wwPDB X-ray Structure Validation Summary Report (i)

Jan 2, 2024 – 02:11 pm GMT

PDB ID	:	4UPE
Title	:	Structure of the unready Ni-A state of the S499C mutant of D. fructosovorans NiFe-hydrogenase
Authors	:	Volbeda, A.; Martin, L.; Barbier, E.; Gutierrez-Sanz, O.; DeLacey, A.L.; Liebgott, P.P.; Dementin, S.; Rousset, M.; Fontecilla-Camps, J.C.
Deposited on	:	2014-06-16
Resolution	:	1.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

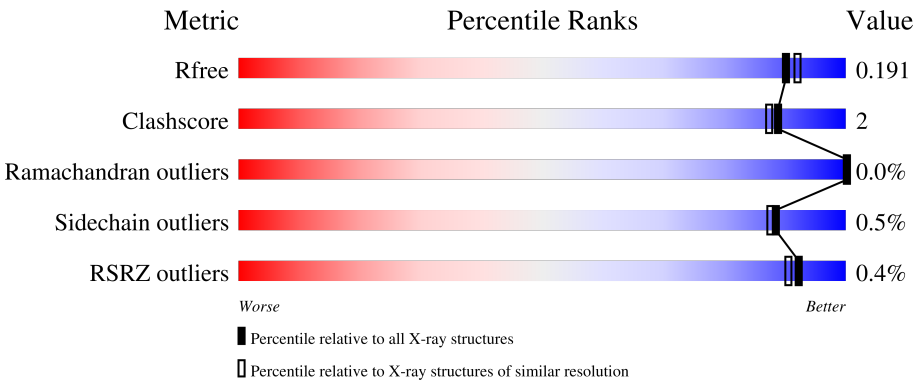
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 1.80 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}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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% 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	265	% 94% 5% •
1	B	265	% 96% • •
1	C	265	94% 5% •
2	Q	548	95% • •
2	R	548	94% 5% •

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Mol	Chain	Length	Quality of chain
2	S	548	% 94% 5%

2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 20844 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 NIFE-HYDROGENASE SMALL SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	262	2015	1287	337	376	15	0	6	0
1	B	262	1986	1265	331	375	15	0	2	0
1	C	261	2004	1280	332	377	15	0	6	0

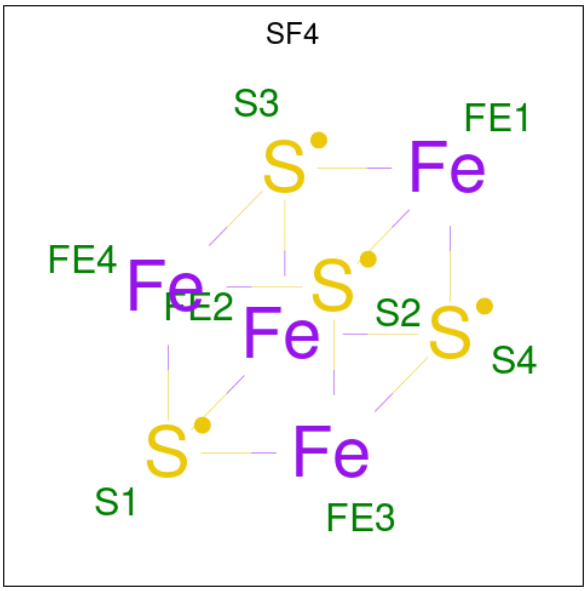
- Molecule 2 is a protein called NICKEL-DEPENDENT HYDROGENASE LARGE SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	Q	545	4219	2692	730	774	23	0	8	0
2	R	544	4223	2698	728	774	23	0	11	0
2	S	544	4206	2681	727	775	23	0	7	0

There are 3 discrepancies between the modelled and reference sequences:

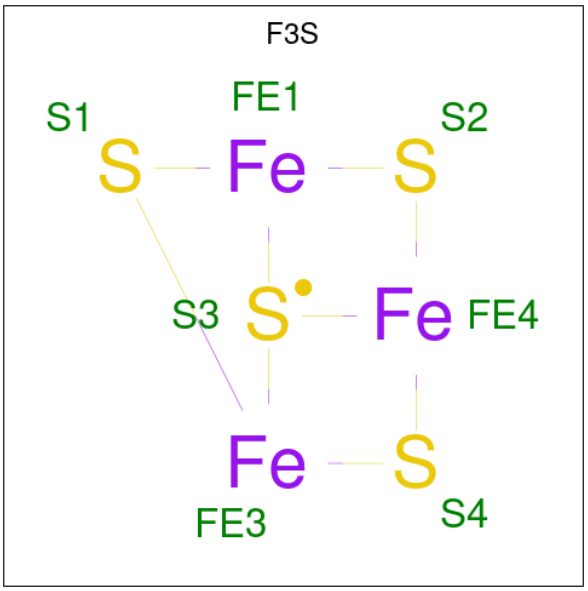
Chain	Residue	Modelled	Actual	Comment	Reference
Q	499	CYS	SER	engineered mutation	UNP P18188
R	499	CYS	SER	engineered mutation	UNP P18188
S	499	CYS	SER	engineered mutation	UNP P18188

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



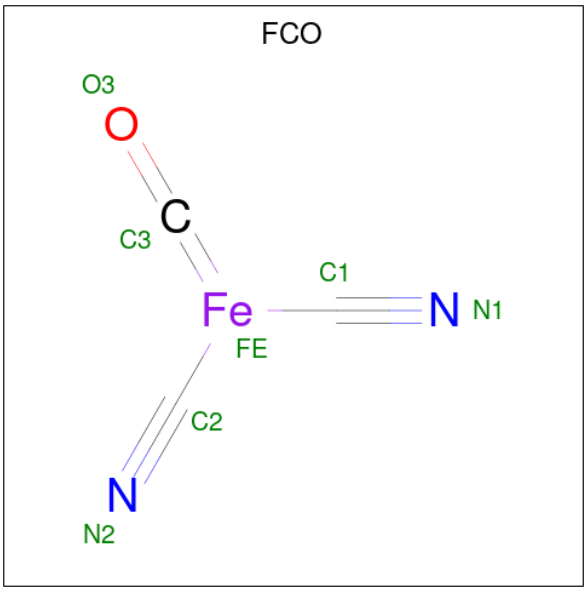
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
3	A	1	8	4	4	0	0
			Total	Fe	S		
3	A	1	8	4	4	0	0
			Total	Fe	S		
3	B	1	8	4	4	0	0
			Total	Fe	S		
3	B	1	8	4	4	0	0
			Total	Fe	S		
3	C	1	8	4	4	0	0
			Total	Fe	S		
3	C	1	8	4	4	0	0

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



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

- Molecule 5 is CARBONMONOXIDE-(DICYANO) IRON (three-letter code: FCO) (formula: C_3FeN_2O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
5	Q	1	7	3	1	2	1	0	0
5	R	1	7	3	1	2	1	0	0
5	S	1	7	3	1	2	1	0	0

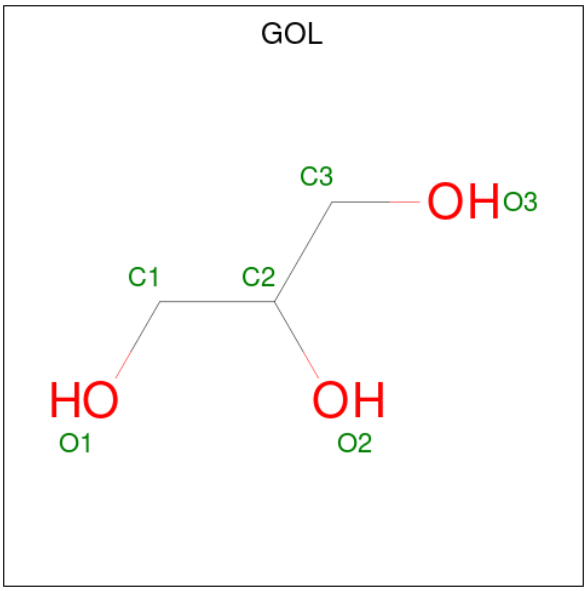
- Molecule 6 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ni		
6	Q	1	1	1	0	0
6	R	1	1	1	0	0
6	S	1	1	1	0	0

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

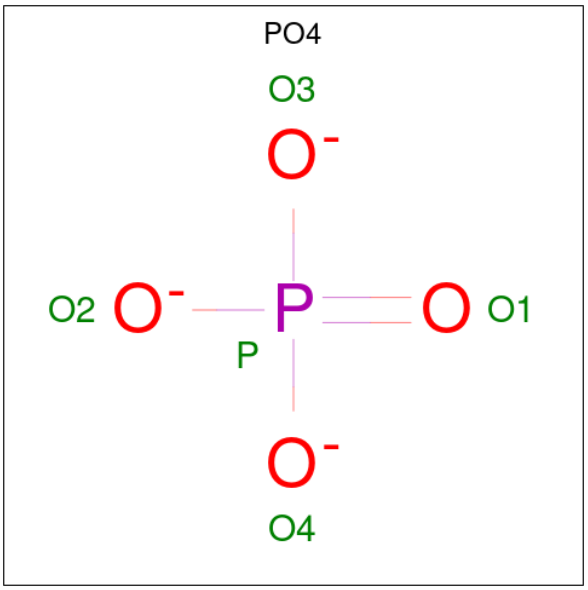
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
7	Q	1	1	1	0	0
7	R	2	2	2	0	0
7	S	1	1	1	0	0

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



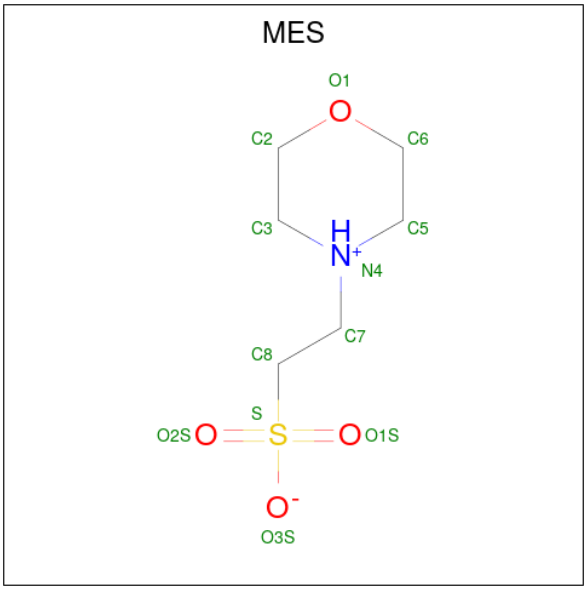
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
8	Q	1	6	3	3	0	0
			Total	C	O		
8	Q	1	6	3	3	0	0
			Total	C	O		
8	R	1	6	3	3	0	0
			Total	C	O		
8	R	1	6	3	3	0	0
			Total	C	O		
8	S	1	6	3	3	0	0

- Molecule 9 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	P			
9	Q	1	5	4	1		0	0
			Total	O	P			
9	R	1	5	4	1		0	0

- Molecule 10 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
10	S	1	12	6	1	4	1	0	0

- Molecule 11 is water.

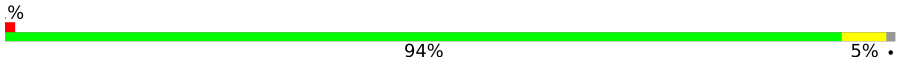
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
11	A	263	264	264	0	1
			Total	O		
11	B	199	199	199	0	0
			Total	O		
11	C	236	237	237	0	1
			Total	O		
11	Q	478	478	478	0	0
			Total	O		
11	R	463	465	465	0	2
			Total	O		
11	S	395	399	399	0	4

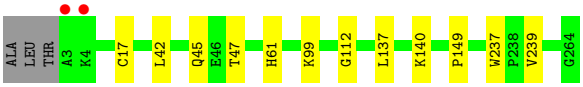
3 Residue-property plots (i)

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 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.

• Molecule 1: NIFE-HYDROGENASE SMALL SUBUNIT

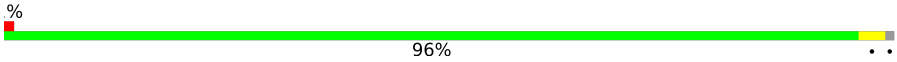
Chain A:

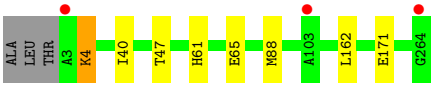




• Molecule 1: NIFE-HYDROGENASE SMALL SUBUNIT

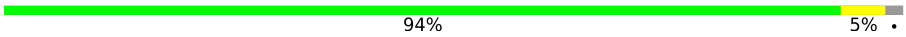
Chain B:





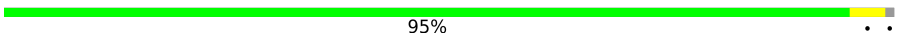
• Molecule 1: NIFE-HYDROGENASE SMALL SUBUNIT

Chain C:



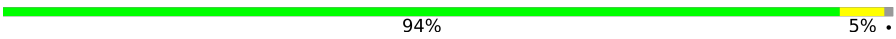
• Molecule 2: NICKEL-DEPENDENT HYDROGENASE LARGE SUBUNIT

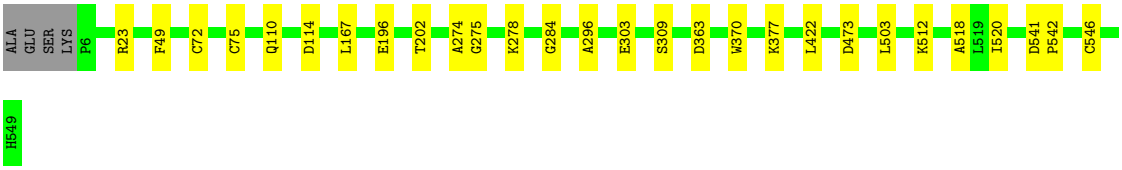
Chain Q:



• Molecule 2: NICKEL-DEPENDENT HYDROGENASE LARGE SUBUNIT

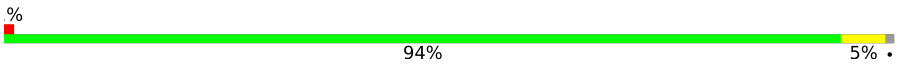
Chain R:

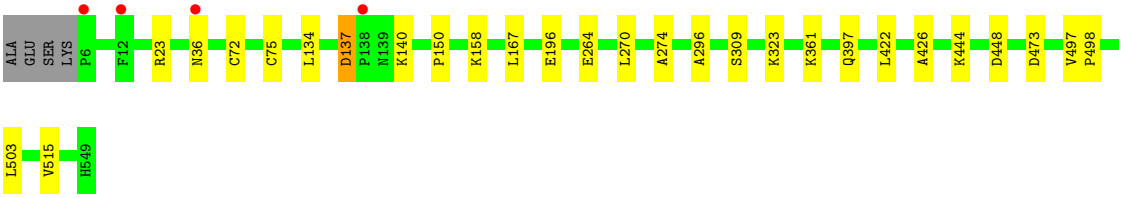




• Molecule 2: NICKEL-DEPENDENT HYDROGENASE LARGE SUBUNIT

Chain S:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	65.43Å 98.96Å 184.95Å 90.00° 91.19° 90.00°	Depositor
Resolution (Å)	29.83 – 1.80 29.83 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.1 (29.83-1.80) 96.1 (29.83-1.80)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.16 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.151 , 0.190 0.153 , 0.191	Depositor DCC
R_{free} test set	10529 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	16.1	Xtriage
Anisotropy	0.441	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 48.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	20844	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: MES, CSX, SF4, GOL, F3S, CA, FCO, PO4, NI

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	0.63	0/2082	0.66	0/2832
1	B	0.58	0/2046	0.63	0/2785
1	C	0.58	0/2077	0.64	0/2826
2	Q	0.63	0/4340	0.68	1/5887 (0.0%)
2	R	0.61	0/4359	0.68	0/5910
2	S	0.62	0/4323	0.69	5/5864 (0.1%)
All	All	0.61	0/19227	0.67	6/26104 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	S	36[A]	ASN	CA-C-O	6.26	133.25	120.10
2	S	36[B]	ASN	CA-C-O	6.26	133.25	120.10
2	Q	50	ARG	NE-CZ-NH2	-5.38	117.61	120.30
2	S	137	ASP	C-N-CD	5.29	139.51	128.40
2	S	36[A]	ASN	CA-C-N	-5.25	105.71	116.20

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	A	2015	0	1974	10	0
1	B	1986	0	1929	5	0
1	C	2004	0	1957	11	0
2	Q	4219	0	4222	17	0
2	R	4223	0	4238	17	0
2	S	4206	0	4193	15	0
3	A	16	0	0	0	0
3	B	16	0	0	0	0
3	C	16	0	0	0	0
4	A	7	0	0	0	0
4	B	7	0	0	0	0
4	C	7	0	0	0	0
5	Q	7	0	0	0	0
5	R	7	0	0	0	0
5	S	7	0	0	0	0
6	Q	1	0	0	0	0
6	R	1	0	0	0	0
6	S	1	0	0	0	0
7	Q	1	0	0	0	0
7	R	2	0	0	0	0
7	S	1	0	0	0	0
8	Q	12	0	16	0	0
8	R	12	0	16	0	0
8	S	6	0	8	0	0
9	Q	5	0	0	0	0
9	R	5	0	0	0	0
10	S	12	0	13	0	0
11	A	264	0	0	4	0
11	B	199	0	0	2	0
11	C	237	0	0	2	0
11	Q	478	0	0	5	0
11	R	465	0	0	5	0
11	S	399	0	0	0	0
All	All	20844	0	18566	69	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 2.

The worst 5 of 69 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:A:61[A]:HIS:HE1	11:A:2102:HOH:O	1.19	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:196[B]:GLU:OE2	11:R:2344:HOH:O	1.57	1.19
2:Q:5:LYS:HB3	2:Q:6:PRO:HA	1.62	0.82
2:R:278[A]:LYS:HG2	11:R:2445:HOH:O	1.80	0.81
1:A:61[A]:HIS:CE1	11:A:2102:HOH:O	2.07	0.74

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	A	266/265 (100%)	260 (98%)	6 (2%)	0	100	100
1	B	262/265 (99%)	254 (97%)	7 (3%)	1 (0%)	34	21
1	C	265/265 (100%)	259 (98%)	6 (2%)	0	100	100
2	Q	550/548 (100%)	534 (97%)	16 (3%)	0	100	100
2	R	552/548 (101%)	543 (98%)	9 (2%)	0	100	100
2	S	548/548 (100%)	535 (98%)	13 (2%)	0	100	100
All	All	2443/2439 (100%)	2385 (98%)	57 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	4	LYS

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	A	214/210 (102%)	214 (100%)	0	100	100
1	B	210/210 (100%)	209 (100%)	1 (0%)	88	87
1	C	214/210 (102%)	214 (100%)	0	100	100
2	Q	443/437 (101%)	440 (99%)	3 (1%)	84	81
2	R	445/437 (102%)	442 (99%)	3 (1%)	84	81
2	S	441/437 (101%)	438 (99%)	3 (1%)	84	81
All	All	1967/1941 (101%)	1957 (100%)	10 (0%)	88	87

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	S	158	LYS
2	S	397	GLN
2	S	473	ASP
2	Q	473	ASP
2	R	473	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	ASN
2	R	36	ASN
2	R	367	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues are 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	CSX	S	75	5,6,2	3,6,7	0.59	0	1,6,8	1.88	0
2	CSX	R	75	5,6,2	3,6,7	1.02	0	1,6,8	0.04	0
2	CSX	Q	75	5,6,2	3,6,7	0.77	0	1,6,8	0.51	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	CSX	S	75	5,6,2	-	0/1/5/7	-
2	CSX	R	75	5,6,2	-	0/1/5/7	-
2	CSX	Q	75	5,6,2	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	S	75	CSX	1	0
2	R	75	CSX	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 27 ligands modelled in this entry, 7 are monoatomic - leaving 20 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	$\#\|Z\| > 2$
10	MES	S	1562	-	12,12,12	2.14	1 (8%)	14,16,16	1.73	3 (21%)
8	GOL	Q	1561	-	5,5,5	0.56	0	5,5,5	0.47	0
3	SF4	A	1267	1	0,12,12	-	-	-		
8	GOL	R	1562	-	5,5,5	0.42	0	5,5,5	0.28	0
5	FCO	S	1550	11,2	0,6,6	-	-	-		
4	F3S	C	1266	1	0,9,9	-	-	-		
5	FCO	Q	1550	11,2	0,6,6	-	-	-		
3	SF4	C	1267	1	0,12,12	-	-	-		
4	F3S	B	1266	1	0,9,9	-	-	-		
9	PO4	Q	1564	-	4,4,4	1.12	0	6,6,6	0.47	0
9	PO4	R	1563	-	4,4,4	0.82	0	6,6,6	0.36	0
8	GOL	Q	1562	-	5,5,5	0.44	0	5,5,5	0.34	0
3	SF4	A	1265	1	0,12,12	-	-	-		
8	GOL	R	1561	-	5,5,5	0.43	0	5,5,5	0.39	0
4	F3S	A	1266	1	0,9,9	-	-	-		
3	SF4	C	1265	1	0,12,12	-	-	-		
3	SF4	B	1265	1	0,12,12	-	-	-		
5	FCO	R	1550	11,2	0,6,6	-	-	-		
8	GOL	S	1561	-	5,5,5	0.50	0	5,5,5	0.36	0
3	SF4	B	1267	1	0,12,12	-	-	-		

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
4	F3S	C	1266	1	-	-	0/3/3/3
10	MES	S	1562	-	-	0/6/14/14	0/1/1/1
3	SF4	B	1265	1	-	-	0/6/5/5
8	GOL	Q	1561	-	-	0/4/4/4	-
3	SF4	A	1265	1	-	-	0/6/5/5
8	GOL	S	1561	-	-	0/4/4/4	-
3	SF4	A	1267	1	-	-	0/6/5/5
3	SF4	C	1267	1	-	-	0/6/5/5
8	GOL	R	1561	-	-	0/4/4/4	-
8	GOL	R	1562	-	-	0/4/4/4	-
4	F3S	A	1266	1	-	-	0/3/3/3
4	F3S	B	1266	1	-	-	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SF4	B	1267	1	-	-	0/6/5/5
3	SF4	C	1265	1	-	-	0/6/5/5
8	GOL	Q	1562	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	S	1562	MES	C8-S	-7.09	1.67	1.77

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	S	1562	MES	O2S-S-C8	3.60	111.24	106.92
10	S	1562	MES	O3S-S-C8	2.80	110.30	105.77
10	S	1562	MES	C2-C3-N4	-2.37	106.51	110.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	262/265 (98%)	-0.54	2 (0%)	86	84	10, 15, 26, 56	6 (2%)
1	B	262/265 (98%)	-0.24	3 (1%)	80	78	13, 21, 35, 62	7 (2%)
1	C	261/265 (98%)	-0.49	1 (0%)	92	90	12, 18, 31, 60	8 (3%)
2	Q	544/548 (99%)	-0.55	0	100	100	10, 16, 27, 49	10 (1%)
2	R	543/548 (99%)	-0.58	0	100	100	10, 16, 26, 41	8 (1%)
2	S	543/548 (99%)	-0.34	4 (0%)	87	86	12, 20, 34, 47	9 (1%)
All	All	2415/2439 (99%)	-0.47	10 (0%)	92	90	10, 17, 31, 62	48 (1%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	264	GLY	5.0
1	A	3	ALA	5.0
1	B	3	ALA	4.5
2	S	6	PRO	2.9
1	C	4	LYS	2.4

6.2 Non-standard residues in protein, DNA, RNA chains (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. 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	B-factors(Å^2)	Q<0.9
2	CSX	R	75	7/8	0.98	0.07	14,15,16,17	1
2	CSX	Q	75	7/8	0.99	0.05	12,15,15,18	1
2	CSX	S	75	7/8	0.99	0.08	13,14,16,18	1

6.3 Carbohydrates (i)

There are no monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
9	PO4	Q	1564	5/5	0.95	0.13	23,23,25,26	5
9	PO4	R	1563	5/5	0.95	0.14	37,40,45,49	0
10	MES	S	1562	12/12	0.95	0.12	30,32,35,35	4
7	CA	R	1564	1/1	0.96	0.07	24,24,24,24	1
8	GOL	Q	1562	6/6	0.96	0.10	18,22,25,27	0
8	GOL	S	1561	6/6	0.96	0.07	17,19,20,21	0
8	GOL	R	1562	6/6	0.97	0.09	17,18,19,20	0
8	GOL	R	1561	6/6	0.98	0.06	16,17,18,19	0
8	GOL	Q	1561	6/6	0.98	0.06	15,15,16,17	0
3	SF4	B	1265	8/8	0.99	0.03	22,24,24,24	0
3	SF4	B	1267	8/8	0.99	0.05	15,16,18,18	0
3	SF4	C	1265	8/8	0.99	0.05	15,16,16,18	0
3	SF4	C	1267	8/8	0.99	0.04	12,15,15,17	0
4	F3S	A	1266	7/7	0.99	0.04	11,13,13,15	0
4	F3S	B	1266	7/7	0.99	0.04	17,17,19,19	0
7	CA	Q	1552	1/1	0.99	0.04	13,13,13,13	0
3	SF4	A	1267	8/8	0.99	0.04	10,12,12,13	0
4	F3S	C	1266	7/7	1.00	0.04	11,13,14,15	0
7	CA	S	1552	1/1	1.00	0.04	14,14,14,14	0
5	FCO	Q	1550	7/7	1.00	0.05	10,11,14,14	0
5	FCO	R	1550	7/7	1.00	0.06	11,11,14,14	0
5	FCO	S	1550	7/7	1.00	0.08	13,15,16,17	0
6	NI	Q	1551	1/1	1.00	0.03	16,16,16,16	0
6	NI	R	1551	1/1	1.00	0.03	14,14,14,14	0
6	NI	S	1551	1/1	1.00	0.05	17,17,17,17	0
3	SF4	A	1265	8/8	1.00	0.03	13,14,15,17	0
7	CA	R	1552	1/1	1.00	0.04	15,15,15,15	0

6.5 Other polymers (i)

There are no such residues in this entry.