



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 03:15 am GMT

PDB ID : 1UBM
Title : Three-dimensional Structure of The Carbon Monoxide Complex of [NiFe]hydrogenase From Desulfovibrio vulgaris Miyazaki F
Authors : Ogata, H.; Mizoguchi, Y.; Mizuno, N.; Miki, K.; Adachi, S.; Yasuoka, N.; Yagi, T.; Yamauchi, O.; Hirota, S.; Higuchi, Y.
Deposited on : 2003-04-04
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

<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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

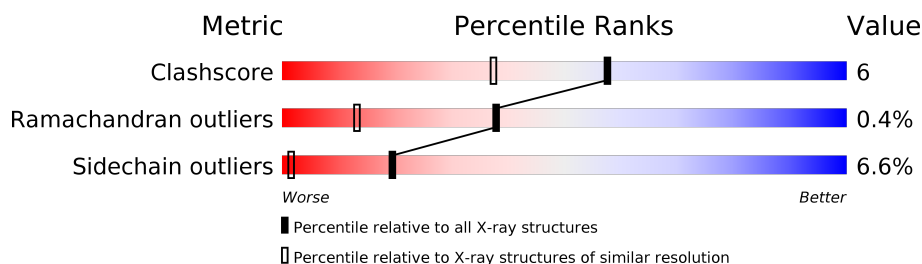
1 Overall quality at a glance

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	112137	1411 (1.40-1.40)
Ramachandran outliers	110173	1373 (1.40-1.40)
Sidechain outliers	110143	1372 (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 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.

Note EDS was not executed.

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

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	MPD	S	2004	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7084 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
			4177	2674	725	763	15			

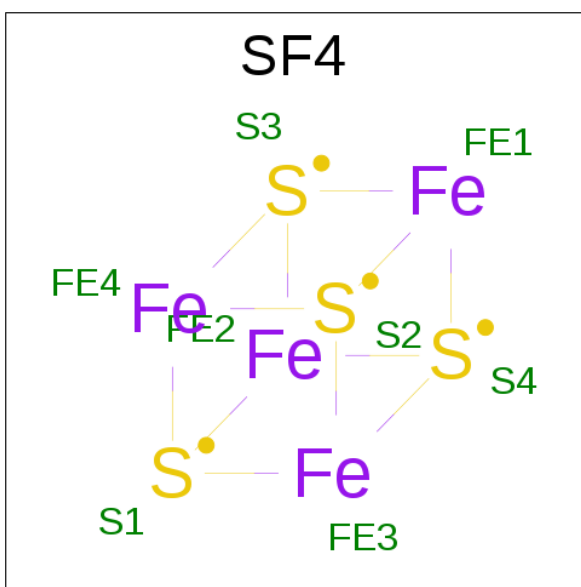
There are 2 discrepancies between the modelled and reference sequences:

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).

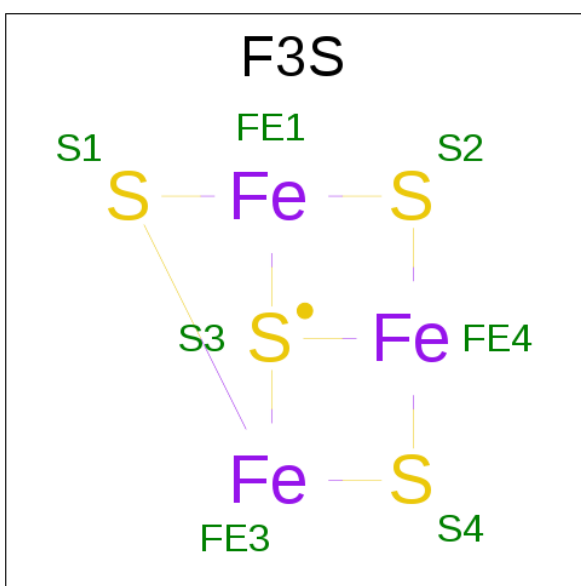
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	1	Total	Mg	0	0
			1	1		

- 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		

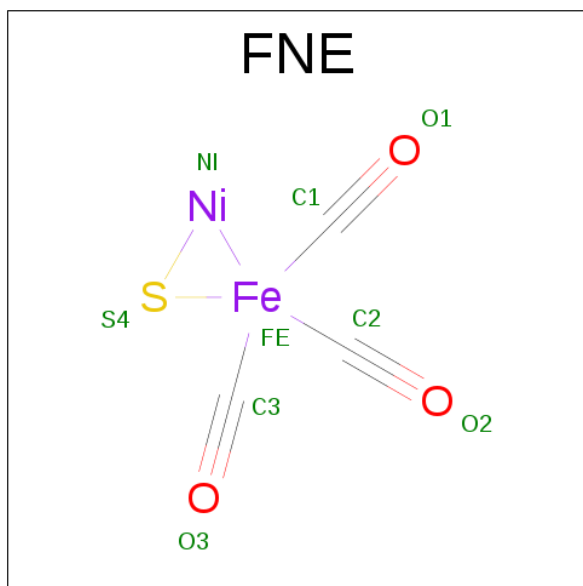
- Molecule 5 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe_3S_4).



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

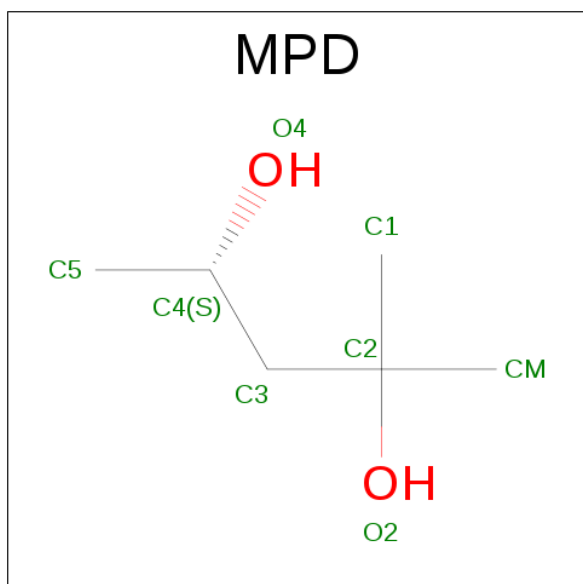
- Molecule 6 is (MU-SULPHIDO)-BIS(MU-CYS,S)-[TRICARBONYLIRON-DI-(CYS,S)NIC

KEL(II)](FE-NI) (three-letter code: FNE) (formula: C_3FeNiO_3S).



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

- Molecule 7 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



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

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

- Molecule 8 is water.

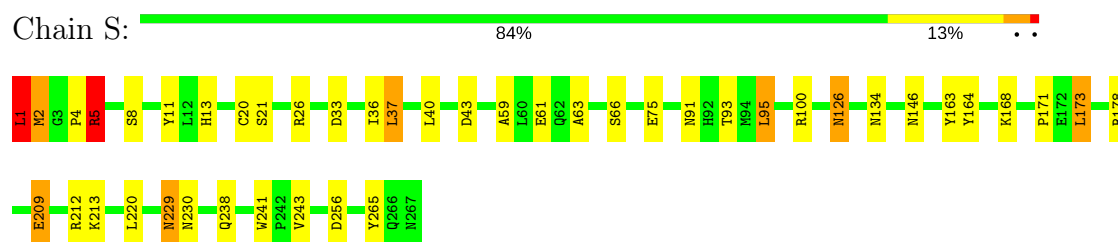
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	L	540	Total	O	0	0
			540	540		
8	S	276	Total	O	0	0
			276	276		

3 Residue-property plots

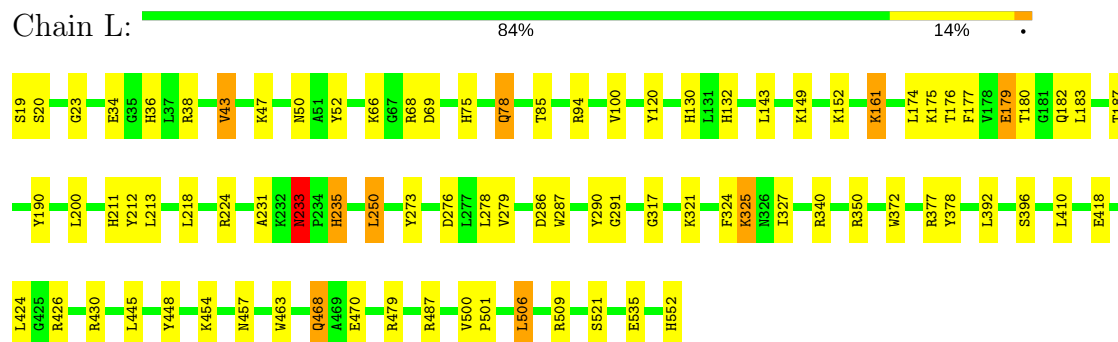
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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



• 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	97.66 Å 125.30 Å 66.41 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.40	Depositor
% Data completeness (in resolution range)	87.3 (20.00-1.40)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.112 , 0.189	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7084	wwPDB-VP
Average B, all atoms (Å ²)	23.0	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: MPD, MG, F3S, FNE, SF4

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	0.51	0/2075	1.38	26/2830 (0.9%)
2	L	0.53	1/4288 (0.0%)	1.38	44/5831 (0.8%)
All	All	0.53	1/6363 (0.0%)	1.38	70/8661 (0.8%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	552	HIS	C-O	10.81	1.43	1.23

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	26	ARG	NE-CZ-NH2	23.17	131.88	120.30
2	L	273	TYR	CB-CG-CD1	14.20	129.52	121.00
2	L	509	ARG	NE-CZ-NH1	13.69	127.14	120.30
2	L	224	ARG	NE-CZ-NH2	11.88	126.24	120.30
1	S	163	TYR	CB-CG-CD1	10.82	127.49	121.00
2	L	233	ASN	CB-CG-OD1	10.45	142.49	121.60
2	L	430	ARG	NE-CZ-NH2	-9.65	115.47	120.30
2	L	426	ARG	NE-CZ-NH2	-9.46	115.57	120.30
2	L	506	LEU	CA-CB-CG	8.86	135.67	115.30
2	L	340	ARG	NE-CZ-NH2	-8.84	115.88	120.30
2	L	377	ARG	NE-CZ-NH1	8.65	124.62	120.30
2	L	273	TYR	CG-CD1-CE1	8.59	128.17	121.30
2	L	430	ARG	NE-CZ-NH1	8.35	124.48	120.30
2	L	224	ARG	NH1-CZ-NH2	-8.05	110.54	119.40
1	S	26	ARG	NH1-CZ-NH2	-7.64	110.99	119.40
1	S	33	ASP	CB-CG-OD1	7.54	125.08	118.30
2	L	509	ARG	NE-CZ-NH2	-7.54	116.53	120.30
1	S	100	ARG	NE-CZ-NH1	7.32	123.96	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	479	ARG	NE-CZ-NH1	7.28	123.94	120.30
1	S	26	ARG	CD-NE-CZ	7.08	133.51	123.60
1	S	100	ARG	NE-CZ-NH2	-7.06	116.77	120.30
2	L	424	LEU	C-N-CA	7.03	137.07	122.30
2	L	100	VAL	CA-CB-CG2	-6.94	100.48	110.90
1	S	11	TYR	CB-CG-CD1	6.81	125.09	121.00
1	S	1	LEU	O-C-N	6.79	133.56	122.70
2	L	350	ARG	NE-CZ-NH2	-6.76	116.92	120.30
2	L	287	TRP	CA-CB-CG	-6.73	100.91	113.70
1	S	238	GLN	CG-CD-OE1	6.58	134.76	121.60
2	L	372	TRP	O-C-N	-6.57	112.19	122.70
1	S	100	ARG	CD-NE-CZ	6.49	132.69	123.60
2	L	190	TYR	CB-CG-CD2	6.42	124.85	121.00
1	S	26	ARG	NE-CZ-NH1	-6.41	117.10	120.30
1	S	95	LEU	C-N-CA	6.28	137.40	121.70
2	L	94	ARG	NE-CZ-NH2	-6.26	117.17	120.30
2	L	52	TYR	CB-CG-CD2	-6.24	117.26	121.00
2	L	68	ARG	NE-CZ-NH1	6.18	123.39	120.30
1	S	95	LEU	O-C-N	-6.08	112.98	122.70
2	L	273	TYR	CB-CG-CD2	-6.07	117.36	121.00
2	L	85	THR	C-N-CA	6.03	136.76	121.70
2	L	426	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	S	126	ASN	CB-CG-OD1	5.86	133.33	121.60
1	S	212	ARG	NE-CZ-NH2	5.86	123.23	120.30
2	L	224	ARG	NE-CZ-NH1	5.83	123.22	120.30
1	S	5	ARG	NE-CZ-NH1	5.81	123.21	120.30
2	L	290	TYR	CG-CD1-CE1	-5.76	116.69	121.30
2	L	250	LEU	CA-CB-CG	5.74	128.49	115.30
2	L	34	GLU	CG-CD-OE1	5.62	129.54	118.30
2	L	378	TYR	CB-CG-CD1	5.58	124.35	121.00
2	L	235	HIS	ND1-CG-CD2	-5.56	98.22	106.00
1	S	163	TYR	CG-CD1-CE1	5.55	125.74	121.30
1	S	5	ARG	NE-CZ-NH2	-5.53	117.54	120.30
2	L	38	ARG	NE-CZ-NH2	-5.53	117.54	120.30
2	L	78	GLN	CG-CD-OE1	5.50	132.59	121.60
1	S	178	ARG	NE-CZ-NH1	5.45	123.03	120.30
2	L	94	ARG	NE-CZ-NH1	5.39	123.00	120.30
2	L	38	ARG	CD-NE-CZ	5.33	131.06	123.60
2	L	448	TYR	CB-CG-CD1	-5.31	117.81	121.00
2	L	212	TYR	CA-CB-CG	5.31	123.49	113.40
2	L	468	GLN	CA-CB-CG	5.30	125.07	113.40
2	L	130	HIS	CA-CB-CG	-5.25	104.67	113.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	120	TYR	CA-CB-CG	5.22	123.32	113.40
2	L	20	SER	CA-C-O	5.21	131.05	120.10
1	S	209	GLU	OE1-CD-OE2	-5.12	117.15	123.30
1	S	229	ASN	O-C-N	-5.12	114.51	122.70
1	S	33	ASP	CB-CG-OD2	-5.12	113.70	118.30
1	S	212	ARG	NE-CZ-NH1	-5.08	117.76	120.30
1	S	163	TYR	CB-CG-CD2	-5.08	117.95	121.00
1	S	93	THR	OG1-CB-CG2	-5.07	98.33	110.00
2	L	340	ARG	NH1-CZ-NH2	5.05	124.96	119.40
2	L	69	ASP	CB-CG-OD1	5.03	122.83	118.30

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	38	0
2	L	4177	0	4128	39	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	16	0	28	7	0
7	S	24	0	42	10	0
8	L	540	0	0	12	0
8	S	276	0	0	5	0
All	All	7084	0	6147	70	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 6.

All (70) 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:146:ASN:HD21	7:S:2004:MPD:H13	1.23	0.97
1:S:2:MET:HB2	2:L:182:GLN:HE21	1.38	0.88
1:S:1:LEU:HG	2:L:187:THR:HG21	1.58	0.85
1:S:2:MET:HA	2:L:182:GLN:HG2	1.63	0.81
1:S:2:MET:HG2	1:S:8:SER:HB2	1.64	0.77
1:S:134:ASN:HB2	7:S:2004:MPD:H12	1.67	0.77
1:S:2:MET:HG3	8:S:3298:HOH:O	1.85	0.74
2:L:175:LYS:O	2:L:179:GLU:HG3	1.87	0.74
2:L:176:THR:O	2:L:180:THR:HG23	1.87	0.73
1:S:5:ARG:HH11	1:S:5:ARG:HA	1.55	0.72
2:L:325:LYS:HD2	8:L:3643:HOH:O	1.91	0.70
1:S:1:LEU:HD21	1:S:59:ALA:O	1.91	0.70
1:S:146:ASN:ND2	7:S:2004:MPD:H13	2.02	0.69
2:L:392:LEU:HD22	7:L:2006:MPD:H11	1.77	0.66
7:L:2010:MPD:HM3	8:L:3335:HOH:O	1.99	0.62
1:S:2:MET:HB3	1:S:43:ASP:OD1	1.99	0.62
1:S:37:LEU:HD12	2:L:177:PHE:CD2	2.36	0.59
1:S:13:HIS:HD2	8:S:3034:HOH:O	1.85	0.58
1:S:256:ASP:HB3	8:S:3418:HOH:O	2.03	0.58
2:L:325:LYS:N	2:L:325:LYS:HE3	2.17	0.58
2:L:454:LYS:HE2	8:L:3326:HOH:O	2.05	0.57
2:L:211:HIS:HE1	8:L:3220:HOH:O	1.87	0.56
1:S:2:MET:HB2	2:L:182:GLN:NE2	2.16	0.55
2:L:75:HIS:HD2	8:L:3074:HOH:O	1.90	0.54
1:S:1:LEU:HA	2:L:187:THR:OG1	2.08	0.54
2:L:535:GLU:HB2	8:L:3725:HOH:O	2.08	0.53
1:S:265:TYR:OH	2:L:75:HIS:HE1	1.92	0.52
1:S:241:TRP:CH2	1:S:243:VAL:HB	2.44	0.52
2:L:392:LEU:HD22	7:L:2006:MPD:H31	1.92	0.52
1:S:164:TYR:OH	7:S:2007:MPD:H53	2.11	0.51
2:L:291:GLY:HA2	2:L:521:SER:O	2.12	0.50
2:L:470:GLU:HB2	8:L:3600:HOH:O	2.12	0.49
1:S:1:LEU:HD22	1:S:43:ASP:HB3	1.94	0.49
1:S:209:GLU:O	1:S:213:LYS:HG3	2.13	0.48
1:S:2:MET:HA	2:L:182:GLN:CG	2.38	0.48
1:S:134:ASN:HD22	7:S:2004:MPD:H12	1.78	0.48
1:S:134:ASN:CB	7:S:2004:MPD:H12	2.41	0.48
2:L:324:PHE:CD2	7:L:2006:MPD:H13	2.48	0.48
1:S:5:ARG:HA	1:S:5:ARG:HD3	1.53	0.48
1:S:37:LEU:HD12	2:L:177:PHE:CE2	2.50	0.47
7:S:2004:MPD:H11	8:S:3119:HOH:O	2.14	0.47
2:L:233:ASN:C	2:L:233:ASN:HD22	2.17	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:317:GLY:HA2	8:L:3788:HOH:O	2.14	0.47
2:L:36:HIS:HD2	8:L:3070:HOH:O	1.97	0.46
1:S:164:TYR:CZ	7:S:2007:MPD:H53	2.51	0.46
2:L:149:LYS:NZ	8:L:3687:HOH:O	2.49	0.46
1:S:171:PRO:O	1:S:173:LEU:HD13	2.15	0.46
2:L:463:TRP:CH2	7:L:2010:MPD:H32	2.51	0.45
2:L:23:GLY:O	2:L:43:VAL:HG13	2.17	0.45
2:L:470:GLU:OE1	2:L:487:ARG:NE	2.49	0.45
1:S:2:MET:CG	1:S:8:SER:HB2	2.40	0.45
1:S:1:LEU:HB3	2:L:187:THR:OG1	2.17	0.45
2:L:211:HIS:HD2	2:L:276:ASP:OD2	1.99	0.45
2:L:327:ILE:HD11	2:L:396:SER:CB	2.47	0.45
1:S:2:MET:HG2	1:S:8:SER:CB	2.41	0.44
1:S:1:LEU:N	1:S:1:LEU:HD12	2.32	0.44
2:L:161:LYS:HG3	8:L:3180:HOH:O	2.17	0.44
1:S:1:LEU:HD13	8:S:3298:HOH:O	2.16	0.44
2:L:78:GLN:HG2	2:L:235:HIS:CD2	2.53	0.43
2:L:500:VAL:CG1	2:L:501:PRO:HD2	2.48	0.43
2:L:535:GLU:N	8:L:3725:HOH:O	2.50	0.43
7:L:2006:MPD:O4	7:L:2006:MPD:O2	2.30	0.43
1:S:13:HIS:HE1	1:S:21:SER:OG	2.01	0.43
1:S:1:LEU:HD22	1:S:63:ALA:HB2	2.01	0.42
1:S:134:ASN:HB3	7:S:2004:MPD:H4	2.01	0.42
2:L:286:ASP:N	2:L:286:ASP:OD2	2.50	0.42
7:S:2007:MPD:H12	7:S:2007:MPD:H4	1.97	0.41
2:L:392:LEU:CD2	7:L:2006:MPD:H31	2.49	0.41
1:S:1:LEU:CG	2:L:187:THR:HG21	2.40	0.41
1:S:20:CYS:HB2	1:S:75:GLU:CD	2.42	0.41

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%)	255 (96%)	8 (3%)	2 (1%)	22	5
2	L	532/534 (100%)	521 (98%)	10 (2%)	1 (0%)	51	21
All	All	797/801 (100%)	776 (97%)	18 (2%)	3 (0%)	38	13

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	S	5	ARG
1	S	4	PRO
2	L	231	ALA

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%)	197 (92%)	16 (8%)	16	1
2	L	438/438 (100%)	411 (94%)	27 (6%)	21	2
All	All	651/651 (100%)	608 (93%)	43 (7%)	19	1

All (43) 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
1	S	37	LEU
1	S	40	LEU
1	S	61	GLU
1	S	66	SER
1	S	91	ASN
1	S	95	LEU
1	S	126	ASN
1	S	168	LYS
1	S	173	LEU

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Mol	Chain	Res	Type
1	S	220	LEU
1	S	229	ASN
1	S	230	ASN
2	L	19	SER
2	L	43	VAL
2	L	47	LYS
2	L	50	ASN
2	L	66	LYS
2	L	132	HIS
2	L	143	LEU
2	L	152	LYS
2	L	161	LYS
2	L	174	LEU
2	L	179	GLU
2	L	183	LEU
2	L	200	LEU
2	L	213	LEU
2	L	218	LEU
2	L	233	ASN
2	L	250	LEU
2	L	278	LEU
2	L	279	VAL
2	L	321	LYS
2	L	325	LYS
2	L	410	LEU
2	L	418	GLU
2	L	445	LEU
2	L	457	ASN
2	L	468	GLN
2	L	506	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	S	13	HIS
1	S	45	HIS
1	S	91	ASN
1	S	92	HIS
1	S	126	ASN
1	S	139	HIS
1	S	146	ASN
1	S	190	GLN

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Mol	Chain	Res	Type
1	S	230	ASN
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	211	HIS
2	L	233	ASN
2	L	235	HIS
2	L	334	GLN
2	L	390	GLN
2	L	446	GLN
2	L	451	ASN
2	L	513	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

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	$\# Z > 2$
6	FNE	L	1004	2	3,7,9	2.62	2 (66%)	0,9,15	0.00	-
7	MPD	L	2006	-	7,7,7	0.42	0	9,10,10	0.51	0
7	MPD	L	2010	-	7,7,7	0.35	0	9,10,10	0.47	0
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	MPD	S	2001	-	7,7,7	0.42	0	9,10,10	0.94	1 (11%)
7	MPD	S	2004	-	7,7,7	0.40	0	9,10,10	0.50	0
7	MPD	S	2007	-	7,7,7	0.41	0	9,10,10	0.72	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	FNE	L	1004	2	-	0/0/9/18	0/0/0/1
7	MPD	L	2006	-	-	0/5/5/5	0/0/0/0
7	MPD	L	2010	-	-	0/5/5/5	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	MPD	S	2001	-	-	0/5/5/5	0/0/0/0
7	MPD	S	2004	-	-	0/5/5/5	0/0/0/0
7	MPD	S	2007	-	-	0/5/5/5	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	L	1004	FNE	O2-C2	-3.94	1.10	1.17
6	L	1004	FNE	O1-C1	2.14	1.20	1.17

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	S	2001	MPD	CM-C2-C1	2.25	115.45	110.42

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

4 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	L	2006	MPD	5	0
7	L	2010	MPD	2	0
7	S	2004	MPD	7	0
7	S	2007	MPD	3	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.