



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:15 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 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 (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

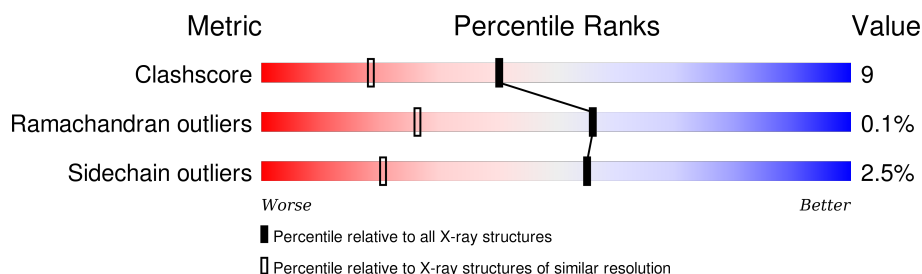
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	102246	2274 (1.50-1.50)
Ramachandran outliers	100387	2218 (1.50-1.50)
Sidechain outliers	100360	2216 (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. 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
8	MPD	S	2004	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 7040 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	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).

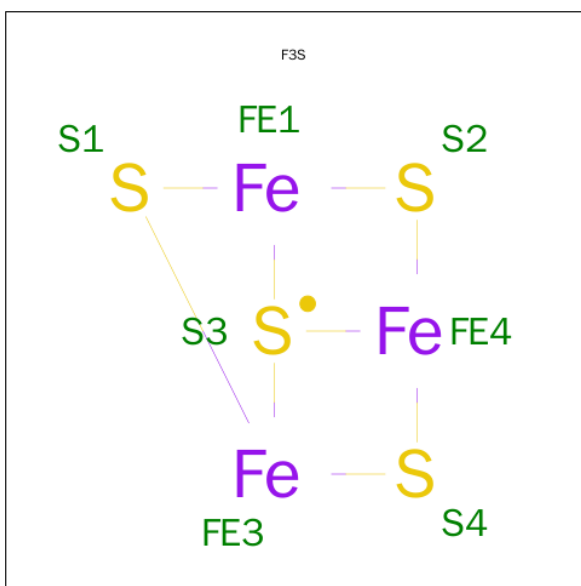
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	1	Total	Mg	0	0
			1	1		

- 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		

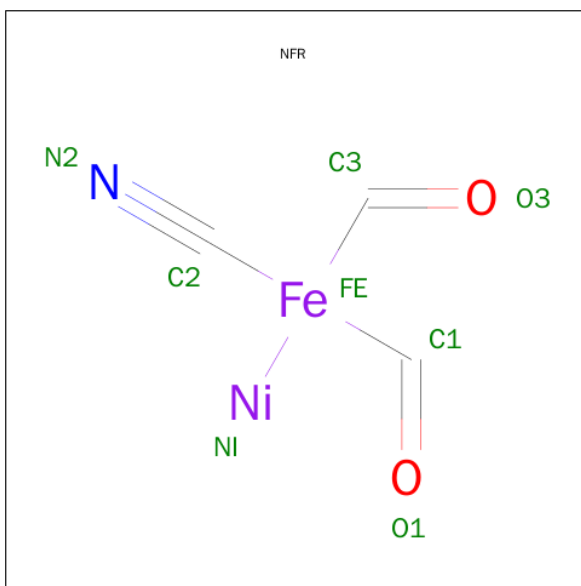
- Molecule 5 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe_3S_4).



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

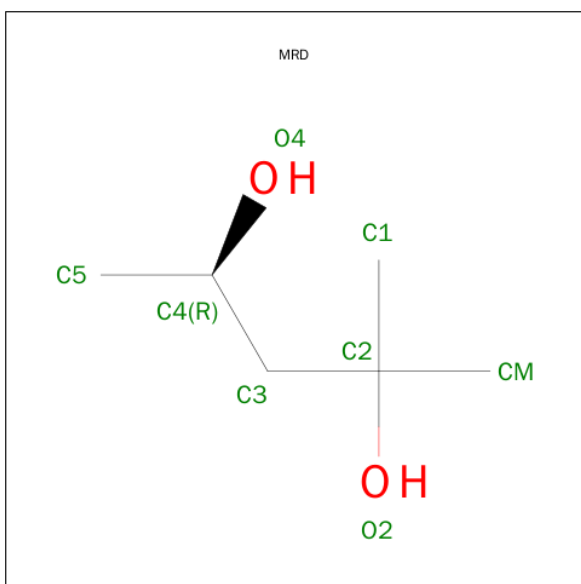
- Molecule 6 is NI-FE REDUCED ACTIVE CENTER (three-letter code: NFR) (formula:

C₃H₂FeNNiO₂).



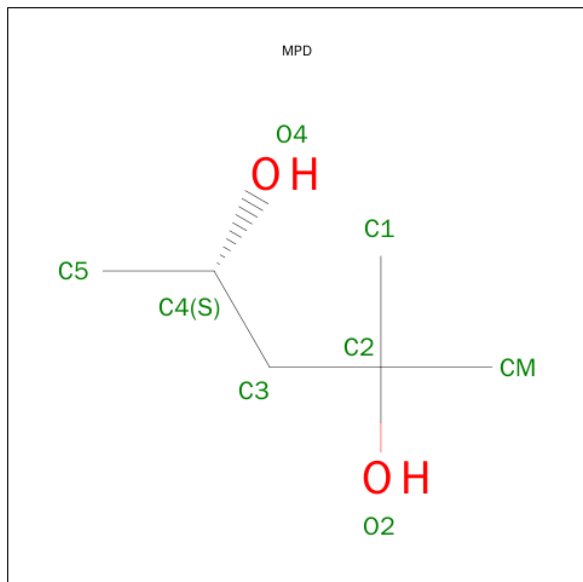
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	Fe	N	Ni	O		
6	L	1	8	3	1	1	1	2	0	0

- Molecule 7 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: C₆H₁₄O₂).



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.

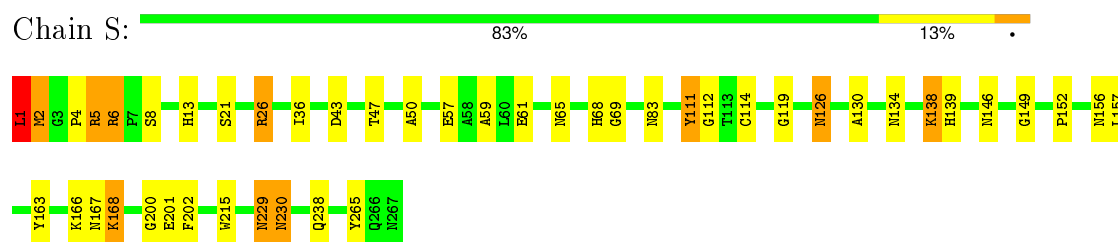
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	L	514	Total	O	0	0
			514	514		
9	S	262	Total	O	0	0
			262	262		

3 Residue-property plots

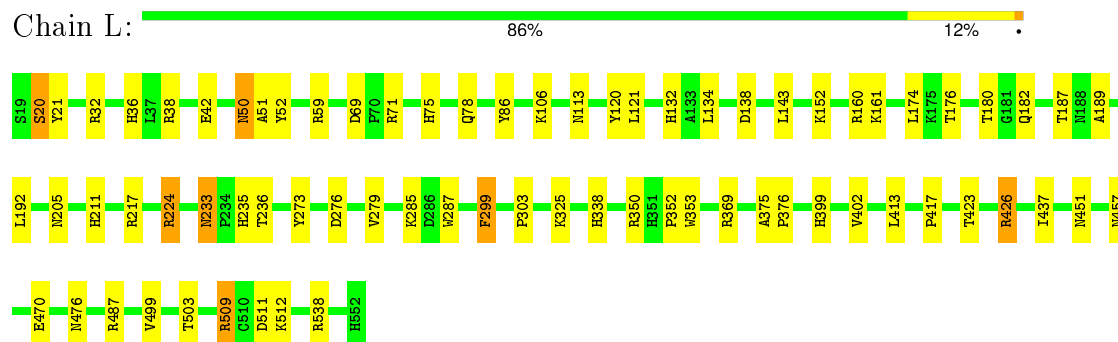
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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 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 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	61	0
2	L	4181	0	4129	61	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	2	0
8	S	24	0	42	6	0
9	L	514	0	0	25	0
9	S	262	0	0	10	0
All	All	7040	0	6134	108	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 (108) 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	8:S:2004:MPD:H13	1.22	1.04
1:S:26:ARG:HH21	2:L:233:ASN:HD21	1.14	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:126:ASN:HD21	1:S:130:ALA:H	1.15	0.90
1:S:238:GLN:HE21	2:L:224:ARG:HH21	1.21	0.87
1:S:134:ASN:HB2	8:S:2004:MPD:H12	1.57	0.86
1:S:2:MET:HA	2:L:182:GLN:HG2	1.59	0.82
2:L:437:ILE:HG23	9:L:5656:HOH:O	1.83	0.79
2:L:426:ARG:HB3	9:L:5526:HOH:O	1.82	0.79
2:L:423:THR:HA	9:L:5526:HOH:O	1.83	0.78
1:S:152:PRO:HG3	9:S:5643:HOH:O	1.82	0.78
1:S:1:LEU:HD21	1:S:59:ALA:O	1.86	0.76
2:L:161:LYS:HG2	9:L:5381:HOH:O	1.84	0.74
2:L:78:GLN:HE21	2:L:86:TYR:H	1.35	0.73
1:S:146:ASN:ND2	8:S:2004:MPD:H13	2.02	0.72
1:S:230:ASN:H	1:S:230:ASN:HD22	1.40	0.70
1:S:5:ARG:HB3	9:L:5580:HOH:O	1.90	0.70
2:L:470:GLU:HG3	2:L:487:ARG:HD3	1.73	0.69
1:S:26:ARG:HH21	2:L:233:ASN:ND2	1.89	0.69
2:L:176:THR:O	2:L:180:THR:HG23	1.92	0.69
2:L:42:GLU:HB3	9:L:5582:HOH:O	1.93	0.67
1:S:238:GLN:NE2	2:L:224:ARG:HH21	1.94	0.65
1:S:1:LEU:HB3	2:L:187:THR:OG1	1.99	0.63
2:L:192:LEU:HG	9:L:5331:HOH:O	2.00	0.62
1:S:2:MET:HB2	2:L:182:GLN:HE21	1.64	0.62
1:S:126:ASN:HD21	1:S:130:ALA:N	1.94	0.62
1:S:2:MET:HE3	1:S:8:SER:HB2	1.81	0.61
2:L:189:ALA:HB3	9:L:5331:HOH:O	2.00	0.61
1:S:68:HIS:HB2	9:S:5460:HOH:O	2.03	0.58
1:S:138:LYS:HE2	8:S:2004:MPD:H51	1.86	0.58
2:L:399:HIS:HD2	2:L:402:VAL:H	1.49	0.58
2:L:299:PHE:H	2:L:476:ASN:ND2	2.01	0.58
1:S:2:MET:HB3	1:S:43:ASP:OD1	2.05	0.57
2:L:211:HIS:HE1	9:L:5287:HOH:O	1.87	0.57
1:S:134:ASN:CB	8:S:2004:MPD:H12	2.33	0.56
2:L:353:TRP:CE2	2:L:470:GLU:HG2	2.41	0.55
2:L:285:LYS:HE2	2:L:413:LEU:O	2.05	0.55
1:S:265:TYR:OH	2:L:75:HIS:HE1	1.90	0.55
1:S:1:LEU:HD12	1:S:1:LEU:H3	1.72	0.54
1:S:202:PHE:HD2	9:S:5558:HOH:O	1.88	0.54
1:S:2:MET:CE	1:S:8:SER:HB2	2.38	0.54
2:L:75:HIS:HD2	9:L:5015:HOH:O	1.90	0.53
2:L:192:LEU:N	9:L:5331:HOH:O	2.41	0.53
1:S:229:ASN:HD22	1:S:230:ASN:H	1.55	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:113:ASN:HD21	2:L:303:PRO:HD2	1.74	0.53
2:L:106:LYS:HE2	2:L:451:ASN:ND2	2.24	0.53
1:S:1:LEU:HA	9:L:5353:HOH:O	2.10	0.52
2:L:121:LEU:HD21	9:L:5581:HOH:O	2.09	0.52
2:L:437:ILE:HG22	9:L:5581:HOH:O	2.10	0.52
1:S:2:MET:HA	2:L:182:GLN:CG	2.35	0.52
2:L:50:ASN:HD21	2:L:509:ARG:NH2	2.07	0.52
2:L:36:HIS:HD2	9:L:5083:HOH:O	1.93	0.52
1:S:139:HIS:CD2	1:S:139:HIS:H	2.28	0.51
1:S:156:ASN:HD21	1:S:230:ASN:HD21	1.57	0.51
2:L:20:SER:HA	9:L:5524:HOH:O	2.10	0.51
2:L:211:HIS:HD2	2:L:276:ASP:OD2	1.94	0.50
1:S:2:MET:HG2	9:S:5231:HOH:O	2.11	0.50
1:S:1:LEU:HD22	1:S:43:ASP:HB3	1.94	0.50
1:S:149:GLY:N	9:S:5643:HOH:O	2.45	0.49
1:S:126:ASN:ND2	1:S:130:ALA:H	1.97	0.49
2:L:299:PHE:H	2:L:476:ASN:HD22	1.61	0.48
1:S:1:LEU:HG	2:L:187:THR:HG21	1.95	0.48
1:S:230:ASN:N	1:S:230:ASN:HD22	2.04	0.48
2:L:399:HIS:CD2	2:L:402:VAL:H	2.30	0.47
2:L:121:LEU:HD11	9:L:5581:HOH:O	2.13	0.47
1:S:166:LYS:HD3	9:S:5516:HOH:O	2.14	0.47
1:S:50:ALA:HB2	2:L:134:LEU:HD13	1.96	0.47
2:L:417:PRO:HB3	7:L:2005:MRD:C5	2.45	0.47
1:S:201:GLU:HB3	1:S:215:TRP:CE3	2.49	0.47
2:L:20:SER:HB2	9:L:5524:HOH:O	2.15	0.47
1:S:134:ASN:HD22	8:S:2004:MPD:H12	1.80	0.47
1:S:26:ARG:NH2	2:L:233:ASN:HD21	1.97	0.46
1:S:167:ASN:O	1:S:168:LYS:HB2	2.14	0.46
1:S:5:ARG:HA	1:S:5:ARG:HD3	1.47	0.46
1:S:13:HIS:HE1	1:S:21:SER:OG	1.98	0.46
1:S:6:ARG:HG3	9:L:5580:HOH:O	2.15	0.46
2:L:426:ARG:NH1	9:L:5526:HOH:O	2.47	0.46
2:L:138:ASP:H	2:L:205:ASN:ND2	2.14	0.45
1:S:5:ARG:HB2	9:L:5528:HOH:O	2.17	0.45
1:S:230:ASN:ND2	1:S:230:ASN:H	2.12	0.45
1:S:200:GLY:HA2	1:S:202:PHE:CE2	2.52	0.45
1:S:36:ILE:HG23	9:S:5067:HOH:O	2.17	0.45
2:L:143:LEU:HD21	2:L:174:LEU:HG	1.99	0.45
1:S:1:LEU:HD12	1:S:1:LEU:N	2.31	0.44
1:S:112:GLY:HA3	9:S:5021:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:78:GLN:HE22	2:L:236:THR:H	1.64	0.44
2:L:338:HIS:HB2	2:L:375:ALA:HB3	2.00	0.44
2:L:512:LYS:HD3	9:L:5213:HOH:O	2.17	0.44
1:S:6:ARG:N	9:L:5580:HOH:O	2.51	0.44
2:L:376:PRO:HD3	2:L:503:THR:HG22	2.00	0.44
1:S:69:GLY:N	9:S:5460:HOH:O	2.50	0.43
2:L:352:PRO:HG3	2:L:499:VAL:HG21	2.01	0.43
2:L:50:ASN:ND2	2:L:51:ALA:H	2.15	0.43
2:L:152:LYS:HD3	9:L:5611:HOH:O	2.19	0.43
2:L:161:LYS:NZ	9:L:5575:HOH:O	2.51	0.42
1:S:114:CYS:HA	1:S:119:GLY:HA3	2.00	0.42
1:S:47:THR:O	2:L:32:ARG:HA	2.19	0.42
2:L:353:TRP:NE1	2:L:470:GLU:HG2	2.35	0.41
1:S:112:GLY:CA	9:S:5643:HOH:O	2.69	0.41
2:L:417:PRO:HB3	7:L:2005:MRD:H5C2	2.02	0.41
1:S:138:LYS:HB2	1:S:138:LYS:HE3	1.18	0.41
1:S:111:TYR:CE1	1:S:157:LEU:HB2	2.55	0.41
2:L:50:ASN:HD21	2:L:509:ARG:HH22	1.69	0.41
2:L:78:GLN:NE2	2:L:235:HIS:HA	2.36	0.40
1:S:61:GLU:OE1	1:S:65:ASN:ND2	2.49	0.40
2:L:106:LYS:HB3	2:L:106:LYS:HE3	1.75	0.40
1:S:5:ARG:HB3	2:L:182:GLN:OE1	2.21	0.40
1:S:111:TYR:CE1	1:S:152:PRO:HG2	2.55	0.40
2:L:50:ASN:HD22	2:L:51:ALA:H	1.69	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%)	8 (3%)	1 (0%)	39 14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	L	532/534 (100%)	519 (98%)	13 (2%)	0	100	100
All	All	797/801 (100%)	775 (97%)	21 (3%)	1 (0%)	56	26

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%)	36	7
2	L	438/437 (100%)	431 (98%)	7 (2%)	70	41
All	All	651/650 (100%)	635 (98%)	16 (2%)	55	20

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

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Mol	Chain	Res	Type
2	L	457	ASN

Some 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	83	ASN
1	S	91	ASN
1	S	126	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	390	GLN
2	L	399	HIS
2	L	446	GLN
2	L	451	ASN
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	0.53	0	1,6,8	2.83	1 (100%)

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.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	546	CSO	O-C-CA	-2.83	118.12	125.49

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 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	1,7,7	0.14	0	0,9,9	0.00	-
7	MRD	L	2005	-	6,7,7	0.55	0	7,10,10	0.50	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	-
8	MPD	S	2001	-	6,7,7	0.48	0	7,10,10	0.64	0
8	MPD	S	2004	-	6,7,7	0.39	0	7,10,10	0.76	0
8	MPD	S	2007	-	6,7,7	0.42	0	7,10,10	0.98	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	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
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

There are no bond length outliers.

There are no bond angle outliers.

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

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

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	L	2005	MRD	2	0
8	S	2004	MPD	6	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.