



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 22, 2023 – 10:06 PM JST

PDB ID : 7XEK
Title : SufS with D-cysteine for 6 h
Authors : Nakamura, R.; Fujishiro, T.
Deposited on : 2022-03-31
Resolution : 1.88 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
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

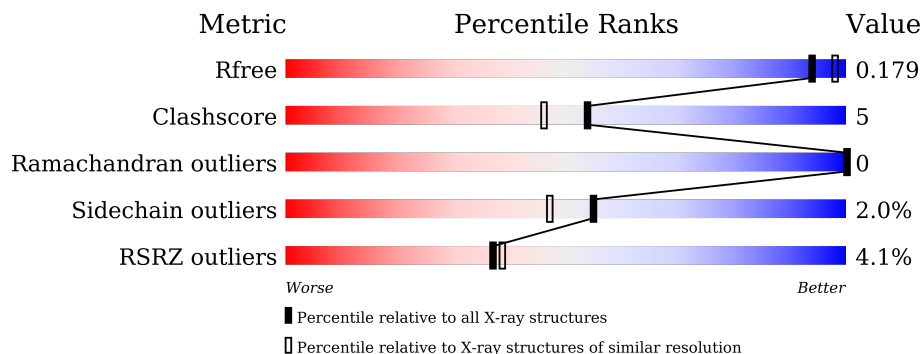
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.88 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	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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	A	419	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 3636 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 Cysteine desulfurase SufS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	413	3225	2044	550	618	13	0	0	0

There are 13 discrepancies between the modelled and reference sequences:

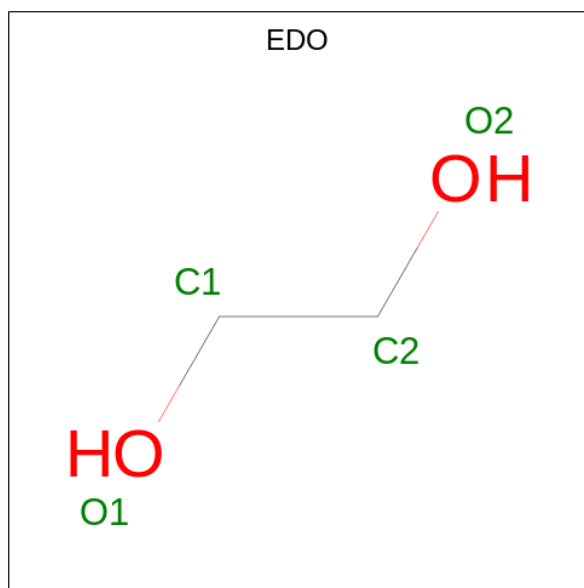
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	initiating methionine	UNP O32164
A	-1	GLY	-	expression tag	UNP O32164
A	0	HIS	-	expression tag	UNP O32164
A	407	VAL	-	expression tag	UNP O32164
A	408	ASP	-	expression tag	UNP O32164
A	409	LEU	-	expression tag	UNP O32164
A	410	GLU	-	expression tag	UNP O32164
A	411	HIS	-	expression tag	UNP O32164
A	412	HIS	-	expression tag	UNP O32164
A	413	HIS	-	expression tag	UNP O32164
A	414	HIS	-	expression tag	UNP O32164
A	415	HIS	-	expression tag	UNP O32164
A	416	HIS	-	expression tag	UNP O32164

- Molecule 2 is (2 {S},4 {S})-2-[2-methyl-3-oxidanyl-5-(phosphonooxymethyl)pyridin-4-yl]-1,3-thiazolidine-4-carboxylic acid (three-letter code: 9YX) (formula: C₁₁H₁₅N₂O₇PS) (labeled as "Ligand of Interest" by depositor).

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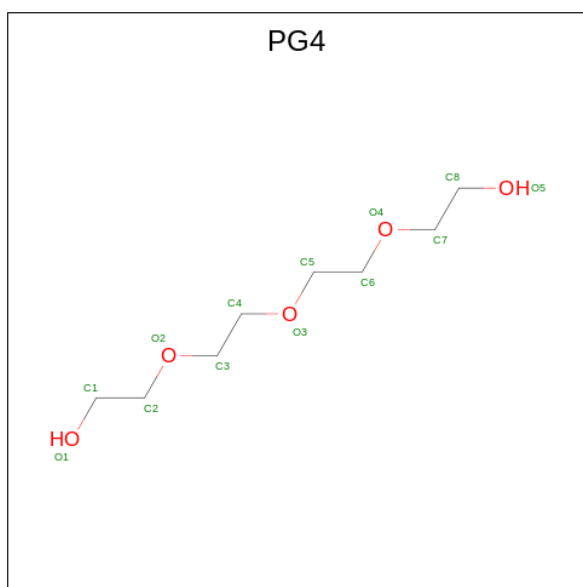
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0
3	A	1	Total C O 7 4 3	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



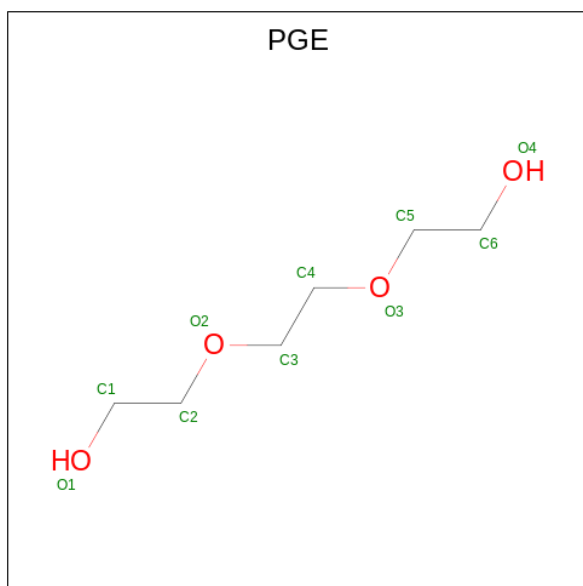
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0

- Molecule 5 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			13	8	5		

- Molecule 6 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			10	6	4		

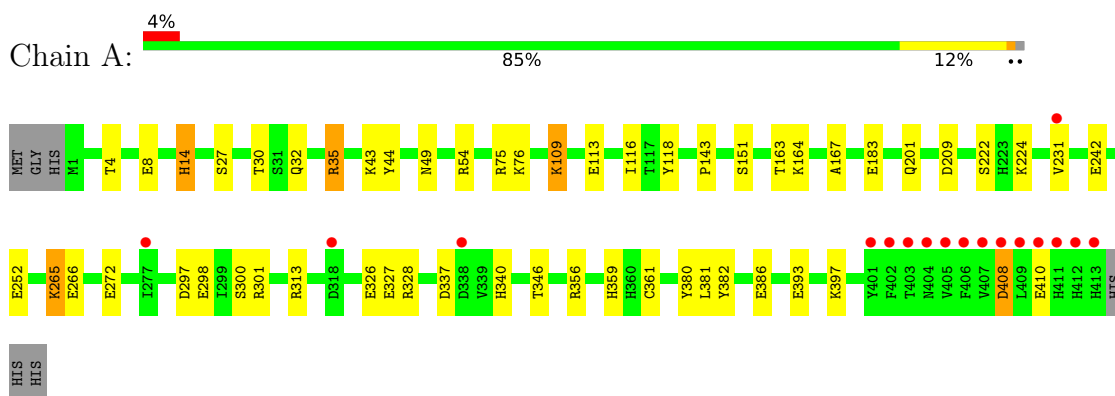
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	288	Total 288	O 288	0	0

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: Cysteine desulfurase SufS



4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	92.80Å 92.80Å 128.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.40 – 1.88 46.40 – 1.88	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.40-1.88) 99.8 (46.40-1.88)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 1.88Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.149 , 0.179 0.149 , 0.179	Depositor DCC
R_{free} test set	2637 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	31.1	Xtrriage
Anisotropy	0.058	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	3636	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% 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: EDO, 9YX, PEG, PG4, PGE

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	1.02	12/3294 (0.4%)	1.19	22/4474 (0.5%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	183	GLU	CD-OE1	9.01	1.35	1.25
1	A	393	GLU	CD-OE2	8.14	1.34	1.25
1	A	326	GLU	CD-OE1	6.75	1.33	1.25
1	A	326	GLU	CD-OE2	6.23	1.32	1.25
1	A	242	GLU	CD-OE2	-6.09	1.19	1.25
1	A	272	GLU	CD-OE1	6.03	1.32	1.25
1	A	327	GLU	CD-OE1	5.72	1.31	1.25
1	A	300	SER	CA-CB	5.65	1.61	1.52
1	A	252	GLU	CD-OE1	-5.42	1.19	1.25
1	A	340	HIS	CE1-NE2	5.16	1.44	1.32
1	A	266	GLU	CD-OE1	5.12	1.31	1.25
1	A	386	GLU	CD-OE2	-5.02	1.20	1.25

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	356	ARG	NE-CZ-NH2	-8.71	115.95	120.30
1	A	313	ARG	NE-CZ-NH2	-8.29	116.16	120.30
1	A	346	THR	CA-CB-OG1	-7.77	92.67	109.00
1	A	54	ARG	NE-CZ-NH1	-7.46	116.57	120.30
1	A	408	ASP	CB-CA-C	7.33	125.07	110.40
1	A	231	VAL	CA-CB-CG2	6.76	121.04	110.90
1	A	313	ARG	NE-CZ-NH1	6.53	123.57	120.30
1	A	337	ASP	C-N-CA	-6.52	105.41	121.70
1	A	209	ASP	CB-CG-OD1	6.17	123.85	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	35	ARG	CD-NE-CZ	-5.99	115.22	123.60
1	A	35	ARG	NE-CZ-NH2	5.78	123.19	120.30
1	A	54	ARG	CB-CG-CD	5.62	126.21	111.60
1	A	222	SER	N-CA-CB	-5.61	102.08	110.50
1	A	297	ASP	CB-CG-OD1	5.50	123.25	118.30
1	A	35	ARG	NE-CZ-NH1	-5.39	117.60	120.30
1	A	328	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	A	35	ARG	CG-CD-NE	-5.37	100.52	111.80
1	A	300	SER	N-CA-CB	5.27	118.41	110.50
1	A	298	GLU	CB-CG-CD	-5.21	100.12	114.20
1	A	231	VAL	CB-CA-C	-5.20	101.52	111.40
1	A	14	HIS	CA-CB-CG	-5.19	104.77	113.60
1	A	265	LYS	CB-CA-C	-5.09	100.21	110.40

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	3225	0	3170	31	0
2	A	22	0	0	0	0
3	A	70	0	100	7	0
4	A	8	0	12	0	0
5	A	13	0	18	3	0
6	A	10	0	14	1	0
7	A	288	0	0	12	0
All	All	3636	0	3314	35	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 5.

All (35) 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:301:ARG:HD3	7:A:853:HOH:O	1.76	0.85
1:A:301:ARG:CD	7:A:853:HOH:O	2.26	0.82
1:A:265:LYS:HE3	5:A:506:PG4:H41	1.70	0.74
3:A:512:PEG:H22	7:A:807:HOH:O	1.90	0.70
3:A:512:PEG:C2	7:A:807:HOH:O	2.39	0.69
3:A:504:PEG:H42	7:A:784:HOH:O	1.97	0.65
1:A:265:LYS:CE	5:A:506:PG4:H41	2.28	0.64
1:A:164:LYS:NZ	7:A:601:HOH:O	2.26	0.62
1:A:301:ARG:HD2	7:A:853:HOH:O	1.98	0.61
1:A:14:HIS:HD2	7:A:807:HOH:O	1.87	0.57
3:A:512:PEG:H21	7:A:807:HOH:O	2.04	0.53
1:A:201:GLN:HE21	1:A:224:LYS:NZ	2.07	0.53
1:A:35:ARG:HH22	3:A:510:PEG:H22	1.73	0.52
1:A:4:THR:OG1	6:A:515:PGE:H32	2.11	0.51
1:A:8:GLU:HG2	7:A:834:HOH:O	2.11	0.51
1:A:109:LYS:HE2	7:A:630:HOH:O	2.11	0.51
1:A:44:TYR:CZ	1:A:49:ASN:HA	2.46	0.50
1:A:381:LEU:H	1:A:381:LEU:HD23	1.78	0.49
1:A:201:GLN:HE21	1:A:224:LYS:HZ1	1.61	0.48
1:A:76:LYS:HE2	7:A:786:HOH:O	2.14	0.47
1:A:27:SER:HA	1:A:30:THR:O	2.15	0.46
1:A:118:TYR:CE2	1:A:143:PRO:HA	2.50	0.46
1:A:43:LYS:HZ1	3:A:502:PEG:H12	1.82	0.45
1:A:113:GLU:HB2	1:A:163:THR:HA	1.97	0.45
1:A:301:ARG:HB3	1:A:301:ARG:CZ	2.46	0.45
1:A:201:GLN:NE2	1:A:224:LYS:NZ	2.65	0.44
1:A:265:LYS:NZ	5:A:506:PG4:H41	2.33	0.43
1:A:359:HIS:HD2	1:A:361:CYS:H	1.64	0.43
1:A:43:LYS:NZ	3:A:502:PEG:H32	2.34	0.43
1:A:32:GLN:HA	1:A:32:GLN:OE1	2.19	0.42
1:A:75:ARG:NH2	1:A:76:LYS:HG2	2.35	0.42
1:A:116:ILE:HG22	1:A:167:ALA:HB3	2.01	0.42
1:A:301:ARG:CB	1:A:301:ARG:NH2	2.83	0.41
1:A:164:LYS:HA	1:A:164:LYS:HD3	1.92	0.41
1:A:35:ARG:CG	1:A:35:ARG:NH1	2.81	0.41

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	411/419 (98%)	398 (97%)	13 (3%)	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	344/349 (99%)	337 (98%)	7 (2%)	55 47

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	109	LYS
1	A	151	SER
1	A	380	TYR
1	A	382	TYR
1	A	397	LYS
1	A	408	ASP
1	A	410	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	HIS

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Mol	Chain	Res	Type
1	A	18	ASN
1	A	191	ASN
1	A	201	GLN
1	A	211	GLN
1	A	243	ASN
1	A	304	HIS
1	A	359	HIS
1	A	363	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

15 ligands 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	$\# Z > 2$
4	EDO	A	505	-	3,3,3	0.26	0	2,2,2	0.58	0
3	PEG	A	511	-	6,6,6	0.29	0	5,5,5	0.31	0
3	PEG	A	509	-	6,6,6	0.21	0	5,5,5	0.26	0
3	PEG	A	512	-	6,6,6	0.14	0	5,5,5	0.33	0
3	PEG	A	508	-	6,6,6	0.13	0	5,5,5	0.27	0
3	PEG	A	503	-	6,6,6	0.21	0	5,5,5	0.15	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PEG	A	504	-	6,6,6	0.24	0	5,5,5	0.20	0
3	PEG	A	502	-	6,6,6	0.21	0	5,5,5	0.22	0
2	9YX	A	501	-	21,23,23	3.37	4 (19%)	25,34,34	2.16	8 (32%)
4	EDO	A	514	-	3,3,3	0.24	0	2,2,2	0.48	0
6	PGE	A	515	-	9,9,9	0.35	0	8,8,8	0.22	0
3	PEG	A	513	-	6,6,6	0.16	0	5,5,5	0.22	0
5	PG4	A	506	-	12,12,12	0.29	0	11,11,11	0.33	0
3	PEG	A	507	-	6,6,6	0.20	0	5,5,5	0.18	0
3	PEG	A	510	-	6,6,6	0.28	0	5,5,5	0.29	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
4	EDO	A	505	-	-	1/1/1/1	-
3	PEG	A	511	-	-	3/4/4/4	-
3	PEG	A	509	-	-	2/4/4/4	-
3	PEG	A	512	-	-	1/4/4/4	-
3	PEG	A	508	-	-	0/4/4/4	-
3	PEG	A	503	-	-	3/4/4/4	-
3	PEG	A	504	-	-	2/4/4/4	-
3	PEG	A	502	-	-	3/4/4/4	-
2	9YX	A	501	-	-	0/13/23/23	0/2/2/2
4	EDO	A	514	-	-	1/1/1/1	-
6	PGE	A	515	-	-	2/7/7/7	-
3	PEG	A	513	-	-	4/4/4/4	-
5	PG4	A	506	-	-	6/10/10/10	-
3	PEG	A	507	-	-	2/4/4/4	-
3	PEG	A	510	-	-	2/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	9YX	CAF-CAI	-11.97	1.42	1.51
2	A	501	9YX	CB-CA	7.30	1.66	1.53
2	A	501	9YX	PAL-OAK	2.98	1.69	1.60
2	A	501	9YX	CAE-CAF	2.07	1.43	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	9YX	CB-SAS-CAI	4.25	98.59	90.91
2	A	501	9YX	OAK-CAJ-CAA	-4.10	101.55	109.35
2	A	501	9YX	CAE-CAF-CAI	4.05	125.26	118.08
2	A	501	9YX	CAG-CAD-CAE	3.78	125.56	120.89
2	A	501	9YX	CAE-CAD-NAC	-3.77	115.89	120.77
2	A	501	9YX	OAN-PAL-OAO	2.66	117.81	107.64
2	A	501	9YX	CAB-NAC-CAD	2.37	123.55	119.17
2	A	501	9YX	CB-CA-C	2.10	114.31	111.32

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	PEG	C1-C2-O2-C3
3	A	504	PEG	C4-C3-O2-C2
5	A	506	PG4	O3-C5-C6-O4
3	A	507	PEG	O2-C3-C4-O4
3	A	509	PEG	O2-C3-C4-O4
5	A	506	PG4	O2-C3-C4-O3
3	A	503	PEG	O2-C3-C4-O4
3	A	504	PEG	O2-C3-C4-O4
3	A	511	PEG	O2-C3-C4-O4
3	A	512	PEG	O2-C3-C4-O4
3	A	513	PEG	O2-C3-C4-O4
3	A	502	PEG	O1-C1-C2-O2
3	A	502	PEG	O2-C3-C4-O4
3	A	510	PEG	O2-C3-C4-O4
3	A	513	PEG	O1-C1-C2-O2
3	A	510	PEG	C1-C2-O2-C3
3	A	511	PEG	C1-C2-O2-C3
3	A	509	PEG	C4-C3-O2-C2
5	A	506	PG4	C6-C5-O3-C4
3	A	511	PEG	C4-C3-O2-C2
5	A	506	PG4	C3-C4-O3-C5
6	A	515	PGE	C1-C2-O2-C3
5	A	506	PG4	C4-C3-O2-C2
3	A	513	PEG	C4-C3-O2-C2
3	A	507	PEG	C4-C3-O2-C2
3	A	503	PEG	C1-C2-O2-C3
4	A	505	EDO	O1-C1-C2-O2
3	A	503	PEG	O1-C1-C2-O2

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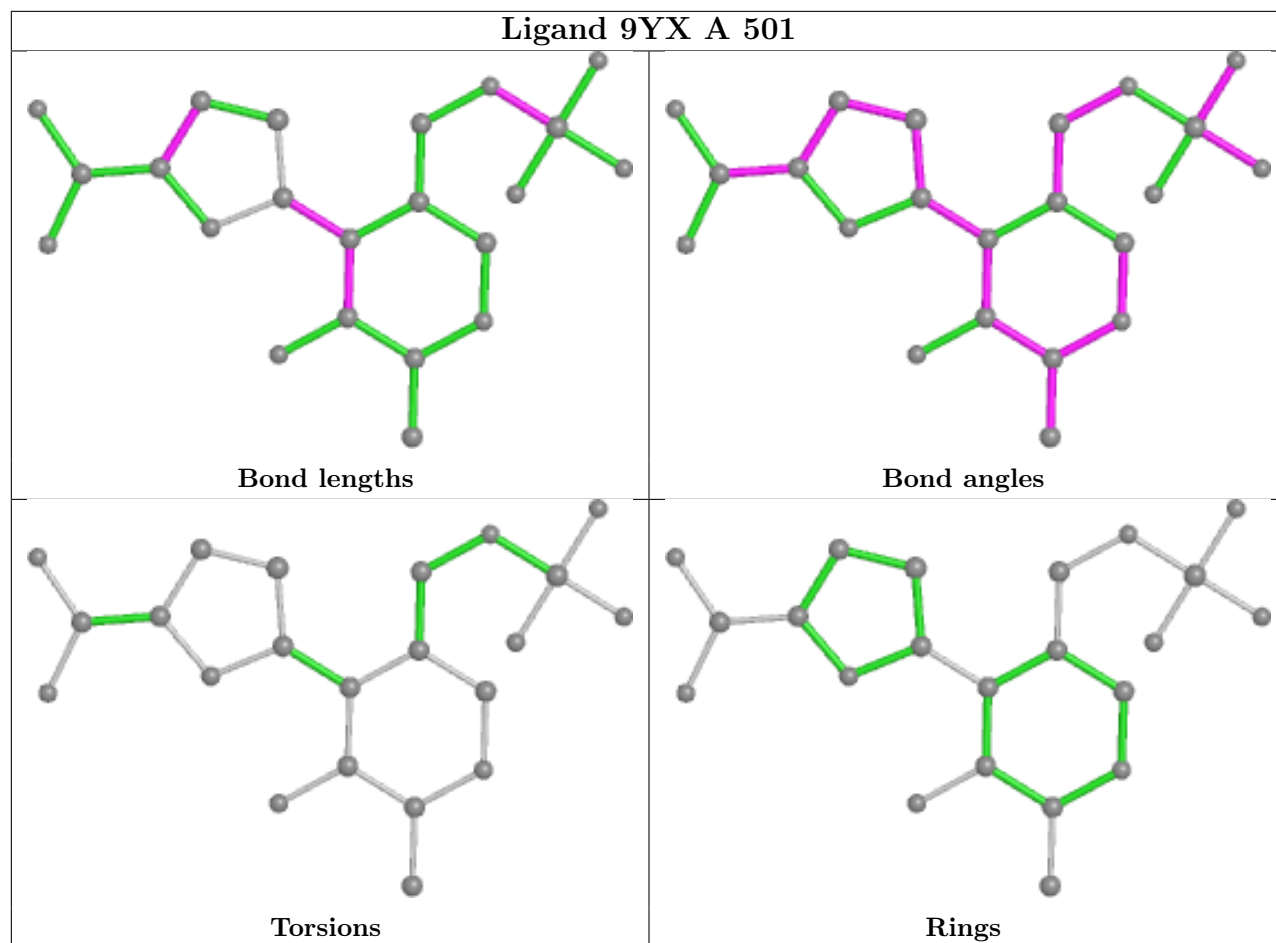
Mol	Chain	Res	Type	Atoms
4	A	514	EDO	O1-C1-C2-O2
6	A	515	PGE	C4-C3-O2-C2
5	A	506	PG4	C5-C6-O4-C7
3	A	513	PEG	C1-C2-O2-C3

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	512	PEG	3	0
3	A	504	PEG	1	0
3	A	502	PEG	2	0
6	A	515	PGE	1	0
5	A	506	PG4	3	0
3	A	510	PEG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	413/419 (98%)	-0.09	17 (4%) 37 39	20, 31, 54, 127	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	411	HIS	9.3
1	A	407	VAL	8.6
1	A	406	PHE	8.4
1	A	409	LEU	7.5
1	A	405	VAL	5.6
1	A	413	HIS	5.1
1	A	412	HIS	4.8
1	A	408	ASP	4.2
1	A	410	GLU	3.9
1	A	401	TYR	3.7
1	A	404	ASN	3.6
1	A	403	THR	3.5
1	A	402	PHE	2.8
1	A	338	ASP	2.7
1	A	277	ILE	2.5
1	A	318	ASP	2.3
1	A	231	VAL	2.3

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](#)

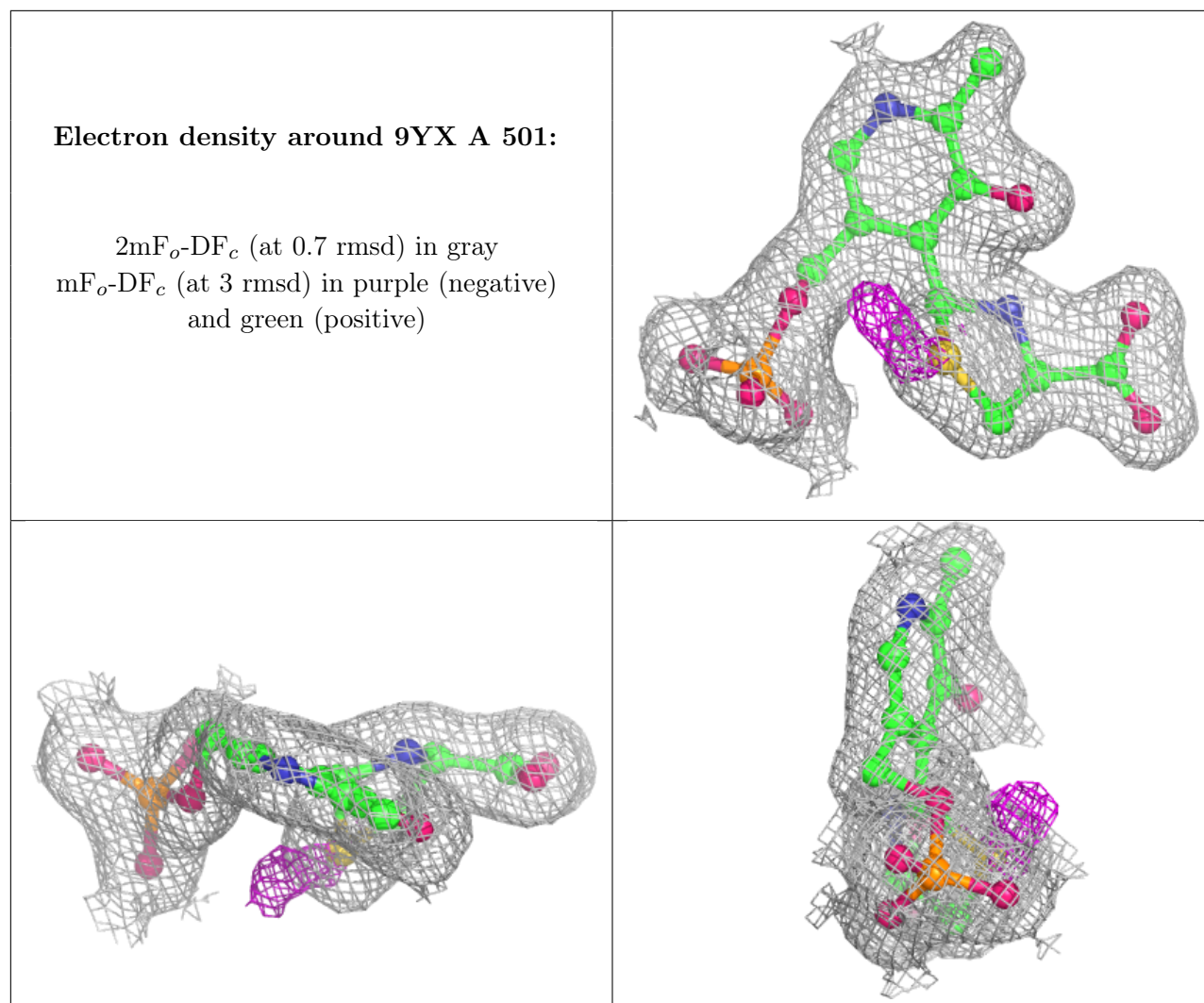
There are no monosaccharides in this entry.

6.4 Ligands

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
3	PEG	A	510	7/7	0.72	0.21	77,82,93,99	0
3	PEG	A	513	7/7	0.83	0.22	70,71,89,96	0
4	EDO	A	514	4/4	0.86	0.22	51,58,61,63	0
3	PEG	A	509	7/7	0.88	0.16	64,72,81,85	0
4	EDO	A	505	4/4	0.89	0.16	48,51,55,58	0
3	PEG	A	512	7/7	0.90	0.16	49,60,68,72	0
3	PEG	A	504	7/7	0.90	0.12	43,60,76,80	0
5	PG4	A	506	13/13	0.90	0.15	49,58,84,85	0
3	PEG	A	507	7/7	0.92	0.16	57,61,73,74	0
3	PEG	A	508	7/7	0.92	0.13	64,67,71,75	0
3	PEG	A	502	7/7	0.92	0.10	60,61,68,69	0
3	PEG	A	511	7/7	0.93	0.11	40,61,70,72	0
6	PGE	A	515	10/10	0.94	0.11	36,49,69,71	0
3	PEG	A	503	7/7	0.95	0.08	55,58,66,73	0
2	9YX	A	501	22/22	0.99	0.11	22,26,30,37	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.