



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 1, 2019 – 06:50 PM EDT

PDB ID : 6FE7  
Title : Crystal structure of human phosphodiesterase 4D2 catalytic domain with inhibitor NPD-356  
Authors : Singh, A.K.; Brown, D.G.  
Deposited on : 2017-12-29  
Resolution : 2.00 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : rb-20031633  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20031633

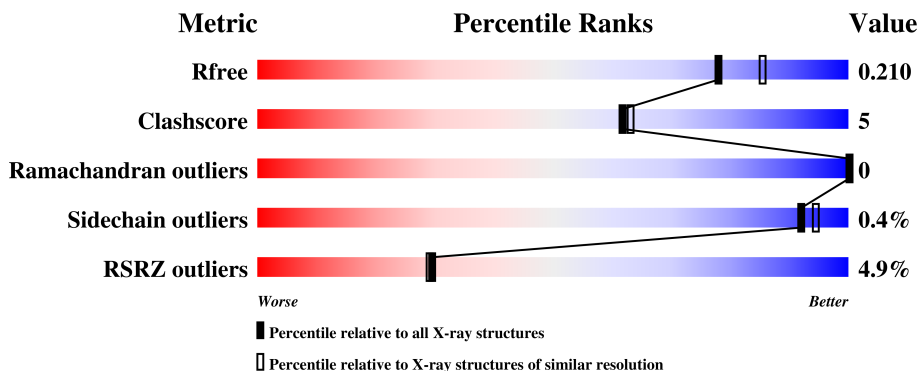
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	111664	7193 (2.00-2.00)
Clashscore	122126	8267 (2.00-2.00)
Ramachandran outliers	120053	8166 (2.00-2.00)
Sidechain outliers	120020	8165 (2.00-2.00)
RSRZ outliers	108989	7011 (2.00-2.00)

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	364	<div> <div>8%</div> <div>84%</div> <div>6%</div> <div>9%</div> </div>
1	B	364	<div> <div>3%</div> <div>85%</div> <div>•</div> <div>11%</div> </div>
1	C	364	<div> <div>5%</div> <div>80%</div> <div>8%</div> <div>•</div> <div>11%</div> </div>
1	D	364	<div> <div>2%</div> <div>83%</div> <div>6%</div> <div>11%</div> </div>

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
4	EDO	C	512	-	-	-	X
4	EDO	D	522	-	X	-	-
8	PG4	C	521	-	-	X	-

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 11789 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 cAMP-specific 3',5'-cyclic phosphodiesterase 4D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	0	0
			2669	1690	455	510	14			
1	B	323	Total	C	N	O	S	0	1	0
			2619	1657	447	501	14			
1	C	324	Total	C	N	O	S	0	0	0
			2622	1659	448	501	14			
1	D	324	Total	C	N	O	S	0	0	0
			2622	1659	448	501	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	75	GLY	-	expression tag	UNP Q08499
A	76	SER	-	expression tag	UNP Q08499
A	77	HIS	-	expression tag	UNP Q08499
A	78	MET	-	expression tag	UNP Q08499
B	75	GLY	-	expression tag	UNP Q08499
B	76	SER	-	expression tag	UNP Q08499
B	77	HIS	-	expression tag	UNP Q08499
B	78	MET	-	expression tag	UNP Q08499
C	75	GLY	-	expression tag	UNP Q08499
C	76	SER	-	expression tag	UNP Q08499
C	77	HIS	-	expression tag	UNP Q08499
C	78	MET	-	expression tag	UNP Q08499
D	75	GLY	-	expression tag	UNP Q08499
D	76	SER	-	expression tag	UNP Q08499
D	77	HIS	-	expression tag	UNP Q08499
D	78	MET	-	expression tag	UNP Q08499

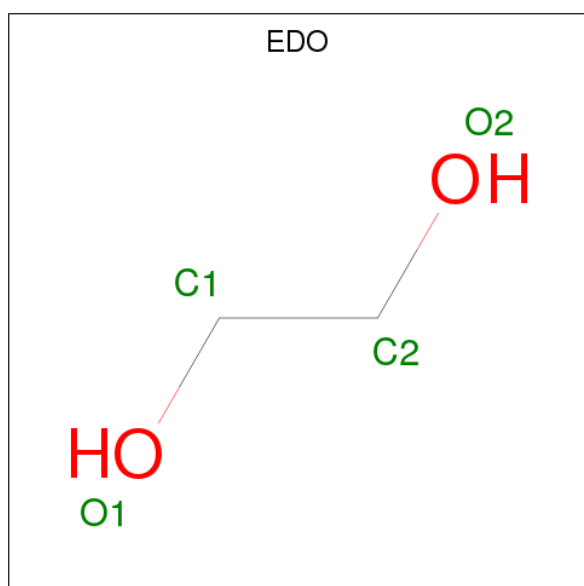
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

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

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

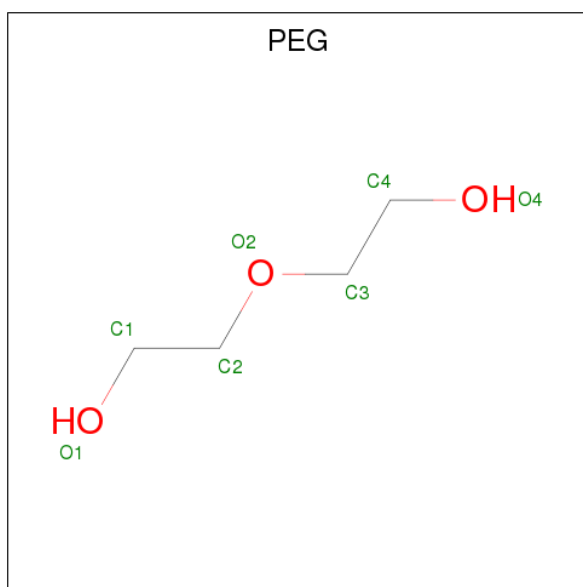
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0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

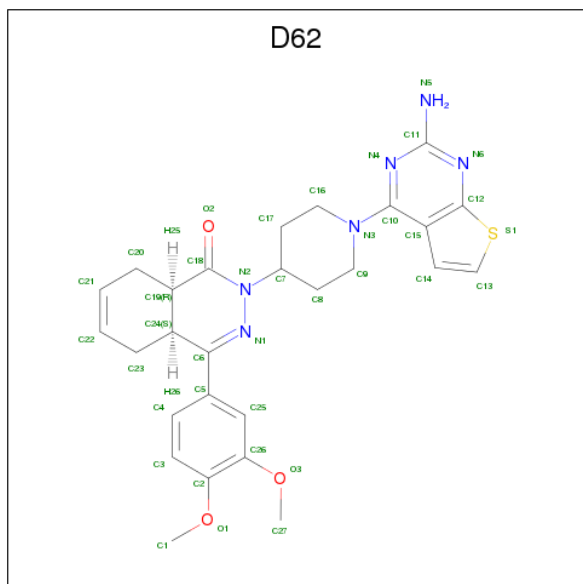
- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).





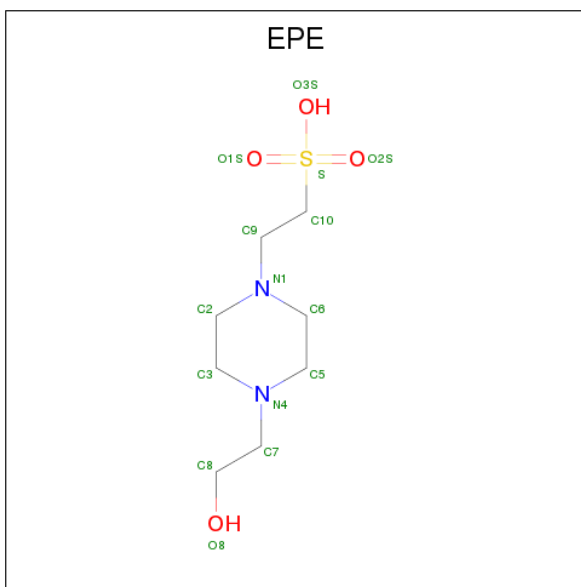
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total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

- Molecule 6 is (4a*S*,8a*R*)-2-(1-{2-aminothieno[2,3-*d*]pyrimidin-4-yl}piperidin-4-yl)-4-(3,4- dimethoxyphenyl)-1,2,4a,5,8,8a-hexahydrophthalazin-1-one (three-letter code: D62) (formula: C<sub>27</sub>H<sub>30</sub>N<sub>6</sub>O<sub>3</sub>S).



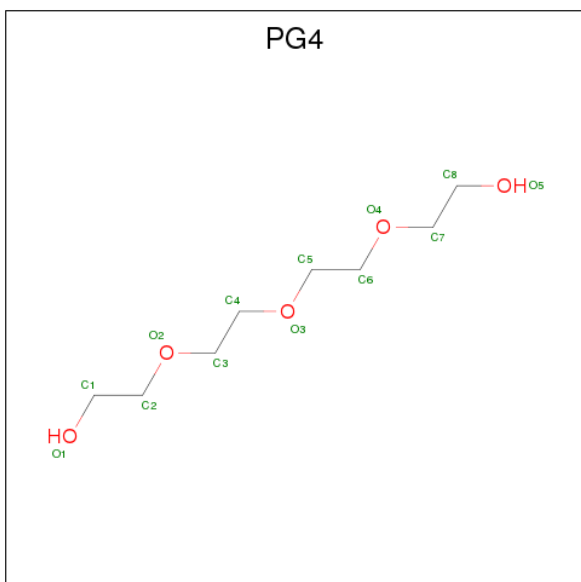
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	S	0	0
			37	27	6	3	1		
6	B	1	Total	C	N	O	S	0	0
			37	27	6	3	1		
6	C	1	Total	C	N	O	S	0	0
			37	27	6	3	1		
6	D	1	Total	C	N	O	S	0	0
			37	27	6	3	1		

- Molecule 7 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
7	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
7	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
7	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
7	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 8 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



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

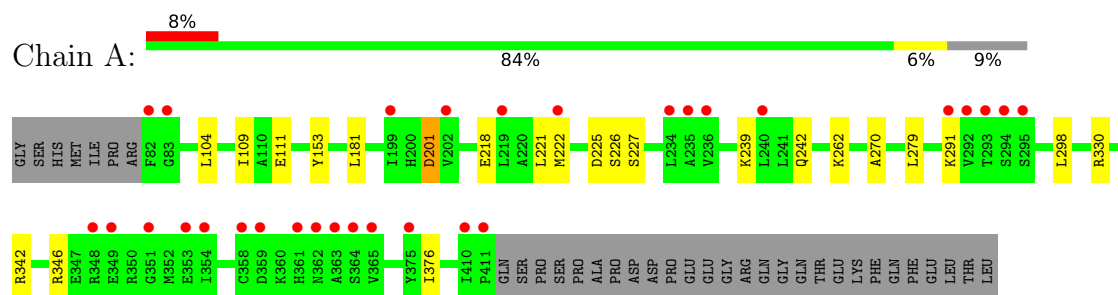
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	172	Total	O	0	0
			172	172		
9	B	182	Total	O	0	0
			182	182		
9	C	119	Total	O	0	0
			119	119		
9	D	197	Total	O	0	0
			197	197		

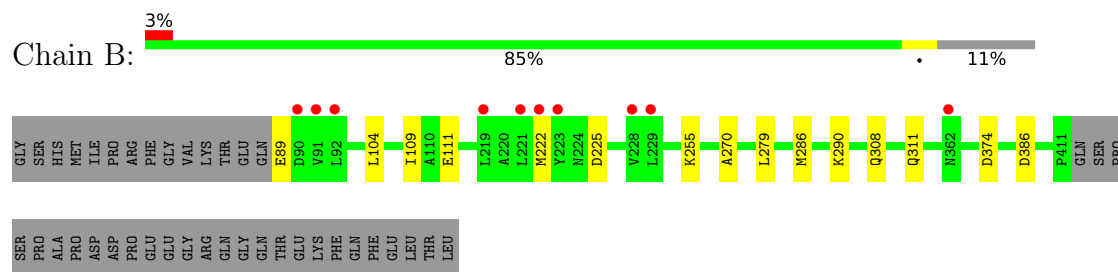
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

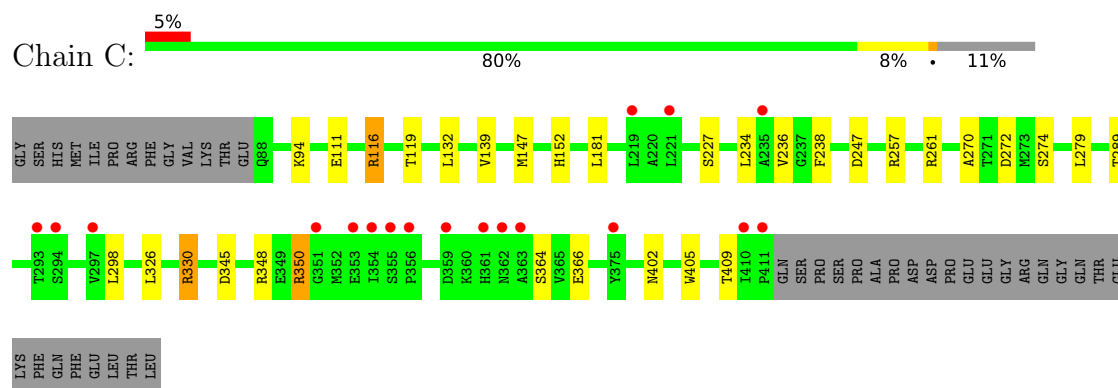
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



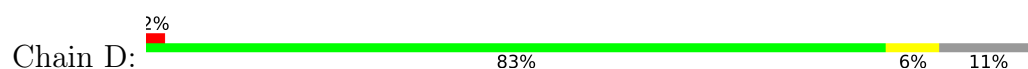
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D

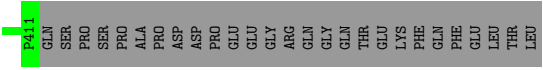
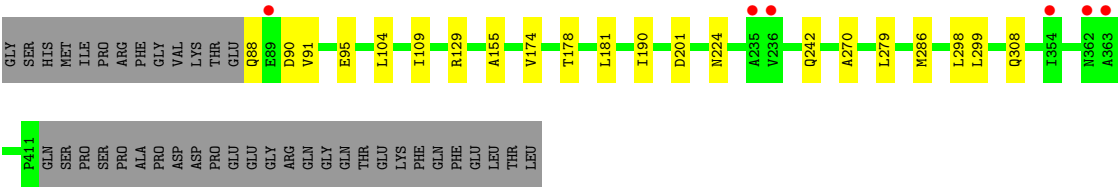


- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.22Å 111.03Å 160.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.30 – 2.00 54.30 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (54.30-2.00) 100.0 (54.30-2.00)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.66 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, $R_{free}$	0.170 , 0.200 0.182 , 0.210	Depositor DCC
$R_{free}$ test set	6067 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.5	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 53.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11789	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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: ZN, PEG, MG, EDO, PG4, EPE, D62

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	0.97	1/2724 (0.0%)	0.88	5/3700 (0.1%)
1	B	0.88	0/2673	0.83	0/3632
1	C	0.86	1/2676 (0.0%)	0.84	1/3636 (0.0%)
1	D	0.91	1/2676 (0.0%)	0.87	1/3636 (0.0%)
All	All	0.91	3/10749 (0.0%)	0.85	7/14604 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	218	GLU	CD-OE1	-5.47	1.19	1.25
1	D	95	GLU	CD-OE2	-5.13	1.20	1.25
1	C	364	SER	CB-OG	5.11	1.48	1.42

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	201	ASP	CB-CG-OD2	12.36	129.42	118.30
1	A	201	ASP	CB-CG-OD1	-9.67	109.59	118.30
1	A	330	ARG	NE-CZ-NH1	-7.62	116.49	120.30
1	C	350	ARG	NE-CZ-NH1	-7.17	116.72	120.30
1	A	330	ARG	NE-CZ-NH2	5.78	123.19	120.30

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	2669	0	2625	21	0
1	B	2619	0	2574	18	0
1	C	2622	0	2578	43	0
1	D	2622	0	2578	19	0
2	A	1	0	0	1	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	60	0	90	4	0
4	B	60	0	90	1	0
4	C	56	0	84	3	0
4	D	56	0	84	4	0
5	A	42	0	60	5	0
5	B	7	0	10	2	0
5	C	14	0	20	3	0
5	D	35	0	50	2	0
6	A	37	0	0	2	0
6	B	37	0	0	0	0
6	C	37	0	0	0	0
6	D	37	0	0	0	0
7	A	15	0	18	1	0
7	B	30	0	36	4	0
7	C	15	0	18	4	0
7	D	15	0	17	2	0
8	C	26	0	36	14	0
9	A	172	0	0	2	0
9	B	182	0	0	4	0
9	C	119	0	0	3	0
9	D	197	0	0	0	0
All	All	11789	0	10968	107	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.

The worst 5 of 107 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:111:GLU:OE2	7:C:514:EPE:H32	1.65	0.95
1:B:111:GLU:OE1	7:B:521:EPE:H72	1.74	0.87
1:B:386:ASP:OD2	4:B:504:EDO:H22	1.75	0.87
1:C:116:ARG:HE	1:C:147:MET:CE	1.90	0.84
1:A:342:ARG:NH2	1:A:346:ARG:HH21	1.76	0.83

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	328/364 (90%)	321 (98%)	7 (2%)	0	100	100
1	B	322/364 (88%)	317 (98%)	5 (2%)	0	100	100
1	C	322/364 (88%)	318 (99%)	4 (1%)	0	100	100
1	D	322/364 (88%)	316 (98%)	6 (2%)	0	100	100
All	All	1294/1456 (89%)	1272 (98%)	22 (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	301/331 (91%)	300 (100%)	1 (0%)	93	95
1	B	296/331 (89%)	295 (100%)	1 (0%)	93	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	296/331 (89%)	293 (99%)	3 (1%)	78	83
1	D	296/331 (89%)	296 (100%)	0	100	100
All	All	1189/1324 (90%)	1184 (100%)	5 (0%)	92	94

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	221	LEU
1	B	89	GLU
1	C	94	LYS
1	C	116	ARG
1	C	330	ARG

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

Mol	Chain	Res	Type
1	A	224	ASN
1	A	308	GLN
1	B	231	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 91 ligands modelled in this entry, 8 are monoatomic - leaving 83 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	EDO	A	503	-	3,3,3	0.37	0	2,2,2	0.72	0
4	EDO	A	504	-	3,3,3	0.41	0	2,2,2	0.91	0
4	EDO	A	505	-	3,3,3	0.52	0	2,2,2	0.26	0
4	EDO	A	506	-	3,3,3	0.71	0	2,2,2	1.03	0
4	EDO	A	507	-	3,3,3	0.31	0	2,2,2	1.49	0
4	EDO	A	508	-	3,3,3	0.45	0	2,2,2	0.38	0
4	EDO	A	509	-	3,3,3	0.55	0	2,2,2	0.37	0
5	PEG	A	510	-	6,6,6	0.50	0	5,5,5	0.74	0
5	PEG	A	511	-	6,6,6	0.40	0	5,5,5	0.58	0
4	EDO	A	512	-	3,3,3	0.30	0	2,2,2	1.22	0
4	EDO	A	513	-	3,3,3	0.28	0	2,2,2	1.49	1 (50%)
4	EDO	A	514	-	3,3,3	0.54	0	2,2,2	0.77	0
4	EDO	A	515	-	3,3,3	1.18	0	2,2,2	0.42	0
5	PEG	A	516	-	6,6,6	0.71	0	5,5,5	1.14	0
5	PEG	A	517	-	6,6,6	0.52	0	5,5,5	0.53	0
5	PEG	A	518	-	6,6,6	0.61	0	5,5,5	0.68	0
5	PEG	A	519	-	6,6,6	0.43	0	5,5,5	0.44	0
6	D62	A	520	-	40,42,42	0.82	2 (5%)	45,61,61	1.18	5 (11%)
4	EDO	A	521	-	3,3,3	0.53	0	2,2,2	0.76	0
4	EDO	A	522	-	3,3,3	0.58	0	2,2,2	0.47	0
4	EDO	A	523	-	3,3,3	0.51	0	2,2,2	0.87	0
7	EPE	A	524	-	15,15,15	2.38	1 (6%)	18,20,20	2.82	7 (38%)
4	EDO	A	525	-	3,3,3	0.78	0	2,2,2	0.10	0
4	EDO	B	503	-	3,3,3	0.44	0	2,2,2	1.18	0
4	EDO	B	504	-	3,3,3	0.28	0	2,2,2	0.62	0
4	EDO	B	505	-	3,3,3	0.46	0	2,2,2	0.52	0
4	EDO	B	506	-	3,3,3	0.39	0	2,2,2	1.47	1 (50%)
4	EDO	B	507	-	3,3,3	0.30	0	2,2,2	1.54	0
5	PEG	B	508	-	6,6,6	0.76	0	5,5,5	1.39	1 (20%)
7	EPE	B	509	-	15,15,15	1.33	1 (6%)	18,20,20	2.48	7 (38%)
4	EDO	B	510	-	3,3,3	0.49	0	2,2,2	0.87	0
4	EDO	B	511	-	3,3,3	0.69	0	2,2,2	1.19	0
4	EDO	B	512	-	3,3,3	0.11	0	2,2,2	1.10	0
4	EDO	B	513	-	3,3,3	0.59	0	2,2,2	0.67	0
4	EDO	B	514	-	3,3,3	0.77	0	2,2,2	0.29	0
4	EDO	B	515	-	3,3,3	0.36	0	2,2,2	0.53	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	D62	B	516	-	40,42,42	0.75	1 (2%)	45,61,61	1.16	6 (13%)
4	EDO	B	517	-	3,3,3	0.20	0	2,2,2	1.36	0
4	EDO	B	518	-	3,3,3	0.84	0	2,2,2	0.27	0
4	EDO	B	519	-	3,3,3	0.29	0	2,2,2	1.11	0
4	EDO	B	520	-	3,3,3	0.43	0	2,2,2	0.64	0
7	EPE	B	521	-	15,15,15	2.04	1 (6%)	18,20,20	1.12	3 (16%)
4	EDO	C	501	-	3,3,3	0.54	0	2,2,2	0.19	0
8	PG4	C	502	-	12,12,12	1.03	0	11,11,11	1.00	0
4	EDO	C	503	-	3,3,3	0.43	0	2,2,2	0.47	0
4	EDO	C	504	-	3,3,3	0.46	0	2,2,2	0.17	0
4	EDO	C	507	-	3,3,3	0.44	0	2,2,2	0.40	0
4	EDO	C	508	-	3,3,3	0.48	0	2,2,2	0.62	0
4	EDO	C	509	-	3,3,3	0.32	0	2,2,2	0.43	0
4	EDO	C	510	-	3,3,3	0.20	0	2,2,2	0.91	0
4	EDO	C	511	-	3,3,3	0.63	0	2,2,2	0.63	0
4	EDO	C	512	-	3,3,3	0.97	0	2,2,2	0.67	0
5	PEG	C	513	-	6,6,6	0.52	0	5,5,5	0.94	0
7	EPE	C	514	-	15,15,15	2.03	1 (6%)	18,20,20	1.10	3 (16%)
4	EDO	C	515	-	3,3,3	0.88	0	2,2,2	0.33	0
4	EDO	C	516	-	3,3,3	1.04	0	2,2,2	0.87	0
4	EDO	C	517	-	3,3,3	0.34	0	2,2,2	0.69	0
4	EDO	C	518	-	3,3,3	0.31	0	2,2,2	0.69	0
5	PEG	C	519	-	6,6,6	0.91	0	5,5,5	1.21	0
6	D62	C	520	-	40,42,42	0.73	2 (5%)	45,61,61	1.20	4 (8%)
8	PG4	C	521	-	12,12,12	1.26	2 (16%)	11,11,11	1.57	2 (18%)
4	EDO	C	522	-	3,3,3	0.46	0	2,2,2	0.47	0
4	EDO	D	501	-	3,3,3	0.77	0	2,2,2	0.35	0
4	EDO	D	504	-	3,3,3	0.78	0	2,2,2	0.21	0
4	EDO	D	505	-	3,3,3	0.51	0	2,2,2	0.45	0
4	EDO	D	506	-	3,3,3	0.32	0	2,2,2	1.15	0
4	EDO	D	507	-	3,3,3	0.48	0	2,2,2	0.45	0
5	PEG	D	508	-	6,6,6	0.49	0	5,5,5	1.21	0
5	PEG	D	509	-	6,6,6	0.97	0	5,5,5	1.63	1 (20%)
5	PEG	D	510	-	6,6,6	0.33	0	5,5,5	0.89	0
4	EDO	D	511	-	3,3,3	0.47	0	2,2,2	0.85	0
4	EDO	D	512	-	3,3,3	0.48	0	2,2,2	0.22	0
4	EDO	D	513	-	3,3,3	0.79	0	2,2,2	1.14	0
4	EDO	D	514	-	3,3,3	1.05	0	2,2,2	0.57	0
4	EDO	D	515	-	3,3,3	0.47	0	2,2,2	1.31	0
4	EDO	D	516	-	3,3,3	0.52	0	2,2,2	1.28	0
6	D62	D	517	-	40,42,42	0.82	1 (2%)	45,61,61	1.34	4 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	PEG	D	518	-	6,6,6	1.08	0	5,5,5	1.30	0
5	PEG	D	519	-	6,6,6	0.47	0	5,5,5	1.27	0
4	EDO	D	520	-	3,3,3	0.34	0	2,2,2	0.89	0
4	EDO	D	521	-	3,3,3	0.62	0	2,2,2	0.87	0
4	EDO	D	522	-	3,3,3	2.62	3 (100%)	2,2,2	2.33	1 (50%)
7	EPE	D	523	-	15,15,15	2.99	4 (26%)	18,20,20	1.86	6 (33%)

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	503	-	-	0/1/1/1	0/0/0/0
4	EDO	A	504	-	-	0/1/1/1	0/0/0/0
4	EDO	A	505	-	-	0/1/1/1	0/0/0/0
4	EDO	A	506	-	-	0/1/1/1	0/0/0/0
4	EDO	A	507	-	-	0/1/1/1	0/0/0/0
4	EDO	A	508	-	-	0/1/1/1	0/0/0/0
4	EDO	A	509	-	-	0/1/1/1	0/0/0/0
5	PEG	A	510	-	-	0/4/4/4	0/0/0/0
5	PEG	A	511	-	-	0/4/4/4	0/0/0/0
4	EDO	A	512	-	-	0/1/1/1	0/0/0/0
4	EDO	A	513	-	-	0/1/1/1	0/0/0/0
4	EDO	A	514	-	-	0/1/1/1	0/0/0/0
4	EDO	A	515	-	-	0/1/1/1	0/0/0/0
5	PEG	A	516	-	-	0/4/4/4	0/0/0/0
5	PEG	A	517	-	-	0/4/4/4	0/0/0/0
5	PEG	A	518	-	-	0/4/4/4	0/0/0/0
5	PEG	A	519	-	-	0/4/4/4	0/0/0/0
6	D62	A	520	-	-	0/16/53/53	0/6/6/6
4	EDO	A	521	-	-	0/1/1/1	0/0/0/0
4	EDO	A	522	-	-	0/1/1/1	0/0/0/0
4	EDO	A	523	-	-	0/1/1/1	0/0/0/0
7	EPE	A	524	-	-	0/9/19/19	0/1/1/1
4	EDO	A	525	-	-	0/1/1/1	0/0/0/0
4	EDO	B	503	-	-	0/1/1/1	0/0/0/0
4	EDO	B	504	-	-	0/1/1/1	0/0/0/0
4	EDO	B	505	-	-	0/1/1/1	0/0/0/0
4	EDO	B	506	-	-	0/1/1/1	0/0/0/0
4	EDO	B	507	-	-	0/1/1/1	0/0/0/0
5	PEG	B	508	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EPE	B	509	-	-	0/9/19/19	0/1/1/1
4	EDO	B	510	-	-	0/1/1/1	0/0/0/0
4	EDO	B	511	-	-	0/1/1/1	0/0/0/0
4	EDO	B	512	-	-	0/1/1/1	0/0/0/0
4	EDO	B	513	-	-	0/1/1/1	0/0/0/0
4	EDO	B	514	-	-	0/1/1/1	0/0/0/0
4	EDO	B	515	-	-	0/1/1/1	0/0/0/0
6	D62	B	516	-	-	0/16/53/53	0/6/6/6
4	EDO	B	517	-	-	0/1/1/1	0/0/0/0
4	EDO	B	518	-	-	0/1/1/1	0/0/0/0
4	EDO	B	519	-	-	0/1/1/1	0/0/0/0
4	EDO	B	520	-	-	0/1/1/1	0/0/0/0
7	EPE	B	521	-	-	0/9/19/19	0/1/1/1
4	EDO	C	501	-	-	0/1/1/1	0/0/0/0
8	PG4	C	502	-	-	0/10/10/10	0/0/0/0
4	EDO	C	503	-	-	0/1/1/1	0/0/0/0
4	EDO	C	504	-	-	0/1/1/1	0/0/0/0
4	EDO	C	507	-	-	0/1/1/1	0/0/0/0
4	EDO	C	508	-	-	0/1/1/1	0/0/0/0
4	EDO	C	509	-	-	0/1/1/1	0/0/0/0
4	EDO	C	510	-	-	0/1/1/1	0/0/0/0
4	EDO	C	511	-	-	0/1/1/1	0/0/0/0
4	EDO	C	512	-	-	0/1/1/1	0/0/0/0
5	PEG	C	513	-	-	0/4/4/4	0/0/0/0
7	EPE	C	514	-	-	0/9/19/19	0/1/1/1
4	EDO	C	515	-	-	0/1/1/1	0/0/0/0
4	EDO	C	516	-	-	0/1/1/1	0/0/0/0
4	EDO	C	517	-	-	0/1/1/1	0/0/0/0
4	EDO	C	518	-	-	0/1/1/1	0/0/0/0
5	PEG	C	519	-	-	0/4/4/4	0/0/0/0
6	D62	C	520	-	-	0/16/53/53	0/6/6/6
8	PG4	C	521	-	-	0/10/10/10	0/0/0/0
4	EDO	C	522	-	-	0/1/1/1	0/0/0/0
4	EDO	D	501	-	-	0/1/1/1	0/0/0/0
4	EDO	D	504	-	-	0/1/1/1	0/0/0/0
4	EDO	D	505	-	-	0/1/1/1	0/0/0/0
4	EDO	D	506	-	-	0/1/1/1	0/0/0/0
4	EDO	D	507	-	-	0/1/1/1	0/0/0/0
5	PEG	D	508	-	-	0/4/4/4	0/0/0/0
5	PEG	D	509	-	-	0/4/4/4	0/0/0/0
5	PEG	D	510	-	-	0/4/4/4	0/0/0/0
4	EDO	D	511	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	D	512	-	-	0/1/1/1	0/0/0/0
4	EDO	D	513	-	-	0/1/1/1	0/0/0/0
4	EDO	D	514	-	-	0/1/1/1	0/0/0/0
4	EDO	D	515	-	-	0/1/1/1	0/0/0/0
4	EDO	D	516	-	-	0/1/1/1	0/0/0/0
6	D62	D	517	-	-	0/16/53/53	0/6/6/6
5	PEG	D	518	-	-	0/4/4/4	0/0/0/0
5	PEG	D	519	-	-	0/4/4/4	0/0/0/0
4	EDO	D	520	-	-	0/1/1/1	0/0/0/0
4	EDO	D	521	-	-	0/1/1/1	0/0/0/0
4	EDO	D	522	-	-	0/1/1/1	0/0/0/0
7	EPE	D	523	-	-	0/9/19/19	0/1/1/1

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	523	EPE	C10-S	-10.83	1.62	1.77
7	A	524	EPE	C10-S	-8.72	1.65	1.77
7	C	514	EPE	C10-S	-7.66	1.66	1.77
7	B	521	EPE	C10-S	-7.66	1.66	1.77
7	B	509	EPE	C10-S	-4.18	1.71	1.77

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	524	EPE	O2S-S-C10	-6.90	98.60	106.92
6	D	517	D62	C8-C7-N2	-4.08	106.15	110.86
7	A	524	EPE	O3S-S-O2S	-3.54	102.62	111.27
6	C	520	D62	C8-C7-N2	-3.41	106.93	110.86
7	D	523	EPE	O2S-S-O1S	-3.29	102.57	113.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

21 monomers are involved in 51 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	508	EDO	1	0
5	A	516	PEG	2	0
5	A	517	PEG	2	0
5	A	518	PEG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	520	D62	2	0
4	A	521	EDO	1	0
7	A	524	EPE	1	0
4	A	525	EDO	2	0
4	B	504	EDO	1	0
5	B	508	PEG	2	0
7	B	521	EPE	4	0
8	C	502	PG4	4	0
4	C	509	EDO	1	0
7	C	514	EPE	4	0
4	C	515	EDO	2	0
5	C	519	PEG	3	0
8	C	521	PG4	10	0
4	D	513	EDO	1	0
5	D	519	PEG	2	0
4	D	521	EDO	3	0
7	D	523	EPE	2	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	330/364 (90%)	0.38	30 (9%) 9 9	24, 37, 67, 98	0
1	B	323/364 (88%)	0.12	10 (3%) 49 48	25, 40, 60, 91	0
1	C	324/364 (89%)	0.21	18 (5%) 24 24	25, 40, 73, 92	0
1	D	324/364 (89%)	-0.09	6 (1%) 66 65	23, 31, 54, 83	0
All	All	1301/1456 (89%)	0.16	64 (4%) 29 29	23, 37, 65, 98	0

The worst 5 of 64 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	294	SER	6.1
1	A	411	PRO	5.8
1	A	362	ASN	5.3
1	A	410	ILE	4.8
1	C	363	ALA	4.6

### 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 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	C	512	4/4	0.63	0.58	63,68,70,75	0
4	EDO	A	525	4/4	0.69	0.35	58,64,64,70	0
5	PEG	C	519	7/7	0.71	0.24	43,57,66,75	0
5	PEG	D	518	7/7	0.75	0.19	50,56,60,68	0
8	PG4	C	502	13/13	0.76	0.33	46,73,84,85	0
4	EDO	B	514	4/4	0.76	0.21	57,62,69,69	0
5	PEG	D	509	7/7	0.78	0.29	44,55,69,75	0
5	PEG	A	511	7/7	0.79	0.28	44,68,77,80	0
4	EDO	D	522	4/4	0.79	0.21	39,40,45,48	0
4	EDO	A	509	4/4	0.79	0.23	66,67,72,76	0
5	PEG	A	519	7/7	0.80	0.16	58,64,71,73	0
4	EDO	D	506	4/4	0.80	0.24	51,52,53,61	0
5	PEG	D	508	7/7	0.81	0.18	43,60,69,72	0
8	PG4	C	521	13/13	0.81	0.28	38,46,59,65	0
4	EDO	B	517	4/4	0.82	0.37	66,69,75,79	0
4	EDO	D	513	4/4	0.82	0.23	43,45,47,55	0
4	EDO	B	505	4/4	0.82	0.23	54,58,63,63	0
4	EDO	C	503	4/4	0.83	0.83	73,78,78,84	0
5	PEG	A	510	7/7	0.84	0.19	55,71,76,78	0
5	PEG	A	518	7/7	0.84	0.38	59,63,70,71	0
4	EDO	B	510	4/4	0.84	0.62	54,57,62,62	0
4	EDO	B	504	4/4	0.84	0.30	70,75,77,82	0
4	EDO	A	508	4/4	0.85	0.31	60,69,69,80	0
4	EDO	C	501	4/4	0.85	0.48	48,48,60,66	0
4	EDO	D	515	4/4	0.86	0.25	53,65,68,76	0
4	EDO	B	518	4/4	0.86	0.35	48,54,57,67	0
4	EDO	C	516	4/4	0.86	0.16	43,47,50,52	0
4	EDO	C	515	4/4	0.86	0.25	58,66,70,70	0
5	PEG	B	508	7/7	0.86	0.40	49,67,72,80	0
4	EDO	D	520	4/4	0.87	0.20	64,65,68,74	0
6	D62	A	520	37/37	0.87	0.18	32,40,96,104	0
4	EDO	C	510	4/4	0.87	0.23	59,67,72,72	0
4	EDO	C	518	4/4	0.88	0.18	64,64,67,77	0
4	EDO	B	513	4/4	0.88	0.55	47,55,62,63	0
4	EDO	B	511	4/4	0.88	0.27	52,58,58,62	0
4	EDO	D	521	4/4	0.89	0.24	34,42,48,51	0
4	EDO	A	503	4/4	0.89	0.23	51,53,54,56	0
6	D62	C	520	37/37	0.90	0.15	33,39,100,107	0
5	PEG	A	516	7/7	0.90	0.20	39,59,73,75	0
4	EDO	A	521	4/4	0.90	0.14	54,65,68,78	0
4	EDO	C	508	4/4	0.90	0.16	57,58,63,66	0
4	EDO	A	522	4/4	0.90	0.47	49,56,64,69	0
4	EDO	B	515	4/4	0.90	0.20	50,54,61,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	A	523	4/4	0.90	0.23	51,56,56,58	0
4	EDO	B	512	4/4	0.90	0.16	60,62,67,80	0
4	EDO	A	514	4/4	0.91	0.13	49,50,55,57	0
5	PEG	C	513	7/7	0.91	0.12	53,58,64,68	0
4	EDO	B	520	4/4	0.91	0.19	50,52,59,65	0
4	EDO	C	511	4/4	0.91	0.14	52,56,60,61	0
4	EDO	B	507	4/4	0.91	0.22	52,55,61,62	0
5	PEG	D	510	7/7	0.91	0.21	56,69,80,92	0
4	EDO	B	519	4/4	0.91	0.28	63,63,68,70	0
4	EDO	A	504	4/4	0.91	0.27	53,65,67,78	0
4	EDO	D	501	4/4	0.91	0.13	51,53,53,54	0
4	EDO	C	517	4/4	0.91	0.11	66,67,71,76	0
4	EDO	C	509	4/4	0.92	0.25	54,55,59,59	0
4	EDO	C	504	4/4	0.92	0.17	51,56,56,60	0
4	EDO	A	515	4/4	0.92	0.28	36,48,53,53	0
7	EPE	B	521	15/15	0.93	0.23	52,77,92,93	0
4	EDO	C	507	4/4	0.93	0.19	52,52,63,63	0
6	D62	D	517	37/37	0.93	0.12	26,32,74,89	0
4	EDO	D	504	4/4	0.93	0.13	31,32,32,33	0
4	EDO	A	505	4/4	0.93	0.18	42,49,54,65	0
5	PEG	A	517	7/7	0.93	0.17	31,43,48,53	0
4	EDO	B	503	4/4	0.93	0.14	37,41,41,43	0
4	EDO	A	506	4/4	0.93	0.11	39,43,46,50	0
4	EDO	D	514	4/4	0.93	0.13	30,41,43,47	0
4	EDO	C	522	4/4	0.94	0.21	49,49,58,68	0
4	EDO	B	506	4/4	0.94	0.12	54,57,60,62	0
5	PEG	D	519	7/7	0.94	0.22	37,42,49,51	0
4	EDO	D	511	4/4	0.94	0.35	42,43,43,61	0
4	EDO	A	512	4/4	0.94	0.26	44,47,48,49	0
6	D62	B	516	37/37	0.94	0.12	27,33,74,78	0
4	EDO	D	505	4/4	0.95	0.09	41,43,43,48	0
4	EDO	A	513	4/4	0.95	0.21	45,51,53,64	0
4	EDO	A	507	4/4	0.95	0.15	50,61,65,67	0
4	EDO	D	507	4/4	0.95	0.16	38,50,52,55	0
4	EDO	D	516	4/4	0.95	0.14	37,39,45,47	0
7	EPE	B	509	15/15	0.96	0.14	53,62,70,73	0
7	EPE	A	524	15/15	0.96	0.23	44,77,92,96	0
2	ZN	A	501	1/1	0.97	0.07	33,33,33,33	0
4	EDO	D	512	4/4	0.97	0.07	38,41,43,46	0
7	EPE	D	523	15/15	0.97	0.14	36,72,91,103	0
7	EPE	C	514	15/15	0.98	0.15	40,46,80,101	0
3	MG	B	502	1/1	0.98	0.17	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	B	501	1/1	0.99	0.08	33,33,33,33	0
3	MG	A	502	1/1	0.99	0.15	19,19,19,19	0
3	MG	D	503	1/1	0.99	0.15	18,18,18,18	0
2	ZN	C	505	1/1	1.00	0.10	33,33,33,33	0
3	MG	C	506	1/1	1.00	0.17	21,21,21,21	0
2	ZN	D	502	1/1	1.00	0.11	30,30,30,30	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.