



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 11:39 PM GMT

PDB ID : 1Y5L
Title : The crystal structure of the NarGHI mutant NarI-H66Y
Authors : Bertero, M.G.; Rothery, R.A.; Boroumand, N.; Palak, M.; Blasco, F.; Ginet, N.; Weiner, J.H.; Strynadka, N.C.J.
Deposited on : 2004-12-02
Resolution : 2.50 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 (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

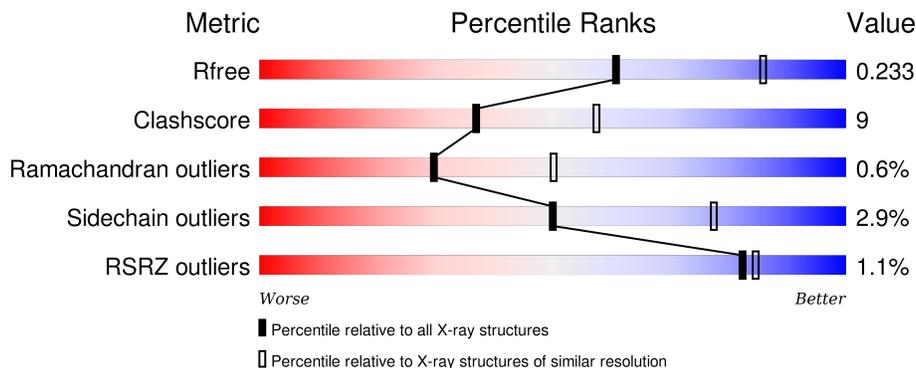
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	1246	 79% 19% •
2	B	512	 84% 14% ••
3	C	225	 67% 26% • 6%

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
7	SF4	A	1801	-	-	X	-
7	SF4	B	1803	-	-	X	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 16150 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
			Total	C	N	O	S			
1	A	1244	9869	6232	1731	1858	48	0	0	0

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	211	1676	1109	283	272	12	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

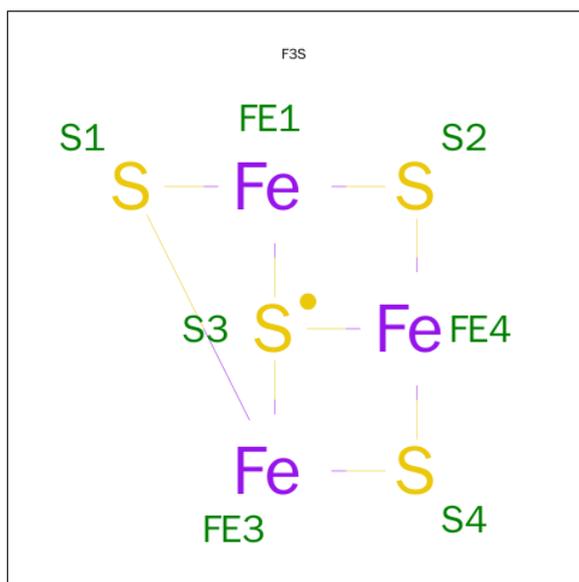
Chain	Residue	Modelled	Actual	Comment	Reference
C	1	FME	MET	MODIFIED RESIDUE	UNP P11350
C	66	TYR	HIS	ENGINEERED	UNP P11350

- 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: C₂₀H₂₆N₁₀O₁₃P₂S₂).

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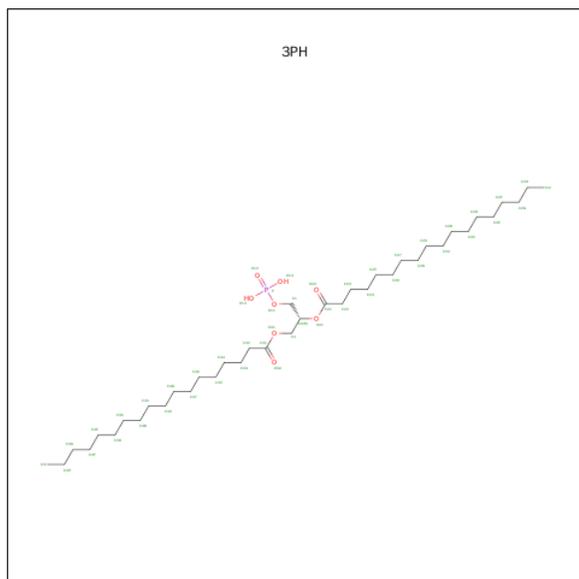
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
7	B	1	8	4	4	0	0

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



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

- Molecule 9 is 1,2-DIACYL-GLYCEROL-3-SN-PHOSPHATE (three-letter code: 3PH) (formula: C₃₉H₇₇O₈P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
9	A	1	27	18	8	1	0	0

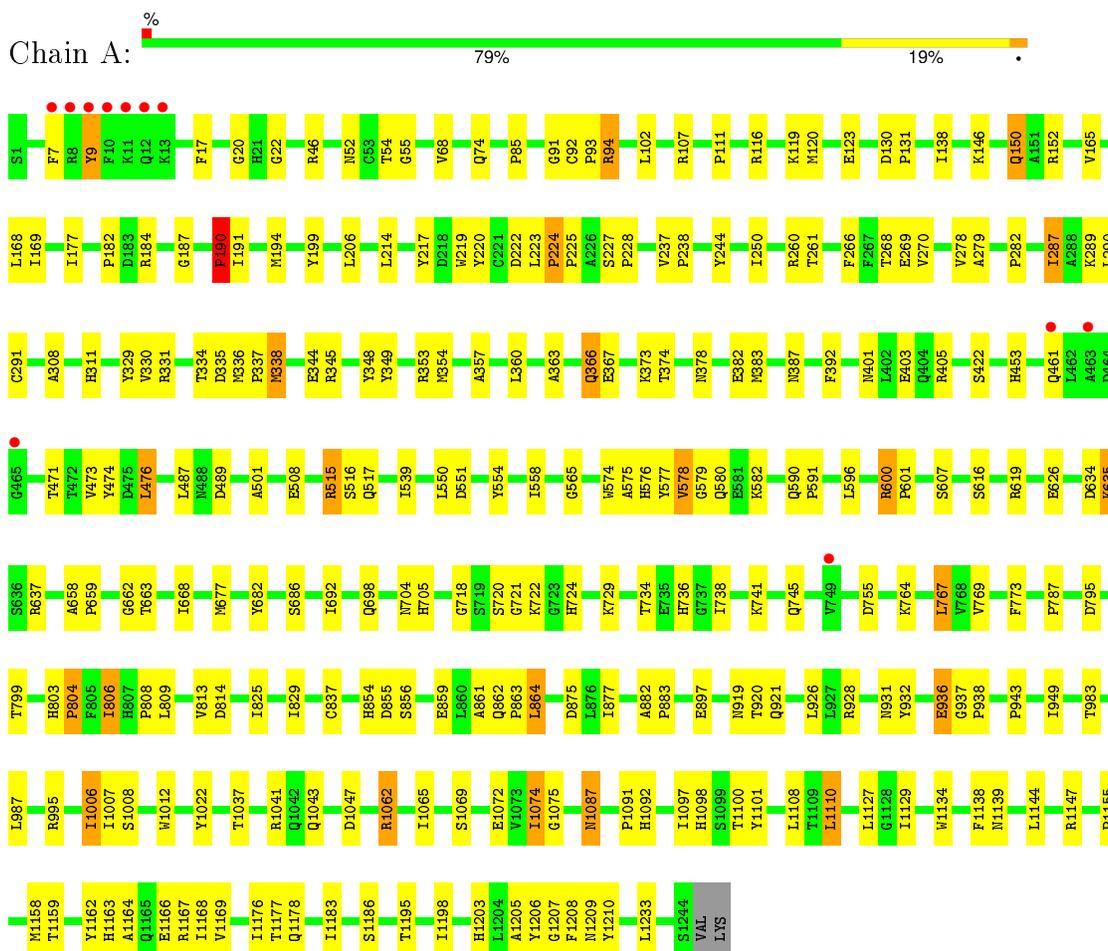
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	174	Total 174	O 174	0	0
10	B	145	Total 145	O 145	0	0
10	C	32	Total 32	O 32	0	0

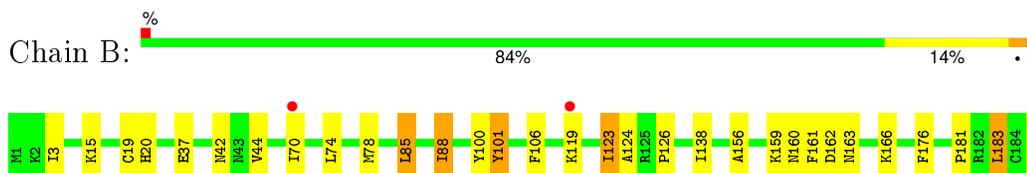
3 Residue-property plots [i](#)

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

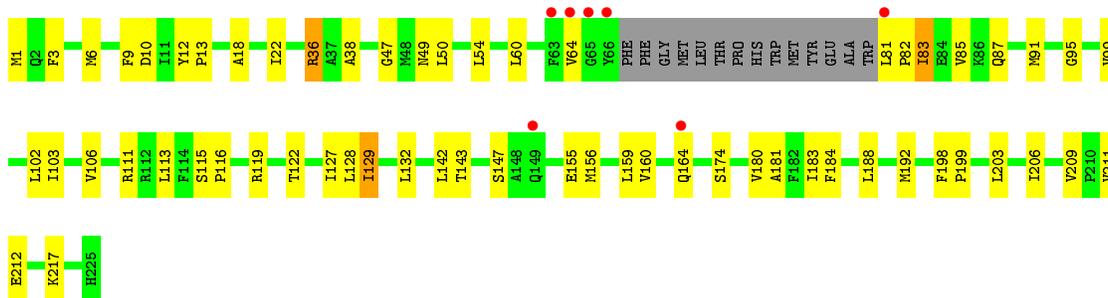


- Molecule 2: Respiratory nitrate reductase 1 beta chain





- Molecule 3: Respiratory nitrate reductase 1 gamma chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	154.16Å 241.90Å 139.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.79 – 2.50 24.79 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.4 (24.79-2.50) 99.5 (24.79-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.34 (at 2.50Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.188 , 0.237 0.185 , 0.233	Depositor DCC
R_{free} test set	7209 reflections (8.75%)	DCC
Wilson B-factor (Å ²)	25.8	Xtrriage
Anisotropy	0.999	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.8	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Outliers	0 of 89584 reflections	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16150	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtrriage'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.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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, 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	0.33	0/10128	0.61	1/13749 (0.0%)
2	B	0.36	0/4146	0.62	0/5609
3	C	0.37	0/1709	0.54	0/2309
All	All	0.34	0/15983	0.61	1/21667 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1097	ILE	N-CA-C	-5.19	96.99	111.00

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	9869	0	9527	197	0
2	B	4050	0	3973	55	0
3	C	1676	0	1726	44	0
4	A	94	0	42	6	0
5	A	1	0	0	0	0
6	C	43	0	30	1	0
7	A	8	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	24	0	0	2	0
8	B	7	0	0	0	0
9	A	27	0	27	0	0
10	A	174	0	0	2	1
10	B	145	0	0	4	0
10	C	32	0	0	3	0
All	All	16150	0	15325	293	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 9.

The worst 5 of 293 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	1.34	0.92
3:C:129:ILE:HD11	3:C:203:LEU:HD11	1.50	0.91
2:B:123:ILE:HD13	2:B:124:ALA:H	1.36	0.89
1:A:165:VAL:O	1:A:169:ILE:HG12	1.83	0.78
1:A:508:GLU:OE1	1:A:515:ARG:HD2	1.83	0.78

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)
10:A:3889:HOH:O	10:A:3889:HOH:O[3_354]	1.70	0.50

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	1242/1246 (100%)	1150 (93%)	82 (7%)	10 (1%)	24 41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	507/512 (99%)	487 (96%)	19 (4%)	1 (0%)	52	75
3	C	207/225 (92%)	198 (96%)	9 (4%)	0	100	100
All	All	1956/1983 (99%)	1835 (94%)	110 (6%)	11 (1%)	30	50

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	501	ALA
1	A	422	SER
1	A	1166	GLU
2	B	101	TYR
1	A	718	GLY

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	1039/1043 (100%)	1008 (97%)	31 (3%)	48	76
2	B	436/439 (99%)	425 (98%)	11 (2%)	55	82
3	C	174/186 (94%)	169 (97%)	5 (3%)	50	77
All	All	1649/1668 (99%)	1602 (97%)	47 (3%)	50	77

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	936	GLU
1	A	1072	GLU
3	C	49	ASN
1	A	1006	ILE
1	A	1074	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	704	ASN
1	A	942	GLN
3	C	149	GLN
1	A	708	ASN
1	A	179	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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	1.98	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	-	0/6/9/11	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	-2.82	1.48	1.53
3	C	1	FME	CB-CG	2.15	1.60	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	FME	O1-CN-N	-3.18	120.17	124.76
3	C	1	FME	CA-N-CN	2.99	127.42	122.82

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	FME	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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$
9	3PH	A	1309	-	26,26,47	0.73	1 (3%)	29,31,52	1.54	4 (13%)
4	MD1	A	1800	5	39,51,51	3.84	11 (28%)	37,78,78	2.42	10 (27%)
7	SF4	A	1801	1	0,12,12	0.00	-	0,24,24	0.00	-
4	MD1	A	2800	5	39,51,51	3.57	9 (23%)	37,78,78	2.34	11 (29%)
7	SF4	B	1802	2	0,12,12	0.00	-	0,24,24	0.00	-
7	SF4	B	1803	2	0,12,12	0.00	-	0,24,24	0.00	-
7	SF4	B	1804	2	0,12,12	0.00	-	0,24,24	0.00	-
8	F3S	B	1805	2	0,9,9	0.00	-	0,15,15	0.00	-
6	HEM	C	806	3	30,50,50	2.32	12 (40%)	24,82,82	2.67	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
9	3PH	A	1309	-	-	0/28/28/49	0/0/0/0
4	MD1	A	1800	5	-	0/18/59/59	0/5/5/5
7	SF4	A	1801	1	-	0/0/48/48	0/6/5/5
4	MD1	A	2800	5	-	0/18/59/59	0/5/5/5
7	SF4	B	1802	2	-	0/0/48/48	0/6/5/5
7	SF4	B	1803	2	-	0/0/48/48	0/6/5/5
7	SF4	B	1804	2	-	0/0/48/48	0/6/5/5
8	F3S	B	1805	2	-	0/0/24/24	0/0/3/3
6	HEM	C	806	3	-	0/10/54/54	0/0/8/8

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	806	HEM	C2D-C3D	-6.15	1.36	1.54
6	C	806	HEM	C3B-C4B	-4.82	1.47	1.51
6	C	806	HEM	C2C-C1C	-2.84	1.47	1.52
6	C	806	HEM	C3D-C4D	-2.32	1.48	1.51
4	A	1800	MD1	PA-O1A	-2.05	1.46	1.54

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1800	MD1	C5-C6-N1	-6.61	114.55	123.59
4	A	2800	MD1	C5-C6-N1	-5.61	115.92	123.59
4	A	2800	MD1	N3-C2-N1	-5.34	119.32	127.44
4	A	1800	MD1	N17-C17-N18	-4.38	118.35	125.53
4	A	1800	MD1	N3-C2-N1	-4.23	121.00	127.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1800	MD1	4	0
7	A	1801	SF4	2	0
4	A	2800	MD1	2	0
7	B	1803	SF4	2	0
6	C	806	HEM	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 [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	1244/1246 (99%)	-0.56	11 (0%) 85 88	13, 26, 46, 83	0
2	B	509/512 (99%)	-0.75	3 (0%) 90 91	10, 21, 38, 63	0
3	C	210/225 (93%)	-0.28	7 (3%) 50 55	18, 33, 59, 65	0
All	All	1963/1983 (98%)	-0.58	21 (1%) 82 84	10, 25, 48, 83	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	9	TYR	8.2
1	A	10	PHE	7.8
3	C	64	VAL	4.4
3	C	66	TYR	3.5
1	A	11	LYS	3.5

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	0.89	0.28	-	54,60,75,76	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
9	3PH	A	1309	27/48	0.95	0.13	1.27	20,28,50,54	0
6	HEM	C	806	43/43	0.97	0.12	-0.01	12,24,29,45	0
4	MD1	A	2800	47/47	0.97	0.09	-0.55	13,25,34,37	0
4	MD1	A	1800	47/47	0.97	0.09	-0.99	17,25,36,38	0
7	SF4	B	1803	8/8	0.99	0.07	-1.56	15,17,18,18	0
7	SF4	B	1802	8/8	0.98	0.06	-1.93	21,24,25,26	0
8	F3S	B	1805	7/7	0.99	0.08	-2.37	17,18,20,21	0
5	6MO	A	3800	1/1	0.98	0.07	-3.11	38,38,38,38	0
7	SF4	B	1804	8/8	0.99	0.06	-3.27	19,21,25,25	0
7	SF4	A	1801	8/8	0.98	0.04	-4.69	20,21,25,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.