



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2018 – 07:49 pm GMT

PDB ID : 2PY5  
Title : Phi29 DNA polymerase complexed with single-stranded DNA  
Authors : Berman, A.J.; Kamtekar, S.; Goodman, J.L.; Lazaro, J.M.; de Vega, M.;  
Blanco, L.; Salas, M.; Steitz, T.A.  
Deposited on : 2007-05-15  
Resolution : 1.60 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](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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : (not set)  
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) : trunk30967

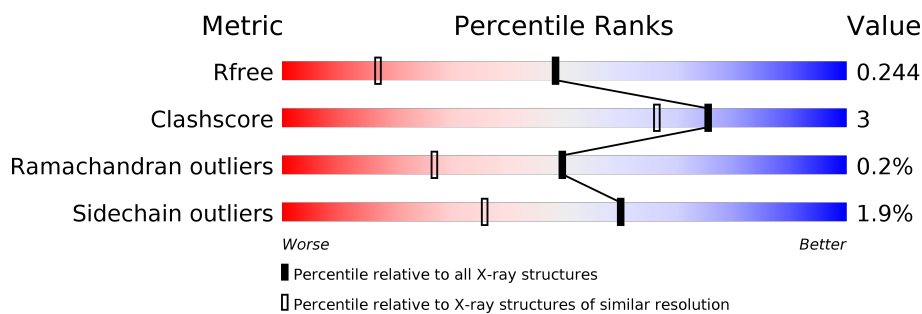
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	2957 (1.60-1.60)
Clashscore	122126	3202 (1.60-1.60)
Ramachandran outliers	120053	3117 (1.60-1.60)
Sidechain outliers	120020	3116 (1.60-1.60)

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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	D	7	29% 57% 14%
1	E	7	57% 29% 14%
1	J	7	71% 14% 14%
1	L	7	43% 14% 43%
1	Y	7	71% 14% 14%
2	A	575	91% 6% ..
2	B	575	89% 9% ..

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11400 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 DNA chain called 5'-d(GGACTTT)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	J	6	Total	C	N	O	P	0	0	0
			122	59	19	38	6			
1	Y	6	Total	C	N	O	P	0	0	0
			105	49	20	31	5			
1	D	6	Total	C	N	O	P	0	0	0
			121	59	22	35	5			
1	E	6	Total	C	N	O	P	0	0	0
			105	49	20	31	5			
1	L	4	Total	C	N	O	P	0	0	0
			79	39	9	27	4			

- Molecule 2 is a protein called DNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	564	Total	C	N	O	S	28	11	0
			4650	3037	741	850	22			
2	B	562	Total	C	N	O	S	11	7	0
			4617	3014	737	844	22			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	ALA	ASP	ENGINEERED	UNP P03680
A	66	ALA	ASP	ENGINEERED	UNP P03680
B	12	ALA	ASP	ENGINEERED	UNP P03680
B	66	ALA	ASP	ENGINEERED	UNP P03680

- Molecule 3 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
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	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		

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	J	31	Total O 31 31	0	0
4	Y	9	Total O 9 9	0	0
4	D	20	Total O 20 20	0	0
4	E	20	Total O 20 20	0	0
4	L	20	Total O 20 20	0	0
4	A	768	Total O 768 768	0	0

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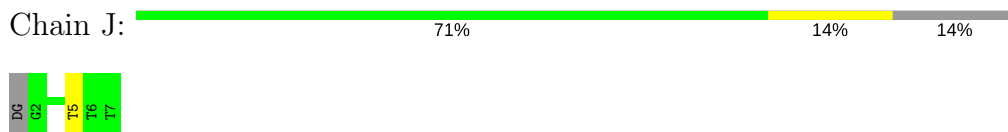
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	625	Total 625	O 625	0	0

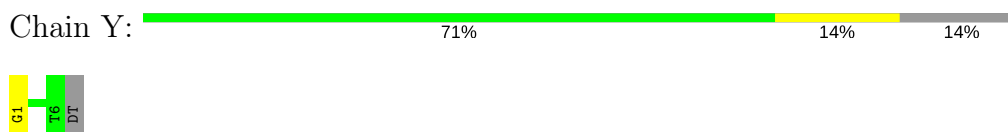
### 3 Residue-property plots [i](#)

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. 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. 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: 5'-d(GGACTTT)-3'



- Molecule 1: 5'-d(GGACTTT)-3'



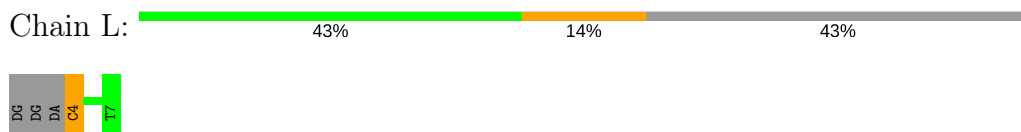
- Molecule 1: 5'-d(GGACTTT)-3'



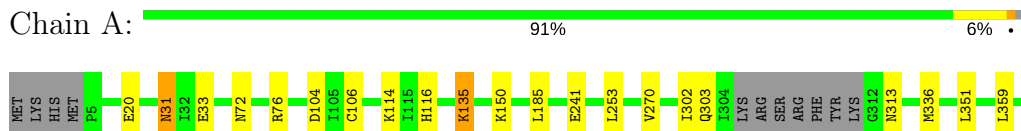
- Molecule 1: 5'-d(GGACTTT)-3'

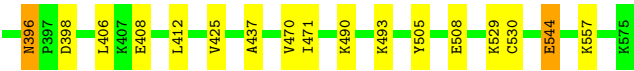


- Molecule 1: 5'-d(GGACTTT)-3'

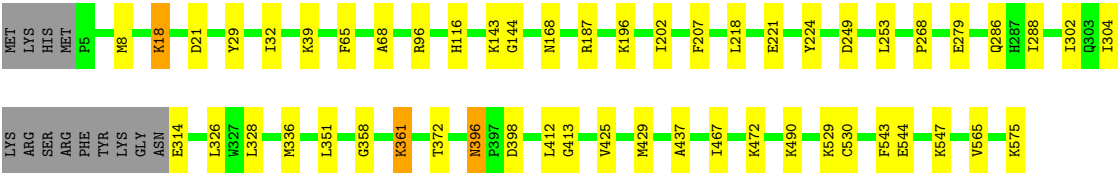
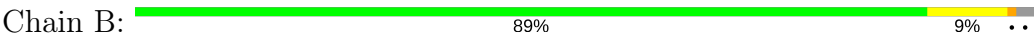


- Molecule 2: DNA polymerase





● Molecule 2: DNA polymerase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.20Å 200.18Å 66.99Å 90.00° 109.40° 90.00°	Depositor
Resolution (Å)	40.59 – 1.60 40.58 – 1.60	Depositor EDS
% Data completeness (in resolution range)	97.8 (40.59-1.60) 97.8 (40.58-1.60)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.23 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, $R_{free}$	0.164 , 0.194 0.224 , 0.244	Depositor DCC
$R_{free}$ test set	8614 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.8	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 53.3	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	11400	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO

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	D	0.85	0/135	1.54	2/207 (1.0%)
1	E	0.95	0/117	1.52	2/180 (1.1%)
1	J	0.85	0/135	1.30	1/206 (0.5%)
1	L	1.19	1/86 (1.2%)	1.68	0/130
1	Y	0.69	0/117	1.29	1/180 (0.6%)
2	A	0.66	7/4801 (0.1%)	0.67	4/6477 (0.1%)
2	B	0.45	1/4755 (0.0%)	0.57	0/6418
All	All	0.59	9/10146 (0.1%)	0.71	10/13798 (0.1%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	135	LYS	CB-CG	-19.61	0.99	1.52
2	A	544	GLU	CB-CG	-13.40	1.26	1.52
2	A	241	GLU	CB-CG	-9.14	1.34	1.52
2	B	314	GLU	CD-OE2	7.14	1.33	1.25
1	L	4	DC	C3'-O3'	-6.58	1.35	1.44
2	A	375	GLU	CG-CD	5.84	1.60	1.51
2	A	557	LYS	CB-CG	-5.70	1.37	1.52
2	A	408	GLU	CB-CG	-5.31	1.42	1.52
2	A	241	GLU	CG-CD	5.10	1.59	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	135	LYS	CA-CB-CG	15.16	146.76	113.40
1	D	3	DA	O4'-C1'-N9	-8.52	102.04	108.00
2	A	241	GLU	CA-CB-CG	8.12	131.25	113.40
2	A	544	GLU	CA-CB-CG	7.98	130.96	113.40
1	E	3	DA	O4'-C1'-N9	-7.82	102.53	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	2	DG	O4'-C1'-N9	-7.81	102.53	108.00
2	A	408	GLU	CA-CB-CG	6.55	127.81	113.40
1	Y	1	DG	P-O3'-C3'	6.17	127.11	119.70
1	E	5	DT	O4'-C4'-C3'	6.04	109.63	106.00
1	J	5	DT	O4'-C1'-N1	-5.02	104.49	108.00

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	D	121	0	70	1	0
1	E	105	0	57	0	0
1	J	122	0	70	0	0
1	L	79	0	48	1	0
1	Y	105	0	57	0	0
2	A	4650	0	4683	25	0
2	B	4617	0	4642	39	0
3	A	72	0	108	4	0
3	B	36	0	54	0	0
4	A	768	0	0	4	2
4	B	625	0	0	4	2
4	D	20	0	0	0	0
4	E	20	0	0	0	0
4	J	31	0	0	0	0
4	L	20	0	0	1	0
4	Y	9	0	0	0	0
All	All	11400	0	9789	66	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (66) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:328:LEU:CD1	2:B:336:MET:HE1	1.79	1.12
2:B:328:LEU:HD11	2:B:336:MET:HE1	1.06	1.06
2:B:302:ILE:CD1	2:B:336:MET:HE2	1.99	0.93
2:B:302:ILE:HD11	2:B:336:MET:CE	2.05	0.87
2:A:72:ASN:HD22	2:A:76:ARG:HH12	1.31	0.78
2:B:328:LEU:HD11	2:B:336:MET:CE	2.03	0.77
2:A:106:CYS:SG	2:A:114:LYS:NZ	2.59	0.76
2:B:328:LEU:CD1	2:B:336:MET:CE	2.63	0.75
2:B:302:ILE:HD11	2:B:336:MET:HE3	1.67	0.74
2:B:302:ILE:CD1	2:B:336:MET:CE	2.65	0.72
2:A:529:LYS:O	2:A:530[B]:CYS:SG	2.48	0.70
2:B:372:THR:HG22	4:B:9498:HOH:O	1.91	0.70
2:B:396:ASN:HD22	2:B:398:ASP:H	1.39	0.69
2:B:302:ILE:HD12	2:B:336:MET:HE2	1.74	0.69
2:B:18:LYS:HG3	2:B:21:ASP:HB3	1.75	0.68
2:B:304:ILE:CD1	2:B:326:LEU:HD21	2.25	0.67
2:A:383:LYS:HG2	3:A:8001:EDO:H22	1.80	0.61
2:A:396:ASN:HD22	2:A:398:ASP:H	1.47	0.61
2:A:470[B]:VAL:HG13	4:A:9252:HOH:O	2.03	0.59
2:A:470[B]:VAL:HG23	2:A:471:ILE:HG23	1.85	0.58
2:B:218[B]:LEU:HD11	2:B:351:LEU:CD2	2.34	0.57
2:A:104:ASP:OD2	2:A:116:HIS:HD2	1.88	0.56
2:B:304:ILE:HD11	2:B:326:LEU:HD21	1.88	0.56
2:A:72:ASN:HD22	2:A:76:ARG:NH1	2.03	0.56
2:B:286:GLN:HG3	2:B:288:ILE:HG23	1.88	0.56
2:A:270:VAL:HG22	2:A:351[B]:LEU:CD2	2.36	0.55
2:A:359:LEU:HD23	3:A:9006:EDO:H12	1.87	0.55
2:A:529:LYS:C	2:A:530[B]:CYS:SG	2.84	0.55
2:B:187:ARG:HD2	2:B:196:LYS:HD2	1.89	0.54
2:B:218[B]:LEU:HD21	2:B:268:PRO:HG2	1.90	0.53
2:A:470[A]:VAL:HG23	4:A:9252:HOH:O	2.08	0.52
2:B:467:ILE:O	2:B:472:LYS:NZ	2.44	0.50
2:A:31:ASN:C	2:A:31:ASN:HD22	2.15	0.50
2:B:490:LYS:NZ	4:B:9424:HOH:O	2.46	0.48
2:B:8:MET:HB3	2:B:32:ILE:HD12	1.94	0.48
2:B:143:LYS:HG2	2:B:144:GLY:CA	2.44	0.48
2:B:253:LEU:HD21	2:B:437:ALA:HB1	1.96	0.47
2:A:406:LEU:HD23	2:A:412:LEU:HD23	1.97	0.47
2:B:218[B]:LEU:HD11	2:B:351:LEU:HD22	1.97	0.47
2:A:396:ASN:ND2	2:A:398:ASP:H	2.13	0.46
2:A:302:ILE:HD11	2:A:336:MET:HG3	1.98	0.46
2:B:65:PHE:CE1	2:B:565[B]:VAL:HG23	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:372:THR:CG2	4:B:9498:HOH:O	2.59	0.46
2:A:303:GLN:NE2	2:A:313:ASN:O	2.47	0.45
2:B:202:ILE:HD11	2:B:207:PHE:HD1	1.82	0.45
2:B:328:LEU:HD13	2:B:336:MET:CE	2.43	0.45
2:A:253:LEU:HD21	2:A:437:ALA:HB1	1.99	0.44
2:B:29:TYR:CZ	2:B:39:LYS:HB3	2.52	0.44
2:B:221:GLU:HA	2:B:224:TYR:CD1	2.53	0.44
2:B:187:ARG:HD2	2:B:196:LYS:CD	2.47	0.44
2:A:150[A]:LYS:NZ	4:A:9585:HOH:O	2.51	0.43
2:A:364:ILE:HG22	3:A:8012:EDO:H11	2.01	0.43
2:A:31:ASN:HD22	2:A:33:GLU:H	1.67	0.43
2:A:359:LEU:CD2	3:A:9006:EDO:H12	2.49	0.43
1:D:4:DC:H3'	1:D:5:DT:H71	1.99	0.43
2:B:529:LYS:O	2:B:530[B]:CYS:SG	2.74	0.43
2:B:168[A]:ASN:ND2	4:B:9316:HOH:O	2.52	0.43
2:B:304:ILE:HD13	2:B:326:LEU:HD21	2.00	0.43
2:A:493:LYS:HD2	4:A:9272:HOH:O	2.18	0.42
1:L:4:DC:OP1	4:L:999:HOH:O	2.22	0.42
2:B:412[B]:LEU:HD13	2:B:413:GLY:O	2.20	0.41
2:B:218[B]:LEU:HD11	2:B:351:LEU:HD21	2.02	0.41
2:A:490:LYS:HD3	2:A:505:TYR:OH	2.22	0.40
2:B:68:ALA:CB	2:B:565[A]:VAL:HG23	2.52	0.40
2:B:218[B]:LEU:HD21	2:B:268:PRO:CG	2.50	0.40
2:B:358:GLY:HA2	2:B:361:LYS:HD3	2.04	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:9650:HOH:O	4:B:9051:HOH:O[2_646]	1.61	0.59
4:A:9184:HOH:O	4:B:9568:HOH:O[2_646]	1.99	0.21

## 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	
2	A	571/575 (99%)	560 (98%)	10 (2%)	1 (0%)	49	27
2	B	565/575 (98%)	553 (98%)	11 (2%)	1 (0%)	49	27
All	All	1136/1150 (99%)	1113 (98%)	21 (2%)	2 (0%)	49	27

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	425	VAL
2	A	425	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	
2	A	506/506 (100%)	499 (99%)	7 (1%)	69	50
2	B	501/506 (99%)	488 (97%)	13 (3%)	49	22
All	All	1007/1012 (100%)	987 (98%)	20 (2%)	60	33

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	20	GLU
2	A	31	ASN
2	A	135	LYS
2	A	185	LEU
2	A	396	ASN
2	A	508	GLU
2	A	544	GLU
2	B	18	LYS
2	B	96	ARG
2	B	116	HIS
2	B	249[A]	ASP

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Mol	Chain	Res	Type
2	B	249[B]	ASP
2	B	279	GLU
2	B	361	LYS
2	B	396	ASN
2	B	429	MET
2	B	543	PHE
2	B	544	GLU
2	B	547	LYS
2	B	575	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	31	ASN
2	A	72	ASN
2	A	116	HIS
2	A	171	GLN
2	A	396	ASN
2	A	497	GLN
2	A	560	GLN
2	B	303	GLN
2	B	387	ASN
2	B	396	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

27 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
3	EDO	A	8001	-	3,3,3	0.59	0	2,2,2	0.45	0
3	EDO	A	8004	-	3,3,3	0.51	0	2,2,2	0.23	0
3	EDO	A	8008	-	3,3,3	0.51	0	2,2,2	0.18	0
3	EDO	A	8009	-	3,3,3	0.50	0	2,2,2	0.08	0
3	EDO	A	8010	-	3,3,3	0.45	0	2,2,2	0.41	0
3	EDO	A	8011	-	3,3,3	0.50	0	2,2,2	0.16	0
3	EDO	A	8012	-	3,3,3	0.39	0	2,2,2	0.35	0
3	EDO	A	8013	-	3,3,3	0.55	0	2,2,2	0.16	0
3	EDO	A	9001	-	3,3,3	0.50	0	2,2,2	0.18	0
3	EDO	A	9005	-	3,3,3	0.46	0	2,2,2	0.27	0
3	EDO	A	9006	-	3,3,3	0.47	0	2,2,2	0.25	0
3	EDO	A	9007	-	3,3,3	0.46	0	2,2,2	0.36	0
3	EDO	A	9008	-	3,3,3	0.50	0	2,2,2	0.17	0
3	EDO	A	9010	-	3,3,3	0.54	0	2,2,2	0.10	0
3	EDO	A	9011	-	3,3,3	0.46	0	2,2,2	0.20	0
3	EDO	A	9012	-	3,3,3	0.50	0	2,2,2	0.25	0
3	EDO	A	9013	-	3,3,3	0.54	0	2,2,2	0.16	0
3	EDO	A	9014	-	3,3,3	0.51	0	2,2,2	0.18	0
3	EDO	B	8002	-	3,3,3	0.45	0	2,2,2	0.25	0
3	EDO	B	8003	-	3,3,3	0.40	0	2,2,2	0.38	0
3	EDO	B	8005	-	3,3,3	0.44	0	2,2,2	0.32	0
3	EDO	B	8006	-	3,3,3	0.36	0	2,2,2	0.50	0
3	EDO	B	8007	-	3,3,3	0.51	0	2,2,2	0.38	0
3	EDO	B	9002	-	3,3,3	0.44	0	2,2,2	0.24	0
3	EDO	B	9003	-	3,3,3	0.46	0	2,2,2	0.32	0
3	EDO	B	9004	-	3,3,3	0.51	0	2,2,2	0.29	0
3	EDO	B	9009	-	3,3,3	0.52	0	2,2,2	0.22	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	EDO	A	8001	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	A	8004	-	-	0/1/1/1	0/0/0/0
3	EDO	A	8008	-	-	0/1/1/1	0/0/0/0
3	EDO	A	8009	-	-	0/1/1/1	0/0/0/0
3	EDO	A	8010	-	-	0/1/1/1	0/0/0/0
3	EDO	A	8011	-	-	0/1/1/1	0/0/0/0
3	EDO	A	8012	-	-	0/1/1/1	0/0/0/0
3	EDO	A	8013	-	-	0/1/1/1	0/0/0/0
3	EDO	A	9001	-	-	0/1/1/1	0/0/0/0
3	EDO	A	9005	-	-	0/1/1/1	0/0/0/0
3	EDO	A	9006	-	-	0/1/1/1	0/0/0/0
3	EDO	A	9007	-	-	0/1/1/1	0/0/0/0
3	EDO	A	9008	-	-	0/1/1/1	0/0/0/0
3	EDO	A	9010	-	-	0/1/1/1	0/0/0/0
3	EDO	A	9011	-	-	0/1/1/1	0/0/0/0
3	EDO	A	9012	-	-	0/1/1/1	0/0/0/0
3	EDO	A	9013	-	-	0/1/1/1	0/0/0/0
3	EDO	A	9014	-	-	0/1/1/1	0/0/0/0
3	EDO	B	8002	-	-	0/1/1/1	0/0/0/0
3	EDO	B	8003	-	-	0/1/1/1	0/0/0/0
3	EDO	B	8005	-	-	0/1/1/1	0/0/0/0
3	EDO	B	8006	-	-	0/1/1/1	0/0/0/0
3	EDO	B	8007	-	-	0/1/1/1	0/0/0/0
3	EDO	B	9002	-	-	0/1/1/1	0/0/0/0
3	EDO	B	9003	-	-	0/1/1/1	0/0/0/0
3	EDO	B	9004	-	-	0/1/1/1	0/0/0/0
3	EDO	B	9009	-	-	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.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	8001	EDO	1	0
3	A	8012	EDO	1	0
3	A	9006	EDO	2	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.