



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:21 PM GMT

PDB ID : 4OGB
Title : Crystal structure of the catalytic domain of PDE4D2 with compound 2
Authors : Feil, S.C.; Parker, M.W.
Deposited on : 2014-01-15
Resolution : 2.03 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

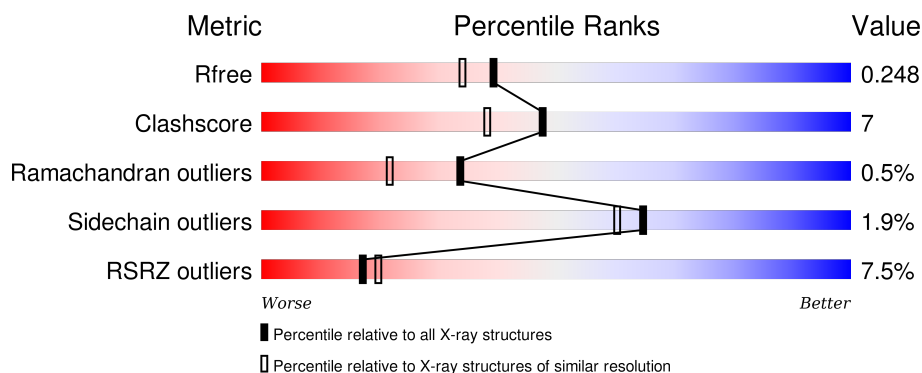
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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}	91344	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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 ≥ 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	361	<div> <div>7%</div> <div>77%</div> <div>12%</div> <div>•</div> <div>9%</div> </div>
1	B	361	<div> <div>9%</div> <div>77%</div> <div>11%</div> <div>•</div> <div>11%</div> </div>
1	C	361	<div> <div>7%</div> <div>74%</div> <div>15%</div> <div>•</div> <div>10%</div> </div>
1	D	361	<div> <div>3%</div> <div>80%</div> <div>10%</div> <div>10%</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
2	2SR	A	501	-	-	-	X
2	2SR	B	501	-	-	-	X
2	2SR	C	502	-	-	-	X
2	2SR	D	502	-	-	-	X
3	EDO	A	503	-	-	-	X
3	EDO	A	507	-	-	-	X
3	EDO	A	508	-	-	-	X
3	EDO	A	514	-	-	-	X
3	EDO	B	507	-	-	-	X
3	EDO	B	509	-	-	-	X
3	EDO	C	503	-	-	-	X
3	EDO	C	504	-	-	-	X
3	EDO	C	507	-	-	-	X
3	EDO	C	509	-	-	-	X
3	EDO	C	512	-	-	X	-
3	EDO	D	503	-	-	-	X
3	EDO	D	510	-	-	-	X
4	PEG	A	504	-	-	-	X
4	PEG	D	515	-	-	-	X
4	PEG	D	516	-	-	X	X
6	DMS	A	513	-	-	X	X
6	DMS	B	510	-	-	-	X
6	DMS	B	512	-	-	-	X
6	DMS	D	508	-	-	-	X
7	EPE	C	506	-	-	-	X

2 Entry composition [i](#)

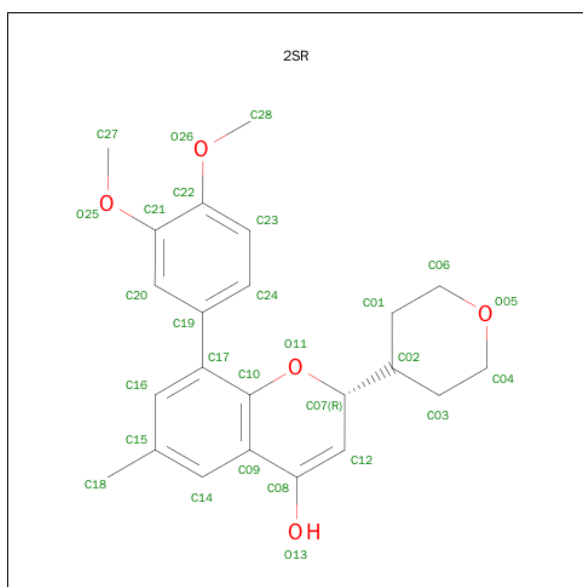
There are 8 unique types of molecules in this entry. The entry contains 11286 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	328	Total	C	N	O	S	0	0	0
			2651	1676	453	508	14			
1	B	321	Total	C	N	O	S	0	1	0
			2606	1649	447	496	14			
1	C	325	Total	C	N	O	S	0	1	0
			2642	1669	453	506	14			
1	D	324	Total	C	N	O	S	0	2	0
			2640	1669	452	505	14			

- Molecule 2 is (2R)-8-(3,4-DIMETHOXYPHENYL)-6-METHYL-2-(TETRAHYDRO-2H-PYRAN-4-YL)-2H-CHROMEN-4-OL (three-letter code: 2SR) (formula: C₂₃H₂₆O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			28	23	5		
2	B	1	Total	C	O	0	0
			28	23	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			28	23	5		
2	D	1	Total	C	O	0	0
			28	23	5		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

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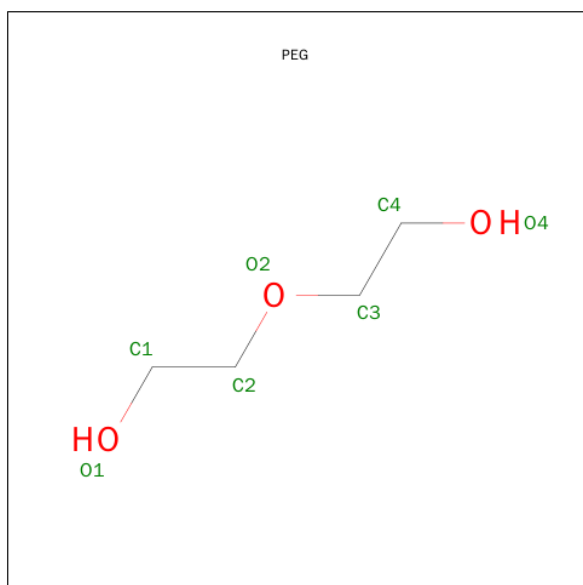
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0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

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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



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

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

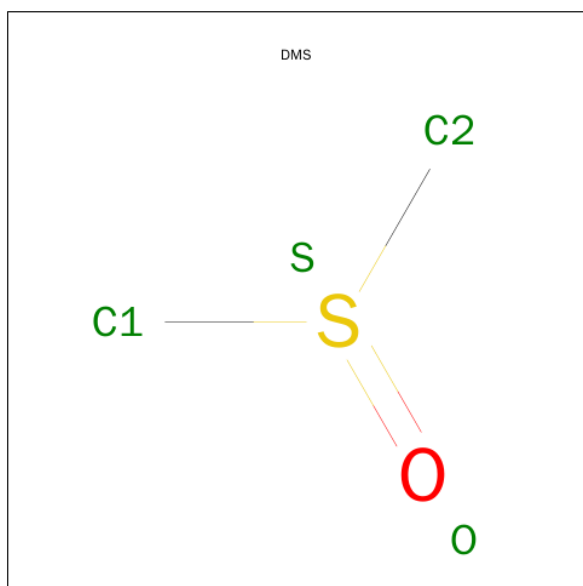
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Zn	0	0
			2	2		
5	A	2	Total	Zn	0	0
			2	2		
5	D	2	Total	Zn	0	0
			2	2		

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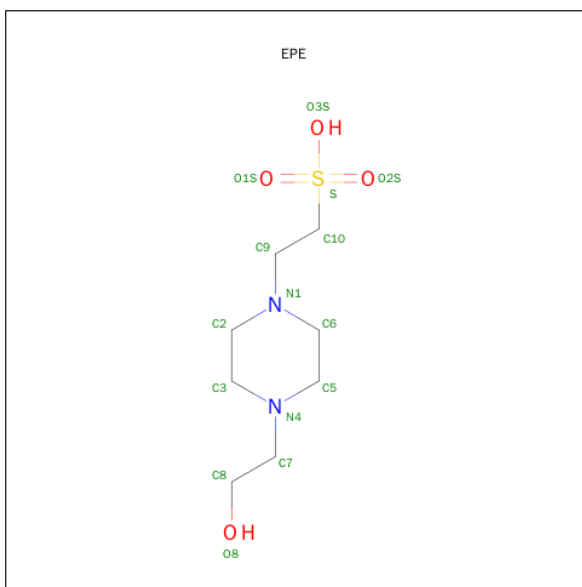
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	2	Total	Zn	0	0
			2	2		

- Molecule 6 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



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

- Molecule 7 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



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

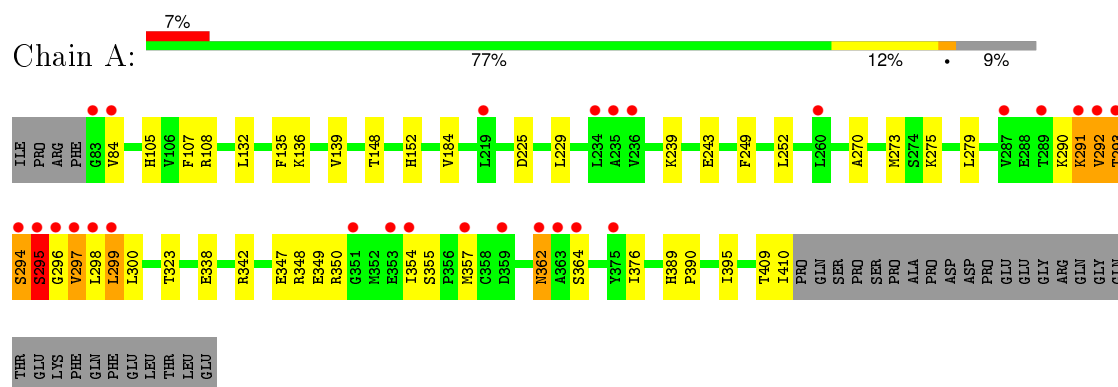
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	120	Total	O	0	0
			120	120		
8	B	104	Total	O	0	0
			104	104		
8	C	77	Total	O	0	0
			77	77		
8	D	131	Total	O	0	0
			131	131		

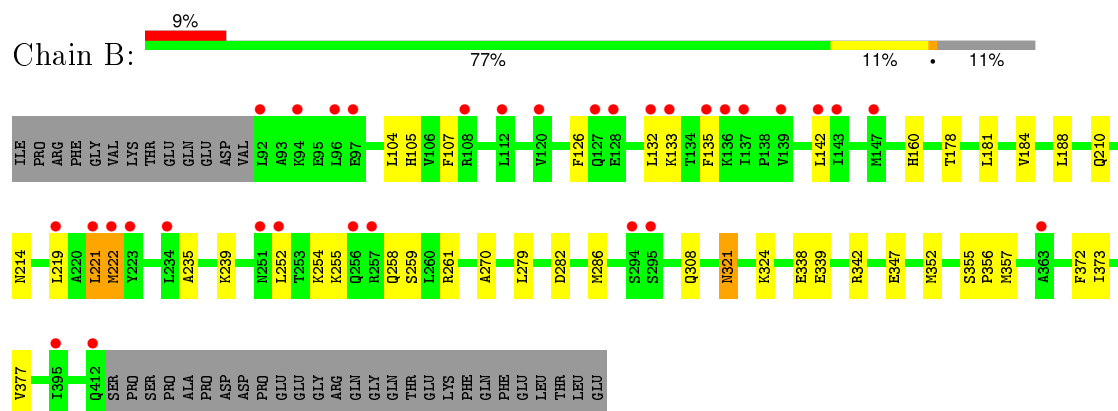
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

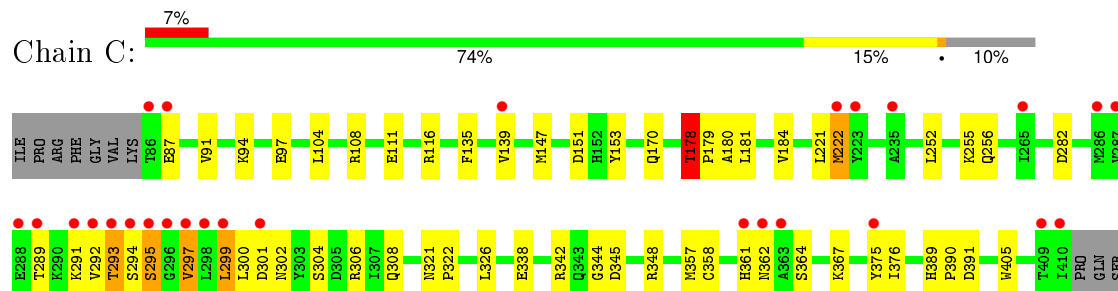
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



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

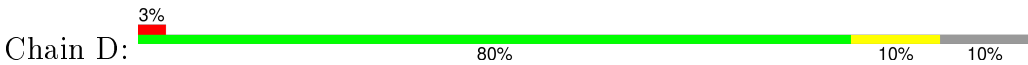


- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



PRO	SER	PRO	ALA	PRO	ASP	ASP	PRO	GLU	GLY	GLY	ARG	GLN	GLY	GLN	THR	GLU	LYS	PHE	GLN	PHE	GLU	LEU	THR	LEU	GLU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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



ILE	PRO	ARG	PHE	GLY	VAL	LYS	THR	GLU	Q88	E89	D90	W102	G103	L104	H105	V106	F107	V120	H123	D140	Q170	V202	L212	L219	A220	L221	M222	V228	L229	K262	A270	M273	L279	M286	V287	E288	N302	R306	I307	Q308	N321	P322		
F340	F341	F342	R348	E349	R350	I354	D359	K360	H361	N362	A363	K367	V375	I376	I410	P411	GLN	SER	PRO	SER	PRO	ALA	PRO	ASP	ASP	PRO	GLU	GLU	GLY	GLY	ARG	GLN	GLY	THR	GLU	LYS	PHE	GLN	PHE	GLU	LEU	THR	LEU	GLU

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	98.84Å 111.55Å 160.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.22 – 2.03 48.13 – 2.03	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.22-2.03) 99.9 (48.13-2.03)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.03Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.202 , 0.243 0.210 , 0.248	Depositor DCC
R_{free} test set	5713 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	31.6	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 114169 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11286	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, EPE, EDO, DMS, PEG, 2SR

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	0.51	0/2704	0.55	0/3672
1	B	0.47	0/2660	0.57	1/3615 (0.0%)
1	C	0.57	0/2695	0.57	1/3660 (0.0%)
1	D	0.54	0/2695	0.59	2/3662 (0.1%)
All	All	0.52	0/10754	0.57	4/14609 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	410	ILE	C-N-CD	5.92	140.84	128.40
1	C	178	THR	C-N-CD	5.55	140.06	128.40
1	B	355	SER	C-N-CD	5.36	139.66	128.40
1	D	367	LYS	CB-CA-C	-5.17	100.05	110.40

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	2651	0	2609	47	0
1	B	2606	0	2565	34	0
1	C	2642	0	2596	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2640	0	2587	34	0
2	A	28	0	26	4	0
2	B	28	0	26	2	0
2	C	28	0	26	1	0
2	D	28	0	26	3	0
3	A	32	0	48	6	0
3	B	28	0	42	5	0
3	C	36	0	54	9	0
3	D	32	0	48	2	0
4	A	7	0	10	0	0
4	D	21	0	30	7	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
6	A	8	0	12	5	0
6	B	8	0	12	3	0
6	D	8	0	12	0	0
7	C	15	0	17	0	0
8	A	120	0	0	2	0
8	B	104	0	0	5	0
8	C	77	0	0	1	0
8	D	131	0	0	2	0
All	All	11286	0	10746	159	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 159 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:222:MET:CE	1:D:222:MET:SD	2.25	1.25
1:C:222:MET:HE1	1:D:222:MET:SD	1.80	1.22
1:C:222:MET:HG3	3:C:512:EDO:H21	1.18	1.17
1:C:222:MET:HG3	3:C:512:EDO:C2	1.85	1.05
1:C:222:MET:HE2	1:D:222:MET:SD	2.04	0.98

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	326/361 (90%)	312 (96%)	10 (3%)	4 (1%)	16	6
1	B	320/361 (89%)	310 (97%)	10 (3%)	0	100	100
1	C	324/361 (90%)	313 (97%)	9 (3%)	2 (1%)	30	18
1	D	324/361 (90%)	318 (98%)	6 (2%)	0	100	100
All	All	1294/1444 (90%)	1253 (97%)	35 (3%)	6 (0%)	34	22

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	297	VAL
1	C	294	SER
1	A	295	SER
1	A	292	VAL
1	A	294	SER

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	299/329 (91%)	291 (97%)	8 (3%)	52	45
1	B	294/329 (89%)	287 (98%)	7 (2%)	57	50
1	C	298/329 (91%)	290 (97%)	8 (3%)	52	45
1	D	298/329 (91%)	297 (100%)	1 (0%)	94	95
All	All	1189/1316 (90%)	1165 (98%)	24 (2%)	65	58

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	222	MET
1	B	321[A]	ASN
1	C	301	ASP
1	B	259	SER
1	B	286	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	210	GLN
1	C	308	GLN
1	C	362	ASN
1	C	389	HIS
1	D	308	GLN

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 55 ligands modelled in this entry, 8 are monoatomic - leaving 47 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
2	2SR	A	501	-	29,31,31	3.04	10 (34%)	38,44,44	1.65	6 (15%)
3	EDO	A	502	-	3,3,3	0.49	0	2,2,2	0.63	0
3	EDO	A	503	-	3,3,3	0.55	0	2,2,2	0.45	0
4	PEG	A	504	-	6,6,6	0.26	0	5,5,5	0.50	0
3	EDO	A	505	-	3,3,3	0.44	0	2,2,2	0.59	0
3	EDO	A	506	-	3,3,3	0.38	0	2,2,2	0.72	0
3	EDO	A	507	-	3,3,3	0.54	0	2,2,2	0.32	0
3	EDO	A	508	-	3,3,3	0.48	0	2,2,2	0.36	0
6	DMS	A	511	-	3,3,3	0.65	0	3,3,3	0.67	0
3	EDO	A	512	-	3,3,3	0.49	0	2,2,2	0.48	0
6	DMS	A	513	-	3,3,3	0.51	0	3,3,3	0.52	0
3	EDO	A	514	-	3,3,3	0.64	0	2,2,2	0.42	0
2	2SR	B	501	-	29,31,31	3.18	12 (41%)	38,44,44	1.65	5 (13%)
3	EDO	B	504	-	3,3,3	0.50	0	2,2,2	0.60	0
3	EDO	B	505	-	3,3,3	0.51	0	2,2,2	0.41	0
3	EDO	B	506	-	3,3,3	0.51	0	2,2,2	0.17	0
3	EDO	B	507	-	3,3,3	0.53	0	2,2,2	0.07	0
3	EDO	B	508	-	3,3,3	0.47	0	2,2,2	0.41	0
3	EDO	B	509	-	3,3,3	0.50	0	2,2,2	0.31	0
6	DMS	B	510	-	3,3,3	0.64	0	3,3,3	0.56	0
3	EDO	B	511	-	3,3,3	0.47	0	2,2,2	0.49	0
6	DMS	B	512	-	3,3,3	0.61	0	3,3,3	0.45	0
3	EDO	C	501	-	3,3,3	0.69	0	2,2,2	0.03	0
2	2SR	C	502	-	29,31,31	3.10	12 (41%)	38,44,44	1.91	8 (21%)
3	EDO	C	503	-	3,3,3	0.42	0	2,2,2	0.59	0
3	EDO	C	504	-	3,3,3	0.47	0	2,2,2	0.67	0
3	EDO	C	505	-	3,3,3	0.50	0	2,2,2	0.54	0
7	EPE	C	506	-	14,15,15	0.42	0	18,20,20	2.27	5 (27%)
3	EDO	C	507	-	3,3,3	0.55	0	2,2,2	0.34	0
3	EDO	C	508	-	3,3,3	0.46	0	2,2,2	0.49	0
3	EDO	C	509	-	3,3,3	0.50	0	2,2,2	0.49	0
3	EDO	C	512	-	3,3,3	0.54	0	2,2,2	0.34	0
3	EDO	C	513	-	3,3,3	0.49	0	2,2,2	0.30	0
3	EDO	D	501	-	3,3,3	0.49	0	2,2,2	0.72	0
2	2SR	D	502	-	29,31,31	3.06	12 (41%)	38,44,44	1.81	8 (21%)
3	EDO	D	503	-	3,3,3	0.37	0	2,2,2	0.50	0
6	DMS	D	504	-	3,3,3	0.68	0	3,3,3	0.57	0
3	EDO	D	505	-	3,3,3	0.54	0	2,2,2	0.33	0
3	EDO	D	506	-	3,3,3	0.57	0	2,2,2	0.21	0
4	PEG	D	507	-	6,6,6	0.40	0	5,5,5	0.35	0
6	DMS	D	508	-	3,3,3	0.64	0	3,3,3	0.65	0
3	EDO	D	509	-	3,3,3	0.50	0	2,2,2	0.33	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	D	510	-	3,3,3	0.50	0	2,2,2	0.53	0
3	EDO	D	511	-	3,3,3	0.53	0	2,2,2	0.34	0
3	EDO	D	514	-	3,3,3	0.58	0	2,2,2	0.20	0
4	PEG	D	515	-	6,6,6	0.31	0	5,5,5	0.33	0
4	PEG	D	516	-	6,6,6	0.33	0	5,5,5	0.57	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	2SR	A	501	-	-	0/12/32/32	0/4/4/4
3	EDO	A	502	-	-	0/1/1/1	0/0/0/0
3	EDO	A	503	-	-	0/1/1/1	0/0/0/0
4	PEG	A	504	-	-	0/4/4/4	0/0/0/0
3	EDO	A	505	-	-	0/1/1/1	0/0/0/0
3	EDO	A	506	-	-	0/1/1/1	0/0/0/0
3	EDO	A	507	-	-	0/1/1/1	0/0/0/0
3	EDO	A	508	-	-	0/1/1/1	0/0/0/0
6	DMS	A	511	-	-	0/0/0/0	0/0/0/0
3	EDO	A	512	-	-	0/1/1/1	0/0/0/0
6	DMS	A	513	-	-	0/0/0/0	0/0/0/0
3	EDO	A	514	-	-	0/1/1/1	0/0/0/0
2	2SR	B	501	-	-	0/12/32/32	0/4/4/4
3	EDO	B	504	-	-	0/1/1/1	0/0/0/0
3	EDO	B	505	-	-	0/1/1/1	0/0/0/0
3	EDO	B	506	-	-	0/1/1/1	0/0/0/0
3	EDO	B	507	-	-	0/1/1/1	0/0/0/0
3	EDO	B	508	-	-	0/1/1/1	0/0/0/0
3	EDO	B	509	-	-	0/1/1/1	0/0/0/0
6	DMS	B	510	-	-	0/0/0/0	0/0/0/0
3	EDO	B	511	-	-	0/1/1/1	0/0/0/0
6	DMS	B	512	-	-	0/0/0/0	0/0/0/0
3	EDO	C	501	-	-	0/1/1/1	0/0/0/0
2	2SR	C	502	-	-	0/12/32/32	0/4/4/4
3	EDO	C	503	-	-	0/1/1/1	0/0/0/0
3	EDO	C	504	-	-	0/1/1/1	0/0/0/0
3	EDO	C	505	-	-	0/1/1/1	0/0/0/0
7	EPE	C	506	-	-	0/9/19/19	0/1/1/1
3	EDO	C	507	-	-	0/1/1/1	0/0/0/0
3	EDO	C	508	-	-	0/1/1/1	0/0/0/0
3	EDO	C	509	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	C	512	-	-	0/1/1/1	0/0/0/0
3	EDO	C	513	-	-	0/1/1/1	0/0/0/0
3	EDO	D	501	-	-	0/1/1/1	0/0/0/0
2	2SR	D	502	-	-	0/12/32/32	0/4/4/4
3	EDO	D	503	-	-	0/1/1/1	0/0/0/0
6	DMS	D	504	-	-	0/0/0/0	0/0/0/0
3	EDO	D	505	-	-	0/1/1/1	0/0/0/0
3	EDO	D	506	-	-	0/1/1/1	0/0/0/0
4	PEG	D	507	-	-	0/4/4/4	0/0/0/0
6	DMS	D	508	-	-	0/0/0/0	0/0/0/0
3	EDO	D	509	-	-	0/1/1/1	0/0/0/0
3	EDO	D	510	-	-	0/1/1/1	0/0/0/0
3	EDO	D	511	-	-	0/1/1/1	0/0/0/0
3	EDO	D	514	-	-	0/1/1/1	0/0/0/0
4	PEG	D	515	-	-	0/4/4/4	0/0/0/0
4	PEG	D	516	-	-	0/4/4/4	0/0/0/0

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	502	2SR	C09-C10	-2.55	1.35	1.40
2	D	502	2SR	C03-C02	-2.47	1.47	1.53
2	B	501	2SR	C09-C10	-2.41	1.35	1.40
2	A	501	2SR	C09-C10	-2.32	1.35	1.40
2	D	502	2SR	C01-C02	-2.29	1.47	1.53

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	502	2SR	C06-C01-C02	-3.55	105.07	110.46
2	B	501	2SR	O26-C22-C23	-3.40	118.63	124.35
2	A	501	2SR	O26-C22-C23	-3.30	118.79	124.35
2	D	502	2SR	C04-C03-C02	-3.23	105.56	110.46
2	B	501	2SR	O25-C21-C20	-3.11	118.91	124.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

20 monomers are involved in 47 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	2SR	4	0
3	A	503	EDO	1	0
3	A	506	EDO	1	0
3	A	507	EDO	1	0
3	A	508	EDO	3	0
6	A	513	DMS	5	0
2	B	501	2SR	2	0
3	B	507	EDO	3	0
3	B	509	EDO	2	0
6	B	510	DMS	2	0
6	B	512	DMS	1	0
2	C	502	2SR	1	0
3	C	504	EDO	1	0
3	C	505	EDO	1	0
3	C	509	EDO	2	0
3	C	512	EDO	5	0
2	D	502	2SR	3	0
3	D	505	EDO	2	0
4	D	507	PEG	3	0
4	D	516	PEG	4	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	A	328/361 (90%)	0.57	27 (8%) 14 16	17, 32, 59, 115	0
1	B	321/361 (88%)	0.66	32 (9%) 9 10	21, 43, 61, 77	0
1	C	325/361 (90%)	0.55	27 (8%) 14 16	22, 39, 66, 106	0
1	D	324/361 (89%)	0.25	11 (3%) 49 55	16, 29, 56, 75	0
All	All	1298/1444 (89%)	0.50	97 (7%) 17 20	16, 36, 61, 115	0

The worst 5 of 97 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	295	SER	6.9
1	C	294	SER	6.5
1	A	293	THR	6.2
1	C	292	VAL	6.0
1	A	296	GLY	5.9

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. 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, 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	LLDF	B-factors(Å ²)	Q<0.9
4	PEG	D	515	7/7	0.65	0.47	16.03	53,67,90,105	0
3	EDO	A	503	4/4	0.61	0.33	10.24	40,40,48,51	0
6	DMS	B	510	4/4	0.95	0.37	10.22	59,64,73,74	0
3	EDO	C	503	4/4	0.89	0.24	9.25	39,41,44,55	0
2	2SR	B	501	28/28	0.70	0.27	8.45	45,56,68,76	0
6	DMS	B	512	4/4	0.92	0.29	8.18	33,45,52,66	0
4	PEG	D	516	7/7	0.86	0.27	7.65	36,44,59,69	0
3	EDO	B	509	4/4	0.83	0.40	7.37	40,46,48,54	0
3	EDO	B	507	4/4	0.90	0.31	6.58	30,30,38,41	0
2	2SR	A	501	28/28	0.77	0.35	5.75	51,62,70,72	0
3	EDO	D	510	4/4	0.92	0.25	5.53	38,40,45,52	0
7	EPE	C	506	15/15	0.96	0.24	4.51	41,52,71,74	0
3	EDO	C	504	4/4	0.91	0.29	4.45	45,45,50,53	0
2	2SR	D	502	28/28	0.81	0.23	4.38	47,54,58,59	0
3	EDO	A	514	4/4	0.86	0.23	4.25	27,38,38,45	0
3	EDO	A	507	4/4	0.76	0.21	4.12	46,49,53,54	0
3	EDO	C	509	4/4	0.84	0.18	3.52	34,41,43,47	0
4	PEG	A	504	7/7	0.89	0.20	3.43	33,36,46,51	0
2	2SR	C	502	28/28	0.78	0.26	3.30	46,58,63,67	0
3	EDO	D	503	4/4	0.94	0.16	2.94	34,35,36,43	0
3	EDO	C	507	4/4	0.84	0.29	2.75	45,46,47,48	0
6	DMS	D	508	4/4	0.89	0.19	2.21	38,42,53,61	0
6	DMS	A	513	4/4	0.89	0.18	2.11	29,46,51,55	0
3	EDO	A	508	4/4	0.91	0.21	2.06	30,31,36,51	0
3	EDO	C	508	4/4	0.76	0.22	1.93	57,57,60,60	0
3	EDO	D	509	4/4	0.86	0.17	1.64	38,47,49,52	0
3	EDO	A	512	4/4	0.92	0.20	0.90	28,30,30,31	0
4	PEG	D	507	7/7	0.87	0.18	0.88	29,33,37,42	0
3	EDO	B	504	4/4	0.92	0.13	0.72	35,40,40,50	0
3	EDO	C	501	4/4	0.89	0.16	0.59	35,38,41,43	0
5	ZN	C	510	1/1	0.99	0.12	0.34	33,33,33,33	0
5	ZN	A	509	1/1	0.99	0.14	0.09	28,28,28,28	0
3	EDO	A	506	4/4	0.94	0.18	0.02	31,31,32,34	0
3	EDO	C	513	4/4	0.91	0.12	-0.11	41,53,55,58	0
3	EDO	B	511	4/4	0.74	0.17	-0.15	58,58,58,66	0
3	EDO	D	514	4/4	0.97	0.11	-0.54	25,28,29,30	0
5	ZN	D	512	1/1	1.00	0.12	-0.71	27,27,27,27	0
3	EDO	D	501	4/4	0.97	0.12	-0.79	30,31,33,37	0
5	ZN	C	511	1/1	0.99	0.11	-1.03	32,32,32,32	1
3	EDO	C	505	4/4	0.92	0.12	-1.11	44,44,52,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	ZN	D	513	1/1	0.99	0.10	-1.67	33,33,33,33	1
3	EDO	B	506	4/4	0.94	0.11	-2.29	40,41,42,43	0
5	ZN	A	510	1/1	0.99	0.10	-2.58	30,30,30,30	1
5	ZN	B	502	1/1	0.99	0.08	-2.90	34,34,34,34	0
5	ZN	B	503	1/1	0.98	0.08	-2.96	35,35,35,35	1
3	EDO	A	505	4/4	0.92	0.14	-	27,32,36,39	0
3	EDO	D	506	4/4	0.84	0.22	-	41,42,43,48	0
3	EDO	A	502	4/4	0.90	0.29	-	52,52,53,54	0
3	EDO	B	508	4/4	0.94	0.14	-	55,57,63,64	0
6	DMS	A	511	4/4	0.90	0.23	-	45,59,63,71	0
3	EDO	D	505	4/4	0.80	0.16	-	41,50,51,52	0
3	EDO	D	511	4/4	0.85	0.18	-	49,49,50,55	0
3	EDO	B	505	4/4	0.84	0.32	-	45,46,49,54	0
3	EDO	C	512	4/4	0.74	0.35	-	43,45,52,54	0
6	DMS	D	504	4/4	0.92	0.29	-	41,42,55,63	0

6.5 Other polymers

There are no such residues in this entry.