Full wwPDB X-ray Structure Validation Report

Aug 25, 2026 – 06:13 am BST

PDB ID	:	4UQL / pdb_00004uql
Title	:	High-resolution structure of a Ni-A Ni-Sox mixture of the D. fructosovorans NiFe-hydrogenase L122A mutant
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	:	2014-06-24
Resolution	:	1.22 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:

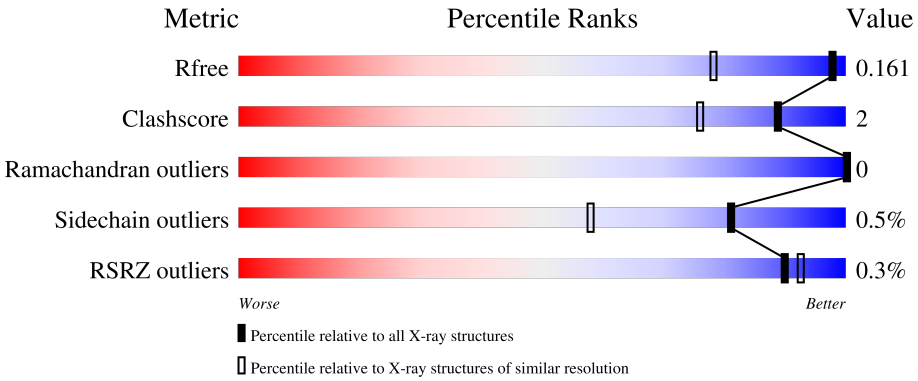
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

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

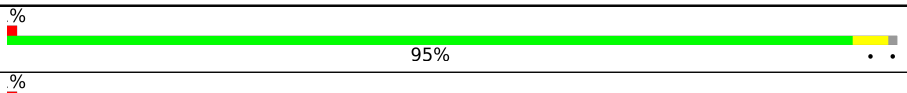
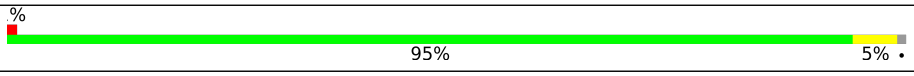
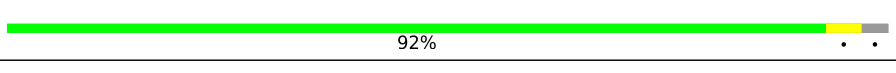
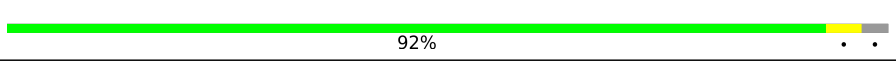
The reported resolution of this entry is 1.22 Å.

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}	180053	2002 (1.24-1.20)
Clashscore	190562	2061 (1.24-1.20)
Ramachandran outliers	187476	2009 (1.24-1.20)
Sidechain outliers	187428	2008 (1.24-1.20)
RSRZ outliers	180081	2000 (1.24-1.20)

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	
1	B	265	
2	Q	563	
2	R	563	

2 Entry composition (i)

There are 13 unique types of molecules in this entry. The entry contains 14688 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 HYDROGENASE (NIFE) SMALL SUBUNIT HYDA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	262	Total	C	N	O	S	0	12	0
			2031	1296	336	383	16			
1	B	263	Total	C	N	O	S	0	16	0
			2061	1316	339	390	16			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Q	544	Total	C	N	O	S	0	31	0
			4300	2748	744	783	25			
2	R	545	Total	C	N	O	S	0	35	0
			4328	2765	742	796	25			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	-13	ALA	-	expression tag	UNP E1K247
Q	-12	SER	-	expression tag	UNP E1K247
Q	-11	TRP	-	expression tag	UNP E1K247
Q	-10	SER	-	expression tag	UNP E1K247
Q	-9	HIS	-	expression tag	UNP E1K247
Q	-8	PRO	-	expression tag	UNP E1K247
Q	-7	GLN	-	expression tag	UNP E1K247
Q	-6	PHE	-	expression tag	UNP E1K247
Q	-5	GLU	-	expression tag	UNP E1K247
Q	-4	LYS	-	expression tag	UNP E1K247
Q	-3	GLY	-	expression tag	UNP E1K247
Q	-2	ALA	-	expression tag	UNP E1K247
Q	-1	SER	-	expression tag	UNP E1K247
Q	0	GLY	-	expression tag	UNP E1K247
Q	1	ALA	-	expression tag	UNP E1K247
Q	122	ALA	LEU	engineered mutation	UNP E1K247

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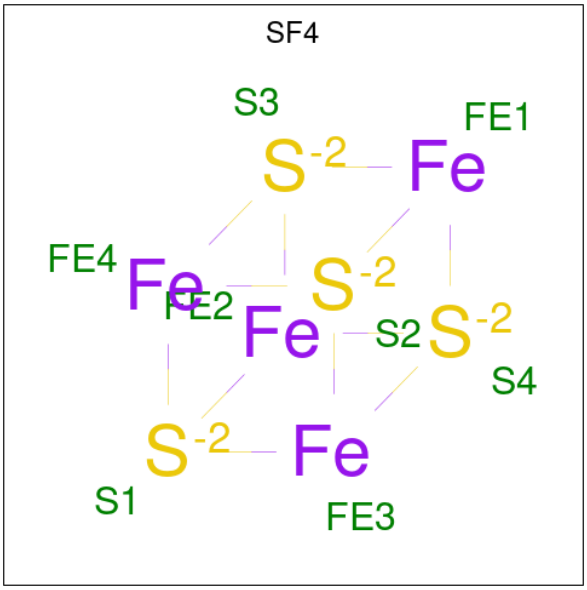
Chain	Residue	Modelled	Actual	Comment	Reference
R	-13	ALA	-	expression tag	UNP E1K247
R	-12	SER	-	expression tag	UNP E1K247
R	-11	TRP	-	expression tag	UNP E1K247
R	-10	SER	-	expression tag	UNP E1K247
R	-9	HIS	-	expression tag	UNP E1K247
R	-8	PRO	-	expression tag	UNP E1K247
R	-7	GLN	-	expression tag	UNP E1K247
R	-6	PHE	-	expression tag	UNP E1K247
R	-5	GLU	-	expression tag	UNP E1K247
R	-4	LYS	-	expression tag	UNP E1K247
R	-3	GLY	-	expression tag	UNP E1K247
R	-2	ALA	-	expression tag	UNP E1K247
R	-1	SER	-	expression tag	UNP E1K247
R	0	GLY	-	expression tag	UNP E1K247
R	1	ALA	-	expression tag	UNP E1K247
R	122	ALA	LEU	engineered mutation	UNP E1K247

- Molecule 3 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



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

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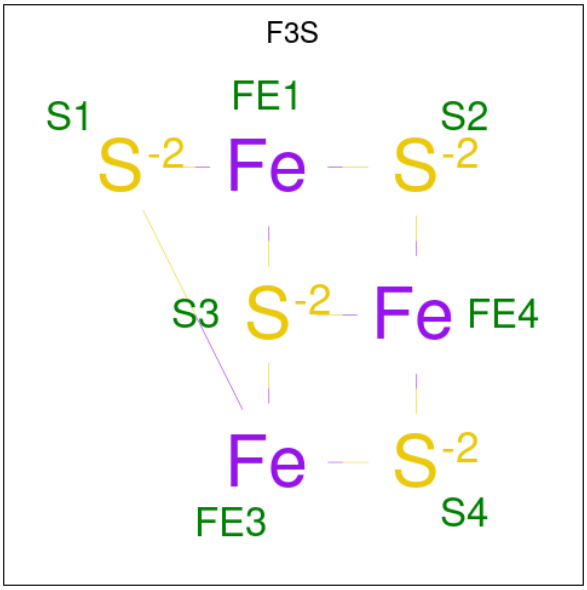
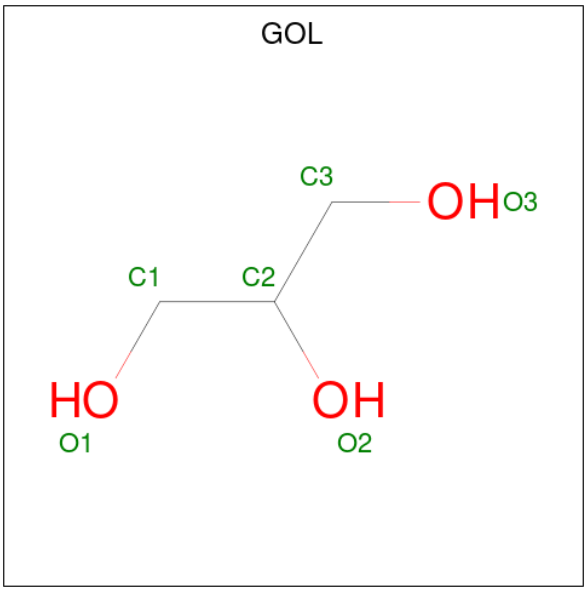
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Fe S 8 4 4	0	0

- Molecule 4 is FE3-S4 CLUSTER (CCD ID: F3S) (formula: Fe_3S_4).



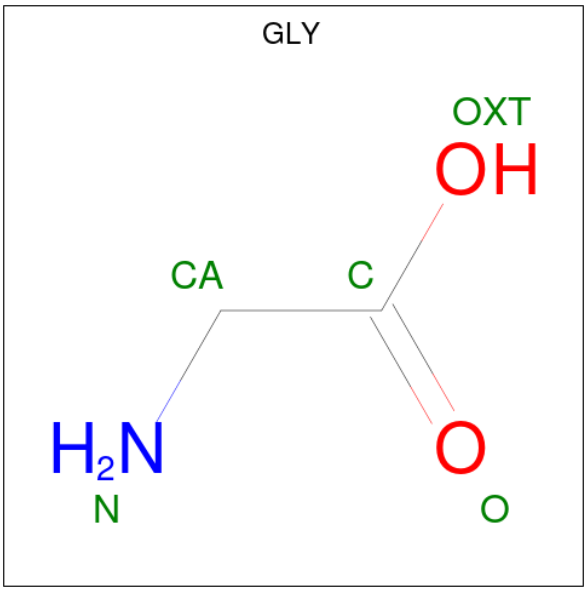
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Fe S 7 3 4	0	0
4	B	1	Total Fe S 7 3 4	0	0

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



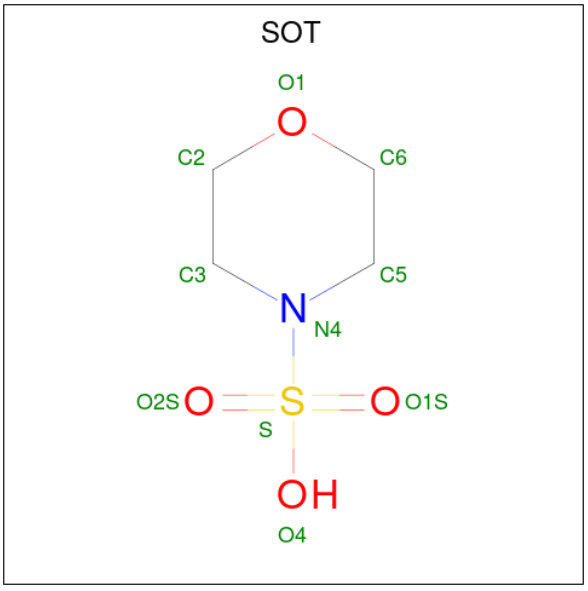
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	Q	1	Total C O 6 3 3	0	0
5	R	1	Total C O 6 3 3	0	0
5	R	1	Total C O 6 3 3	0	0
5	R	1	Total C O 7 3 4	0	1
5	R	1	Total C O 6 3 3	0	0
5	R	1	Total C O 6 3 3	0	0

- Molecule 6 is GLYCINE (CCD ID: GLY) (formula: $C_2H_5NO_2$).



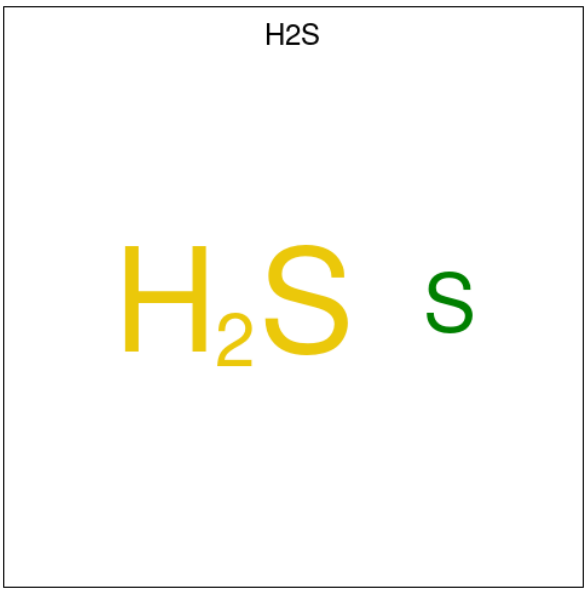
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			5	2	1	2		
6	Q	1	Total	C	N	O	0	0
			5	2	1	2		
6	R	1	Total	C	N	O	0	0
			5	2	1	2		

- Molecule 7 is morpholine-4-sulfonic acid (CCD ID: SOT) (formula: $C_4H_9NO_4S$).



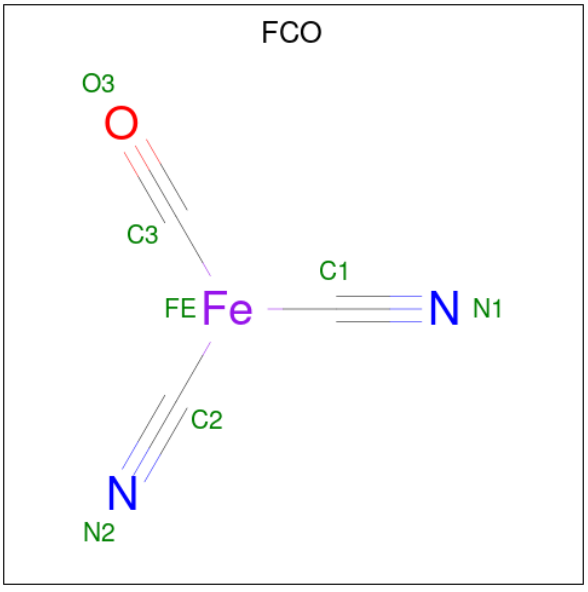
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	B	1	Total	C	N	O	S	0	1
			18	8	2	6	2		

- Molecule 8 is HYDROSULFURIC ACID (CCD ID: H2S) (formula: H_2S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	1	Total S 1 1	0	0

- Molecule 9 is CARBONMONOXIDE-(DICYANO) IRON (CCD ID: FCO) (formula: C_3FeN_2O).



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

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

- Molecule 10 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	Q	1	Total Ni 2 2	0	1
10	R	1	Total Ni 2 2	0	1

- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	Q	1	Total Mg 1 1	0	0
11	R	1	Total Mg 1 1	0	0

- Molecule 12 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	Q	1	Total Cl 1 1	0	0

- Molecule 13 is water.

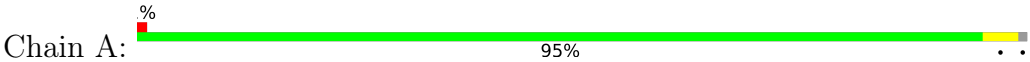
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	A	283	Total O 295 295	0	12
13	B	307	Total O 316 316	0	9
13	Q	544	Total O 557 557	0	13
13	R	618	Total O 632 632	0	14

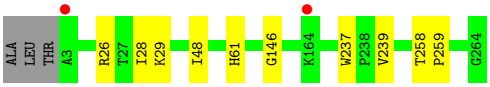
3 Residue-property plots (i)

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: HYDROGENASE (NIFE) SMALL SUBUNIT HYDA

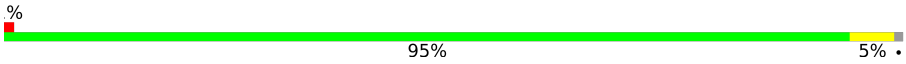
Chain A:

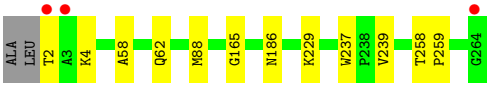




• Molecule 1: HYDROGENASE (NIFE) SMALL SUBUNIT HYDA

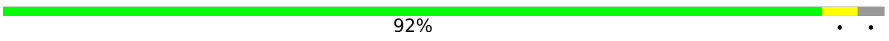
Chain B:

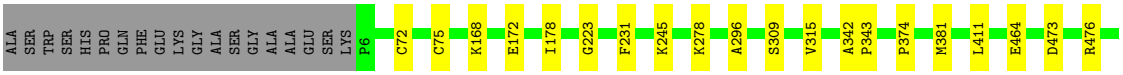


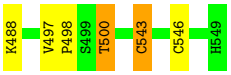


• Molecule 2: NICKEL-DEPENDENT HYDROGENASE LARGE SUBUNIT

Chain Q:

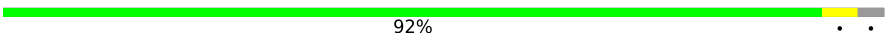


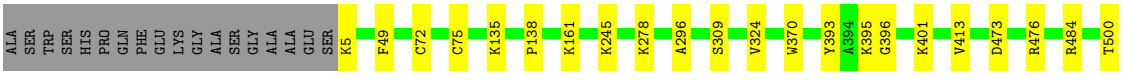


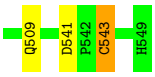


• Molecule 2: NICKEL-DEPENDENT HYDROGENASE LARGE SUBUNIT

Chain R:







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	64.69Å 100.85Å 116.70Å 90.00° 105.96° 90.00°	Depositor
Resolution (Å)	30.00 – 1.22 30.00 – 1.22	Depositor EDS
% Data completeness (in resolution range)	97.4 (30.00-1.22) 97.4 (30.00-1.22)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.52 (at 1.15Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.120 , 0.152 0.132 , 0.161	Depositor DCC
R_{free} test set	24508 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	6.4	Xtriage
Anisotropy	0.342	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 54.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.018 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	14688	wwPDB-VP
Average B, all atoms (Å^2)	11.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FCO, SF4, F3S, SOT, H2S, NI, MG, CL, GOL, CSX, CSS

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	0.82	0/2137	0.84	1/2904 (0.0%)
1	B	0.78	0/2181	0.86	0/2958
2	Q	0.80	0/4495	0.88	0/6081
2	R	0.79	1/4555 (0.0%)	0.87	3/6166 (0.0%)
All	All	0.80	1/13368 (0.0%)	0.87	4/18109 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	541	ASP	C-O	-5.80	1.21	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	R	5	LYS	CA-C-N	-7.09	112.67	119.76
2	R	5	LYS	C-N-CA	-7.09	112.67	119.76
1	A	146	GLY	N-CA-C	-5.19	107.02	111.95
2	R	245	LYS	N-CA-C	5.11	116.53	111.07

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	26	ARG	Sidechain

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	2031	0	1971	8	0
1	B	2061	0	1998	10	0
2	Q	4300	0	4316	19	0
2	R	4328	0	4320	14	0
3	A	16	0	0	0	0
3	B	16	0	0	0	0
4	A	7	0	0	0	0
4	B	7	0	0	0	0
5	A	12	0	16	0	0
5	B	18	0	24	1	0
5	Q	6	0	8	0	0
5	R	31	0	38	0	0
6	B	5	0	2	0	0
6	Q	5	0	2	0	0
6	R	5	0	2	0	0
7	B	18	0	16	0	0
8	B	1	0	0	0	0
9	Q	7	0	0	0	0
9	R	7	0	0	0	0
10	Q	2	0	0	0	0
10	R	2	0	0	0	0
11	Q	1	0	0	0	0
11	R	1	0	0	0	0
12	Q	1	0	0	0	0
13	A	295	0	0	1	0
13	B	316	0	0	5	0
13	Q	557	0	0	3	0
13	R	632	0	0	2	0
All	All	14688	0	12713	49	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.

All (49) 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:48[B]:ILE:HD11	2:Q:178:ILE:HG21	1.50	0.92
2:Q:172[A]:GLU:HG2	13:Q:2513:HOH:O	1.70	0.92
2:Q:72:CYS:HB3	2:Q:75:CSX:OD	1.95	0.65
2:Q:72:CYS:CB	2:Q:75:CSX:OD	2.46	0.63
2:R:324:VAL:HG11	2:R:395[B]:LYS:HE2	1.82	0.61
1:A:61[A]:HIS:HE1	13:A:2156:HOH:O	1.83	0.60
2:R:396:GLY:HA2	2:R:401[A]:LYS:HE3	1.86	0.58
2:R:138:PRO:HG3	2:R:161[A]:LYS:HG2	1.84	0.58
2:R:72:CYS:HB3	2:R:75:CSX:OD	2.04	0.57
2:R:484[A]:ARG:HD2	13:R:2370:HOH:O	2.03	0.57
2:Q:342[A]:ALA:HB1	2:Q:343[A]:PRO:HD2	1.88	0.55
1:A:48[B]:ILE:CD1	2:Q:178:ILE:HG21	2.33	0.55
2:Q:464[B]:GLU:OE2	2:Q:488:LYS:HE3	2.07	0.55
1:A:48[B]:ILE:CD1	2:Q:178:ILE:HD13	2.37	0.54
1:B:62[A]:GLN:HG3	13:B:2166:HOH:O	2.07	0.54
1:A:28:ILE:HG13	1:A:29[B]:LYS:HG3	1.90	0.53
2:R:509[A]:GLN:HG3	13:R:2140:HOH:O	2.07	0.53
1:B:165:GLY:HA2	13:B:2264:HOH:O	2.10	0.50
2:Q:168:LYS:O	2:Q:172[A]:GLU:HG3	2.12	0.50
1:B:4[B]:LYS:HE3	13:B:2215:HOH:O	2.12	0.49
2:R:278[A]:LYS:HE3	2:R:413:VAL:HG12	1.94	0.48
2:R:393:TYR:O	2:R:401[A]:LYS:CE	2.61	0.48
2:R:278[A]:LYS:HE3	2:R:413:VAL:CG1	2.46	0.46
5:B:1269:GOL:C3	13:B:2305:HOH:O	2.38	0.46
2:R:296:ALA:HA	2:R:309:SER:HA	1.97	0.46
1:B:237:TRP:CZ2	1:B:239:VAL:HB	2.51	0.46
1:B:186:ASN:ND2	1:B:229[A]:LYS:HD2	2.30	0.45
1:B:58:ALA:O	1:B:62[A]:GLN:HG3	2.16	0.45
1:A:237:TRP:CZ2	1:A:239:VAL:HB	2.51	0.45
2:R:138:PRO:HG3	2:R:161[A]:LYS:CG	2.46	0.45
1:B:4[B]:LYS:CE	13:B:2215:HOH:O	2.66	0.44
1:B:258:THR:HA	1:B:259:PRO:C	2.43	0.44
1:B:2:THR:CG2	1:B:4[A]:LYS:HE3	2.48	0.43
2:Q:245[A]:LYS:NZ	13:Q:2230:HOH:O	2.31	0.43
1:A:258:THR:HA	1:A:259:PRO:C	2.42	0.43
1:B:237:TRP:CH2	1:B:239:VAL:HB	2.53	0.43
2:R:476:ARG:CZ	2:R:543[B]:CSS:SD	3.07	0.42
2:Q:278[B]:LYS:HE3	13:Q:2342:HOH:O	2.19	0.42
2:Q:497:VAL:CG1	2:Q:498:PRO:HD2	2.50	0.42
2:Q:278[B]:LYS:HE2	2:Q:411:LEU:O	2.20	0.41
2:Q:497:VAL:HG11	2:Q:546:CYS:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:476:ARG:HD2	2:R:543[B]:CSS:SD	2.61	0.41
2:Q:296:ALA:HA	2:Q:309:SER:HA	2.02	0.41
2:Q:315:VAL:HG13	2:Q:381[B]:MET:HE2	2.03	0.41
2:Q:476:ARG:CZ	2:Q:543[B]:CSS:SD	3.09	0.40
1:A:237:TRP:CH2	1:A:239:VAL:HB	2.57	0.40
2:Q:374:PRO:HD3	2:Q:500:THR:HG22	2.03	0.40
2:R:49:PHE:HB2	2:R:370:TRP:CD2	2.56	0.40
2:Q:223:GLY:HA2	2:Q:231:PHE:CD1	2.56	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	A	273/265 (103%)	266 (97%)	7 (3%)	0	100	100
1	B	277/265 (104%)	271 (98%)	6 (2%)	0	100	100
2	Q	570/563 (101%)	554 (97%)	16 (3%)	0	100	100
2	R	576/563 (102%)	566 (98%)	10 (2%)	0	100	100
All	All	1696/1656 (102%)	1657 (98%)	39 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	221/210 (105%)	221 (100%)	0	100 100
1	B	225/210 (107%)	223 (99%)	2 (1%)	70 40
2	Q	459/445 (103%)	457 (100%)	2 (0%)	84 63
2	R	467/445 (105%)	463 (99%)	4 (1%)	70 40
All	All	1372/1310 (105%)	1364 (99%)	8 (1%)	81 52

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	88[A]	MET
1	B	88[B]	MET
2	Q	473	ASP
2	Q	500	THR
2	R	135[A]	LYS
2	R	135[B]	LYS
2	R	473	ASP
2	R	500	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	ASN
1	A	85	GLN
1	A	234	GLN
1	A	240	GLN
1	B	5	HIS
1	B	14	ASN
1	B	129	GLN
1	B	240	GLN
2	Q	139	ASN
2	Q	241	GLN
2	Q	250	ASN
2	Q	509	GLN
2	R	139	ASN
2	R	241	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

6 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	R	75	2,10,9	3,6,7	0.67	0	1,6,8	1.37	0
2	CSX	Q	75	2,10,9	3,6,7	0.51	0	1,6,8	0.55	0
2	CSS	R	543[B]	10	4,6,7	1.09	0	1,6,8	0.36	0
2	CSS	R	543[A]	10	4,5,7	1.53	1 (25%)	1,5,8	1.09	0
2	CSS	Q	543[B]	10	4,6,7	0.73	0	1,6,8	0.13	0
2	CSS	Q	543[A]	10	4,5,7	1.55	1 (25%)	1,5,8	1.60	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	R	75	2,10,9	-	0/1/5/7	-
2	CSX	Q	75	2,10,9	-	0/1/5/7	-
2	CSS	R	543[B]	10	-	0/1/5/7	-
2	CSS	R	543[A]	10	-	0/1/4/7	-
2	CSS	Q	543[B]	10	-	0/1/5/7	-
2	CSS	Q	543[A]	10	-	0/1/4/7	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Q	543[A]	CSS	CB-SG	-2.73	1.72	1.81
2	R	543[A]	CSS	CB-SG	-2.32	1.74	1.81

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	R	75	CSX	1	0
2	Q	75	CSX	2	0
2	R	543[B]	CSS	2	0
2	Q	543[B]	CSS	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 33 ligands modelled in this entry, 1 is modelled with single atom and 7 are monoatomic - leaving 25 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	$\#\|Z\| > 2$
4	F3S	B	1266	1	0,9,9	-	-	-		
5	GOL	B	1272	-	5,5,5	0.36	0	5,5,5	0.79	0
7	SOT	B	1268[B]	-	6,9,10	0.50	0	3,11,14	1.36	0
5	GOL	R	1553	-	5,5,5	0.43	0	5,5,5	0.33	0
5	GOL	R	1555[B]	-	5,5,5	0.52	0	5,5,5	1.24	1 (20%)
6	GLY	R	601	-	4,4,4	1.02	0	3,4,4	1.36	0
6	GLY	Q	601	-	4,4,4	1.11	0	3,4,4	1.23	0
4	F3S	A	1266	1	0,9,9	-	-	-		
9	FCO	R	1550	2,13	1,6,6	1.65	0	-		
5	GOL	R	1556	-	5,5,5	0.31	0	5,5,5	0.87	0
9	FCO	Q	1550	2,13	1,6,6	1.09	0	-		
7	SOT	B	1268[A]	1	6,9,10	0.70	0	3,11,14	3.73	3 (100%)
5	GOL	B	1270	-	5,5,5	0.26	0	5,5,5	0.42	0
5	GOL	A	1269	-	5,5,5	0.56	0	5,5,5	0.69	0
5	GOL	R	1557	-	5,5,5	0.16	0	5,5,5	0.69	0
5	GOL	R	1554	-	5,5,5	0.73	0	5,5,5	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	SF4	B	1267	1	0,12,12	-	-	-		
6	GLY	B	301	-	4,4,4	1.22	1 (25%)	3,4,4	1.78	1 (33%)
3	SF4	B	1265	1	0,12,12	-	-	-		
5	GOL	R	1555[A]	-	5,5,5	0.44	0	5,5,5	0.85	0
5	GOL	Q	1553	-	5,5,5	0.35	0	5,5,5	0.29	0
5	GOL	A	1268	-	5,5,5	0.16	0	5,5,5	0.90	0
3	SF4	A	1267	1	0,12,12	-	-	-		
5	GOL	B	1269	-	5,5,5	0.49	0	5,5,5	0.68	0
3	SF4	A	1265	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	B	1266	1	-	-	0/3/3/3
5	GOL	B	1272	-	-	0/4/4/4	-
7	SOT	B	1268[B]	-	-	0/0/12/14	0/1/1/1
5	GOL	R	1553	-	-	0/4/4/4	-
5	GOL	R	1555[B]	-	-	0/4/4/4	-
6	GLY	R	601	-	-	2/2/2/2	-
6	GLY	Q	601	-	-	2/2/2/2	-
4	F3S	A	1266	1	-	-	0/3/3/3
5	GOL	R	1556	-	-	1/4/4/4	-
7	SOT	B	1268[A]	1	-	0/0/12/14	0/1/1/1
5	GOL	B	1270	-	-	0/4/4/4	-
5	GOL	A	1269	-	-	4/4/4/4	-
5	GOL	R	1557	-	-	1/4/4/4	-
5	GOL	R	1554	-	-	0/4/4/4	-
3	SF4	B	1267	1	-	-	0/6/5/5
6	GLY	B	301	-	-	0/2/2/2	-
3	SF4	B	1265	1	-	-	0/6/5/5
5	GOL	R	1555[A]	-	-	2/4/4/4	-
5	GOL	Q	1553	-	-	0/4/4/4	-
5	GOL	A	1268	-	-	0/4/4/4	-
3	SF4	A	1267	1	-	-	0/6/5/5
5	GOL	B	1269	-	-	1/4/4/4	-
3	SF4	A	1265	1	-	-	0/6/5/5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	301	GLY	OXT-C	-2.36	1.22	1.30

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	B	1268[A]	SOT	O1-C2-C3	4.23	121.10	111.80
7	B	1268[A]	SOT	C6-O1-C2	3.47	121.46	109.89
7	B	1268[A]	SOT	O1-C6-C5	3.44	119.38	111.80
5	R	1555[B]	GOL	O1-C1-C2	-2.64	97.56	110.20
6	B	301	GLY	OXT-C-O	-2.40	117.31	123.30

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1269	GOL	O1-C1-C2-C3
5	R	1555[A]	GOL	O1-C1-C2-C3
6	R	601	GLY	O-C-CA-N
6	R	601	GLY	OXT-C-CA-N
6	Q	601	GLY	O-C-CA-N
6	Q	601	GLY	OXT-C-CA-N
5	B	1269	GOL	O1-C1-C2-C3
5	R	1556	GOL	C1-C2-C3-O3
5	R	1555[A]	GOL	O1-C1-C2-O2
5	A	1269	GOL	O1-C1-C2-O2
5	A	1269	GOL	O2-C2-C3-O3
5	A	1269	GOL	C1-C2-C3-O3
5	R	1557	GOL	C1-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1269	GOL	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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%)	-0.59	2 (0%)	82	85	4, 8, 18, 48	16 (6%)
1	B	263/265 (99%)	-0.66	3 (1%)	78	80	4, 7, 16, 32	19 (7%)
2	Q	542/563 (96%)	-0.63	0	100	100	4, 8, 18, 37	36 (6%)
2	R	543/563 (96%)	-0.76	0	100	100	4, 7, 15, 40	38 (6%)
All	All	1610/1656 (97%)	-0.67	5 (0%)	90	92	4, 8, 17, 48	109 (6%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	ALA	5.3
1	A	164[A]	LYS	3.0
1	B	264[A]	GLY	2.7
1	B	2	THR	2.6
1	B	3	ALA	2.3

6.2 Non-standard residues in protein, DNA, RNA chains

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	CSS	Q	543[A]	6/8	0.99	0.03	5,5,6,8	2
2	CSS	Q	543[B]	7/8	0.99	0.03	5,5,8,9	3
2	CSS	R	543[A]	6/8	0.99	0.03	3,4,5,7	2
2	CSS	R	543[B]	7/8	0.99	0.03	3,4,7,8	3
2	CSX	Q	75	7/8	1.00	0.03	4,4,5,6	1
2	CSX	R	75	7/8	1.00	0.02	3,4,5,5	1

6.3 Carbohydrates (i)

There are no oligosaccharides 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
5	GOL	B	1270	6/6	0.70	0.21	20,22,27,33	6
5	GOL	R	1557	6/6	0.83	0.23	14,23,25,26	6
6	GLY	B	301	5/5	0.83	0.13	14,16,16,18	5
5	GOL	B	1269	6/6	0.85	0.11	20,22,27,28	1
5	GOL	A	1268	6/6	0.89	0.11	26,27,30,33	0
12	CL	Q	1554	1/1	0.91	0.11	32,32,32,32	1
6	GLY	R	601	5/5	0.92	0.12	9,10,12,14	5
5	GOL	B	1272	6/6	0.94	0.08	17,20,25,37	0
6	GLY	Q	601	5/5	0.95	0.12	12,12,14,16	5
5	GOL	A	1269	6/6	0.95	0.08	18,27,30,32	0
5	GOL	R	1556	6/6	0.95	0.09	11,14,15,17	6
8	H2S	B	1271	1/1	0.96	0.07	18,18,18,18	1
5	GOL	R	1554	6/6	0.96	0.07	14,15,17,20	1
7	SOT	B	1268[A]	9/10	0.97	0.07	11,12,14,16	9
7	SOT	B	1268[B]	9/10	0.97	0.07	15,17,22,22	9
5	GOL	R	1555[B]	6/6	0.98	0.06	11,18,22,24	1
5	GOL	R	1555[A]	6/6	0.98	0.06	11,18,22,24	1
5	GOL	Q	1553	6/6	0.99	0.03	6,7,8,8	0
5	GOL	R	1553	6/6	0.99	0.04	6,6,7,8	0
3	SF4	A	1267	8/8	1.00	0.01	4,4,4,4	0
3	SF4	B	1265	8/8	1.00	0.01	5,5,5,5	0
3	SF4	B	1267	8/8	1.00	0.01	4,4,4,4	0
4	F3S	A	1266	7/7	1.00	0.01	4,4,5,5	0
4	F3S	B	1266	7/7	1.00	0.01	4,4,5,5	0
9	FCO	Q	1550	7/7	1.00	0.02	5,5,6,7	0
9	FCO	R	1550	7/7	1.00	0.03	5,5,5,6	0
10	NI	Q	1551[A]	1/1	1.00	0.02	8,8,8,8	1
10	NI	Q	1551[B]	1/1	1.00	0.02	7,7,7,7	1
10	NI	R	1551[A]	1/1	1.00	0.02	7,7,7,7	1
10	NI	R	1551[B]	1/1	1.00	0.02	8,8,8,8	1
11	MG	Q	1552	1/1	1.00	0.01	4,4,4,4	0
11	MG	R	1552	1/1	1.00	0.02	4,4,4,4	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SF4	A	1265	8/8	1.00	0.01	5,5,5,6	0

6.5 Other polymers (i)

There are no such residues in this entry.