



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 10:39 pm GMT

PDB ID : 4O1X  
Title : Crystal structure of human thymidylate synthase double mutant C195S-Y202C  
Authors : Pozzi, C.; Mangani, S.  
Deposited on : 2013-12-16  
Resolution : 2.32 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

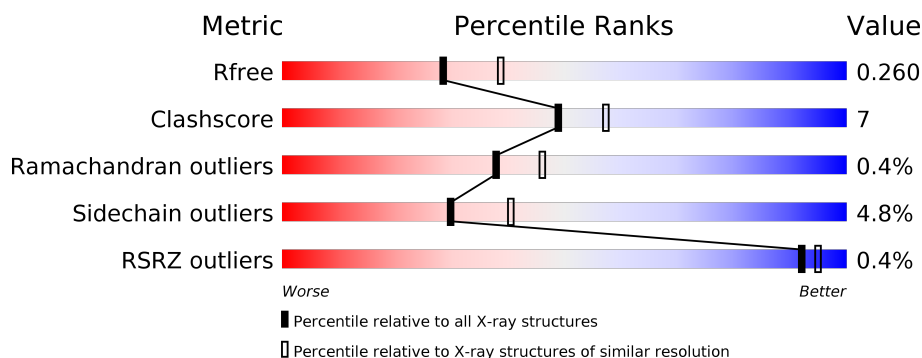
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.32 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))
$R_{free}$	100719	4787 (2.34-2.30)
Clashscore	112137	5439 (2.34-2.30)
Ramachandran outliers	110173	5386 (2.34-2.30)
Sidechain outliers	110143	5385 (2.34-2.30)
RSRZ outliers	101464	4814 (2.34-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	325	
1	B	325	
1	C	325	
2	D	325	

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	EDO	A	406	-	-	X	X
5	EDO	D	403	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9482 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 Thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	0	0
			2327	1484	408	420	15			
1	B	288	Total	C	N	O	S	0	0	0
			2308	1474	400	419	15			
1	C	286	Total	C	N	O	S	0	0	0
			2293	1465	397	416	15			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	INITIATING METHIONINE	UNP P04818
A	-10	ARG	-	EXPRESSION TAG	UNP P04818
A	-9	GLY	-	EXPRESSION TAG	UNP P04818
A	-8	SER	-	EXPRESSION TAG	UNP P04818
A	-7	HIS	-	EXPRESSION TAG	UNP P04818
A	-6	HIS	-	EXPRESSION TAG	UNP P04818
A	-5	HIS	-	EXPRESSION TAG	UNP P04818
A	-4	HIS	-	EXPRESSION TAG	UNP P04818
A	-3	HIS	-	EXPRESSION TAG	UNP P04818
A	-2	HIS	-	EXPRESSION TAG	UNP P04818
A	-1	GLY	-	EXPRESSION TAG	UNP P04818
A	0	SER	-	EXPRESSION TAG	UNP P04818
A	195	SER	CYS	ENGINEERED MUTATION	UNP P04818
A	202	CME	TYR	ENGINEERED MUTATION	UNP P04818
B	-11	MET	-	INITIATING METHIONINE	UNP P04818
B	-10	ARG	-	EXPRESSION TAG	UNP P04818
B	-9	GLY	-	EXPRESSION TAG	UNP P04818
B	-8	SER	-	EXPRESSION TAG	UNP P04818
B	-7	HIS	-	EXPRESSION TAG	UNP P04818
B	-6	HIS	-	EXPRESSION TAG	UNP P04818
B	-5	HIS	-	EXPRESSION TAG	UNP P04818
B	-4	HIS	-	EXPRESSION TAG	UNP P04818
B	-3	HIS	-	EXPRESSION TAG	UNP P04818

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	EXPRESSION TAG	UNP P04818
B	-1	GLY	-	EXPRESSION TAG	UNP P04818
B	0	SER	-	EXPRESSION TAG	UNP P04818
B	195	SER	CYS	ENGINEERED MUTATION	UNP P04818
B	202	CME	TYR	ENGINEERED MUTATION	UNP P04818
C	-11	MET	-	INITIATING METHIONINE	UNP P04818
C	-10	ARG	-	EXPRESSION TAG	UNP P04818
C	-9	GLY	-	EXPRESSION TAG	UNP P04818
C	-8	SER	-	EXPRESSION TAG	UNP P04818
C	-7	HIS	-	EXPRESSION TAG	UNP P04818
C	-6	HIS	-	EXPRESSION TAG	UNP P04818
C	-5	HIS	-	EXPRESSION TAG	UNP P04818
C	-4	HIS	-	EXPRESSION TAG	UNP P04818
C	-3	HIS	-	EXPRESSION TAG	UNP P04818
C	-2	HIS	-	EXPRESSION TAG	UNP P04818
C	-1	GLY	-	EXPRESSION TAG	UNP P04818
C	0	SER	-	EXPRESSION TAG	UNP P04818
C	195	SER	CYS	ENGINEERED MUTATION	UNP P04818
C	202	CME	TYR	ENGINEERED MUTATION	UNP P04818

- Molecule 2 is a protein called Thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	278	Total	C	N	O	S	0	0	0
			2241	1432	383	410	16			

There are 14 discrepancies between the modelled and reference sequences:

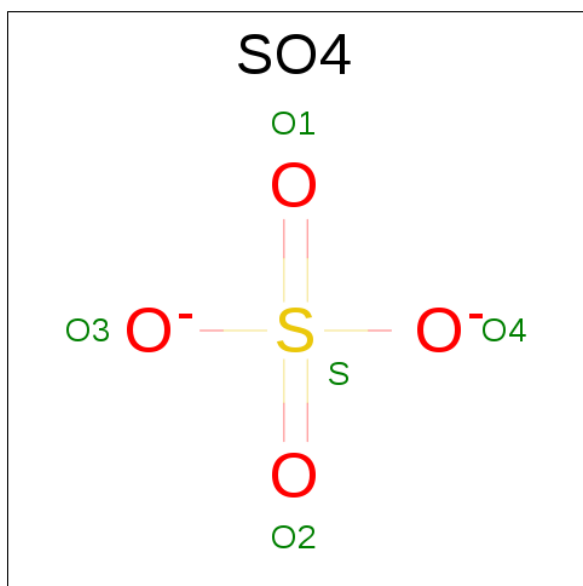
Chain	Residue	Modelled	Actual	Comment	Reference
D	-11	MET	-	INITIATING METHIONINE	UNP P04818
D	-10	ARG	-	EXPRESSION TAG	UNP P04818
D	-9	GLY	-	EXPRESSION TAG	UNP P04818
D	-8	SER	-	EXPRESSION TAG	UNP P04818
D	-7	HIS	-	EXPRESSION TAG	UNP P04818
D	-6	HIS	-	EXPRESSION TAG	UNP P04818
D	-5	HIS	-	EXPRESSION TAG	UNP P04818
D	-4	HIS	-	EXPRESSION TAG	UNP P04818
D	-3	HIS	-	EXPRESSION TAG	UNP P04818
D	-2	HIS	-	EXPRESSION TAG	UNP P04818
D	-1	GLY	-	EXPRESSION TAG	UNP P04818
D	0	SER	-	EXPRESSION TAG	UNP P04818
D	195	SER	CYS	ENGINEERED MUTATION	UNP P04818

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Chain	Residue	Modelled	Actual	Comment	Reference
D	202	CME	TYR	ENGINEERED MUTATION	UNP P04818

- Molecule 3 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).

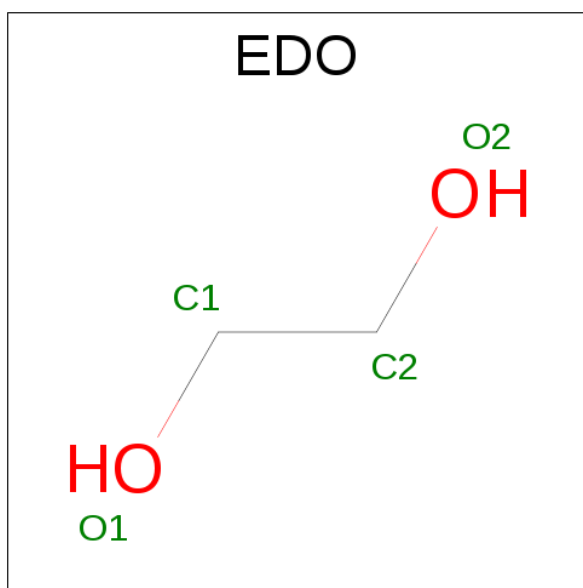


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	72	Total	O	0	0
			72	72		
6	B	60	Total	O	0	0
			60	60		
6	C	59	Total	O	0	0
			59	59		
6	D	59	Total	O	0	0
			59	59		





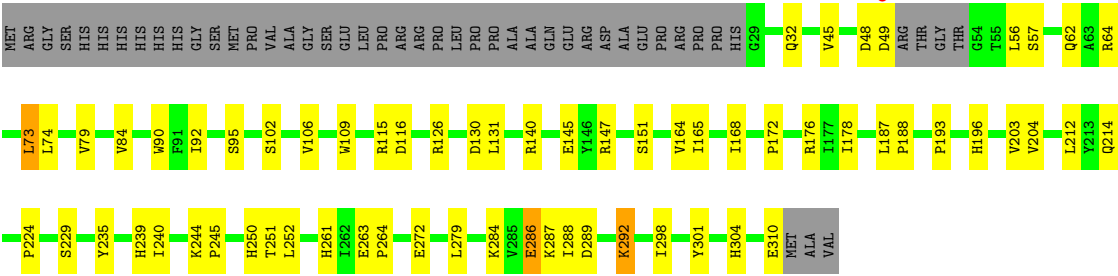
Chain D: 

65%

19%

•

14%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.93Å 95.52Å 131.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.49 – 2.32 38.49 – 2.32	Depositor EDS
% Data completeness (in resolution range)	98.6 (38.49-2.32) 96.8 (38.49-2.32)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.10 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, $R_{free}$	0.206 , 0.260 0.205 , 0.260	Depositor DCC
$R_{free}$ test set	2628 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	32.8	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 15.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.287 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	9482	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: SO4, CME, EDO, SCH, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.57	0/2356	0.74	0/3182
1	B	0.57	0/2337	0.73	1/3160 (0.0%)
1	C	0.57	0/2321	0.74	1/3137 (0.0%)
2	D	0.55	0/2256	0.72	0/3045
All	All	0.57	0/9270	0.73	2/12524 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	254	ASP	CB-CG-OD1	5.68	123.41	118.30
1	B	192	LEU	CA-CB-CG	5.08	126.98	115.30

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	2327	0	2295	27	0
1	B	2308	0	2258	35	0
1	C	2293	0	2249	35	0
2	D	2241	0	2192	36	0
3	A	15	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	5	0	0	0	0
3	C	10	0	0	0	0
3	D	10	0	0	0	0
4	A	3	0	0	0	0
5	A	8	0	12	5	0
5	B	4	0	6	0	0
5	C	4	0	6	0	0
5	D	4	0	6	1	0
6	A	72	0	0	1	0
6	B	60	0	0	2	0
6	C	59	0	0	3	0
6	D	59	0	0	2	0
All	All	9482	0	9024	124	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 7.

The worst 5 of 124 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:C:280:ARG:HH11	1:C:280:ARG:HG3	1.19	1.04
1:B:165:ILE:HG21	1:B:240:ILE:HD11	1.36	1.02
1:C:280:ARG:HH11	1:C:280:ARG:CG	1.76	0.96
1:B:165:ILE:CG2	1:B:240:ILE:HD11	1.97	0.95
1:A:308:LYS:H	1:A:308:LYS:HE2	1.33	0.93

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	283/325 (87%)	270 (95%)	13 (5%)	0	100	100
1	B	283/325 (87%)	264 (93%)	18 (6%)	1 (0%)	38	46
1	C	281/325 (86%)	260 (92%)	18 (6%)	3 (1%)	17	17
2	D	270/325 (83%)	249 (92%)	21 (8%)	0	100	100
All	All	1117/1300 (86%)	1043 (93%)	70 (6%)	4 (0%)	38	46

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	53	THR
1	C	260	ASN
1	B	134	VAL
1	C	134	VAL

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	247/278 (89%)	237 (96%)	10 (4%)	36	49
1	B	243/278 (87%)	228 (94%)	15 (6%)	21	28
1	C	242/278 (87%)	235 (97%)	7 (3%)	48	63
2	D	236/277 (85%)	222 (94%)	14 (6%)	23	30
All	All	968/1111 (87%)	922 (95%)	46 (5%)	30	40

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	240	ILE
1	C	55	THR
2	D	288	ILE
1	B	259	LEU
1	B	297	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such

sidechains are listed below:

Mol	Chain	Res	Type
1	C	38	GLN
2	D	260	ASN
1	C	156	GLN
1	B	211	GLN
1	C	297	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

13 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	$\# Z  > 2$
1	CME	A	199	1	9,9,10	1.00	0	6,9,11	0.97	0
1	CME	A	202	1	9,9,10	0.81	0	6,9,11	1.39	1 (16%)
1	SCH	A	43	1	7,7,8	0.69	0	3,7,9	1.71	1 (33%)
1	CME	B	199	1	9,9,10	0.88	0	6,9,11	0.90	0
1	CME	B	202	1	9,9,10	1.03	0	6,9,11	1.81	2 (33%)
1	SCH	B	43	1	7,7,8	0.84	0	3,7,9	1.50	0
1	CME	C	199	1	9,9,10	0.78	0	6,9,11	0.81	0
1	CME	C	202	1	9,9,10	0.84	0	6,9,11	0.89	0
1	SCH	C	43	1	7,7,8	0.91	0	3,7,9	1.59	1 (33%)
2	SCH	D	180	2	7,7,8	0.96	0	3,7,9	2.18	1 (33%)
2	CME	D	199	2	9,9,10	0.79	0	6,9,11	0.75	0
2	CME	D	202	2	9,9,10	0.76	0	6,9,11	0.80	0
2	SCH	D	43	2	7,7,8	0.79	0	3,7,9	1.24	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
1	CME	A	199	1	-	0/5/8/10	0/0/0/0
1	CME	A	202	1	-	0/5/8/10	0/0/0/0
1	SCH	A	43	1	-	0/2/6/8	0/0/0/0
1	CME	B	199	1	-	0/5/8/10	0/0/0/0
1	CME	B	202	1	-	0/5/8/10	0/0/0/0
1	SCH	B	43	1	-	0/2/6/8	0/0/0/0
1	CME	C	199	1	-	0/5/8/10	0/0/0/0
1	CME	C	202	1	-	0/5/8/10	0/0/0/0
1	SCH	C	43	1	-	0/2/6/8	0/0/0/0
2	SCH	D	180	2	-	0/2/6/8	0/0/0/0
2	CME	D	199	2	-	0/5/8/10	0/0/0/0
2	CME	D	202	2	-	0/5/8/10	0/0/0/0
2	SCH	D	43	2	-	0/2/6/8	0/0/0/0

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	180	SCH	CB-SG-SD	-3.06	97.89	103.83
1	B	202	CME	CZ-CE-SD	-2.95	102.76	113.24
1	B	202	CME	CB-SG-SD	-2.49	98.99	103.83
1	C	43	SCH	CB-SG-SD	2.00	107.73	103.83
1	A	43	SCH	CB-SG-SD	2.01	107.75	103.83

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
1	C	199	CME	1	0
1	C	202	CME	2	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 16 ligands modelled in this entry, 3 are monoatomic - leaving 13 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	$\# Z  > 2$
3	SO4	A	401	-	4,4,4	0.33	0	6,6,6	0.31	0
5	EDO	A	405	-	3,3,3	0.48	0	2,2,2	0.81	0
5	EDO	A	406	-	3,3,3	0.68	0	2,2,2	0.50	0
3	SO4	A	407	-	4,4,4	0.36	0	6,6,6	0.53	0
3	SO4	A	408	-	4,4,4	0.42	0	6,6,6	0.39	0
3	SO4	B	401	-	4,4,4	0.37	0	6,6,6	0.48	0
5	EDO	B	402	-	3,3,3	0.19	0	2,2,2	0.78	0
3	SO4	C	401	-	4,4,4	0.47	0	6,6,6	0.19	0
3	SO4	C	402	-	4,4,4	0.48	0	6,6,6	0.38	0
5	EDO	C	403	-	3,3,3	0.64	0	2,2,2	0.61	0
3	SO4	D	401	-	4,4,4	0.43	0	6,6,6	0.20	0
3	SO4	D	402	-	4,4,4	0.40	0	6,6,6	0.12	0
5	EDO	D	403	-	3,3,3	0.62	0	2,2,2	0.10	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
3	SO4	A	401	-	-	0/0/0/0	0/0/0/0
5	EDO	A	405	-	-	0/1/1/1	0/0/0/0
5	EDO	A	406	-	-	0/1/1/1	0/0/0/0
3	SO4	A	407	-	-	0/0/0/0	0/0/0/0
3	SO4	A	408	-	-	0/0/0/0	0/0/0/0
3	SO4	B	401	-	-	0/0/0/0	0/0/0/0
5	EDO	B	402	-	-	0/1/1/1	0/0/0/0
3	SO4	C	401	-	-	0/0/0/0	0/0/0/0
3	SO4	C	402	-	-	0/0/0/0	0/0/0/0
5	EDO	C	403	-	-	0/1/1/1	0/0/0/0
3	SO4	D	401	-	-	0/0/0/0	0/0/0/0
3	SO4	D	402	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	D	403	-	-	0/1/1/1	0/0/0/0

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.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	SO4	1	0
5	A	405	EDO	1	0
5	A	406	EDO	4	0
5	D	403	EDO	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	285/325 (87%)	-0.17	0 100 100	13, 29, 52, 76	0
1	B	285/325 (87%)	-0.15	1 (0%) 92 95	14, 31, 54, 91	0
1	C	283/325 (87%)	-0.16	3 (1%) 80 84	14, 30, 54, 96	0
2	D	274/325 (84%)	-0.09	1 (0%) 92 95	15, 34, 52, 79	0
All	All	1127/1300 (86%)	-0.14	5 (0%) 92 95	13, 31, 53, 96	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	26	PRO	3.1
1	C	51	THR	2.8
1	B	117	PHE	2.7
2	D	49	ASP	2.2
1	C	311	MET	2.2

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	SCH	D	43	8/9	0.88	0.12	-	40,41,50,57	0
1	SCH	A	43	8/9	0.94	0.13	-	38,40,55,56	0
1	SCH	C	43	8/9	0.93	0.13	-	43,46,59,66	0
1	CME	A	202	10/11	0.97	0.10	-	18,23,37,38	0
1	CME	C	202	10/11	0.97	0.09	-	19,26,35,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	CME	A	199	10/11	0.97	0.09	-	15,18,25,26	0
1	CME	B	199	10/11	0.97	0.08	-	17,19,24,25	0
1	CME	C	199	10/11	0.96	0.10	-	18,24,31,34	0
2	CME	D	199	10/11	0.97	0.09	-	19,23,29,33	0
2	SCH	D	180	8/9	0.91	0.13	-	24,28,51,62	0
1	CME	B	202	10/11	0.96	0.10	-	19,25,38,39	0
2	CME	D	202	10/11	0.95	0.09	-	23,26,38,38	0
1	SCH	B	43	8/9	0.89	0.11	-	49,55,73,79	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	EDO	A	406	4/4	0.81	0.34	9.15	29,36,37,44	0
5	EDO	D	403	4/4	0.78	0.20	2.24	24,25,26,31	0
3	SO4	A	401	5/5	0.96	0.14	1.14	35,35,41,43	0
5	EDO	C	403	4/4	0.85	0.14	0.86	22,24,28,28	0
5	EDO	A	405	4/4	0.93	0.15	0.75	20,21,22,30	0
5	EDO	B	402	4/4	0.95	0.13	0.28	15,17,18,19	0
3	SO4	D	401	5/5	0.94	0.14	-0.54	58,61,64,64	0
3	SO4	D	402	5/5	0.98	0.13	-0.63	50,51,54,55	0
3	SO4	B	401	5/5	0.98	0.10	-1.19	34,35,35,39	0
3	SO4	A	407	5/5	0.97	0.09	-2.58	44,47,50,50	0
4	CL	A	403	1/1	0.95	0.07	-	48,48,48,48	0
3	SO4	A	408	5/5	0.97	0.11	-	29,31,33,35	0
4	CL	A	404	1/1	0.88	0.07	-	59,59,59,59	0
3	SO4	C	401	5/5	0.91	0.17	-	58,67,68,68	0
4	CL	A	402	1/1	0.89	0.14	-	59,59,59,59	0
3	SO4	C	402	5/5	0.91	0.13	-	68,69,73,76	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.