



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:46 PM UTC

PDB ID : 4KL8 / pdb_00004kl8
Title : High-resolution structure of anaerobically purified Dm. baculatum [NiFeSe]-hydrogenase after crystallization under air
Authors : Volbeda, A.; Cavazza, C.; Fontecilla-Camps, J.C.
Deposited on : 2013-05-07
Resolution : 1.52 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

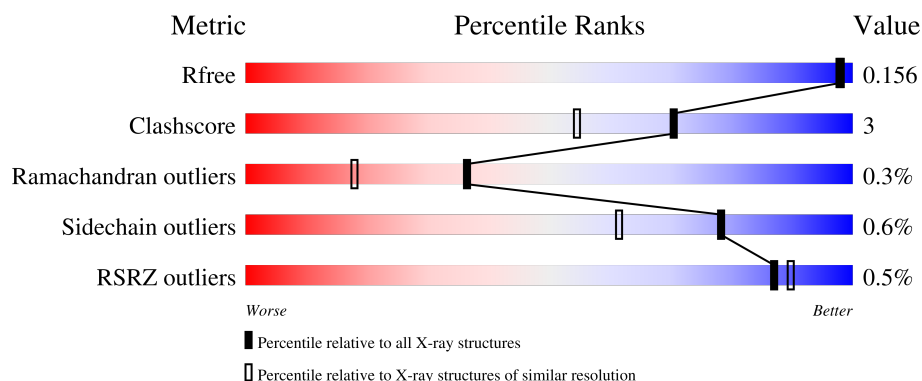
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.52 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	5890 (1.54-1.50)
Clashscore	190562	6116 (1.54-1.50)
Ramachandran outliers	187476	6002 (1.54-1.50)
Sidechain outliers	187428	5999 (1.54-1.50)
RSRZ outliers	180081	5891 (1.54-1.50)

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 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 $\leq 5\%$. 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	S	283	92% 6% .
1	T	283	2% 94% 5% .
2	L	501	91% 6% ..
2	M	501	90% 8% .

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
6	GOL	M	506	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 14237 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 [NiFeSe] hydrogenase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	S	279	Total	C	N	O	S	44	15	0
			2207	1403	364	422	18			
1	T	279	Total	C	N	O	S	4	10	0
			2184	1393	364	409	18			

- Molecule 2 is a protein called Nickel-dependent hydrogenase large subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	L	489	Total	C	N	O	S	Se	0	25	0
			3938	2514	669	727	25	3			
2	M	489	Total	C	N	O	S	Se	0	28	0
			3945	2520	671	728	23	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	492	SE7	U	SEE REMARK 999	UNP C7LN88
M	492	SE7	U	SEE REMARK 999	UNP C7LN88

- Molecule 3 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



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

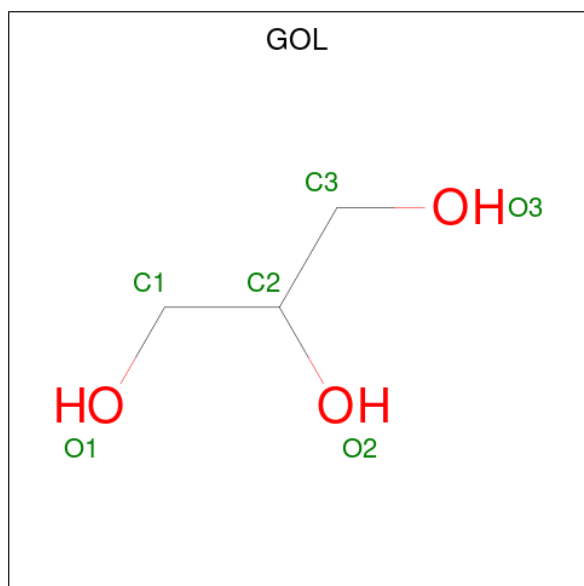
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	S	2	Total Ca 2 2	0	0
4	L	1	Total Ca 1 1	0	0
4	T	3	Total Ca 3 3	0	0
4	M	2	Total Ca 2 2	0	0

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

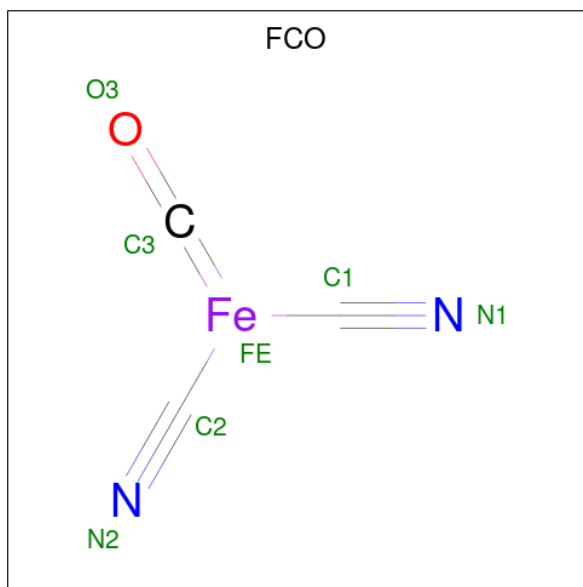
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	S	1	Total	Cl	0	0
			1	1		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	S	1	Total	C	O	0	0
			6	3	3		
6	S	1	Total	C	O	0	0
			6	3	3		
6	M	1	Total	C	O	0	0
			6	3	3		
6	M	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is CARBONMONOXIDE-(DICYANO) IRON (CCD ID: FCO) (formula: C_3FeN_2O).

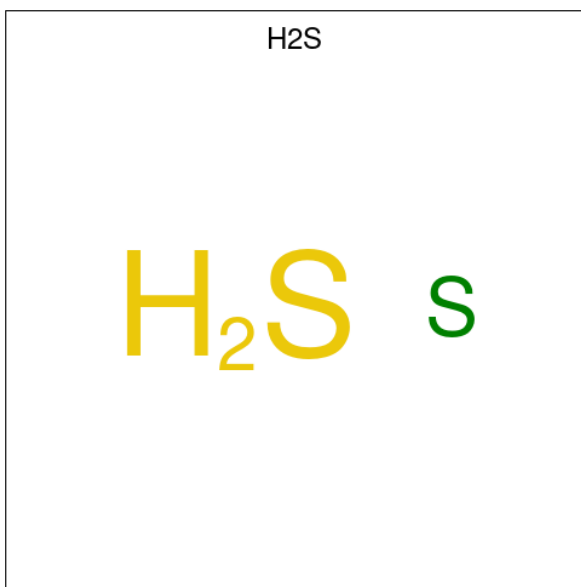


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	L	1	Total	C	Fe	N	O	0	1
			14	6	2	4	2		
7	M	1	Total	C	Fe	N	O	0	1
			14	6	2	4	2		

- Molecule 8 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	L	1	Total	Ni	0	1
			3	3		
8	M	1	Total	Ni	0	1
			3	3		

- Molecule 9 is HYDROSULFURIC ACID (CCD ID: H2S) (formula: H₂S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	L	1	Total S 1 1	0	0
9	M	1	Total S 1 1	0	0

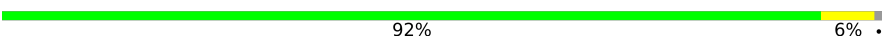
- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	S	373	Total O 374 374	0	5
10	L	595	Total O 595 595	0	1
10	T	358	Total O 359 359	0	1
10	M	518	Total O 518 518	0	3

3 Residue-property plots [i](#)

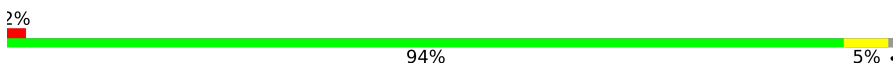
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

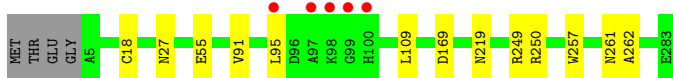
- Molecule 1: Periplasmic [NiFeSe] hydrogenase small subunit

Chain S: 



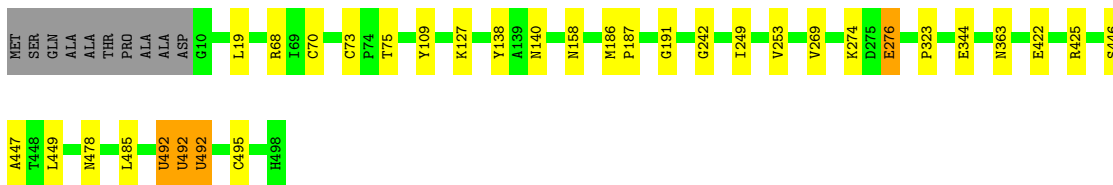
- Molecule 1: Periplasmic [NiFeSe] hydrogenase small subunit

Chain T: 

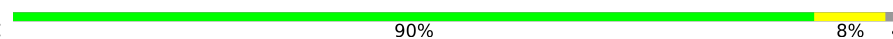


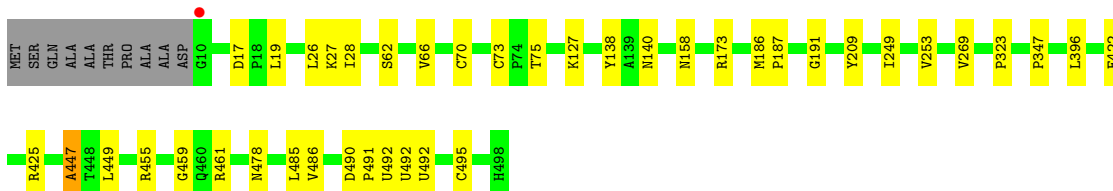
- Molecule 2: Nickel-dependent hydrogenase large subunit

Chain L: 



- Molecule 2: Nickel-dependent hydrogenase large subunit

Chain M: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	106.20Å 108.72Å 136.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.52 25.00 – 1.52	Depositor EDS
% Data completeness (in resolution range)	93.7 (25.00-1.52) 93.6 (25.00-1.52)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 1.52Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.122 , 0.171 (Not available) , 0.156	Depositor DCC
R_{free} test set	11463 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	8.6	Xtriage
Anisotropy	0.390	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.012 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14237	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.85% 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, 0.333 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: SEC, SE7, SF4, H2S, UOX, FCO, CA, GOL, NI, 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	S	0.68	0/2324	0.77	0/3153
1	T	0.63	0/2289	0.79	0/3109
2	L	0.66	0/4113	0.78	0/5565
2	M	0.62	0/4132	0.76	0/5591
All	All	0.64	0/12858	0.77	0/17418

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S	2207	0	2101	13	0
1	T	2184	0	2111	8	0
2	L	3938	0	3904	25	0
2	M	3945	0	3920	39	0
3	S	24	0	0	0	0
3	T	24	0	0	0	0
4	L	1	0	0	0	0
4	M	2	0	0	0	0
4	S	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	T	3	0	0	0	0
5	S	1	0	0	0	0
6	M	12	0	16	6	0
6	S	12	0	16	0	0
7	L	14	0	0	0	0
7	M	14	0	0	1	0
8	L	3	0	0	0	0
8	M	3	0	0	0	0
9	L	1	0	0	0	0
9	M	1	0	0	0	0
10	L	595	0	0	0	0
10	M	518	0	0	1	0
10	S	374	0	0	5	0
10	T	359	0	0	2	0
All	All	14237	0	12068	79	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 3.

All (79) 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)
2:L:274[B]:LYS:NZ	2:L:276[B]:GLU:OE2	1.76	1.16
2:L:127:LYS:H	2:L:158:ASN:HD21	1.10	0.97
2:M:127:LYS:H	2:M:158:ASN:HD21	1.15	0.92
1:S:248[B]:LYS:HG3	10:S:608:HOH:O	1.72	0.88
2:M:19[B]:LEU:CD2	2:M:486:VAL:HG11	2.16	0.76
1:S:102[B]:HIS:HD2	10:S:744:HOH:O	1.70	0.74
2:M:19[B]:LEU:HD23	2:M:26:LEU:HD23	1.72	0.71
2:L:274[B]:LYS:CE	2:L:276[B]:GLU:OE2	2.39	0.70
2:M:19[B]:LEU:HD21	2:M:486:VAL:HG11	1.78	0.66
1:S:118:LEU:HD21	1:S:182:VAL:HG21	1.78	0.64
1:T:250[A]:ARG:HD2	1:T:257:TRP:CD1	2.36	0.60
2:M:73[P]:CYS:SG	2:M:495[P]:CYS:SG	2.99	0.60
2:M:73[O]:CYS:SG	2:M:495[O]:CYS:SG	3.00	0.60
2:L:249[B]:ILE:HG22	2:L:269:VAL:HG22	1.84	0.59
2:M:138:TYR:HB3	2:M:478:ASN:HD22	1.68	0.59
2:M:19[B]:LEU:HD22	2:M:28:ILE:CG1	2.33	0.59
2:L:127:LYS:N	2:L:158:ASN:HD21	1.92	0.58
1:S:102[B]:HIS:CD2	10:S:744:HOH:O	2.51	0.57
2:L:73[O]:CYS:SG	2:L:495[O]:CYS:SG	3.02	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:274[B]:LYS:HZ3	2:L:276[B]:GLU:CD	2.01	0.56
2:M:19[A]:LEU:HD13	2:M:28:ILE:HG13	1.87	0.56
2:L:73[P]:CYS:SG	2:L:495[P]:CYS:SG	3.04	0.56
2:M:19[B]:LEU:HD22	2:M:28:ILE:HG13	1.86	0.56
2:L:127:LYS:H	2:L:158:ASN:ND2	1.93	0.56
2:L:446[A]:SER:O	2:L:449:LEU:HB3	2.06	0.55
2:M:455:ARG:HE	6:M:506:GOL:H32	1.71	0.54
2:M:127:LYS:N	2:M:158:ASN:HD21	1.95	0.54
2:L:425:ARG:HD2	2:L:492[O]:SE7:OD1	2.07	0.53
2:M:455:ARG:NE	6:M:506:GOL:H32	2.23	0.53
1:S:82:THR:HG21	1:S:143[A]:LYS:HD2	1.90	0.53
2:M:249[B]:ILE:HG22	2:M:269:VAL:HG22	1.90	0.53
2:M:127:LYS:H	2:M:158:ASN:ND2	1.96	0.52
2:L:138:TYR:HB3	2:L:478:ASN:HD22	1.75	0.52
2:M:455:ARG:HE	6:M:506:GOL:C3	2.23	0.51
2:L:253:VAL:HB	2:L:422:GLU:HB2	1.93	0.51
2:M:425:ARG:HD2	2:M:492[O]:SE7:OD1	2.10	0.51
2:M:461:ARG:NH1	6:M:506:GOL:H2	2.27	0.50
1:S:250:ARG:HD2	1:S:257:TRP:CD1	2.47	0.50
2:M:485:LEU:C	2:M:485:LEU:HD13	2.37	0.50
2:M:70[P]:CYS:SG	2:M:495[P]:CYS:SG	3.09	0.49
2:M:253:VAL:HB	2:M:422:GLU:HB2	1.95	0.49
2:L:70[P]:CYS:SG	2:L:495[P]:CYS:SG	3.11	0.49
2:M:347:PRO:HD2	10:M:1094:HOH:O	2.11	0.48
2:L:242:GLY:HA3	2:L:485:LEU:HD23	1.96	0.48
2:M:425:ARG:CD	2:M:492[O]:SE7:SEG	3.12	0.47
2:L:425:ARG:CD	2:L:492[O]:SE7:SEG	3.13	0.46
2:L:323:PRO:HG3	2:L:449:LEU:HG	1.96	0.46
1:T:18:CYS:HB2	2:M:70[P]:CYS:HA	1.97	0.46
2:M:490:ASP:N	2:M:491:PRO:HD3	2.32	0.45
1:S:277:SER:HA	1:S:278:PRO:C	2.40	0.45
1:T:250[B]:ARG:HD2	10:T:412:HOH:O	2.15	0.45
1:S:261:ASN:HD21	2:L:191:GLY:CA	2.29	0.45
1:S:132:ILE:HD12	2:L:68:ARG:HG2	2.00	0.44
1:S:18:CYS:HB2	2:L:70[P]:CYS:HA	2.00	0.44
2:L:274[B]:LYS:NZ	2:L:276[B]:GLU:CD	2.69	0.44
2:M:209:TYR:CD1	2:M:396:LEU:HD21	2.53	0.44
2:M:323:PRO:HG3	2:M:449:LEU:HG	1.99	0.43
2:M:140:ASN:H	2:M:478:ASN:ND2	2.16	0.43
1:T:91:VAL:HG21	1:T:109:LEU:HD22	2.00	0.43
1:T:261:ASN:HD21	2:M:191:GLY:CA	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:19[B]:LEU:HD23	2:M:26:LEU:CD2	2.47	0.43
1:S:143[A]:LYS:HE2	10:S:716:HOH:O	2.19	0.42
1:S:216:LYS:HE2	10:S:747:HOH:O	2.19	0.42
2:L:485:LEU:C	2:L:485:LEU:HD13	2.45	0.42
1:T:55:GLU:CD	10:T:543:HOH:O	2.62	0.42
2:L:140:ASN:H	2:L:478:ASN:ND2	2.17	0.42
2:L:186:MET:HA	2:L:187:PRO:C	2.45	0.42
2:M:19[B]:LEU:HD22	2:M:28:ILE:HG12	1.99	0.42
1:T:169:ASP:HB2	1:T:249:ARG:HD3	2.02	0.41
2:M:447[A]:ALA:HB3	7:M:501[A]:FCO:N1	2.35	0.41
2:M:186:MET:HA	2:M:187:PRO:C	2.46	0.41
2:M:62:SER:O	2:M:66:VAL:HG22	2.21	0.41
1:T:27:ASN:HA	2:M:173:ARG:HG3	2.01	0.41
2:L:344:GLU:HA	2:L:363:ASN:HD22	1.86	0.41
2:M:17:ASP:HB2	2:M:27:LYS:HG3	2.03	0.41
1:S:181:HIS:CD2	1:S:190:LEU:HG	2.56	0.40
2:M:459:GLY:O	6:M:506:GOL:H31	2.22	0.40
2:M:461:ARG:HG3	6:M:506:GOL:C3	2.52	0.40
2:M:425:ARG:NE	2:M:492[O]:SE7:SEG	3.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	291/283 (103%)	283 (97%)	7 (2%)	1 (0%)	36	18
1	T	288/283 (102%)	280 (97%)	7 (2%)	1 (0%)	36	18
2	L	513/501 (102%)	495 (96%)	16 (3%)	2 (0%)	30	12
2	M	515/501 (103%)	496 (96%)	17 (3%)	2 (0%)	30	12
All	All	1607/1568 (102%)	1554 (97%)	47 (3%)	6 (0%)	36	12

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	447[A]	ALA
2	L	447[B]	ALA
2	M	447[A]	ALA
2	M	447[B]	ALA
1	S	262	ALA
1	T	262	ALA

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	245/233 (105%)	244 (100%)	1 (0%)	84	71
1	T	241/233 (103%)	239 (99%)	2 (1%)	73	53
2	L	430/410 (105%)	425 (99%)	5 (1%)	63	37
2	M	432/410 (105%)	431 (100%)	1 (0%)	87	77
All	All	1348/1286 (105%)	1339 (99%)	9 (1%)	78	57

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	S	207	ILE
2	L	19	LEU
2	L	75	THR
2	L	109	TYR
2	L	276[A]	GLU
2	L	276[B]	GLU
1	T	95	LEU
1	T	219	ASN
2	M	75	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	S	210	ASN
1	S	261	ASN
2	L	140	ASN
2	L	158	ASN
2	L	188	HIS
2	L	363	ASN
2	L	478	ASN
1	T	16	GLN
1	T	101	HIS
1	T	261	ASN
2	M	52	GLN
2	M	102	ASN
2	M	140	ASN
2	M	158	ASN
2	M	188	HIS
2	M	400	GLN
2	M	441	ASN
2	M	443	GLN
2	M	478	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	SE7	M	492[O]	8,2	2,7,8	0.95	0	0,8,10	-	-
2	UOX	L	492[P]	-	2,6,7	0.91	0	1,6,8	2.23	1 (100%)
2	SE7	L	492[O]	8,2	2,7,8	0.91	0	0,8,10	-	-
2	UOX	M	492[P]	-	2,6,7	0.95	0	1,6,8	1.67	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	SE7	M	492[O]	8,2	-	0/0/6/8	-
2	UOX	L	492[P]	-	-	0/0/5/7	-
2	SE7	L	492[O]	8,2	-	0/0/6/8	-
2	UOX	M	492[P]	-	-	0/0/5/7	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	492[P]	UOX	SE-CB-CA	2.23	117.41	111.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	M	492[O]	SE7	3	0
2	L	492[O]	SE7	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 31 ligands modelled in this entry, 15 are monoatomic and 2 are modelled with single atom - leaving 14 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
7	FCO	L	501[B]	2	0,6,6	-	-	-		
7	FCO	M	501[B]	2	0,6,6	-	-	-		
6	GOL	S	306	-	5,5,5	0.32	0	5,5,5	0.47	0
6	GOL	M	505	-	5,5,5	0.33	0	5,5,5	0.32	0
7	FCO	L	501[A]	2	0,6,6	-	-	-		
3	SF4	S	301	1	0,12,12	-	-	-		
3	SF4	S	303	1	0,12,12	-	-	-		
7	FCO	M	501[A]	2	0,6,6	-	-	-		
6	GOL	S	307	-	5,5,5	0.27	0	5,5,5	0.57	0
3	SF4	T	302	1	0,12,12	-	-	-		
6	GOL	M	506	-	5,5,5	0.56	0	5,5,5	1.30	0
3	SF4	T	301	1	0,12,12	-	-	-		
3	SF4	T	303	1	0,12,12	-	-	-		
3	SF4	S	302	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
3	SF4	S	302	1	-	-	0/6/5/5
6	GOL	S	306	-	-	0/4/4/4	-
6	GOL	M	505	-	-	0/4/4/4	-
3	SF4	S	301	1	-	-	0/6/5/5
3	SF4	S	303	1	-	-	0/6/5/5
6	GOL	S	307	-	-	0/4/4/4	-
3	SF4	T	302	1	-	-	0/6/5/5
3	SF4	T	301	1	-	-	0/6/5/5
3	SF4	T	303	1	-	-	0/6/5/5
6	GOL	M	506	-	-	0/4/4/4	-

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 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	M	501[A]	FCO	1	0
6	M	506	GOL	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	S	273/283 (96%)	-0.94	1 (0%) 88 91	5, 8, 16, 37	21 (7%)
1	T	279/283 (98%)	-0.70	5 (1%) 67 73	6, 11, 23, 42	27 (9%)
2	L	488/501 (97%)	-1.01	0 100 100	3, 8, 16, 35	35 (7%)
2	M	488/501 (97%)	-0.76	1 (0%) 91 92	5, 12, 22, 37	36 (7%)
All	All	1528/1568 (97%)	-0.86	7 (0%) 87 90	3, 10, 20, 42	119 (7%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	T	97	ALA	4.4
1	T	99	GLY	4.2
1	T	95	LEU	3.9
1	T	100	HIS	3.2
2	M	10[A]	GLY	3.0
1	S	101	HIS	2.4
1	T	98	LYS	2.1

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	SE7	L	492[O]	8/9	0.99	0.04	6,7,11,11	8
2	UOX	L	492[P]	7/8	-	-	6,7,8,9	7
2	SE7	M	492[O]	8/9	0.99	0.04	8,10,13,13	8
2	UOX	M	492[P]	7/8	-	-	8,9,10,13	7
2	SEC	L	492[R]	6/7	-	-	6,7,9,12	6

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SEC	M	492[R]	6/7	-	-	8,9,11,14	6

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($\text{\AA}^2$)	Q<0.9
6	GOL	M	505	6/6	0.79	0.14	43,43,44,47	0
6	GOL	M	506	6/6	0.94	0.11	16,23,25,25	0
4	CA	T	306	1/1	0.97	0.09	47,47,47,47	1
6	GOL	S	307	6/6	0.97	0.07	16,21,23,27	0
6	GOL	S	306	6/6	0.98	0.04	17,18,20,22	0
4	CA	M	507	1/1	0.98	0.12	36,36,36,36	1
4	CA	S	308	1/1	0.99	0.05	22,22,22,22	1
3	SF4	S	301	8/8	1.00	0.01	7,8,8,9	0
4	CA	L	503	1/1	1.00	0.01	7,7,7,7	0
4	CA	T	304	1/1	1.00	0.01	13,13,13,13	1
4	CA	T	305	1/1	1.00	0.14	24,24,24,24	1
3	SF4	S	302	8/8	1.00	0.01	6,6,6,6	0
4	CA	M	503	1/1	1.00	0.01	9,9,9,9	0
3	SF4	S	303	8/8	1.00	0.01	4,5,6,6	0
5	CL	S	305	1/1	1.00	0.07	19,19,19,19	1
3	SF4	T	301	8/8	1.00	0.01	12,12,14,14	0
3	SF4	T	302	8/8	1.00	0.01	8,9,9,10	0
3	SF4	T	303	8/8	1.00	0.01	7,8,9,9	0
4	CA	S	304	1/1	1.00	0.01	9,9,9,9	0
7	FCO	L	501[A]	7/7	1.00	0.02	6,7,8,10	7
7	FCO	L	501[B]	7/7	1.00	0.02	6,7,9,11	7
7	FCO	M	501[A]	7/7	1.00	0.02	8,9,11,11	7
7	FCO	M	501[B]	7/7	1.00	0.02	7,9,11,12	7
8	NI	L	502[O]	1/1	1.00	0.01	12,12,12,12	1
8	NI	L	502[P]	1/1	1.00	0.01	11,11,11,11	1
8	NI	L	502[R]	1/1	1.00	0.01	11,11,11,11	1
8	NI	M	502[O]	1/1	1.00	0.02	14,14,14,14	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	NI	M	502[P]	1/1	1.00	0.02	14,14,14,14	1
8	NI	M	502[R]	1/1	1.00	0.02	13,13,13,13	1
9	H2S	L	504	1/1	1.00	0.01	5,5,5,5	0
9	H2S	M	504	1/1	1.00	0.01	9,9,9,9	0

6.5 Other polymers [i](#)

There are no such residues in this entry.