W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

Jan 31, 2016 – 09:39 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)

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

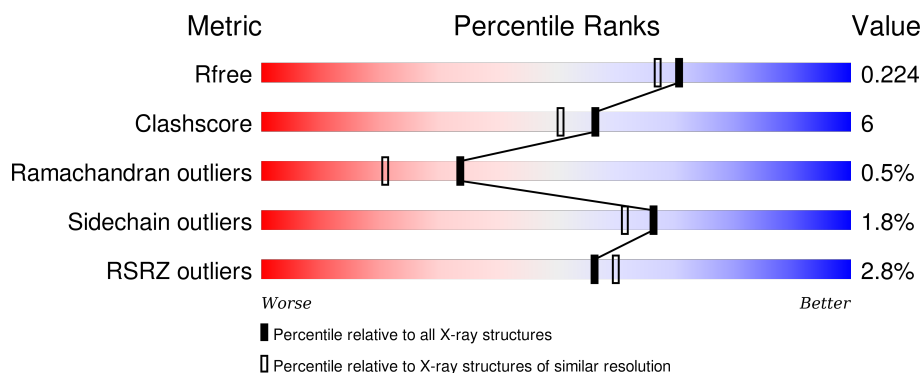|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 1.90 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	Percentile Ranks	Value
Rfree		0.224
Clashscore		6
Ramachandran outliers		0.5%
Sidechain outliers		1.8%
RSRZ outliers		2.8%

Worse ← → *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (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. 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	1247	3% / 84% / 15% •
2	B	512	% / 90% / 8% ••
3	C	225	4% / 80% / 20%

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
10	3PH	B	1310	X	-	-	X
7	SF4	B	1403	-	-	X	-

2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 17199 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 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-YL ESTER GUANYLATE ESTER (three-letter code: MD1) (formula: $C_{20}H_{26}N_{10}O_{13}P_2S_2$).
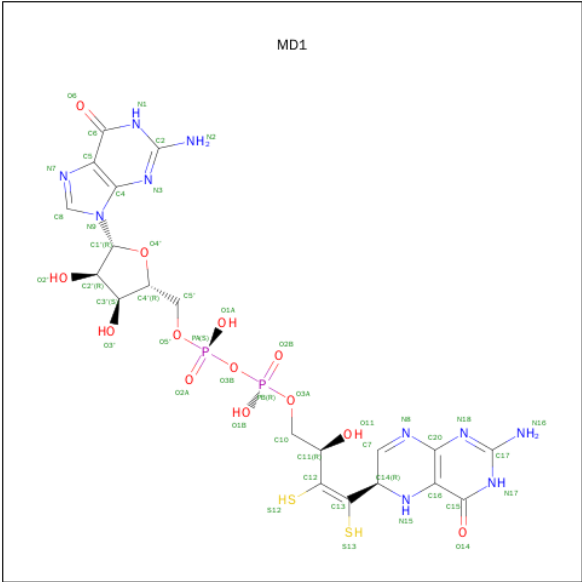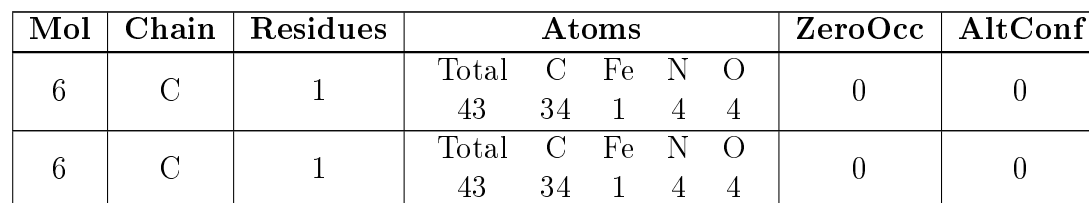
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
4	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		

- 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: $C_{34}H_{32}FeN_4O_4$).

HEM

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).

SF4

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: Fe_3S_4).
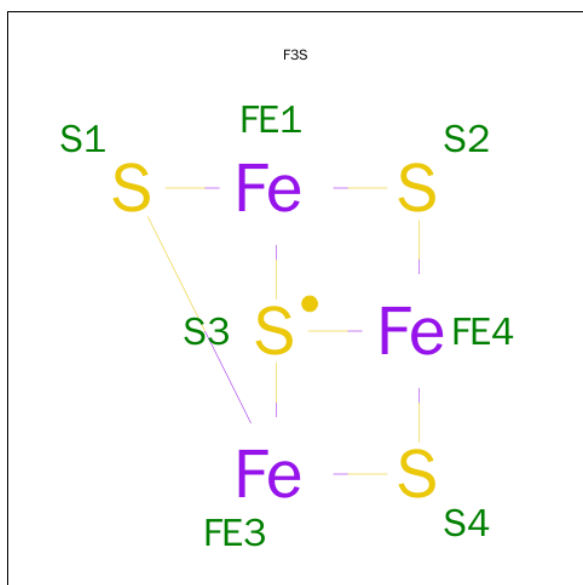
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 9 is (1S)-2-{[{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHO RYL]OXY}-1-[(PENTANOYLOXY)METHYL]ETHYL OCTANOATE (three-letter code: AGA) (formula: $C_{19}H_{36}O_{10}P$).
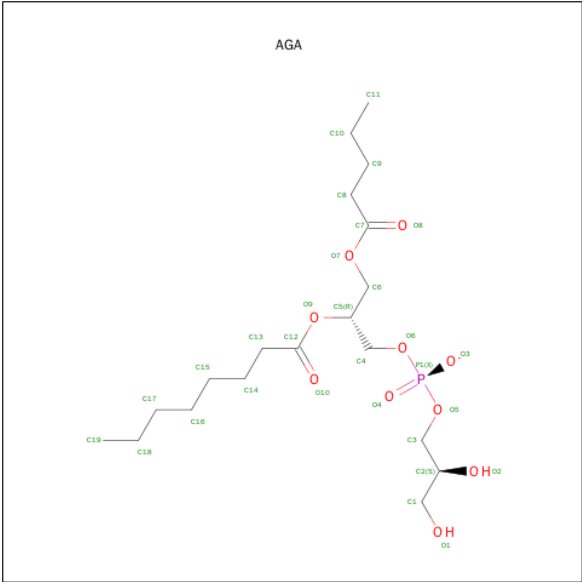
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
9	A	1	30	19	10	1	0	0

- Molecule 10 is 1,2-DIACYL-GLYCEROL-3-SN-PHOSPHATE (three-letter code: 3PH) (formula: $C_{39}H_{77}O_8P$).
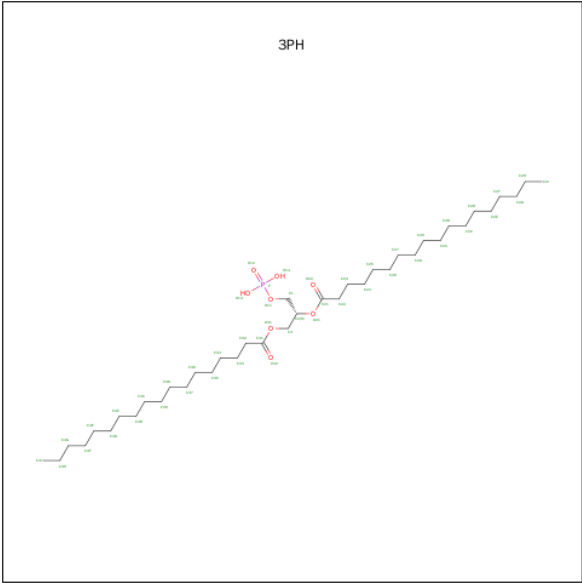
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
10	B	1	18	9	8	1	0	0

- Molecule 11 is water.

| Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	710	Total O 710 710	0	0
11	B	427	Total O 427 427	0	0
11	C	76	Total O 76 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.
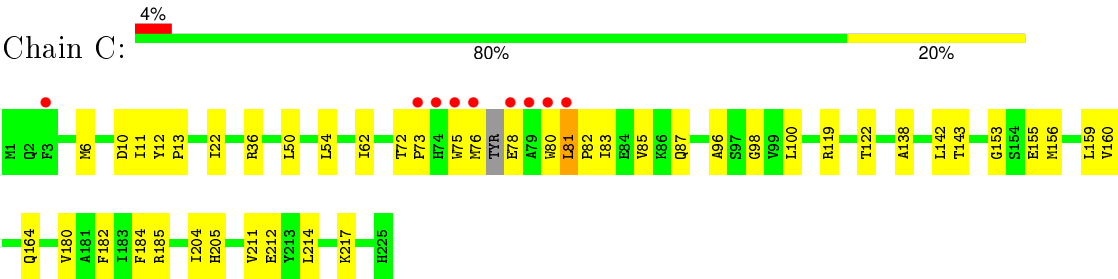
• Molecule 1: Respiratory nitrate reductase 1 alpha chain
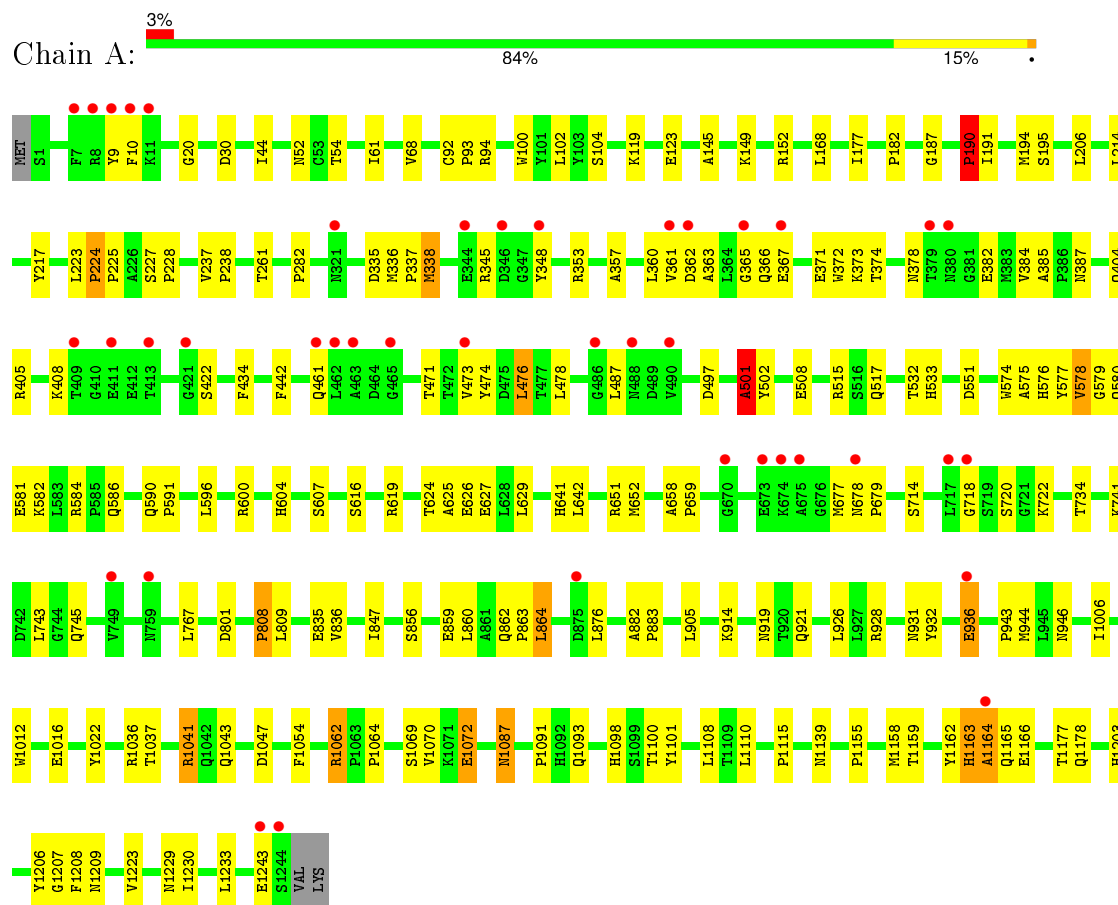
• Molecule 2: Respiratory nitrate reductase 1 beta chain
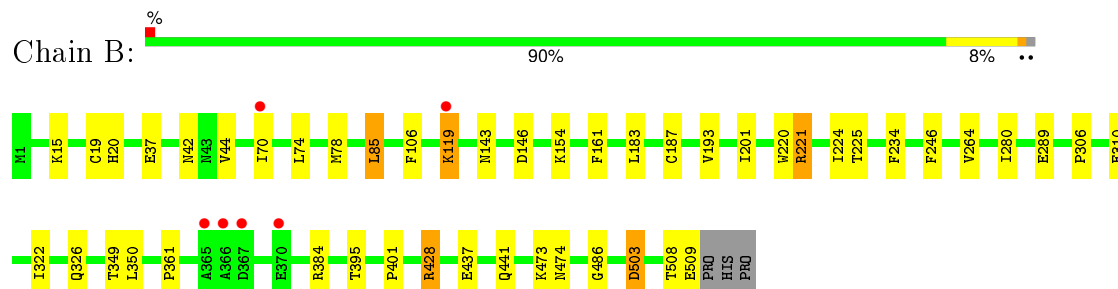
• Molecule 3: Respiratory nitrate reductase 1 gamma chain

Chain C:

4 Data and refinement statistics (i)

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
$< I/\sigma(I) >$ [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 , 56.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.51, < L^2 > = 0.35$	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.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 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(^{o})	Ideal(^{o})
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 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	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

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 192 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: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	Interatomic distance (Å)	Clash overlap (Å)
11:A:1448:HOH:O	11:A:1448:HOH:O[3_354]	0.98	1.22

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	1242/1247 (100%)	1171 (94%)	61 (5%)	10 (1%)	24	11
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%)	34	21

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 (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	1041/1044 (100%)	1022 (98%)	19 (2%)	66	61
2	B	436/439 (99%)	427 (98%)	9 (2%)	61	55
3	C	185/186 (100%)	183 (99%)	2 (1%)	80	79
All	All	1662/1669 (100%)	1632 (98%)	30 (2%)	66	61

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

Mol	Chain	Res	Type
1	A	1062	ARG
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 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	#$|Z| > 2$
3	FME	C	1	3	8,9,10	1.41	2 (25%)	6,9,11	1.93	3 (50%)

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	-	0/6/9/11	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1	FME	CB-CA	-2.88	1.48	1.53
3	C	1	FME	CB-CG	2.16	1.60	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	1	FME	O1-CN-N	-2.96	120.50	124.76
3	C	1	FME	O-C-CA	-2.02	120.11	125.44
3	C	1	FME	CA-N-CN	2.89	127.27	122.82

There are no chirality outliers.

There are no torsion outliers.

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 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	39,51,51	3.93	11 (28%)	37,78,78	2.37	10 (27%)
4	MD1	A	1301	5	39,51,51	3.68	10 (25%)	37,78,78	2.38	11 (29%)
9	AGA	A	1309	-	29,29,29	0.69	1 (3%)	30,35,35	1.46	3 (10%)
7	SF4	A	1401	1	0,12,12	0.00	-	0,24,24	0.00	-
10	3PH	B	1310	-	17,17,47	0.84	0	19,21,52	2.13	5 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
7	SF4	B	1402	2	0,12,12	0.00	-	0,24,24	0.00	-
7	SF4	B	1403	2	0,12,12	0.00	-	0,24,24	0.00	-
7	SF4	B	1404	2	0,12,12	0.00	-	0,24,24	0.00	-
8	F3S	B	1405	2	0,9,9	0.00	-	0,15,15	0.00	-
6	HEM	C	806	3	30,50,50	2.32	10 (33%)	24,82,82	2.66	10 (41%)
6	HEM	C	807	3	30,50,50	2.44	12 (40%)	24,82,82	2.79	11 (45%)

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	-	0/18/59/59	0/5/5/5
4	MD1	A	1301	5	-	0/18/59/59	0/5/5/5
9	AGA	A	1309	-	-	0/34/34/34	0/0/0/0
7	SF4	A	1401	1	-	0/0/48/48	0/6/5/5
10	3PH	B	1310	-	1/1/3/4	1/18/18/49	0/0/0/0
7	SF4	B	1402	2	-	0/0/48/48	0/6/5/5
7	SF4	B	1403	2	-	0/0/48/48	0/6/5/5
7	SF4	B	1404	2	-	0/0/48/48	0/6/5/5
8	F3S	B	1405	2	-	0/0/24/24	0/0/3/3
6	HEM	C	806	3	-	0/10/54/54	0/0/8/8
6	HEM	C	807	3	-	0/10/54/54	0/0/8/8

The worst 5 of 44 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	806	HEM	C2D-C3D	-6.25	1.35	1.54
6	C	807	HEM	C2D-C3D	-6.08	1.36	1.54
6	C	806	HEM	C3B-C4B	-5.27	1.47	1.51
6	C	807	HEM	C3B-C4B	-5.12	1.47	1.51
6	C	807	HEM	C3D-C4D	-3.34	1.47	1.51

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1300	MD1	C5-C6-N1	-6.46	114.76	123.59
4	A	1301	MD1	C5-C6-N1	-5.70	115.79	123.59
4	A	1301	MD1	N3-C2-N1	-5.23	119.48	127.44
4	A	1301	MD1	O3B-PB-O3A	-4.41	91.23	102.94
4	A	1300	MD1	N17-C17-N18	-4.36	118.38	125.53

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
10	B	1310	3PH	C2

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	B	1310	3PH	C2-O21-C21-O22

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1300	MD1	3	0
4	A	1301	MD1	2	0
7	B	1403	SF4	2	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	1244/1247 (99%)	0.12	41 (3%)	50	53	12, 24, 42, 59	0
2	B	509/512 (99%)	-0.28	6 (1%)	81	83	11, 18, 31, 51	0
3	C	223/225 (99%)	0.12	9 (4%)	42	46	13, 24, 41, 55	0
All	All	1976/1984 (99%)	0.02	56 (2%)	56	60	11, 22, 41, 59	0

The worst 5 of 56 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	10	PHE	12.3
3	C	75	TRP	10.9
1	A	9	TYR	9.4
3	C	80	TRP	7.0
1	A	362	ASP	6.3

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
3	FME	C	1	10/11	0.91	0.22	-	37,44,53,54	0

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
10	3PH	B	1310	18/48	0.78	0.19	19.46	42,55,60,62	0
6	HEM	C	806	43/43	0.97	0.11	1.82	11,16,19,30	0
6	HEM	C	807	43/43	0.95	0.12	0.85	20,25,37,45	0
9	AGA	A	1309	30/30	0.93	0.13	0.09	19,23,55,60	0
4	MD1	A	1300	47/47	0.94	0.11	0.06	14,22,35,39	0
4	MD1	A	1301	47/47	0.95	0.09	-0.27	16,21,29,34	0
8	F3S	B	1405	7/7	0.99	0.07	-1.38	13,14,15,15	0
5	6MO	A	1302	1/1	0.92	0.10	-1.47	40,40,40,40	0
7	SF4	B	1403	8/8	0.99	0.05	-1.58	13,13,14,15	0
7	SF4	B	1402	8/8	0.98	0.05	-1.64	19,21,21,23	0
7	SF4	A	1401	8/8	0.98	0.05	-2.15	19,22,22,24	0
7	SF4	B	1404	8/8	0.99	0.06	-4.23	17,19,20,21	0

6.5 Other polymers (i)

There are no such residues in this entry.