



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 09:26 AM EDT

PDB ID : 1WUJ / pdb_00001wuj
Title : Three-Dimensional Structure Of The Ni-B 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 : 1.40 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

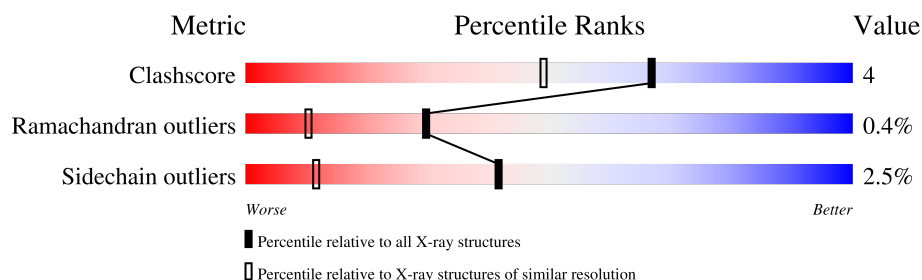
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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	190562	2660 (1.40-1.40)
Ramachandran outliers	187476	2611 (1.40-1.40)
Sidechain outliers	187428	2610 (1.40-1.40)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	S	267	 86% 12% ..
2	L	534	 88% 10% •

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7064 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	0	0
			2019	1282	342	378	17			

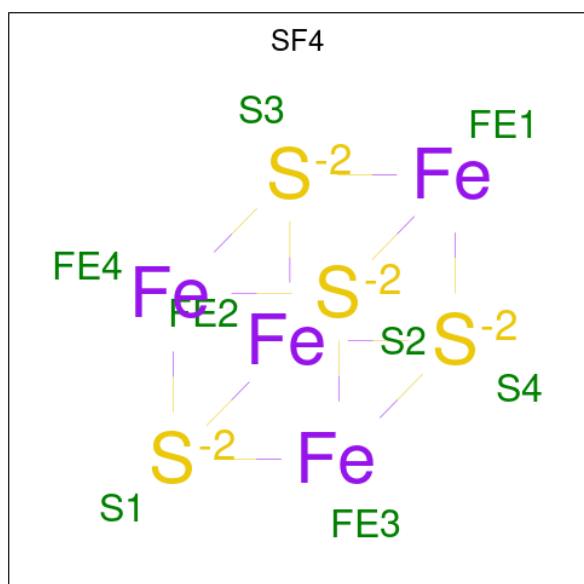
- Molecule 2 is a protein called Periplasmic [NiFe] hydrogenase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	534	Total	C	N	O	S	0	0	0
			4178	2674	725	764	15			

There are 2 discrepancies between the modelled and reference sequences:

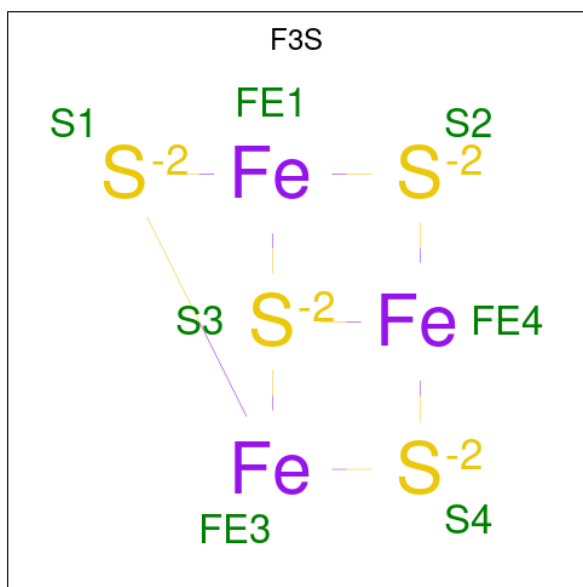
Chain	Residue	Modelled	Actual	Comment	Reference
L	514	LYS	ASN	SEE REMARK 999	UNP P21852
L	515	LEU	VAL	SEE REMARK 999	UNP P21852

- Molecule 3 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



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

- Molecule 4 is FE3-S4 CLUSTER (CCD ID: F3S) (formula: Fe_3S_4).

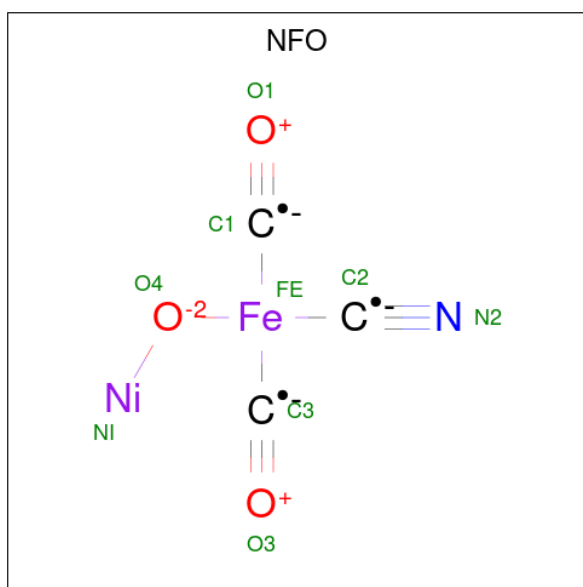


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	S	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 6 is NI-FE OXIDIZED ACTIVE CENTER (CCD ID: NFO) (formula: $\text{C}_3\text{FeNNiO}_3$).



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 water.

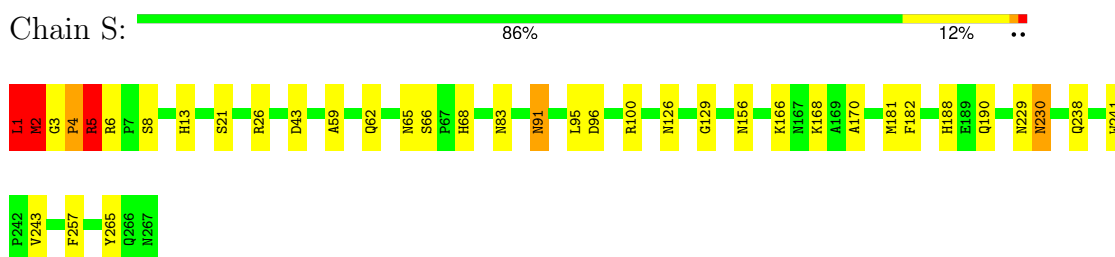
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	S	287	Total	O	0	0
			287	287		
7	L	547	Total	O	0	0
			547	547		

3 Residue-property plots

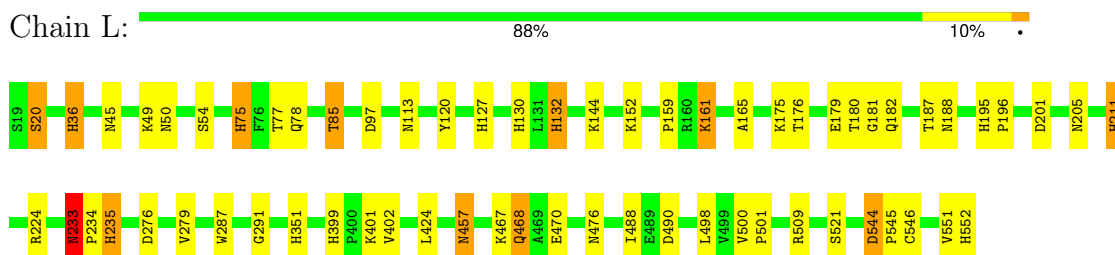
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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



- Molecule 2: Periplasmic [NiFe] hydrogenase large subunit



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	98.16Å 125.92Å 66.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.40	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-1.40)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.115 , 0.162	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7064	wwPDB-VP
Average B, all atoms (Å ²)	17.0	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, SF4, F3S, NFO, CSO

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	0.78	1/2075 (0.0%)	1.60	38/2830 (1.3%)
2	L	0.76	2/4281 (0.0%)	1.57	74/5820 (1.3%)
All	All	0.77	3/6356 (0.0%)	1.58	112/8650 (1.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S	126	ASN	C-O	7.04	1.27	1.23
2	L	552	HIS	C-O	5.43	1.34	1.23
2	L	399	HIS	CD2-NE2	-5.17	1.32	1.37

All (112) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	224	ARG	NE-CZ-NH2	13.69	131.52	119.20
1	S	229	ASN	O-C-N	-12.77	110.82	123.46
1	S	129	GLY	O-C-N	-12.19	112.63	122.51
1	S	2	MET	CA-C-N	11.67	140.19	121.87
1	S	2	MET	C-N-CA	11.67	140.19	121.87
2	L	424	LEU	O-C-N	-10.86	110.88	122.07
2	L	233	ASN	CB-CG-OD1	10.83	142.46	120.80
2	L	233	ASN	OD1-CG-ND2	-10.76	111.84	122.60
1	S	95	LEU	CA-C-N	10.61	134.88	120.44
1	S	95	LEU	C-N-CA	10.61	134.88	120.44
1	S	1	LEU	O-C-N	10.55	139.88	123.00
1	S	26	ARG	NE-CZ-NH2	10.20	128.38	119.20
1	S	129	GLY	CA-C-N	10.13	135.53	121.05
1	S	129	GLY	C-N-CA	10.13	135.53	121.05
2	L	424	LEU	CA-C-N	10.02	141.05	121.41
2	L	424	LEU	C-N-CA	10.02	141.05	121.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	238	GLN	OE1-CD-NE2	-9.93	112.67	122.60
1	S	229	ASN	CA-C-N	9.67	138.29	122.73
1	S	229	ASN	C-N-CA	9.67	138.29	122.73
2	L	234	PRO	CA-C-N	9.39	139.48	121.54
2	L	234	PRO	C-N-CA	9.39	139.48	121.54
2	L	401	LYS	CA-C-N	8.99	131.89	120.56
2	L	401	LYS	C-N-CA	8.99	131.89	120.56
2	L	224	ARG	NH1-CZ-NH2	-8.99	107.61	119.30
2	L	78	GLN	OE1-CD-NE2	-8.98	113.62	122.60
2	L	85	THR	CA-C-N	8.63	138.02	121.54
2	L	85	THR	C-N-CA	8.63	138.02	121.54
2	L	165	ALA	CA-C-N	8.52	131.52	120.44
2	L	165	ALA	C-N-CA	8.52	131.52	120.44
2	L	78	GLN	CG-CD-OE1	8.33	137.46	120.80
2	L	20	SER	CA-C-N	8.25	132.42	120.71
2	L	20	SER	C-N-CA	8.25	132.42	120.71
2	L	509	ARG	NE-CZ-NH1	8.17	129.67	121.50
2	L	54	SER	CA-C-N	8.06	133.48	122.77
2	L	54	SER	C-N-CA	8.06	133.48	122.77
1	S	230	ASN	CA-CB-CG	7.99	120.59	112.60
2	L	195	HIS	CB-CG-CD2	7.98	141.57	131.20
2	L	113	ASN	CA-CB-CG	7.95	120.55	112.60
2	L	399	HIS	CG-CD2-NE2	7.84	115.04	107.20
1	S	95	LEU	O-C-N	-7.78	114.06	122.07
2	L	130	HIS	CA-CB-CG	-7.74	106.06	113.80
2	L	544	ASP	CA-CB-CG	7.57	120.17	112.60
2	L	201	ASP	CA-CB-CG	7.52	120.12	112.60
2	L	75	HIS	CB-CG-CD2	-7.51	121.44	131.20
1	S	229	ASN	CA-CB-CG	7.44	120.04	112.60
1	S	83	ASN	CA-CB-CG	-7.31	105.29	112.60
2	L	144	LYS	CA-C-O	7.30	127.90	119.35
2	L	75	HIS	CB-CG-ND1	7.21	133.52	122.70
2	L	233	ASN	CB-CG-ND2	-7.18	105.63	116.40
1	S	229	ASN	OD1-CG-ND2	-7.16	115.44	122.60
2	L	50	ASN	CA-CB-CG	6.87	119.47	112.60
2	L	233	ASN	CA-CB-CG	6.84	119.44	112.60
2	L	127	HIS	CA-CB-CG	-6.79	107.02	113.80
2	L	205	ASN	OD1-CG-ND2	-6.75	115.85	122.60
1	S	26	ARG	NH1-CZ-NH2	-6.75	110.53	119.30
2	L	196	PRO	CA-C-N	6.74	134.72	121.58
2	L	196	PRO	C-N-CA	6.74	134.72	121.58
2	L	36	HIS	CB-CG-CD2	-6.73	122.45	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	196	PRO	O-C-N	-6.64	113.35	122.24
1	S	229	ASN	CA-C-O	6.57	128.33	121.10
2	L	54	SER	O-C-N	-6.53	114.91	123.13
1	S	1	LEU	CA-C-O	-6.50	109.76	120.80
2	L	97	ASP	CA-CB-CG	6.37	118.97	112.60
2	L	401	LYS	O-C-N	-6.32	114.95	122.15
2	L	161	LYS	O-C-N	-6.29	116.05	123.22
2	L	551	VAL	CB-CA-C	-6.27	104.34	111.55
2	L	402	VAL	N-CA-C	-6.24	104.43	110.42
1	S	96	ASP	N-CA-C	-6.22	104.42	111.14
2	L	161	LYS	CA-C-O	6.18	127.52	120.54
2	L	476	ASN	CA-CB-CG	-6.13	106.47	112.60
1	S	156	ASN	OD1-CG-ND2	6.08	128.68	122.60
1	S	257	PHE	CA-CB-CG	6.01	119.81	113.80
2	L	195	HIS	ND1-CG-CD2	-5.98	100.12	106.10
2	L	287	TRP	CA-CB-CG	-5.98	102.25	113.60
1	S	1	LEU	CD1-CG-CD2	5.96	123.91	110.80
2	L	195	HIS	ND1-CE1-NE2	-5.96	102.44	108.40
1	S	129	GLY	CA-C-O	5.95	128.03	120.29
2	L	132	HIS	CB-CG-CD2	-5.95	123.47	131.20
2	L	181	GLY	CA-C-O	5.93	125.33	119.04
2	L	36	HIS	CB-CG-ND1	5.91	131.56	122.70
2	L	161	LYS	CB-CA-C	5.90	119.48	109.80
2	L	159	PRO	CA-C-N	5.86	129.69	121.02
2	L	159	PRO	C-N-CA	5.86	129.69	121.02
1	S	100	ARG	NE-CZ-NH2	5.85	124.47	119.20
2	L	161	LYS	CA-C-N	5.79	131.15	122.99
2	L	161	LYS	C-N-CA	5.79	131.15	122.99
1	S	91	ASN	CB-CG-ND2	5.71	124.96	116.40
1	S	238	GLN	CG-CD-OE1	5.65	132.10	120.80
1	S	95	LEU	CA-C-O	5.64	126.74	120.82
2	L	490	ASP	CA-CB-CG	5.60	118.20	112.60
1	S	26	ARG	CG-CD-NE	-5.58	99.72	112.00
2	L	457	ASN	CB-CG-ND2	5.56	124.75	116.40
2	L	50	ASN	OD1-CG-ND2	-5.54	117.06	122.60
1	S	170	ALA	O-C-N	5.51	127.59	121.53
1	S	126	ASN	OD1-CG-ND2	-5.48	117.12	122.60
2	L	188	ASN	CA-CB-CG	5.42	118.02	112.60
2	L	195	HIS	CG-ND1-CE1	5.42	118.51	109.30
1	S	188	HIS	CA-CB-CG	5.42	119.22	113.80
2	L	120	TYR	CA-CB-CG	5.39	123.61	113.90
1	S	100	ARG	CD-NE-CZ	5.36	131.90	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	211	HIS	CG-CD2-NE2	5.35	112.55	107.20
2	L	399	HIS	ND1-CG-CD2	-5.33	100.77	106.10
2	L	77	THR	CA-CB-OG1	-5.30	101.65	109.60
2	L	85	THR	O-C-N	-5.29	116.56	122.75
1	S	126	ASN	CA-CB-CG	5.29	117.89	112.60
1	S	65	ASN	CA-CB-CG	-5.27	107.33	112.60
2	L	85	THR	CA-C-O	5.25	127.65	121.87
2	L	159	PRO	O-C-N	-5.16	115.31	122.27
2	L	488	ILE	O-C-N	5.12	128.78	122.95
1	S	190	GLN	OE1-CD-NE2	5.08	127.68	122.60
2	L	132	HIS	CB-CG-ND1	5.08	130.32	122.70
2	L	351	HIS	CA-CB-CG	-5.08	108.72	113.80

There are no chirality outliers.

There are no planarity outliers.

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	2019	0	1949	28	0
2	L	4178	0	4129	24	0
3	S	16	0	0	0	0
4	S	7	0	0	0	0
5	L	1	0	0	0	0
6	L	9	0	0	1	0
7	L	547	0	0	7	0
7	S	287	0	0	1	0
All	All	7064	0	6078	45	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 4.

All (45) 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:HE1	1:S:68:HIS:HB2	1.54	0.89
1:S:2:MET:HA	2:L:182:GLN:HG2	1.53	0.89
1:S:2:MET:HB2	2:L:182:GLN:HE21	1.40	0.86
1:S:1:LEU:HD21	1:S:59:ALA:O	1.90	0.70
2:L:176:THR:O	2:L:180:THR:HG23	1.91	0.70
1:S:5:ARG:NH1	1:S:5:ARG:HA	2.06	0.70
1:S:166:LYS:HD3	7:S:5490:HOH:O	1.91	0.69
2:L:175:LYS:O	2:L:179:GLU:HG3	1.98	0.64
1:S:2:MET:HB3	1:S:43:ASP:OD1	1.98	0.63
1:S:5:ARG:HA	1:S:5:ARG:HH11	1.66	0.60
2:L:211:HIS:HE1	7:L:5242:HOH:O	1.87	0.58
2:L:233:ASN:C	2:L:233:ASN:HD22	2.12	0.58
1:S:5:ARG:HB3	2:L:182:GLN:OE1	2.05	0.56
1:S:2:MET:HG2	1:S:8:SER:HB2	1.88	0.55
2:L:211:HIS:HD2	2:L:276:ASP:OD2	1.90	0.55
1:S:2:MET:HE3	1:S:66:SER:CB	2.36	0.54
2:L:36:HIS:HD2	7:L:5087:HOH:O	1.90	0.54
1:S:1:LEU:HA	2:L:187:THR:OG1	2.09	0.53
1:S:2:MET:HA	2:L:182:GLN:CG	2.33	0.53
1:S:5:ARG:HB2	7:L:5523:HOH:O	2.09	0.53
1:S:2:MET:CE	1:S:68:HIS:HB2	2.34	0.52
2:L:75:HIS:HD2	7:L:5015:HOH:O	1.92	0.51
1:S:2:MET:HE3	1:S:66:SER:HB3	1.92	0.51
1:S:1:LEU:HB3	2:L:187:THR:OG1	2.10	0.51
1:S:1:LEU:HD22	1:S:43:ASP:HB3	1.94	0.50
1:S:3:GLY:O	1:S:4:PRO:O	2.30	0.50
1:S:265:TYR:OH	2:L:75:HIS:HE1	1.96	0.48
2:L:20:SER:HA	7:L:5689:HOH:O	2.14	0.47
1:S:3:GLY:HA2	1:S:68:HIS:CD2	2.50	0.46
1:S:1:LEU:HD11	1:S:62:GLN:HG2	1.98	0.46
2:L:291:GLY:HA2	2:L:521:SER:O	2.16	0.45
2:L:85:THR:OG1	2:L:235:HIS:HD2	2.00	0.45
1:S:241:TRP:CH2	1:S:243:VAL:HB	2.51	0.44
2:L:500:VAL:CG1	2:L:501:PRO:HD2	2.48	0.44
2:L:467:LYS:NZ	7:L:5491:HOH:O	2.51	0.43
2:L:498:LEU:HD12	2:L:498:LEU:N	2.33	0.43
1:S:181:MET:HE3	1:S:182:PHE:CE2	2.53	0.43
2:L:468:GLN:NE2	7:L:5621:HOH:O	2.51	0.43
1:S:1:LEU:HD12	1:S:1:LEU:N	2.33	0.42
1:S:13:HIS:HE1	1:S:21:SER:OG	2.01	0.42
1:S:5:ARG:HH11	1:S:5:ARG:HD3	1.66	0.42
2:L:544:ASP:N	2:L:545:PRO:HD3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:5:ARG:HB3	1:S:6:ARG:H	1.81	0.40
2:L:211:HIS:CD2	2:L:276:ASP:OD2	2.73	0.40
2:L:546:CSO:CB	6:L:1004:NFO:O4	2.65	0.40

There are no symmetry-related clashes.

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	S	265/267 (99%)	256 (97%)	7 (3%)	2 (1%)	16	3
2	L	531/534 (99%)	519 (98%)	11 (2%)	1 (0%)	43	19
All	All	796/801 (99%)	775 (97%)	18 (2%)	3 (0%)	30	10

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	S	4	PRO
2	L	235	HIS
1	S	5	ARG

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	S	213/213 (100%)	207 (97%)	6 (3%)	38 9
2	L	437/437 (100%)	427 (98%)	10 (2%)	44 13
All	All	650/650 (100%)	634 (98%)	16 (2%)	42 11

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	91	ASN
1	S	168	LYS
1	S	230	ASN
2	L	45	ASN
2	L	49	LYS
2	L	132	HIS
2	L	152	LYS
2	L	161	LYS
2	L	233	ASN
2	L	279	VAL
2	L	457	ASN
2	L	468	GLN
2	L	470	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	S	13	HIS
1	S	45	HIS
1	S	68	HIS
1	S	126	ASN
1	S	139	HIS
1	S	229	ASN
1	S	230	ASN
2	L	36	HIS
2	L	50	ASN
2	L	75	HIS
2	L	78	GLN

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Mol	Chain	Res	Type
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	289	GLN
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	6,2	3,6,7	0.51	0	1,6,8	0.81	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	6,2	-	1/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L	546	CSO	N-CA-CB-SG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	546	CSO	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\# Z > 2$
3	SF4	S	1002	1	0,12,12	-	-	-		
3	SF4	S	1001	1	0,12,12	-	-	-		
4	F3S	S	1003	1	0,9,9	-	-	-		
6	NFO	L	1004	2	3,8,8	3.49	2 (66%)	-		

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	SF4	S	1002	1	-	-	0/6/5/5
3	SF4	S	1001	1	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	F3S	S	1003	1	-	-	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	L	1004	NFO	C2-N2	-5.57	1.02	1.13
6	L	1004	NFO	O3-C3	-2.36	1.11	1.16

There are no bond angle outliers.

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
6	L	1004	NFO	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.