MGD	A	1804	47/47	0.99	0.05	-1.10	2,5,7,8	0
5	MGD	A	1803	47/47	0.99	0.05	-1.17	2,4,6,6	0
4	MOS	A	1802	2/4	1.00	0.03	-2.27	5,5,5,8	0
6	FMT	A	810	3/3	0.67	0.29	-	42,42,43,44	0
6	FMT	B	140	3/3	0.82	0.17	-	44,44,44,44	0
6	FMT	A	813	3/3	0.82	0.18	-	39,39,42,43	0
6	FMT	A	815	3/3	0.84	0.17	-	42,42,42,43	0
6	FMT	A	811	3/3	0.73	0.21	-	38,38,38,38	0
6	FMT	A	809	3/3	0.53	0.24	-	42,42,43,44	0
6	FMT	A	808	3/3	0.81	0.14	-	36,36,37,37	0
6	FMT	B	135	3/3	0.89	0.18	-	33,33,35,37	0
6	FMT	A	812	3/3	0.81	0.20	-	41,41,42,42	0

6.5 Other polymers ⓘ

There are no such residues in this entry.