



Full wwPDB X-ray Structure Validation Report i

Feb 27, 2014 – 11:12 PM GMT

PDB ID : 1WUL
Title : High Resolution Structure Of The Reduced State Of [Nife]Hydrogenase From Desulfovibrio Vulgaris Miyazaki F
Authors : Ogata, H.; Hirota, S.; Nakahara, A.; Komori, H.; Shibata, N.; Kato, T.; Kano, K.; Higuchi, Y.
Deposited on : 2004-12-07
Resolution : 1.50 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

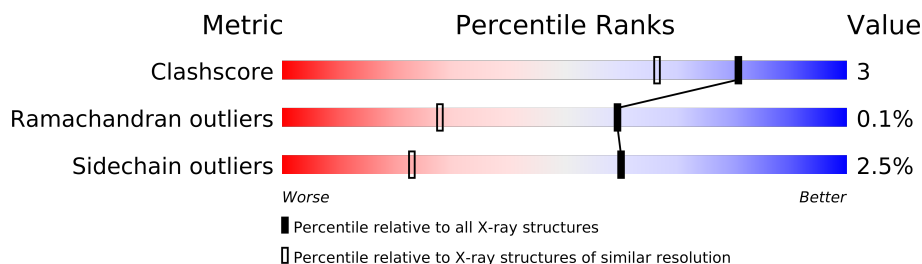
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
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 1.50 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))
Clashscore	79885	1768 (1.50-1.50)
Ramachandran outliers	78287	1720 (1.50-1.50)
Sidechain outliers	78261	1718 (1.50-1.50)

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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	S	267	
2	L	534	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 7040 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 Periplasmic [NiFe] hydrogenase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	S	267	Total	C	N	O	S	0	0	0
			2019	1282	342	378	17			

- Molecule 2 is a protein called Periplasmic [NiFe] hydrogenase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	534	Total	C	N	O	S	0	1	0
			4181	2675	726	765	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	514	LYS	ASN	SEE REMARK 999	UNP P21852
L	515	LEU	VAL	SEE REMARK 999	UNP P21852

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

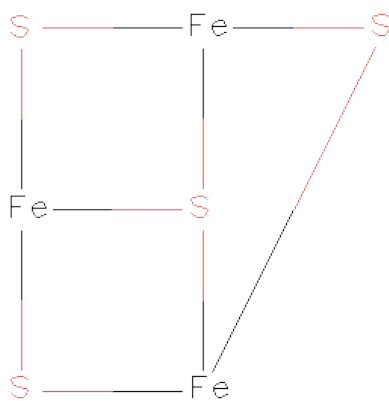
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	1	Total	Mg	0	0
			1	1		

- Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



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

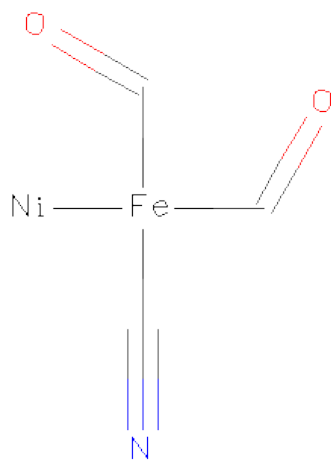
- Molecule 5 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe_3S_4).



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

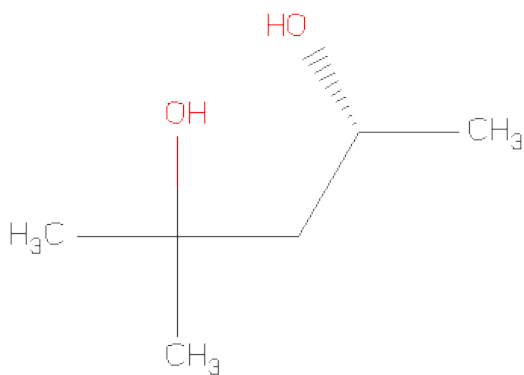
- Molecule 6 is NI-FE REDUCED ACTIVE CENTER (three-letter code: NFR) (formula:

$\text{C}_3\text{H}_2\text{FeNNiO}_2$).



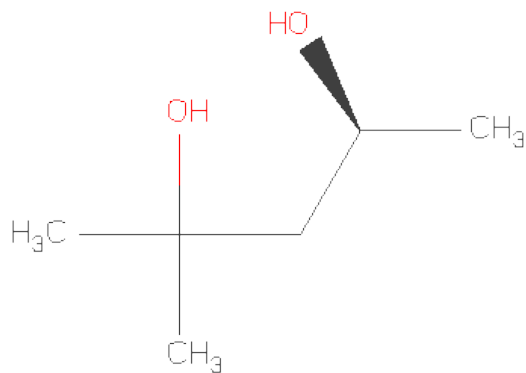
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	Fe	N	Ni	O		
6	L	1	8	3	1	1	1	2	0	0

- Molecule 7 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: $\text{C}_6\text{H}_{14}\text{O}_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	L	1	8	6	2	0	0

- Molecule 8 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	S	1	Total	C	O	0	0
			8	6	2		
8	S	1	Total	C	O	0	0
			8	6	2		
8	S	1	Total	C	O	0	0
			8	6	2		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	L	514	Total	O	0	0
			514	514		
9	S	262	Total	O	0	0
			262	262		

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.

Note EDS was not executed.

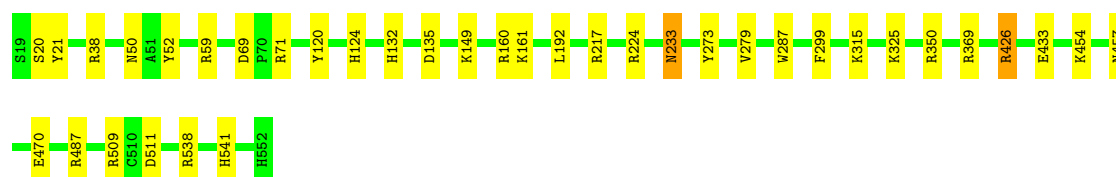
- Molecule 1: Periplasmic [NiFe] hydrogenase small subunit

Chain S: 



- Molecule 2: Periplasmic [NiFe] hydrogenase large subunit

Chain L: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	98.12Å 126.02Å 66.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.50	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-1.50)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.119 , 0.169	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7040	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CSO, SF4, MG, F3S, NFR, MRD, MPD

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	S	0.54	0/2075	1.09	8/2830 (0.3%)
2	L	0.55	0/4290	1.13	22/5832 (0.4%)
All	All	0.55	0/6365	1.12	30/8662 (0.3%)

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	273	TYR	CB-CG-CD1	12.40	128.44	121.00
2	L	160	ARG	NE-CZ-NH2	-8.77	115.91	120.30
1	S	1	LEU	O-C-N	8.41	136.15	122.70
1	S	163	TYR	CB-CG-CD1	7.84	125.70	121.00
2	L	38	ARG	NE-CZ-NH2	-7.00	116.80	120.30
2	L	509	ARG	NE-CZ-NH2	6.86	123.73	120.30
2	L	287	TRP	CA-CB-CG	-6.75	100.86	113.70
2	L	299	PHE	CB-CG-CD2	6.75	125.53	120.80
1	S	6	ARG	NE-CZ-NH1	6.68	123.64	120.30
2	L	224	ARG	NE-CZ-NH1	6.59	123.60	120.30
2	L	511	ASP	CB-CG-OD2	6.45	124.10	118.30
1	S	163	TYR	CG-CD1-CE1	6.43	126.45	121.30
1	S	26	ARG	CG-CD-NE	-6.38	98.39	111.80
2	L	69	ASP	CB-CG-OD1	6.32	123.99	118.30
2	L	350	ARG	NE-CZ-NH2	6.30	123.45	120.30
2	L	273	TYR	CG-CD1-CE1	6.20	126.26	121.30
2	L	217	ARG	NE-CZ-NH1	-6.10	117.25	120.30
2	L	426	ARG	NE-CZ-NH2	-5.85	117.37	120.30
2	L	426	ARG	NE-CZ-NH1	5.74	123.17	120.30
2	L	369	ARG	NE-CZ-NH1	5.71	123.16	120.30
2	L	59	ARG	NE-CZ-NH1	5.70	123.15	120.30
2	L	52	TYR	CB-CG-CD2	-5.63	117.62	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	111	TYR	C-N-CA	-5.62	110.49	122.30
1	S	57	GLU	CA-CB-CG	5.47	125.44	113.40
2	L	538	ARG	NE-CZ-NH2	-5.41	117.60	120.30
2	L	21	TYR	CB-CG-CD2	-5.40	117.76	121.00
1	S	1	LEU	CA-C-N	-5.28	105.58	117.20
2	L	71	ARG	NE-CZ-NH2	-5.10	117.75	120.30
2	L	273	TYR	CB-CG-CD2	-5.07	117.96	121.00
2	L	120	TYR	CA-CB-CG	5.04	122.97	113.40

There are no chirality outliers.

There are no planarity outliers.

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	S	2019	0	0	12	0
2	L	4181	0	0	10	0
3	L	1	0	0	0	0
4	S	16	0	0	0	0
5	S	7	0	0	0	0
6	L	8	0	0	0	0
7	L	8	0	14	0	0
8	S	24	0	42	2	0
9	L	514	0	0	7	0
9	S	262	0	0	5	0
All	All	7040	0	56	21	0

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 3.

All (21) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:S:146:ASN:ND2	8:S:2004:MPD:H13	2.02	0.73
1:S:134:ASN:CB	8:S:2004:MPD:H12	2.33	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:L:192:LEU:N	9:L:5331:HOH:O	2.41	0.53
1:S:149:GLY:N	9:S:5643:HOH:O	2.45	0.49
2:L:426:ARG:NH1	9:L:5526:HOH:O	2.47	0.47
1:S:196:HIS:ND1	1:S:201:GLU:OE1	2.49	0.46
1:S:61:GLU:OE1	1:S:65:ASN:ND2	2.49	0.46
2:L:315:LYS:NZ	9:L:5418:HOH:O	2.49	0.46
2:L:470:GLU:OE1	2:L:487:ARG:NE	2.50	0.45
2:L:149:LYS:NZ	9:L:5597:HOH:O	2.50	0.45
1:S:1:LEU:N	1:S:62:GLN:OE1	2.49	0.45
1:S:88:LYS:NZ	9:S:5784:HOH:O	2.50	0.44
1:S:91:ASN:ND2	9:S:5784:HOH:O	2.49	0.44
2:L:454:LYS:NZ	9:L:5295:HOH:O	2.50	0.44
2:L:135:ASP:OD2	2:L:541:HIS:ND1	2.50	0.44
1:S:6:ARG:N	9:L:5580:HOH:O	2.51	0.44
1:S:69:GLY:N	9:S:5460:HOH:O	2.50	0.43
2:L:161:LYS:NZ	9:L:5575:HOH:O	2.51	0.42
1:S:112:GLY:CA	9:S:5643:HOH:O	2.69	0.41
1:S:26:ARG:NH2	2:L:233:ASN:ND2	2.68	0.41
2:L:124:HIS:NE2	2:L:433:GLU:OE1	2.55	0.40

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	S	265/267 (99%)	256 (97%)	8 (3%)	1 (0%)	43	15
2	L	532/534 (100%)	519 (98%)	13 (2%)	0	100	100
All	All	797/801 (100%)	775 (97%)	21 (3%)	1 (0%)	59	28

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	S	4	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	S	213/213 (100%)	204 (96%)	9 (4%)	40 8
2	L	438/437 (100%)	431 (98%)	7 (2%)	75 44
All	All	651/650 (100%)	635 (98%)	16 (2%)	60 23

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	S	1	LEU
1	S	2	MET
1	S	5	ARG
1	S	83	ASN
1	S	126	ASN
1	S	138	LYS
1	S	168	LYS
1	S	229	ASN
1	S	230	ASN
2	L	20	SER
2	L	50	ASN
2	L	132	HIS
2	L	233	ASN
2	L	279	VAL
2	L	325	LYS
2	L	457	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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	$\# Z > 2$
2	CSO	L	546	2,6	6,6,7	7.54	2 (33%)	3,6,8	4.99	1 (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
2	CSO	L	546	2,6	-	0/2/5/7	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	546	CSO	O-C	18.29	1.24	1.11
2	L	546	CSO	CA-C	2.27	1.52	1.48

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	546	CSO	C-CA-N	-8.57	105.27	113.83

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 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 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
6	NFR	L	1004	2	4,7,7	3.46	1 (25%)	0,9,9	0.00	-
7	MRD	L	2005	-	7,7,7	0.53	0	10,10,10	0.80	0
4	SF4	S	1001	1	12,12,12	133.38	8 (66%)	0,24,24	0.00	-
4	SF4	S	1002	1	12,12,12	133.88	10 (83%)	0,24,24	0.00	-
5	F3S	S	1003	1	3,9,9	5.11	3 (100%)	0,15,15	0.00	-
8	MPD	S	2001	-	7,7,7	0.44	0	10,10,10	0.62	0
8	MPD	S	2004	-	7,7,7	0.40	0	10,10,10	0.64	0
8	MPD	S	2007	-	7,7,7	0.42	0	10,10,10	0.89	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
6	NFR	L	1004	2	-	0/0/9/9	0/0/0/0
7	MRD	L	2005	-	-	0/5/5/5	0/0/0/0
4	SF4	S	1001	1	-	0/0/48/48	0/0/5/5
4	SF4	S	1002	1	-	0/0/48/48	0/0/5/5
5	F3S	S	1003	1	-	0/0/24/24	0/0/3/3
8	MPD	S	2001	-	-	0/5/5/5	0/0/0/0
8	MPD	S	2004	-	-	0/5/5/5	0/0/0/0
8	MPD	S	2007	-	-	0/5/5/5	0/0/0/0

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	S	1001	SF4	S2-FE4	242.88	3.96	2.33
4	S	1002	SF4	S2-FE4	242.40	3.96	2.33
4	S	1002	SF4	S3-FE2	232.94	3.89	2.33
4	S	1001	SF4	S1-FE3	228.93	3.87	2.33
4	S	1001	SF4	S4-FE1	228.28	3.86	2.33
4	S	1002	SF4	S1-FE3	228.20	3.86	2.33
4	S	1001	SF4	S3-FE2	222.92	3.83	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	S	1002	SF4	S4-FE1	222.91	3.83	2.33
4	S	1001	SF4	S2-FE1	-12.23	2.25	2.33
4	S	1002	SF4	S3-FE4	-9.84	2.26	2.33
4	S	1002	SF4	S2-FE1	-8.97	2.27	2.33
4	S	1002	SF4	S4-FE3	-8.33	2.27	2.33
4	S	1001	SF4	S1-FE2	-7.47	2.28	2.33
4	S	1001	SF4	S3-FE4	-7.04	2.28	2.33
6	L	1004	NFR	C2-FE	-6.89	1.99	2.00
5	S	1003	F3S	S3-FE1	-6.12	2.29	2.33
4	S	1002	SF4	S1-FE2	-5.76	2.29	2.33
4	S	1001	SF4	S4-FE3	-5.13	2.29	2.33
5	S	1003	F3S	S3-FE4	-5.04	2.29	2.33
5	S	1003	F3S	S3-FE3	-3.96	2.30	2.33
4	S	1002	SF4	S2-FE3	3.01	2.35	2.33
4	S	1002	SF4	S3-FE1	-2.38	2.31	2.33

There are no bond angle outliers.

There are no chirality outliers.

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.