



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:15 PM GMT

PDB ID : 1WUK  
Title : High resolution Structure Of The Oxidized 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 : 1.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

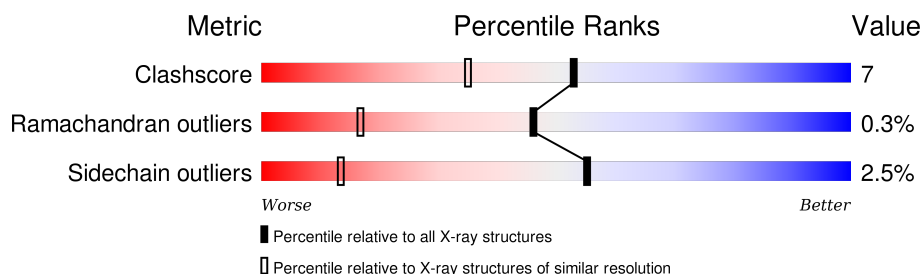
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.10 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	102246	1055 (1.14-1.06)
Ramachandran outliers	100387	1016 (1.14-1.06)
Sidechain outliers	100360	1014 (1.14-1.06)

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  $\geq 3$ , 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.

Note EDS was not executed.

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

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7122 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 [NiFe] hydrogenase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	S	267	Total	C	N	O	S	0	3	0
			2022	1284	342	378	18			

- 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	2	0
			4187	2681	726	765	15			

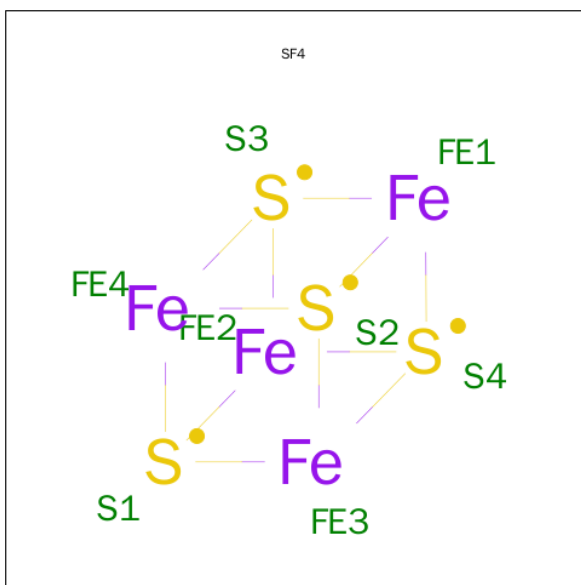
There are 2 discrepancies between the modelled and reference sequences:

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).

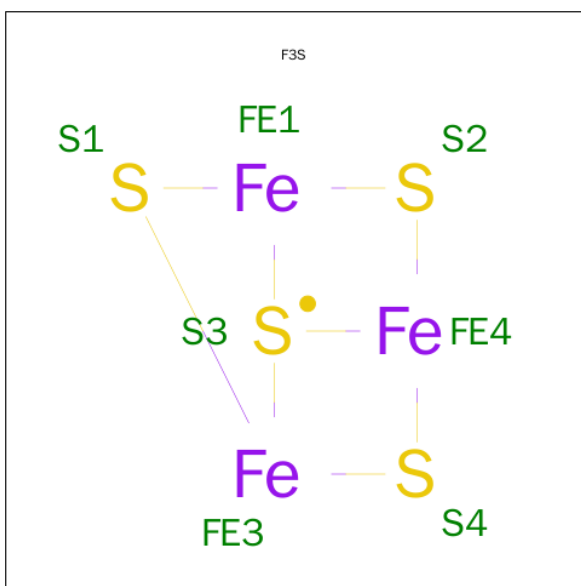
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	1	Total	Mg	0	0
			1	1		

- Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



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		

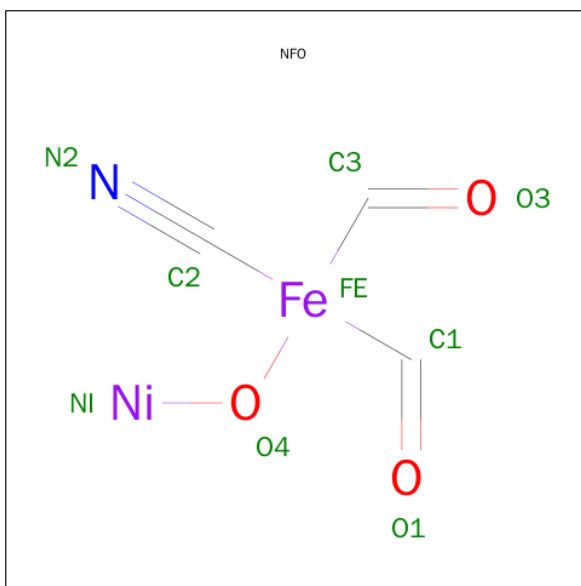
- Molecule 5 is FE3-S4 CLUSTER (three-letter code: F3S) (formula:  $\text{Fe}_3\text{S}_4$ ).



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

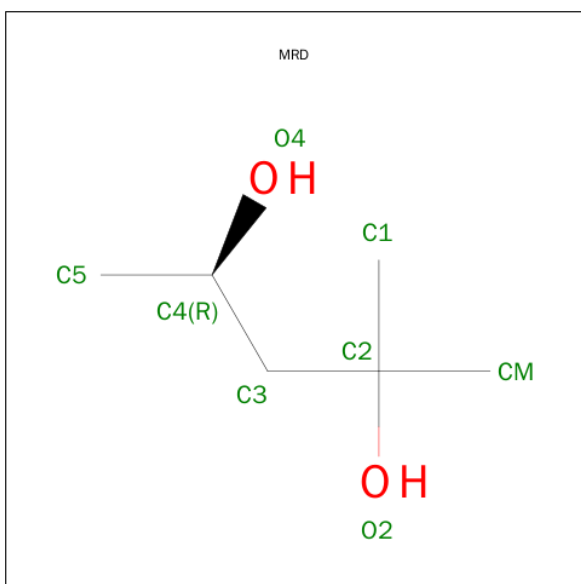
- Molecule 6 is NI-FE OXIDIZED ACTIVE CENTER (three-letter code: NFO) (formula:

C<sub>3</sub>H<sub>2</sub>FeNNiO<sub>3</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	L	1	Total	C	Fe	N	Ni	O	0	0
			9	3	1	1	1	3		

- Molecule 7 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



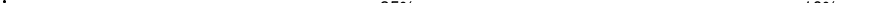

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	S	1	Total	C	O	0	0
			8	6	2		


- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	L	570	Total 570	O 570	0	0
8	S	302	Total 302	O 302	0	0



Note EDS was not executed.

- Chain S:  85% 10% ..
- 

- 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, $\alpha$ , $\beta$ , $\gamma$	98.29Å 125.84Å 66.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.10	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-1.10)	Depositor
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.094 , 0.123	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7122	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	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: MG, NFO, SF4, CSO, F3S, MRD

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	0.82	0/2099	1.32	24/2862 (0.8%)
2	L	0.78	1/4302 (0.0%)	1.21	35/5848 (0.6%)
All	All	0.79	1/6401 (0.0%)	1.24	59/8710 (0.7%)

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	S	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	509	ARG	CZ-NH2	-5.99	1.25	1.33

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	224	ARG	NE-CZ-NH2	17.47	129.04	120.30
1	S	100	ARG	CD-NE-CZ	16.86	147.20	123.60
1	S	1	LEU	O-C-N	14.98	146.67	122.70
1	S	2	MET	C-N-CA	14.03	151.76	122.30
1	S	209	GLU	OE1-CD-OE2	-9.91	111.40	123.30
1	S	1	LEU	CB-CG-CD1	-9.81	94.32	111.00
2	L	487	ARG	CD-NE-CZ	9.77	137.28	123.60
2	L	224	ARG	NH1-CZ-NH2	-9.49	108.97	119.40
2	L	195	HIS	CG-ND1-CE1	9.41	121.38	108.20
1	S	256	ASP	CB-CG-OD1	8.80	126.22	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	1	LEU	CA-C-O	-8.67	101.89	120.10
1	S	212	ARG	NE-CZ-NH2	8.19	124.39	120.30
2	L	136[A]	PHE	CB-CG-CD2	-8.18	115.08	120.80
2	L	136[B]	PHE	CB-CG-CD2	-8.18	115.08	120.80
2	L	38	ARG	NE-CZ-NH2	-8.12	116.24	120.30
2	L	106	LYS	CD-CE-NZ	8.06	130.23	111.70
1	S	2	MET	CB-CG-SD	7.85	135.96	112.40
1	S	6	ARG	NE-CZ-NH1	7.64	124.12	120.30
2	L	144	LYS	CA-CB-CG	7.63	130.18	113.40
2	L	350	ARG	NE-CZ-NH1	7.49	124.05	120.30
2	L	199	TYR	CB-CG-CD1	7.34	125.41	121.00
2	L	20	SER	N-CA-CB	7.33	121.49	110.50
2	L	136[A]	PHE	CB-CG-CD1	7.28	125.89	120.80
2	L	136[B]	PHE	CB-CG-CD1	7.28	125.89	120.80
1	S	1	LEU	CB-CA-C	-7.26	96.40	110.20
2	L	287	TRP	CE3-CZ3-CH2	7.23	129.15	121.20
2	L	430	ARG	NE-CZ-NH1	7.17	123.88	120.30
1	S	26	ARG	NE-CZ-NH1	7.16	123.88	120.30
2	L	489	GLU	OE1-CD-OE2	-6.86	115.06	123.30
1	S	96	ASP	CB-CG-OD2	6.62	124.26	118.30
2	L	433	GLU	CG-CD-OE1	6.54	131.38	118.30
1	S	5	ARG	CD-NE-CZ	-6.48	114.53	123.60
1	S	209	GLU	CB-CG-CD	6.47	131.66	114.20
1	S	61	GLU	OE1-CD-OE2	-6.46	115.55	123.30
2	L	159	PRO	O-C-N	-6.44	112.39	122.70
1	S	181	MET	CG-SD-CE	6.41	110.46	100.20
2	L	273	TYR	CB-CG-CD1	6.24	124.74	121.00
1	S	33	ASP	CB-CG-OD1	6.16	123.85	118.30
2	L	68	ARG	NE-CZ-NH1	6.05	123.33	120.30
2	L	45	ASN	CB-CG-OD1	-5.88	109.84	121.60
2	L	38	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	S	2	MET	CB-CA-C	5.84	122.08	110.40
2	L	21	TYR	CB-CG-CD2	-5.81	117.51	121.00
2	L	487	ARG	NE-CZ-NH1	5.81	123.20	120.30
1	S	26	ARG	NH1-CZ-NH2	-5.64	113.19	119.40
2	L	433	GLU	CG-CD-OE2	-5.57	107.17	118.30
1	S	5	ARG	NE-CZ-NH2	-5.55	117.52	120.30
1	S	218	TYR	CB-CG-CD2	-5.48	117.71	121.00
2	L	509	ARG	NE-CZ-NH1	5.41	123.00	120.30
2	L	287	TRP	CA-CB-CG	-5.34	103.55	113.70
1	S	209	GLU	CG-CD-OE2	5.25	128.81	118.30
2	L	135	ASP	CB-CG-OD2	-5.14	113.67	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	160	ARG	NE-CZ-NH1	-5.12	117.74	120.30
2	L	195	HIS	ND1-CG-CD2	-5.07	98.90	106.00
2	L	32	ARG	NE-CZ-NH1	5.04	122.82	120.30
2	L	426	ARG	NE-CZ-NH1	5.04	122.82	120.30
2	L	279	VAL	CA-CB-CG1	-5.03	103.35	110.90
1	S	26	ARG	NE-CZ-NH2	5.03	122.81	120.30
2	L	299	PHE	CB-CG-CD2	5.02	124.32	120.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	S	4	PRO	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	S	2022	0	1947	37	0
2	L	4187	0	4133	54	0
3	L	1	0	0	0	0
4	S	16	0	0	0	0
5	S	7	0	0	0	0
6	L	9	0	0	0	0
7	S	8	0	13	1	0
8	L	570	0	0	26	0
8	S	302	0	0	15	0
All	All	7122	0	6093	81	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 7.

All (81) 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:S:2:MET:HA	2:L:182:GLN:HG2	1.40	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:2:MET:HB2	2:L:182:GLN:HE21	1.29	0.96
2:L:390:GLN:HA	8:L:5636:HOH:O	1.72	0.88
2:L:423:THR:HG21	8:L:5622:HOH:O	1.73	0.86
2:L:176:THR:O	2:L:180:THR:HG23	1.84	0.76
1:S:94:MET:HE1	8:S:5589:HOH:O	1.84	0.76
1:S:2:MET:HG2	1:S:8:SER:HB2	1.69	0.75
1:S:1:LEU:HD11	1:S:62:GLN:HG2	1.69	0.75
8:S:5589:HOH:O	2:L:57:LEU:HD13	1.89	0.72
1:S:5:ARG:HB2	8:L:5362:HOH:O	1.90	0.72
8:S:5625:HOH:O	2:L:180:THR:HG21	1.90	0.72
1:S:1:LEU:HD21	1:S:59:ALA:O	1.93	0.69
2:L:86:TYR:HB3	8:L:5641:HOH:O	1.91	0.69
1:S:1:LEU:HG	2:L:187:THR:HG21	1.73	0.69
2:L:175:LYS:O	2:L:179:GLU:HG3	1.94	0.68
2:L:299:PHE:HB3	8:L:5626:HOH:O	1.97	0.64
1:S:26:ARG:HH21	2:L:233:ASN:HD21	1.43	0.64
1:S:68:HIS:HB2	8:S:5285:HOH:O	1.99	0.62
2:L:78:GLN:HE21	2:L:86:TYR:H	1.48	0.61
2:L:539:THR:N	8:L:5622:HOH:O	2.34	0.61
2:L:287:TRP:CZ3	8:L:5622:HOH:O	2.52	0.60
2:L:272:VAL:HG22	8:L:5576:HOH:O	2.02	0.59
2:L:233:ASN:C	2:L:233:ASN:HD22	2.05	0.59
2:L:211:HIS:HD2	2:L:276:ASP:OD2	1.85	0.59
2:L:211:HIS:HE1	8:L:5412:HOH:O	1.86	0.59
2:L:133:ALA:HA	2:L:136[B]:PHE:CZ	2.37	0.59
8:S:5589:HOH:O	2:L:57:LEU:HD22	2.02	0.59
1:S:29:GLU:HG3	8:S:5658:HOH:O	2.02	0.58
2:L:36:HIS:HD2	8:L:5118:HOH:O	1.86	0.58
2:L:290:TYR:HE2	8:L:5650:HOH:O	1.86	0.58
2:L:133:ALA:HA	2:L:136[B]:PHE:CE1	2.39	0.57
2:L:474:PHE:HB3	8:L:5626:HOH:O	2.03	0.57
7:S:2001:MRD:H5C2	8:S:5359:HOH:O	2.04	0.57
2:L:119:GLN:HG2	8:L:5641:HOH:O	2.04	0.57
1:S:2:MET:HB3	1:S:43:ASP:OD1	2.05	0.56
1:S:257:PHE:HB2	1:S:261[B]:MET:HG2	1.86	0.56
1:S:1:LEU:HD22	1:S:43:ASP:HB3	1.87	0.56
2:L:298:THR:HG21	8:L:5636:HOH:O	2.05	0.56
1:S:2:MET:CB	2:L:182:GLN:HE21	2.12	0.55
1:S:238:GLN:HE21	2:L:224:ARG:HH21	1.55	0.54
1:S:2:MET:CG	1:S:8:SER:HB2	2.37	0.54
2:L:233:ASN:HA	8:L:5606:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:1:LEU:CG	2:L:187:THR:HG21	2.40	0.52
2:L:75:HIS:HD2	8:L:5021:HOH:O	1.91	0.52
1:S:265:TYR:OH	2:L:75:HIS:HE1	1.93	0.52
1:S:15:ALA:HA	8:S:5589:HOH:O	2.10	0.51
1:S:1:LEU:HD12	1:S:2:MET:H	1.76	0.50
2:L:136[B]:PHE:CD1	2:L:280:VAL:HG11	2.46	0.50
2:L:111:ILE:HD13	8:L:5642:HOH:O	2.12	0.50
1:S:2:MET:HB2	2:L:182:GLN:NE2	2.12	0.49
1:S:19:GLY:HA3	8:L:5666:HOH:O	2.13	0.48
1:S:29:GLU:N	8:S:5658:HOH:O	2.46	0.48
1:S:1:LEU:HB3	2:L:187:THR:OG1	2.14	0.47
2:L:312:ARG:NH1	8:L:5626:HOH:O	2.48	0.47
1:S:14:ASN:O	8:S:5589:HOH:O	2.20	0.47
1:S:1:LEU:HA	2:L:187:THR:OG1	2.15	0.47
1:S:96:ASP:OD2	1:S:100:ARG:NH1	2.49	0.46
1:S:1:LEU:HD13	8:S:5328:HOH:O	2.14	0.46
2:L:401:LYS:HG2	8:L:5670:HOH:O	2.16	0.45
1:S:5:ARG:HB3	1:S:6:ARG:H	1.65	0.45
2:L:236:THR:N	8:L:5606:HOH:O	2.50	0.45
1:S:36:ILE:HD13	1:S:36:ILE:N	2.32	0.44
2:L:235:HIS:N	8:L:5606:HOH:O	2.50	0.44
2:L:512:LYS:NZ	8:L:5547:HOH:O	2.49	0.44
2:L:356:GLN:N	8:L:5567:HOH:O	2.49	0.44
2:L:287:TRP:HZ3	8:L:5622:HOH:O	1.96	0.44
1:S:36:ILE:HG23	8:S:5075:HOH:O	2.18	0.44
1:S:1:LEU:HD12	1:S:1:LEU:H3	1.83	0.43
8:S:5589:HOH:O	2:L:57:LEU:CD1	2.58	0.43
1:S:241:TRP:CH2	1:S:243:VAL:HB	2.54	0.43
1:S:2:MET:HG3	8:S:5328:HOH:O	2.18	0.43
1:S:13:HIS:HE1	1:S:21:SER:OG	2.02	0.42
1:S:229:ASN:HD22	1:S:230:ASN:H	1.67	0.42
2:L:233:ASN:ND2	2:L:233:ASN:C	2.72	0.42
2:L:418:GLU:H	2:L:418:GLU:CD	2.23	0.42
2:L:500:VAL:CG1	2:L:501:PRO:HD2	2.50	0.42
2:L:86:TYR:HD1	8:L:5641:HOH:O	2.03	0.41
2:L:299:PHE:H	2:L:476:ASN:ND2	2.18	0.41
2:L:291:GLY:HA2	2:L:521:SER:O	2.21	0.41
2:L:211:HIS:CD2	2:L:276:ASP:OD2	2.70	0.40
8:S:5589:HOH:O	2:L:57:LEU:CD2	2.67	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	268/267 (100%)	261 (97%)	5 (2%)	2 (1%)	26	4
2	L	533/534 (100%)	518 (97%)	15 (3%)	0	100	100
All	All	801/801 (100%)	779 (97%)	20 (2%)	2 (0%)	46	19

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	S	5	ARG
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	216/213 (101%)	207 (96%)	9 (4%)	36	4
2	L	439/437 (100%)	432 (98%)	7 (2%)	70	31
All	All	655/650 (101%)	639 (98%)	16 (2%)	55	15

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	36	ILE

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Mol	Chain	Res	Type
1	S	91	ASN
1	S	138	LYS
1	S	168	LYS
1	S	229	ASN
1	S	230	ASN
2	L	50	ASN
2	L	132	HIS
2	L	144	LYS
2	L	161	LYS
2	L	233	ASN
2	L	400	PRO
2	L	457	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	S	13	HIS
1	S	91	ASN
1	S	139	HIS
1	S	190	GLN
1	S	229	ASN
1	S	230	ASN
1	S	238	GLN
1	S	266	GLN
1	S	267	ASN
2	L	36	HIS
2	L	50	ASN
2	L	75	HIS
2	L	78	GLN
2	L	113	ASN
2	L	132	HIS
2	L	188	ASN
2	L	205	ASN
2	L	211	HIS
2	L	233	ASN
2	L	235	HIS
2	L	310	ASN
2	L	334	GLN
2	L	358	GLN
2	L	390	GLN
2	L	446	GLN
2	L	451	ASN

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Mol	Chain	Res	Type
2	L	457	ASN
2	L	476	ASN
2	L	513	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	$\# Z  > 2$
2	CSO	L	546	2,6	3,6,7	0.47	0	1,6,8	1.79	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
2	CSO	L	546	2,6	-	0/1/5/7	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

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

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	NFO	L	1004	2	1,8,8	1.47	0	0,10,10	0.00	-
4	SF4	S	1001	1	0,12,12	0.00	-	0,24,24	0.00	-
4	SF4	S	1002	1	0,12,12	0.00	-	0,24,24	0.00	-
5	F3S	S	1003	1	0,9,9	0.00	-	0,15,15	0.00	-
7	MRD	S	2001	-	6,7,7	0.73	0	7,10,10	2.75	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
6	NFO	L	1004	2	-	0/0/12/12	0/0/0/0
4	SF4	S	1001	1	-	0/0/48/48	2/6/5/5
4	SF4	S	1002	1	-	0/0/48/48	2/6/5/5
5	F3S	S	1003	1	-	0/0/24/24	0/0/3/3
7	MRD	S	2001	-	-	0/5/5/5	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	S	2001	MRD	C2-C3-C4	6.98	149.65	116.66

There are no chirality outliers.

There are no torsion outliers.

All (4) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	S	1001	SF4	FE3-FE4-S1-S2
4	S	1001	SF4	FE1-FE2-S3-S4
4	S	1002	SF4	FE3-FE4-S1-S2
4	S	1002	SF4	FE1-FE2-S3-S4

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	S	2001	MRD	1	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](#)

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

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

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

### 6.3 Carbohydrates [i](#)

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

### 6.4 Ligands [i](#)

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

### 6.5 Other polymers [i](#)

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