Full wwPDB X-ray Structure Validation Report (i)

Oct 18, 2023 – 01:37 PM EDT

PDB ID	:	1UBK
Title	:	Three-dimensional Structure of The Carbon Monoxide Complex of [NiFe]hydrogenase From Desulufovibrio 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	:	1.18 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 (i) 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 (i)) were used in the production of this report:

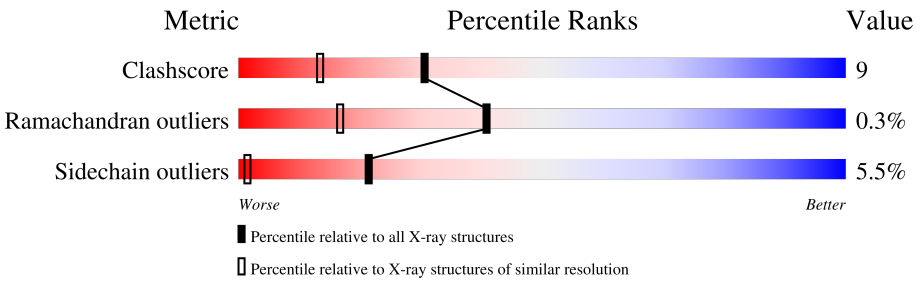
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.18 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	141614	1182 (1.20-1.16)
Ramachandran outliers	138981	1134 (1.20-1.16)
Sidechain outliers	138945	1134 (1.20-1.16)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	S	267	81% 15% • •
2	L	534	82% 15% •

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 7345 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
			Total	C	N	O	S			
1	S	267	2019	1282	342	378	17	0	0	0

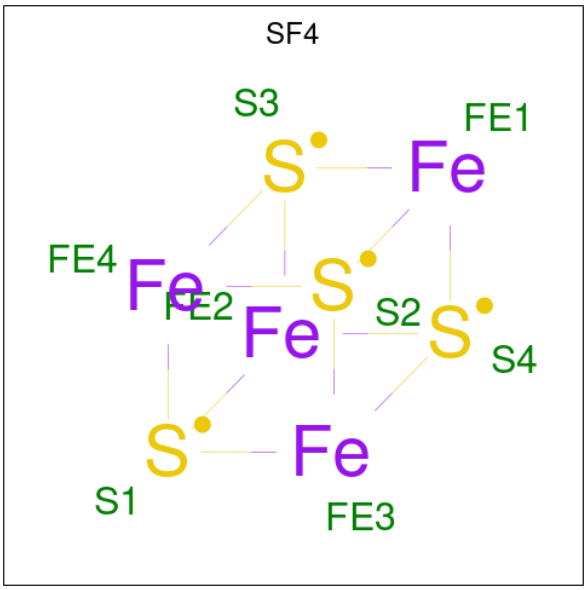
- Molecule 2 is a protein called Periplasmic [NiFe] hydrogenase Large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	534	4177	2674	725	763	15	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

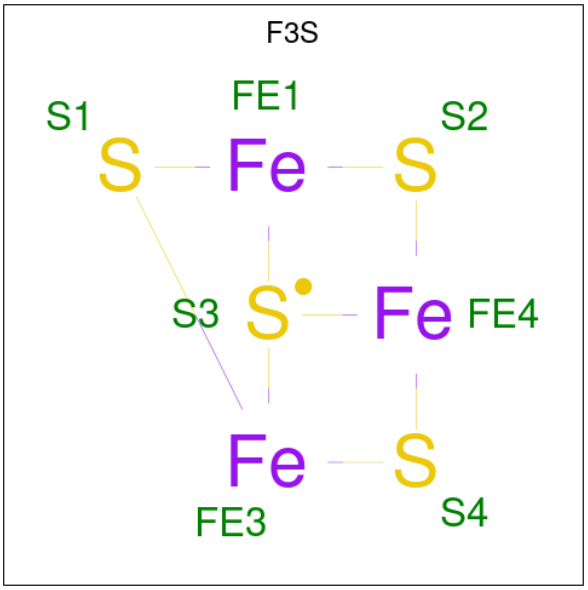
Chain	Residue	Modelled	Actual	Comment	Reference
L	514	LYS	ASN	SEE REMARK 999	UNP P21852
L	515	LEU	VAL	SEE REMARK 999	UNP P21852

- Molecule 3 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



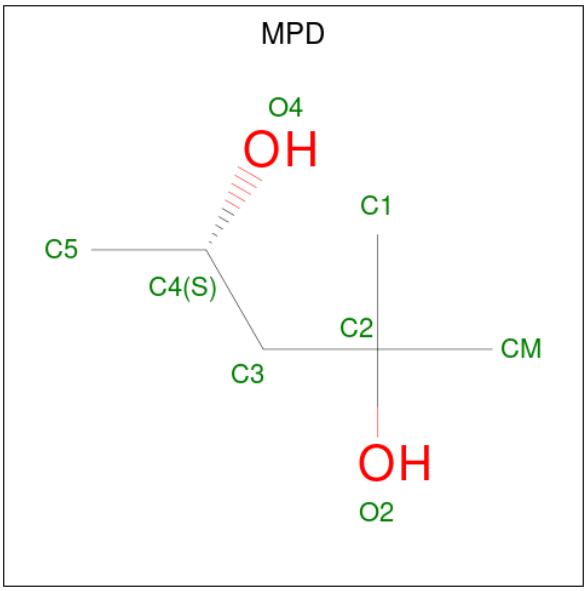
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
3	S	1	8	4	4	0	0
			Total	Fe	S		
3	S	1	8	4	4	0	0

- Molecule 4 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe_3S_4).



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

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).

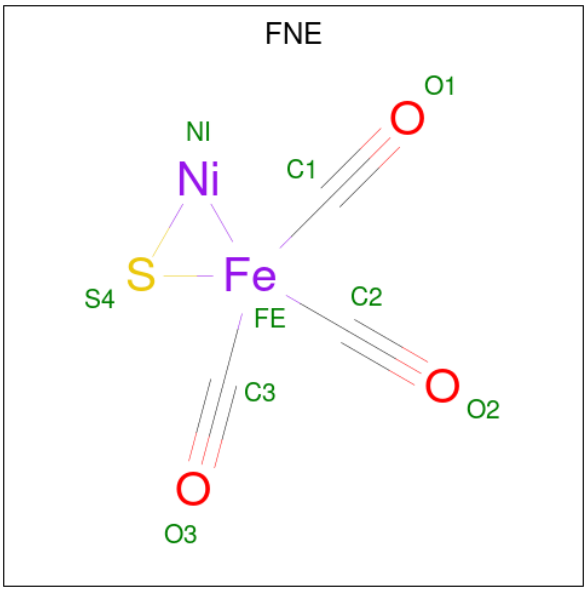


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	S	1	8	6	2	0	0
5	S	1	8	6	2	0	0
5	S	1	8	6	2	0	0
5	L	1	8	6	2	0	0
5	L	1	8	6	2	0	0
5	L	1	8	6	2	0	0
5	L	1	8	6	2	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

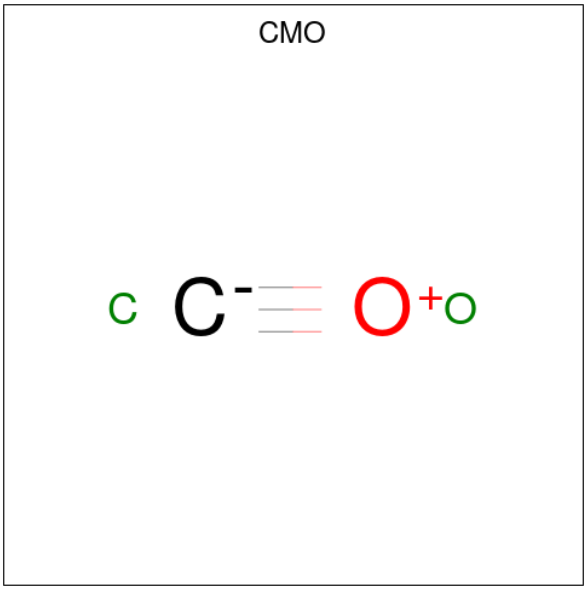
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
6	L	1	1	1	0	0

- Molecule 7 is (MU-SULPHIDO)-BIS(MU-CYS,S)-[TRICARBONYLIRON-DI-(CYS,S)NICKEL(II)](FE-NI) (three-letter code: FNE) (formula: C_3FeNiO_3S).



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

- Molecule 8 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO).



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

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	S	371	371	371	0	0
			Total	O		
9	L	688	688	688	0	0

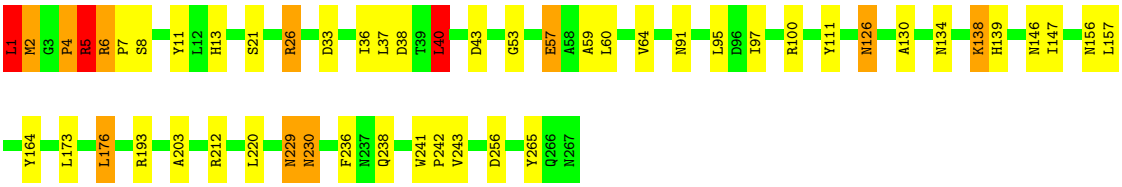
3 Residue-property plots (i)

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.

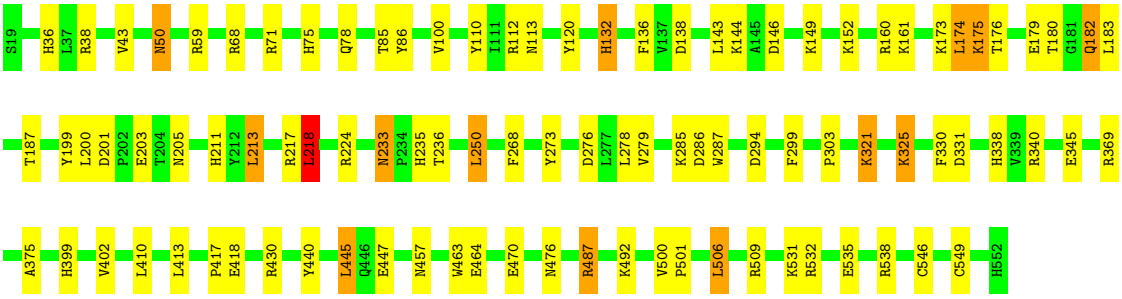
- Molecule 1: Periplasmic [NiFe] hydrogenase Small subunit

Chain S:



- Molecule 2: Periplasmic [NiFe] hydrogenase Large subunit

Chain L:



4 Data and refinement statistics (i)

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	97.60Å 125.26Å 66.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.18	Depositor
% Data completeness (in resolution range)	82.3 (20.00-1.18)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS, SHELXL-97	Depositor
R, R_{free}	0.110 , 0.151	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7345	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

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: MPD, SF4, F3S, MG, FNE, CMO

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	0.77	0/2075	1.30	20/2830 (0.7%)
2	L	0.74	0/4288	1.33	43/5831 (0.7%)
All	All	0.75	0/6363	1.32	63/8661 (0.7%)

There are no bond length outliers.

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	L	273	TYR	CB-CG-CD1	12.44	128.46	121.00
2	L	506	LEU	CA-CB-CG	12.17	143.28	115.30
2	L	369	ARG	NE-CZ-NH1	10.08	125.34	120.30
2	L	59	ARG	NE-CZ-NH2	-9.98	115.31	120.30
1	S	212	ARG	NE-CZ-NH2	9.76	125.18	120.30
1	S	100	ARG	NE-CZ-NH1	9.07	124.84	120.30
2	L	430	ARG	NE-CZ-NH1	8.86	124.73	120.30
2	L	59	ARG	NE-CZ-NH1	8.83	124.72	120.30
1	S	100	ARG	NE-CZ-NH2	-8.63	115.98	120.30
2	L	71	ARG	NE-CZ-NH2	-8.43	116.09	120.30
1	S	5	ARG	CD-NE-CZ	-8.37	111.88	123.60
1	S	6	ARG	NE-CZ-NH2	7.98	124.29	120.30
1	S	33	ASP	CB-CG-OD1	7.68	125.21	118.30
1	S	193	ARG	NE-CZ-NH1	7.54	124.07	120.30
2	L	294	ASP	CB-CG-OD2	7.52	125.07	118.30
2	L	538	ARG	NE-CZ-NH2	-7.28	116.66	120.30
1	S	40	LEU	CA-CB-CG	7.14	131.73	115.30
2	L	112	ARG	NE-CZ-NH1	7.10	123.85	120.30
2	L	38	ARG	NE-CZ-NH1	7.06	123.83	120.30
2	L	201	ASP	CB-CG-OD1	7.01	124.61	118.30
2	L	250	LEU	CA-CB-CG	6.95	131.29	115.30
2	L	273	TYR	CB-CG-CD2	-6.94	116.84	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	S	5	ARG	NE-CZ-NH1	-6.83	116.88	120.30
2	L	71	ARG	NE-CZ-NH1	6.58	123.59	120.30
2	L	487	ARG	NE-CZ-NH2	-6.46	117.07	120.30
2	L	345	GLU	OE1-CD-OE2	-6.45	115.56	123.30
2	L	532	ARG	NE-CZ-NH2	-6.39	117.10	120.30
2	L	340	ARG	NE-CZ-NH2	-6.33	117.14	120.30
1	S	138	LYS	CA-CB-CG	6.33	127.32	113.40
2	L	369	ARG	NE-CZ-NH2	-6.21	117.19	120.30
2	L	68	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	S	164	TYR	CG-CD2-CE2	-6.18	116.36	121.30
2	L	213	LEU	CB-CG-CD1	6.13	121.43	111.00
2	L	182	GLN	OE1-CD-NE2	-6.12	107.82	121.90
2	L	174	LEU	CA-CB-CG	6.11	129.36	115.30
2	L	136	PHE	CG-CD1-CE1	-6.10	114.09	120.80
2	L	218	LEU	CB-CG-CD2	-5.96	100.87	111.00
2	L	287	TRP	CA-CB-CG	-5.96	102.38	113.70
2	L	218	LEU	CD1-CG-CD2	5.95	128.36	110.50
2	L	120	TYR	CB-CG-CD2	-5.89	117.46	121.00
2	L	110	TYR	CG-CD1-CE1	-5.86	116.61	121.30
1	S	176	LEU	CB-CG-CD1	5.73	120.75	111.00
2	L	447	GLU	OE1-CD-OE2	-5.73	116.43	123.30
2	L	146	ASP	CB-CG-OD2	-5.71	113.16	118.30
2	L	199	TYR	CB-CG-CD2	-5.66	117.60	121.00
1	S	26	ARG	CG-CD-NE	-5.66	99.91	111.80
2	L	68	ARG	NE-CZ-NH1	5.65	123.13	120.30
2	L	120	TYR	CG-CD1-CE1	-5.58	116.84	121.30
2	L	330	PHE	CB-CG-CD1	-5.58	116.90	120.80
1	S	193	ARG	NE-CZ-NH2	-5.56	117.52	120.30
2	L	331	ASP	CB-CG-OD2	5.53	123.28	118.30
2	L	38	ARG	NE-CZ-NH2	-5.50	117.55	120.30
2	L	445	LEU	CA-CB-CG	5.38	127.66	115.30
1	S	38	ASP	CB-CG-OD1	5.34	123.10	118.30
2	L	440	TYR	CB-CG-CD1	-5.25	117.85	121.00
1	S	100	ARG	CD-NE-CZ	5.22	130.91	123.60
1	S	11	TYR	CB-CG-CD1	5.21	124.13	121.00
1	S	57	GLU	CA-CB-CG	5.16	124.75	113.40
2	L	144	LYS	CA-CB-CG	5.13	124.69	113.40
1	S	1	LEU	O-C-N	5.08	130.83	122.70
1	S	236	PHE	CB-CG-CD1	-5.04	117.27	120.80
2	L	217	ARG	NE-CZ-NH1	-5.00	117.80	120.30
2	L	199	TYR	CB-CG-CD1	5.00	124.00	121.00

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	S	2019	0	1949	60	0
2	L	4177	0	4129	68	0
3	S	16	0	0	0	0
4	S	7	0	0	0	0
5	L	32	0	56	7	0
5	S	24	0	42	5	0
6	L	1	0	0	0	0
7	L	8	0	0	0	0
8	L	2	0	0	0	0
9	L	688	0	0	18	0
9	S	371	0	0	11	0
All	All	7345	0	6176	115	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 9.

All (115) 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	5:S:2004:MPD:H13	1.25	1.00
1:S:238:GLN:HE21	2:L:224:ARG:HH21	1.22	0.87
1:S:26:ARG:HH21	2:L:233:ASN:HD21	1.21	0.86
1:S:126:ASN:HD21	1:S:130:ALA:H	1.21	0.85
2:L:470:GLU:HG2	2:L:487:ARG:HD3	1.59	0.84
1:S:176:LEU:HD13	9:S:3183:HOH:O	1.80	0.82
2:L:487:ARG:HB3	9:L:4011:HOH:O	1.84	0.77
5:L:2011:MPD:HM1	9:L:3322:HOH:O	1.84	0.76
2:L:78:GLN:HE21	2:L:86:TYR:H	1.31	0.75
1:S:6:ARG:H	2:L:182:GLN:HE22	1.32	0.75
2:L:173:LYS:HB2	5:L:2012:MPD:H11	1.69	0.75
1:S:256:ASP:HB3	9:S:3425:HOH:O	1.85	0.73
2:L:175:LYS:O	2:L:179:GLU:HG3	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:2:MET:HA	2:L:182:GLN:HG2	1.72	0.72
5:L:2010:MPD:HM3	9:L:3337:HOH:O	1.91	0.71
1:S:1:LEU:HB3	2:L:187:THR:OG1	1.91	0.71
1:S:1:LEU:HD21	1:S:59:ALA:O	1.90	0.71
1:S:2:MET:SD	1:S:8:SER:HB2	2.34	0.68
1:S:6:ARG:H	2:L:182:GLN:NE2	1.90	0.68
1:S:146:ASN:ND2	5:S:2004:MPD:H13	2.05	0.68
1:S:134:ASN:HB2	5:S:2004:MPD:H12	1.75	0.68
2:L:176:THR:O	2:L:180:THR:HG23	1.95	0.67
1:S:2:MET:HE2	2:L:182:GLN:HG2	1.76	0.65
1:S:2:MET:HG2	1:S:8:SER:HB2	1.81	0.61
1:S:1:LEU:HG	2:L:187:THR:HG21	1.81	0.61
1:S:5:ARG:HB2	9:L:3193:HOH:O	2.02	0.60
1:S:6:ARG:HB2	2:L:182:GLN:NE2	2.15	0.60
2:L:211:HIS:HE1	9:L:3221:HOH:O	1.84	0.60
1:S:13:HIS:HD2	9:S:3034:HOH:O	1.84	0.60
2:L:173:LYS:CB	5:L:2012:MPD:H11	2.33	0.59
1:S:6:ARG:HB2	2:L:182:GLN:HE22	1.68	0.58
2:L:50:ASN:HD21	2:L:509:ARG:NH2	2.01	0.58
1:S:7:PRO:HG2	1:S:40:LEU:HD12	1.86	0.57
2:L:36:HIS:HD2	9:L:3070:HOH:O	1.86	0.57
1:S:238:GLN:NE2	2:L:224:ARG:HH21	1.98	0.57
2:L:211:HIS:HD2	2:L:276:ASP:OD2	1.88	0.56
1:S:156:ASN:HD21	1:S:230:ASN:HD21	1.52	0.56
1:S:230:ASN:HD22	1:S:230:ASN:H	1.54	0.56
2:L:321:LYS:N	2:L:321:LYS:HD3	2.21	0.56
2:L:535:GLU:HB2	9:L:3816:HOH:O	2.06	0.55
1:S:1:LEU:HD22	1:S:43:ASP:HB3	1.88	0.55
1:S:53:GLY:HA3	9:L:4004:HOH:O	2.07	0.55
1:S:2:MET:HG2	1:S:43:ASP:OD1	2.07	0.55
1:S:1:LEU:HD12	1:S:1:LEU:H3	1.71	0.55
2:L:100:VAL:HG11	2:L:463:TRP:CE3	2.42	0.55
1:S:1:LEU:HD13	9:S:3300:HOH:O	2.07	0.55
2:L:492:LYS:HD2	9:L:3436:HOH:O	2.06	0.55
2:L:299:PHE:H	2:L:476:ASN:ND2	2.06	0.53
1:S:265:TYR:OH	2:L:75:HIS:HE1	1.90	0.53
1:S:134:ASN:HD22	5:S:2004:MPD:H12	1.74	0.53
1:S:2:MET:HA	2:L:182:GLN:CG	2.38	0.53
2:L:399:HIS:HD2	2:L:402:VAL:H	1.56	0.53
1:S:1:LEU:CG	2:L:187:THR:HG21	2.39	0.52
2:L:470:GLU:HG2	2:L:487:ARG:CD	2.36	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:2:MET:CG	1:S:8:SER:HB2	2.39	0.52
2:L:75:HIS:HD2	9:L:3074:HOH:O	1.92	0.51
2:L:138:ASP:H	2:L:205:ASN:ND2	2.08	0.51
1:S:1:LEU:HD12	1:S:1:LEU:N	2.26	0.51
1:S:241:TRP:CH2	1:S:243:VAL:HB	2.45	0.51
1:S:139:HIS:H	1:S:139:HIS:CD2	2.29	0.51
1:S:229:ASN:HD22	1:S:230:ASN:H	1.60	0.50
5:L:2012:MPD:O4	5:L:2012:MPD:O2	2.29	0.50
1:S:5:ARG:HB3	2:L:182:GLN:OE1	2.12	0.50
1:S:13:HIS:HE1	1:S:21:SER:OG	1.93	0.49
2:L:78:GLN:HE22	2:L:236:THR:H	1.60	0.49
2:L:160:ARG:HB3	9:L:4000:HOH:O	2.11	0.49
1:S:2:MET:HE1	1:S:4:PRO:O	2.13	0.49
2:L:285:LYS:HE2	2:L:413:LEU:O	2.13	0.49
2:L:399:HIS:CD2	2:L:402:VAL:H	2.30	0.49
1:S:2:MET:HB3	1:S:43:ASP:OD1	2.11	0.48
1:S:26:ARG:HH21	2:L:233:ASN:ND2	2.00	0.48
1:S:203:ALA:O	1:S:220:LEU:HD13	2.14	0.48
2:L:325:LYS:HD2	2:L:325:LYS:N	2.29	0.48
2:L:50:ASN:HD21	2:L:509:ARG:HH22	1.61	0.48
2:L:233:ASN:C	2:L:233:ASN:HD22	2.16	0.47
2:L:487:ARG:HD2	9:L:4011:HOH:O	2.14	0.47
1:S:5:ARG:HD3	9:S:3903:HOH:O	2.14	0.46
2:L:218:LEU:HD13	2:L:268:PHE:CD2	2.50	0.46
1:S:2:MET:HG3	9:S:3300:HOH:O	2.15	0.46
2:L:175:LYS:NZ	9:L:3656:HOH:O	2.49	0.46
9:S:3617:HOH:O	5:L:2012:MPD:H52	2.15	0.45
2:L:175:LYS:NZ	9:L:3578:HOH:O	2.49	0.45
1:S:134:ASN:CB	5:S:2004:MPD:H12	2.43	0.45
2:L:500:VAL:CG1	2:L:501:PRO:HD2	2.47	0.45
1:S:5:ARG:HA	9:S:3903:HOH:O	2.17	0.45
1:S:6:ARG:N	2:L:182:GLN:HE22	2.08	0.45
2:L:160:ARG:HD2	9:L:3759:HOH:O	2.16	0.45
1:S:126:ASN:HD21	1:S:130:ALA:N	2.00	0.44
2:L:535:GLU:N	9:L:3816:HOH:O	2.49	0.44
1:S:126:ASN:ND2	1:S:130:ALA:H	2.03	0.44
2:L:149:LYS:HD3	2:L:203:GLU:HG2	1.98	0.44
2:L:299:PHE:H	2:L:476:ASN:HD22	1.65	0.44
1:S:2:MET:HE1	1:S:6:ARG:O	2.18	0.44
2:L:338:HIS:HB2	2:L:375:ALA:HB3	2.00	0.43
2:L:78:GLN:NE2	2:L:235:HIS:HA	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:175:LYS:HE2	2:L:175:LYS:HB3	1.54	0.43
2:L:417:PRO:HD2	2:L:418:GLU:OE2	2.18	0.43
2:L:100:VAL:HG13	2:L:464:GLU:O	2.18	0.43
2:L:113:ASN:HD21	2:L:303:PRO:HD2	1.83	0.43
2:L:173:LYS:HG2	5:L:2012:MPD:H31	2.00	0.43
2:L:321:LYS:HD3	2:L:321:LYS:H	1.83	0.43
1:S:5:ARG:NH1	9:S:3903:HOH:O	2.52	0.43
1:S:60:LEU:O	1:S:64:VAL:HG22	2.19	0.42
1:S:111:TYR:CE1	1:S:157:LEU:HB2	2.54	0.42
2:L:85:THR:OG1	2:L:235:HIS:HD2	2.03	0.42
1:S:97:ILE:HD11	9:S:3968:HOH:O	2.19	0.41
2:L:286:ASP:OD2	2:L:286:ASP:N	2.53	0.41
1:S:5:ARG:HD3	1:S:5:ARG:HA	1.33	0.41
1:S:147:ILE:HD13	1:S:157:LEU:HA	2.02	0.41
2:L:531:LYS:NZ	9:L:3763:HOH:O	2.53	0.41
2:L:132:HIS:HD2	9:L:3113:HOH:O	2.03	0.41
2:L:218:LEU:CD1	2:L:268:PHE:HB2	2.51	0.41
1:S:57:GLU:HG2	9:S:3826:HOH:O	2.22	0.40
2:L:100:VAL:HG11	2:L:463:TRP:HE3	1.84	0.40
2:L:546:CYS:SG	2:L:549:CYS:HB2	2.62	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%)	19 3
2	L	532/534 (100%)	519 (98%)	13 (2%)	0	100 100
All	All	797/801 (100%)	775 (97%)	20 (2%)	2 (0%)	41 17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	S	4	PRO
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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	S	213/213 (100%)	199 (93%)	14 (7%)	16 1
2	L	438/438 (100%)	416 (95%)	22 (5%)	24 2
All	All	651/651 (100%)	615 (94%)	36 (6%)	21 1

All (36) 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	91	ASN
1	S	95	LEU
1	S	126	ASN
1	S	138	LYS
1	S	173	LEU
1	S	229	ASN
1	S	230	ASN
1	S	242	PRO
2	L	43	VAL
2	L	50	ASN
2	L	132	HIS
2	L	143	LEU
2	L	152	LYS
2	L	161	LYS
2	L	174	LEU
2	L	175	LYS

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Mol	Chain	Res	Type
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	445	LEU
2	L	457	ASN
2	L	506	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	S	13	HIS
1	S	68	HIS
1	S	91	ASN
1	S	126	ASN
1	S	139	HIS
1	S	146	ASN
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	182	GLN
2	L	188	ASN
2	L	205	ASN
2	L	211	HIS
2	L	233	ASN
2	L	235	HIS

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Mol	Chain	Res	Type
2	L	310	ASN
2	L	334	GLN
2	L	390	GLN
2	L	399	HIS
2	L	451	ASN
2	L	457	ASN
2	L	476	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 13 ligands modelled in this entry, 1 is monoatomic - leaving 12 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	$\#\|Z\| > 2$
5	MPD	S	2004	-	7,7,7	0.83	0	9,10,10	0.90	1 (11%)
5	MPD	S	2007	-	7,7,7	0.55	0	9,10,10	1.05	1 (11%)
5	MPD	L	2011	-	7,7,7	0.44	0	9,10,10	0.75	0
7	FNE	L	1004	8,2	3,7,9	1.50	0	-		
5	MPD	L	2010	-	7,7,7	0.48	0	9,10,10	0.87	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	MPD	L	2006	-	7,7,7	0.45	0	9,10,10	0.45	0
8	CMO	L	1006	7	0,1,1	-	-	-		
3	SF4	S	1001	1	0,12,12	-	-	-		
5	MPD	S	2001	-	7,7,7	0.60	0	9,10,10	1.52	2 (22%)
4	F3S	S	1003	1	0,9,9	-	-	-		
3	SF4	S	1002	1	0,12,12	-	-	-		
5	MPD	L	2012	-	7,7,7	0.48	0	9,10,10	0.70	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
5	MPD	S	2007	-	-	1/5/5/5	-
5	MPD	S	2004	-	-	0/5/5/5	-
5	MPD	L	2011	-	-	2/5/5/5	-
5	MPD	L	2010	-	-	2/5/5/5	-
5	MPD	L	2006	-	-	3/5/5/5	-
3	SF4	S	1001	1	-	-	0/6/5/5
5	MPD	S	2001	-	-	1/5/5/5	-
4	F3S	S	1003	1	-	-	0/3/3/3
3	SF4	S	1002	1	-	-	0/6/5/5
5	MPD	L	2012	-	-	3/5/5/5	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	S	2001	MPD	CM-C2-C1	3.11	117.05	110.57
5	S	2001	MPD	O2-C2-C3	-2.16	101.67	109.80
5	S	2007	MPD	CM-C2-C1	2.10	114.95	110.57
5	S	2004	MPD	O2-C2-CM	2.04	114.63	108.08

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	L	2011	MPD	C2-C3-C4-O4
5	L	2012	MPD	O2-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
5	S	2001	MPD	C1-C2-C3-C4
5	S	2007	MPD	C1-C2-C3-C4
5	L	2006	MPD	CM-C2-C3-C4
5	L	2010	MPD	CM-C2-C3-C4
5	L	2012	MPD	C1-C2-C3-C4
5	L	2012	MPD	CM-C2-C3-C4
5	L	2006	MPD	O2-C2-C3-C4
5	L	2010	MPD	O2-C2-C3-C4
5	L	2011	MPD	C2-C3-C4-C5
5	L	2006	MPD	C2-C3-C4-O4

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	S	2004	MPD	5	0
5	L	2011	MPD	1	0
5	L	2010	MPD	1	0
5	L	2012	MPD	5	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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.