



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:55 PM GMT

PDB ID : 4JY9
Title : X-ray snapshots of possible intermediates in the time course of synthesis and degradation of protein-bound Fe₄S₄ clusters
Authors : Nicolet, Y.; Rohac, R.; Martin, L.; Fontecilla-Camps, J.C.
Deposited on : 2013-03-29
Resolution : 1.60 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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

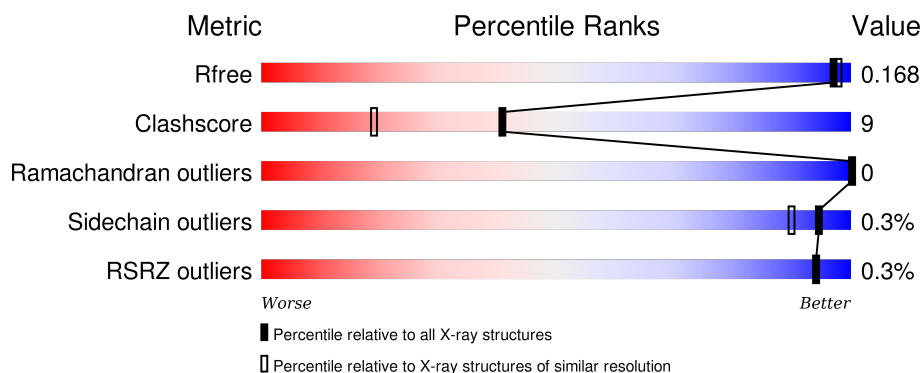
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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))
R_{free}	91344	2475 (1.60-1.60)
Clashscore	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (1.60-1.60)

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.

Mol	Chain	Length	Quality of chain
1	A	348	<div> <div></div> <div>89%</div> <div>11%</div> <div></div> </div>

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
4	1N7	A	407	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	1N7	A	410	-	-	-	X

2 Entry composition [i](#)

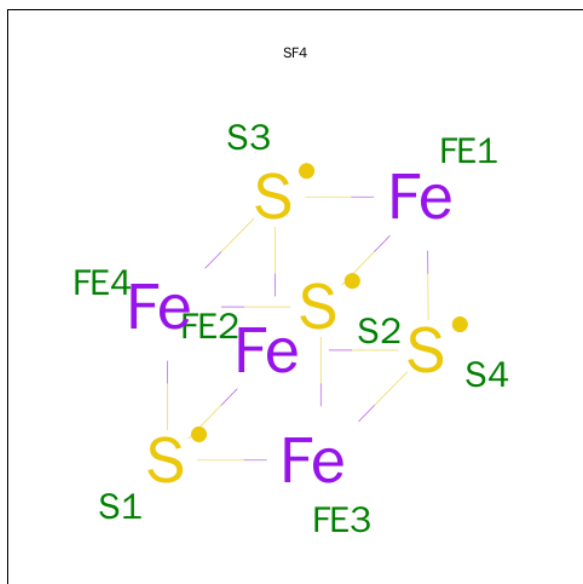
There are 7 unique types of molecules in this entry. The entry contains 3332 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FEFE-HYDROGENASE MATURASE.

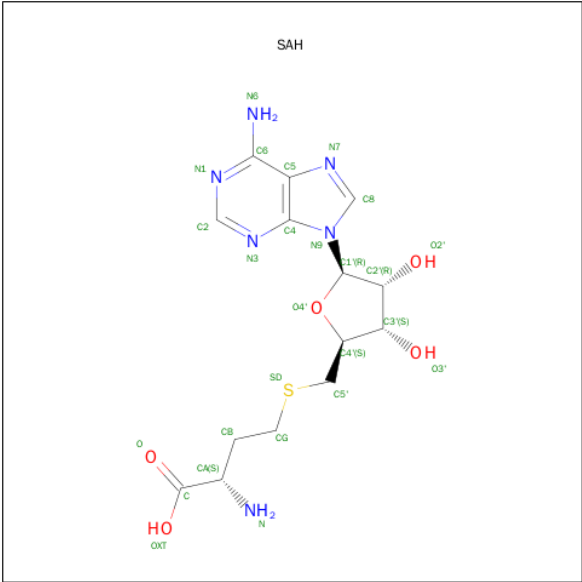
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	346	2775	1783	472	499	21	0	11	0

- Molecule 2 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



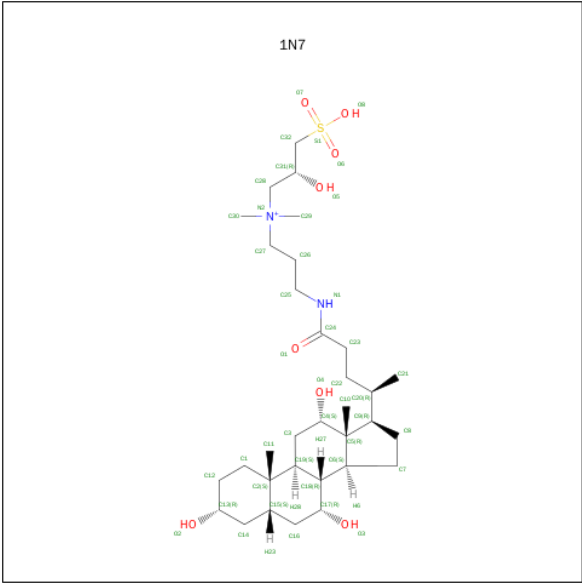
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
2	A	1	8	4	4	0	0

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C₁₄H₂₀N₆O₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 4 is CHAPSO (three-letter code: 1N7) (formula: C₃₂H₅₉N₂O₈S).



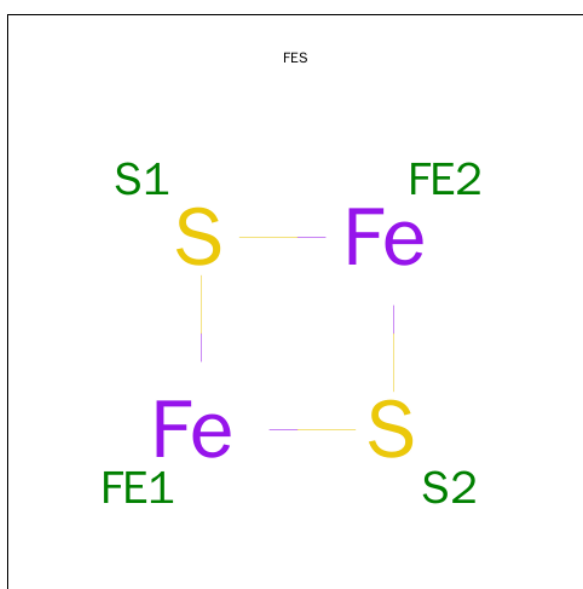
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O		0	0
			36	30	2	4			
4	A	1	Total	C	N	O	S	0	0
			43	32	2	8	1		
4	A	1	Total	C	O			0	0
			26	23	3				

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			29	24	1	4		
4	A	1	Total	C	O		0	0
			22	20	2			
4	A	1	Total	C	N		0	0
			6	5	1			
4	A	1	Total	C	O	S	0	0
			7	2	4	1		

- Molecule 5 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	Cl	0	1
			4	4		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	345	Total	O	0	2
			346	346		

i

• Molecule 1: FEFE-HYDROGENASE MATURASE

Q304	M324	D337	W338	G339	G340	R341	K342	E346	T347	VAL	T2	I6	R12	R17	E22	I26	R29	I66	R64	R74	N78	R94	M115	P116	R142	L157	L158	R159	T162	H168	R172	H220	D221	F222	D223	M224	H233	F246	N264	A270	I274	I290	M291	R300
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.25Å 78.95Å 86.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.22 – 1.60 44.04 – 1.60	Depositor EDS
% Data completeness (in resolution range)	98.6 (58.22-1.60) 98.6 (44.04-1.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.102 , 0.156 0.119 , 0.168	Depositor DCC
R_{free} test set	2361 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	11.7	Xtriage
Anisotropy	0.430	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 55.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 46218 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3332	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.70% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SAH, SF4, 1N7, FES, CL

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	A	0.99	2/2868 (0.1%)	0.96	9/3877 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	346	GLU	CD-OE2	-5.47	1.19	1.25
1	A	300	ARG	CB-CG	-5.15	1.38	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	17	ARG	NE-CZ-NH2	-8.40	116.10	120.30
1	A	64	ARG	NE-CZ-NH1	7.69	124.15	120.30
1	A	159	ARG	NE-CZ-NH2	-6.32	117.14	120.30
1	A	94	ARG	NE-CZ-NH2	5.81	123.21	120.30
1	A	74	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	A	17	ARG	NE-CZ-NH1	5.51	123.06	120.30
1	A	142	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	159	ARG	NE-CZ-NH1	-5.29	117.66	120.30
1	A	159	ARG	NH1-CZ-NH2	5.27	125.20	119.40

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	A	2775	0	2810	42	0
2	A	8	0	0	0	0
3	A	26	0	19	0	0
4	A	169	0	224	22	0
5	A	4	0	0	0	0
6	A	4	0	0	1	0
7	A	346	0	0	7	1
All	All	3332	0	3053	52	1

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 (52) 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)
4:A:403:1N7:H52	4:A:410:1N7:C31	1.51	1.38
6:A:413[B]:CL:CL	7:A:843:HOH:O	1.90	1.22
1:A:324[B]:MET:HE3	4:A:407:1N7:C11	1.93	0.98
4:A:403:1N7:C30	4:A:410:1N7:C31	2.43	0.95
1:A:324[B]:MET:HE2	4:A:407:1N7:H17	1.52	0.90
1:A:324[B]:MET:CE	4:A:407:1N7:C11	2.49	0.89
1:A:246:PHE:HD1	1:A:274[B]:ILE:HD11	1.41	0.85
4:A:407:1N7:H32	7:A:707:HOH:O	1.75	0.84
1:A:157:LEU:CD2	1:A:224[A]:MET:HE2	2.10	0.82
1:A:324[B]:MET:CE	4:A:407:1N7:H17	2.09	0.81
1:A:157:LEU:HD23	1:A:224[A]:MET:HE2	1.63	0.81
4:A:403:1N7:H52	4:A:410:1N7:C32	2.11	0.80
1:A:324[B]:MET:HE3	4:A:407:1N7:H16	1.66	0.78
4:A:403:1N7:C30	4:A:410:1N7:C32	2.65	0.74
1:A:337:ASP:CG	4:A:408:1N7:H51	2.10	0.71
4:A:403:1N7:C30	4:A:410:1N7:H56	2.21	0.70
1:A:342:LYS:NZ	4:A:408:1N7:H49	2.06	0.70
1:A:157:LEU:HD23	1:A:224[A]:MET:CE	2.22	0.70
1:A:340:GLY:H	4:A:408:1N7:H50	1.59	0.68
1:A:246:PHE:CD1	1:A:274[B]:ILE:HD11	2.27	0.68
1:A:157:LEU:CD2	1:A:224[A]:MET:CE	2.74	0.66
1:A:291[B]:MET:HE3	7:A:845:HOH:O	1.97	0.65
1:A:338:TRP:H	4:A:408:1N7:C26	2.11	0.64
1:A:342:LYS:HZ2	4:A:408:1N7:H49	1.62	0.64
1:A:56[B]:ILE:CD1	1:A:291[B]:MET:HB3	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:THR:N	7:A:722:HOH:O	2.31	0.63
1:A:168:HIS:HE1	1:A:172:ARG:HH11	1.45	0.63
1:A:29:ARG:NE	7:A:603:HOH:O	2.31	0.62
1:A:56[B]:ILE:HD11	1:A:291[B]:MET:CE	2.30	0.61
4:A:403:1N7:H53	4:A:410:1N7:H56	1.83	0.60
1:A:6:ILE:HD11	1:A:22:GLU:CG	2.32	0.59
1:A:56[B]:ILE:HD11	1:A:291[B]:MET:SD	2.42	0.59
1:A:56[B]:ILE:HD11	1:A:291[B]:MET:HB3	1.85	0.58
1:A:168:HIS:CE1	1:A:172:ARG:HH11	2.20	0.58
1:A:6:ILE:HD11	1:A:22:GLU:HG2	1.86	0.56
1:A:270:ALA:O	1:A:274[B]:ILE:HG23	2.07	0.53
1:A:337:ASP:HB2	4:A:408:1N7:C26	2.39	0.53
1:A:78:ASN:ND2	7:A:733:HOH:O	2.43	0.51
1:A:168:HIS:CE1	1:A:172:ARG:HD3	2.47	0.50
1:A:233:HIS:HE2	1:A:304:GLN:HE21	1.60	0.50
1:A:338:TRP:HB2	4:A:408:1N7:H46	1.95	0.49
4:A:404:1N7:H5	4:A:404:1N7:H31	1.95	0.49
1:A:12:ARG:CD	7:A:746:HOH:O	2.62	0.48
4:A:407:1N7:H5	4:A:407:1N7:H31	1.99	0.44
1:A:342:LYS:HZ1	4:A:408:1N7:H49	1.80	0.44
1:A:6:ILE:CD1	1:A:26:ILE:HD11	2.48	0.44
1:A:115:MET:HA	1:A:116:PRO:HA	1.88	0.42
1:A:224[B]:MET:HA	1:A:264:ASN:O	2.20	0.41
1:A:224[A]:MET:HA	1:A:264:ASN:O	2.20	0.41
1:A:56[B]:ILE:HD11	1:A:291[B]:MET:CB	2.51	0.41
1:A:220:HIS:HB2	1:A:222:PHE:CE1	2.56	0.41
1:A:162:THR:O	1:A:168:HIS:HD2	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:602:HOH:O	7:A:760:HOH:O[2_655]	1.94	0.26

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	A	355/348 (102%)	345 (97%)	10 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	A	296/304 (97%)	295 (100%)	1 (0%)	94	90

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	290	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	168	HIS
1	A	304	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 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$
2	SF4	A	401	1,3	0,12,12	0.00	-	0,24,24	0.00	-
3	SAH	A	402	2	20,28,28	1.22	3 (15%)	19,40,40	2.32	3 (15%)
4	1N7	A	403	-	39,39,46	1.02	2 (5%)	61,61,72	1.34	5 (8%)
4	1N7	A	404	-	44,46,46	0.98	1 (2%)	66,72,72	1.37	6 (9%)
4	1N7	A	405	-	29,29,46	0.85	1 (3%)	47,47,72	1.13	5 (10%)
4	1N7	A	406	-	32,32,46	1.09	2 (6%)	51,51,72	0.96	2 (3%)
4	1N7	A	407	-	24,24,46	1.07	3 (12%)	38,40,72	1.62	6 (15%)
4	1N7	A	408	-	4,5,46	2.44	2 (50%)	6,7,72	1.00	0
5	FES	A	409	1,7	0,4,4	0.00	-	0,4,4	0.00	-
4	1N7	A	410	-	4,6,46	2.12	2 (50%)	6,8,72	6.77	3 (50%)

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	SF4	A	401	1,3	-	0/0/48/48	0/6/5/5
3	SAH	A	402	2	-	0/7/31/31	0/3/3/3
4	1N7	A	403	-	-	0/17/82/92	0/4/4/4
4	1N7	A	404	-	-	0/27/92/92	0/4/4/4
4	1N7	A	405	-	-	0/6/71/92	0/4/4/4
4	1N7	A	406	-	-	0/9/74/92	0/4/4/4
4	1N7	A	407	-	-	0/4/59/92	0/3/3/4
4	1N7	A	408	-	-	0/3/3/92	0/0/0/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FES	A	409	1,7	-	0/0/4/4	0/1/1/1
4	1N7	A	410	-	-	0/4/4/92	0/0/0/4

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	408	1N7	C29-N2	-4.22	1.37	1.50
4	A	404	1N7	C32-S1	-3.01	1.73	1.77
4	A	408	1N7	C30-N2	-2.23	1.43	1.50
4	A	407	1N7	C5-C9	-2.13	1.51	1.55
4	A	407	1N7	C16-C17	-2.12	1.49	1.52
4	A	405	1N7	C5-C6	-2.01	1.52	1.55
3	A	402	SAH	C5'-SD	2.07	1.85	1.81
4	A	403	1N7	C3-C19	2.08	1.57	1.53
4	A	406	1N7	C16-C17	2.37	1.56	1.52
4	A	410	1N7	O6-S1	2.47	1.53	1.45
4	A	403	1N7	C14-C13	2.47	1.56	1.51
3	A	402	SAH	C5-C4	2.50	1.46	1.40
3	A	402	SAH	O4'-C1'	2.65	1.44	1.41
4	A	407	1N7	C3-C4	2.79	1.58	1.53
4	A	406	1N7	O4-C4	2.92	1.48	1.43
4	A	410	1N7	O7-S1	3.24	1.55	1.45

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	410	1N7	O6-S1-C32	-13.62	95.28	106.91
3	A	402	SAH	N3-C2-N1	-8.18	122.63	128.89
4	A	404	1N7	O8-S1-O6	-3.62	103.18	111.61
4	A	403	1N7	C3-C19-C2	-3.14	110.53	113.79
4	A	407	1N7	C10-C5-C9	-3.14	106.27	111.22
4	A	407	1N7	C14-C15-C16	-2.95	103.67	110.38
3	A	402	SAH	C1'-N9-C4	-2.84	122.65	126.94
4	A	407	1N7	C8-C9-C5	-2.83	100.78	103.60
3	A	402	SAH	C2'-C1'-N9	-2.64	110.26	114.29
4	A	403	1N7	C30-N2-C27	-2.57	99.67	109.90
4	A	406	1N7	C15-C16-C17	-2.49	111.66	114.44
4	A	403	1N7	C29-N2-C28	-2.45	102.66	108.98
4	A	405	1N7	C21-C20-C22	-2.44	105.66	111.87
4	A	405	1N7	C11-C2-C1	-2.37	104.22	108.20
4	A	410	1N7	O5-C31-C32	-2.34	105.33	109.98
4	A	405	1N7	C19-C18-C17	-2.26	109.26	111.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	404	1N7	C5-C9-C20	-2.21	116.81	119.50
4	A	407	1N7	C22-C20-C9	-2.19	106.46	112.32
4	A	404	1N7	O1-C24-C23	-2.18	118.23	121.98
4	A	405	1N7	O2-C13-C14	-2.14	105.62	109.86
4	A	403	1N7	C15-C14-C13	-2.10	109.79	112.91
4	A	405	1N7	O3-C17-C18	2.01	113.69	109.26
4	A	406	1N7	C10-C5-C4	2.12	111.16	109.09
4	A	404	1N7	C7-C6-C5	2.14	105.72	103.60
4	A	407	1N7	C5-C9-C20	2.21	122.19	119.49
4	A	407	1N7	C11-C2-C15	2.31	114.39	110.08
4	A	404	1N7	C23-C24-N1	2.54	120.87	116.46
4	A	403	1N7	C30-N2-C28	5.14	122.20	108.98
4	A	404	1N7	O6-S1-C32	6.33	112.28	106.94
4	A	410	1N7	O7-S1-C32	9.10	114.67	106.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	403	1N7	6	0
4	A	404	1N7	1	0
4	A	407	1N7	7	0
4	A	408	1N7	8	0
4	A	410	1N7	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](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	346/348 (99%)	-0.59	1 (0%) 94 94	7, 13, 27, 37	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	78	ASN	2.4

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	1N7	A	407	22/43	0.84	0.13	6.93	20,27,32,35	0
4	1N7	A	410	7/43	0.90	0.17	6.61	25,36,58,90	0
5	FES	A	409	4/4	0.99	0.07	1.23	12,13,14,18	4
4	1N7	A	403	36/43	0.96	0.07	0.61	7,12,21,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	1N7	A	404	43/43	0.96	0.08	0.46	10,13,33,36	0
4	1N7	A	406	29/43	0.95	0.07	0.12	13,15,22,34	0
4	1N7	A	405	26/43	0.97	0.06	-0.32	10,12,17,32	0
3	SAH	A	402	26/26	0.98	0.06	-0.77	10,12,18,23	0
6	CL	A	411	1/1	1.00	0.06	-1.80	13,13,13,13	0
6	CL	A	412	1/1	0.99	0.04	-1.95	27,27,27,27	1
2	SF4	A	401	8/8	1.00	0.04	-2.17	10,10,11,11	0
4	1N7	A	408	6/43	0.94	0.14	-	18,25,33,34	0
6	CL	A	413[B]	1/1	0.99	0.04	-	30,30,30,30	1
6	CL	A	413[A]	1/1	0.99	0.04	-	24,24,24,24	1

6.5 Other polymers [i](#)

There are no such residues in this entry.