



wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 06:23 PM GMT

PDB ID : 1Q16
Title : Crystal structure of Nitrate Reductase A, NarGHI, from Escherichia coli
Authors : Bertero, M.G.; Strynadka, N.C.J.
Deposited on : 2003-07-18
Resolution : 1.90 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

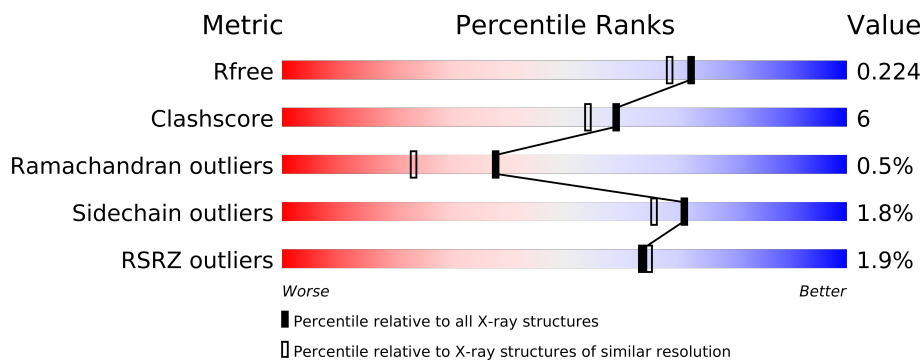
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.90 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}	66092	3684 (1.90-1.90)
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)
RSRZ outliers	66119	3686 (1.90-1.90)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	1247	
2	B	512	
3	C	225	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
10	3PH	B	1310	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 17199 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Respiratory nitrate reductase 1 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1244	Total	C	N	O	S	0	0	0
			9878	6239	1731	1860	48			

- Molecule 2 is a protein called Respiratory nitrate reductase 1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	509	Total	C	N	O	S	0	0	0
			4050	2562	701	755	32			

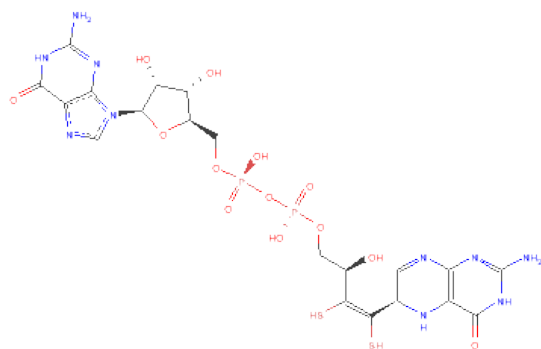
- Molecule 3 is a protein called Respiratory nitrate reductase 1 gamma chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	224	Total	C	N	O	S	0	0	0
			1790	1187	302	287	14			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	FME	MET	MODIFIED RESIDUE	UNP P11350

- Molecule 4 is PHOSPHORIC ACID 4-(2-AMINO-4-OXO-3,4,5,6,-TETRAHYDRO-PTE RIDIN-6-YL)-2-HYDROXY-3,4-DIMERCAPTO-BUT-3-EN-YLESTER GUANYLATE ESTER (three-letter code: MD1) (formula: C₂₀H₂₆N₁₀O₁₃P₂S₂).



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

- Molecule 5 is MOLYBDENUM(VI) ION (three-letter code: 6MO) (formula: Mo).

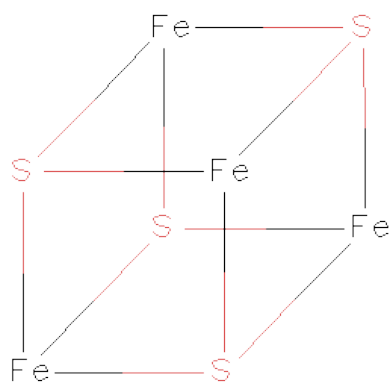
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mo	0	0
			1	1		

- Molecule 6 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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

- Molecule 7 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



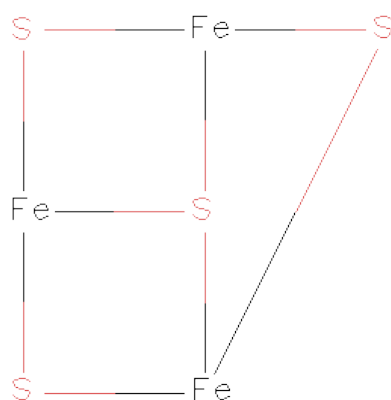
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	Fe	S	0	0
			8	4	4		
7	B	1	Total	Fe	S	0	0
			8	4	4		

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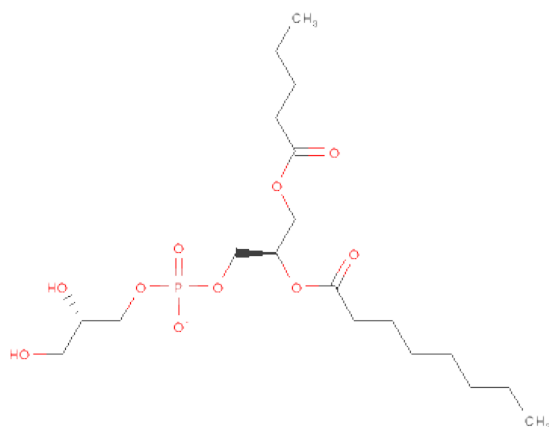
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	Fe	S	0	0
			8	4	4		
7	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 8 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe₃S₄).



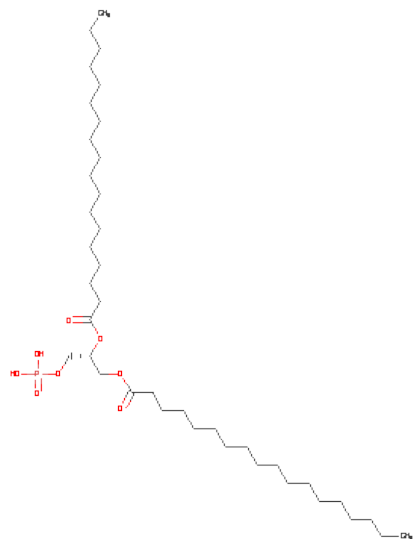
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 9 is (1S)-2-{{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PENTANOYLOXY)METHYL]ETHYLOCTANOATE (three-letter code: AGA) (formula: C₁₉H₃₆O₁₀P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
9	A	1	30	19	10	1	0	0

- Molecule 10 is 1,2-DIACYL-GLYCEROL-3-SN-PHOSPHATE (three-letter code: 3PH) (formula: $C_{39}H_{77}O_8P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
10	B	1	18	9	8	1	0	0

- Molecule 11 is water.

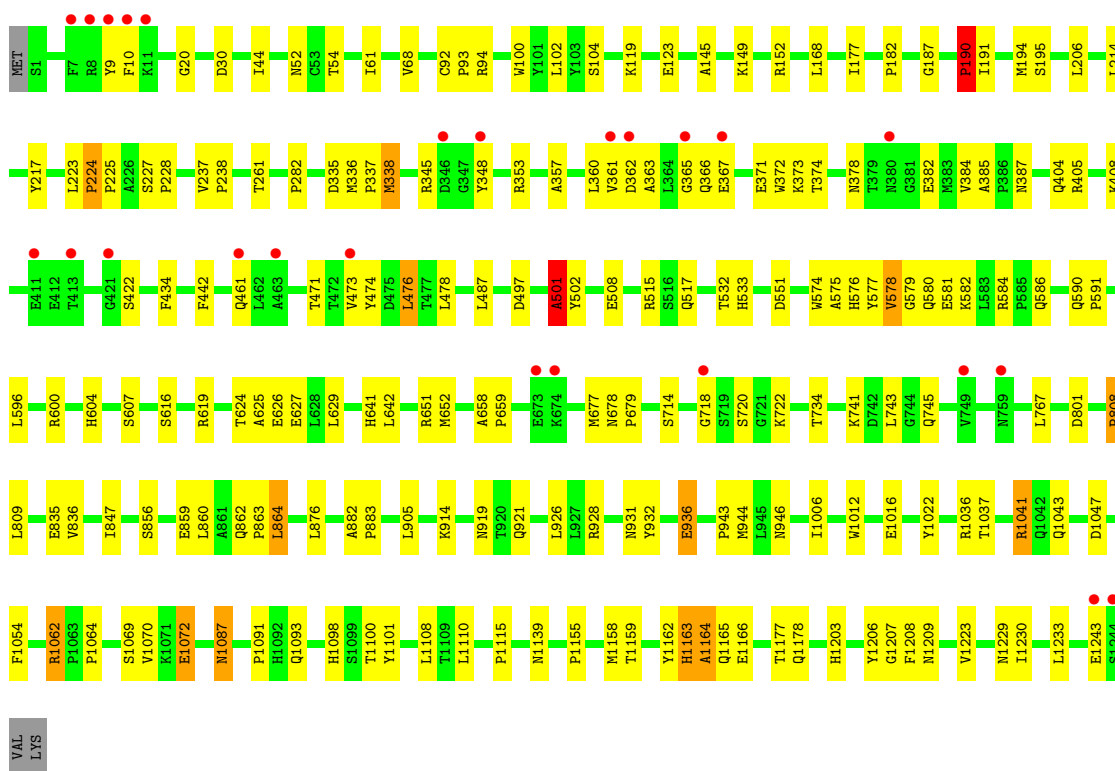
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	710	Total 710	O 710	0	0
11	B	427	Total 427	O 427	0	0
11	C	76	Total 76	O 76	0	0

3 Residue-property plots


These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

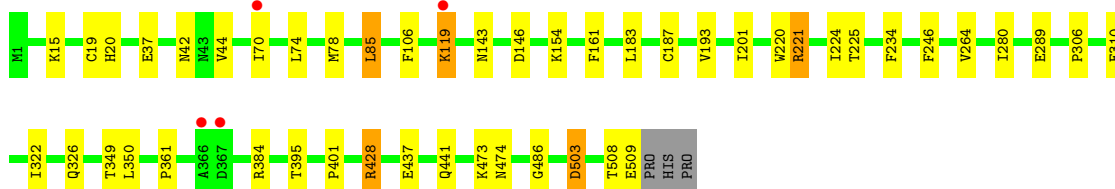
- Molecule 1: Respiratory nitrate reductase 1 alpha chain

Chain A: 



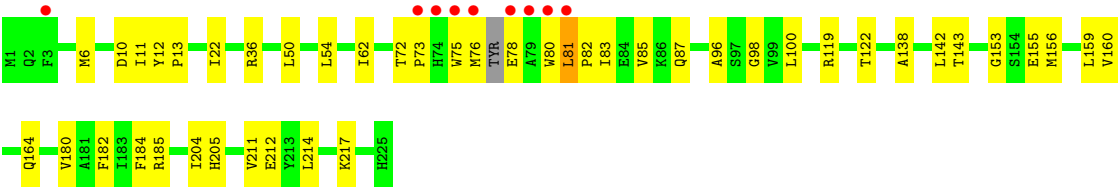
- Molecule 2: Respiratory nitrate reductase 1 beta chain

Chain B: 



- Molecule 3: Respiratory nitrate reductase 1 gamma chain

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	154.18Å 241.38Å 139.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.68 – 1.90 29.67 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.4 (29.68-1.90) 99.6 (29.67-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 1.91Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.202 , 0.230 0.195 , 0.224	Depositor DCC
R_{free} test set	10078 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	18.7	Xtriage
Anisotropy	0.732	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 202288 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17199	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 6MO, FME, SF4, AGA, 3PH, F3S, HEM, MD1

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	0.31	0/10138	0.64	11/13762 (0.1%)
2	B	0.33	0/4146	0.61	0/5609
3	C	0.32	0/1831	0.53	0/2476
All	All	0.32	0/16115	0.62	11/21847 (0.1%)

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	3

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1163	HIS	C-N-CA	13.34	155.04	121.70
1	A	502	TYR	CB-CG-CD1	-10.86	114.48	121.00
1	A	502	TYR	CB-CG-CD2	10.19	127.11	121.00
1	A	501	ALA	C-N-CA	10.11	146.96	121.70
1	A	1163	HIS	O-C-N	-8.48	109.13	122.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1163	HIS	Peptide
1	A	501	ALA	Mainchain,Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9878	0	9534	133	0
2	B	4050	0	3973	31	0
3	C	1790	0	1826	31	0
4	A	94	0	42	5	0
5	A	1	0	0	0	0
6	C	86	0	60	0	0
7	A	8	0	0	0	0
7	B	24	0	0	2	0
8	B	7	0	0	0	0
9	A	30	0	36	0	0
10	B	18	0	10	0	0
11	A	710	0	0	10	1
11	B	427	0	0	6	0
11	C	76	0	0	2	0
All	All	17199	0	15481	192	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

The worst 5 of 192 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:378:ASN:HD21	1:A:382:GLU:HB2	1.18	1.00
1:A:378:ASN:ND2	1:A:382:GLU:HB2	1.93	0.84
3:C:73:PRO:HG2	3:C:76:MET:HG3	1.57	0.84
1:A:863:PRO:HG2	1:A:864:LEU:HD22	1.60	0.83
2:B:503:ASP:HB3	11:B:1830:HOH:O	1.82	0.80

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:A:1448:HOH:O	11:A:1448:HOH:O[3_354]	0.98	1.22

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	1242/1247 (100%)	1171 (94%)	61 (5%)	10 (1%)	27	12
2	B	507/512 (99%)	495 (98%)	12 (2%)	0	100	100
3	C	220/225 (98%)	216 (98%)	4 (2%)	0	100	100
All	All	1969/1984 (99%)	1882 (96%)	77 (4%)	10 (0%)	38	23

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	361	VAL
1	A	1166	GLU
1	A	501	ALA
1	A	578	VAL
1	A	190	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	1041/1044 (100%)	1022 (98%)	19 (2%)	71	66
2	B	436/439 (99%)	427 (98%)	9 (2%)	66	59
3	C	185/186 (100%)	183 (99%)	2 (1%)	84	82
All	All	1662/1669 (100%)	1632 (98%)	30 (2%)	71	66

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1062	ARG

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Mol	Chain	Res	Type
1	A	1110	LEU
2	B	503	ASP
1	A	1087	ASN
1	A	1233	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	586	GLN
1	A	708	ASN
3	C	149	GLN
1	A	604	HIS
1	A	704	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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	$\# Z > 2$
3	FME	C	1	3	9,9,10	5.66	4 (44%)	6,9,11	1.55	2 (33%)

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	FME	C	1	3	-	0/7/9/11	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1	FME	O-C	15.13	1.21	1.11
3	C	1	FME	CB-CA	-6.23	1.48	1.53
3	C	1	FME	CA-C	3.54	1.55	1.48
3	C	1	FME	CB-CG	2.18	1.60	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	FME	CA-N-CN	2.60	127.27	122.97
3	C	1	FME	CB-CA-N	2.03	114.79	111.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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
4	MD1	A	1300	5	51,51,51	3.78	16 (31%)	64,78,78	2.78	10 (15%)
4	MD1	A	1301	5	51,51,51	3.51	17 (33%)	64,78,78	2.21	14 (21%)
9	AGA	A	1309	-	29,29,29	0.93	2 (6%)	35,35,35	1.45	3 (8%)
7	SF4	A	1401	1	12,12,12	8.50	12 (100%)	0,24,24	0.00	-
10	3PH	B	1310	-	16,17,47	2.11	1 (6%)	19,21,52	1.95	4 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	SF4	B	1402	2	12,12,12	7.28	12 (100%)	0,24,24	0.00	-
7	SF4	B	1403	2	12,12,12	9.09	12 (100%)	0,24,24	0.00	-
7	SF4	B	1404	2	12,12,12	7.88	12 (100%)	0,24,24	0.00	-
8	F3S	B	1405	2	3,9,9	7.39	3 (100%)	0,15,15	0.00	-
6	HEM	C	806	3	49,50,50	3.64	18 (36%)	46,82,82	1.45	5 (10%)
6	HEM	C	807	3	49,50,50	4.13	21 (42%)	46,82,82	1.51	6 (13%)

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
4	MD1	A	1300	5	-	0/22/59/59	0/1/5/5
4	MD1	A	1301	5	-	0/22/59/59	0/1/5/5
9	AGA	A	1309	-	-	0/34/34/34	0/0/0/0
7	SF4	A	1401	1	-	0/0/48/48	0/0/5/5
10	3PH	B	1310	-	1/1/3/4	0/17/18/49	0/0/0/0
7	SF4	B	1402	2	-	0/0/48/48	0/0/5/5
7	SF4	B	1403	2	-	0/0/48/48	0/0/5/5
7	SF4	B	1404	2	-	0/0/48/48	0/0/5/5
8	F3S	B	1405	2	-	0/0/24/24	0/0/3/3
6	HEM	C	806	3	-	0/14/114/114	0/0/8/8
6	HEM	C	807	3	-	0/14/114/114	0/0/8/8

The worst 5 of 126 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1300	MD1	C7-N8	22.11	1.50	1.27
4	A	1301	MD1	C7-N8	20.95	1.49	1.27
6	C	807	HEM	C2D-C1D	17.07	1.48	1.44
7	B	1403	SF4	S2-FE3	-14.28	2.23	2.33
6	C	806	HEM	C3D-C4D	13.91	1.48	1.44

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1300	MD1	C6-C5-N7	-18.99	131.58	134.14
4	A	1301	MD1	C6-C5-N7	-10.27	132.76	134.14
4	A	1301	MD1	C14-C7-N8	-8.44	104.58	124.80
6	C	806	HEM	C3B-C4B-NB	-5.24	110.25	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1309	AGA	C14-C13-C12	5.13	133.61	113.51

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
10	B	1310	3PH	C2

There are no torsion outliers.

There are no ring outliers.

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	1244/1247 (99%)	0.08	25 (2%) 62 63	12, 24, 42, 59	0
2	B	509/512 (99%)	-0.27	4 (0%) 83 85	11, 18, 31, 51	0
3	C	224/225 (99%)	0.09	9 (4%) 36 37	13, 24, 41, 55	0
All	All	1977/1984 (99%)	-0.01	38 (1%) 64 65	11, 22, 41, 59	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	10	PHE	10.5
3	C	75	TRP	9.2
1	A	9	TYR	8.9
3	C	80	TRP	6.0
1	A	362	ASP	5.8

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

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	FME	C	1	10/11	0.22	1.88	37,44,53,54	0

6.3 Carbohydrates ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
10	3PH	B	1310	18/48	0.19	22.66	42,55,60,62	0
6	HEM	C	806	43/43	0.11	1.85	11,16,19,30	0
6	HEM	C	807	43/43	0.12	0.89	20,25,37,45	0
9	AGA	A	1309	30/30	0.13	0.11	19,23,55,60	0
4	MD1	A	1300	47/47	0.11	0.09	14,22,35,39	0
4	MD1	A	1301	47/47	0.09	-0.21	16,21,29,34	0
8	F3S	B	1405	7/7	0.08	-1.11	13,14,15,15	0
5	6MO	A	1302	1/1	0.10	-1.16	40,40,40,40	0
7	SF4	B	1403	8/8	0.06	-1.20	13,13,14,15	0
7	SF4	B	1402	8/8	0.05	-1.50	19,21,21,23	0
7	SF4	A	1401	8/8	0.05	-2.05	19,22,22,24	0
7	SF4	B	1404	8/8	0.06	-3.35	17,19,20,21	0

6.5 Other polymers ⓘ

There are no such residues in this entry.