



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:10 PM UTC

PDB ID : 3ECB / pdb\_00003ecb  
Title : Crystal structure of mouse H-2Dd in complex with peptide P18-I10 derived from human immunodeficiency virus envelope glycoprotein 120  
Authors : Natarajan, K.; Wang, R.; Margulies, D.H.  
Deposited on : 2008-08-29  
Resolution : 1.70 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

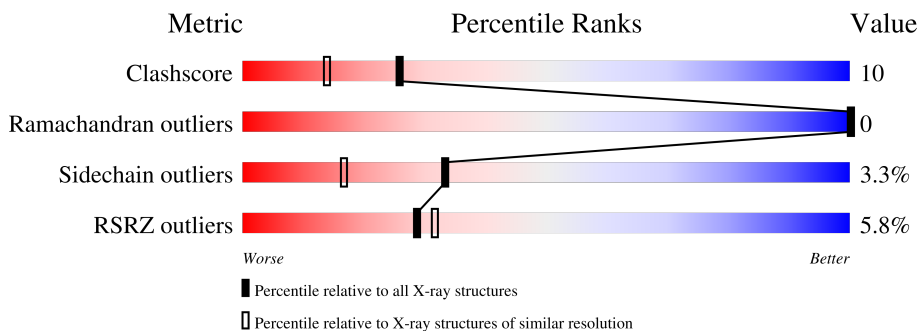
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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))
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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

Mol	Chain	Length	Quality of chain
1	A	277	 4% 86% 11% ..
2	B	100	 9% 77% 17% . ..
3	P	10	 10% 80% 10% 10%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3476 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 H-2 class I histocompatibility antigen, D-D alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	273	2244	1409	406	420	9	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP P01900

- Molecule 2 is a protein called Beta-2 microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	99	817	523	138	149	7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	expression tag	UNP Q91XJ8

- Molecule 3 is a protein called Peptide P18-I10 from HIV gp160.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	P	10	75	48	16	11	0	0	0

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: 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 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Mg 1 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	236	Total O 236 236	0	0
6	B	69	Total O 69 69	0	0

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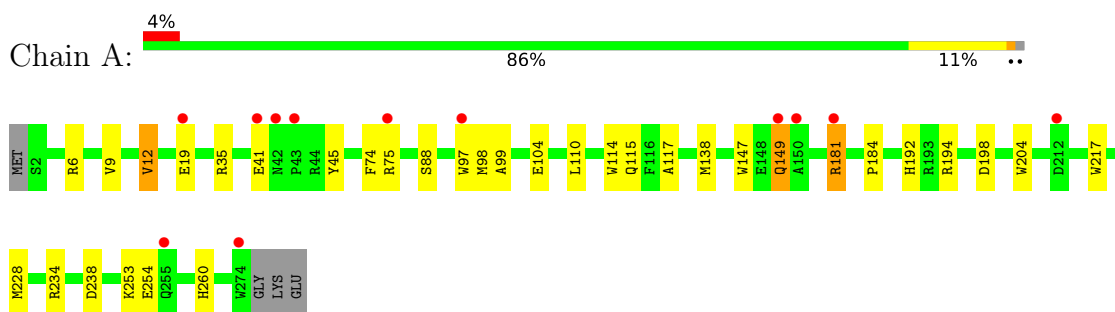
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
6	P	10	Total	O	0	0
			10	10		

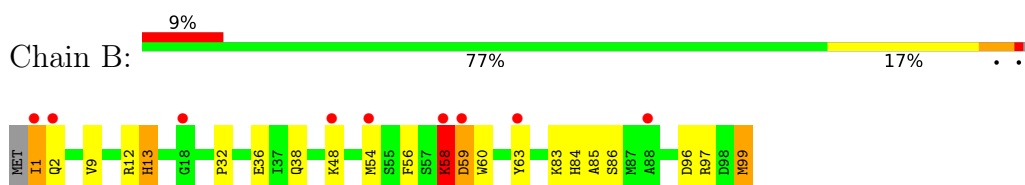
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

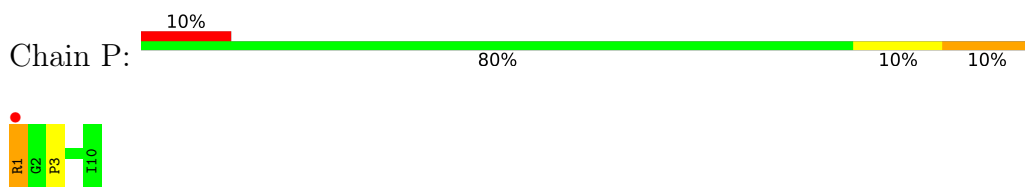
- Molecule 1: H-2 class I histocompatibility antigen, D-D alpha chain



- Molecule 2: Beta-2 microglobulin



- Molecule 3: Peptide P18-I10 from HIV gp160



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.73Å 89.45Å 109.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.80 – 1.70 28.80 – 1.70	Depositor EDS
% Data completeness (in resolution range)	94.9 (28.80-1.70) 95.1 (28.80-1.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.67 (at 1.70Å)	Xtrriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.182 , 0.227 0.185 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.7	Xtrriage
Anisotropy	0.759	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 49.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3476	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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: MG, 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	A	0.55	5/2307 (0.2%)	0.75	5/3133 (0.2%)
2	B	0.63	3/843 (0.4%)	1.00	9/1144 (0.8%)
3	P	0.38	0/76	0.73	0/101
All	All	0.57	8/3226 (0.2%)	0.82	14/4378 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	253	LYS	C-N	8.19	1.44	1.33
1	A	254	GLU	C-N	-7.02	1.24	1.33
1	A	260	HIS	ND1-CE1	5.46	1.38	1.32
2	B	13	HIS	ND1-CE1	5.39	1.38	1.32
1	A	149	GLN	CD-OE1	5.38	1.33	1.23
1	A	192	HIS	ND1-CE1	5.27	1.37	1.32
2	B	84	HIS	ND1-CE1	5.23	1.37	1.32
2	B	38	GLN	CD-OE1	5.13	1.33	1.23

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	58	LYS	N-CA-C	10.56	125.90	111.54
2	B	58	LYS	CA-C-N	-7.44	107.33	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	58	LYS	C-N-CA	-7.44	107.33	121.54
2	B	2	GLN	N-CA-C	6.69	125.05	110.80
2	B	13	HIS	CB-CG-CD2	-6.63	122.58	131.20
1	A	192	HIS	CB-CG-CD2	-6.52	122.72	131.20
2	B	84	HIS	CB-CG-CD2	-6.49	122.77	131.20
1	A	260	HIS	CB-CG-CD2	-6.45	122.81	131.20
2	B	59	ASP	N-CA-C	6.02	123.63	110.80
2	B	84	HIS	CB-CG-ND1	5.70	131.25	122.70
2	B	13	HIS	CB-CG-ND1	5.69	131.23	122.70
1	A	192	HIS	CB-CG-ND1	5.61	131.12	122.70
1	A	260	HIS	CB-CG-ND1	5.44	130.86	122.70
1	A	184	PRO	O-C-N	5.23	123.61	121.15

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	58	LYS	Peptide

## 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	2244	0	2111	31	5
2	B	817	0	797	29	0
3	P	75	0	82	8	0
4	A	16	0	24	3	0
4	B	8	0	12	2	0
5	A	1	0	0	0	0
6	A	236	0	0	3	5
6	B	69	0	0	3	0
6	P	10	0	0	0	0
All	All	3476	0	3026	59	5

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 10.

All (59) 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:58:LYS:HA	2:B:60:TRP:N	1.66	1.09
2:B:58:LYS:HA	2:B:60:TRP:H	1.19	1.05
2:B:58:LYS:CA	2:B:60:TRP:H	1.82	0.93
2:B:58:LYS:N	2:B:60:TRP:H	1.68	0.90
1:A:181:ARG:HD2	6:A:383:HOH:O	1.72	0.89
1:A:97:TRP:HH2	1:A:114:TRP:CE2	1.93	0.86
3:P:1:ARG:CG	3:P:1:ARG:HH11	1.97	0.78
3:P:1:ARG:HH11	3:P:1:ARG:HG3	1.52	0.74
1:A:238:ASP:HB3	2:B:12:ARG:HD2	1.69	0.74
1:A:181:ARG:HD3	6:A:453:HOH:O	1.90	0.71
1:A:97:TRP:CH2	1:A:114:TRP:CE2	2.78	0.71
3:P:1:ARG:HH11	3:P:1:ARG:HB2	1.58	0.69
1:A:35:ARG:HH11	2:B:54:MET:HE1	1.61	0.65
3:P:1:ARG:HH11	3:P:1:ARG:CB	2.11	0.63
2:B:58:LYS:H	2:B:60:TRP:H	1.45	0.60
1:A:6:ARG:HB3	1:A:98:MET:HE3	1.85	0.58
2:B:96:ASP:N	4:B:100:EDO:O1	2.37	0.57
2:B:48:LYS:O	2:B:48:LYS:HG3	2.03	0.57
1:A:204:TRP:HZ2	2:B:99:MET:HB2	1.69	0.56
2:B:1:ILE:HG22	2:B:86:SER:HB3	1.87	0.56
2:B:9:VAL:O	4:B:100:EDO:H12	2.05	0.56
2:B:1:ILE:HG21	2:B:32:PRO:HD2	1.86	0.56
1:A:138:MET:HA	1:A:138:MET:HE2	1.88	0.55
1:A:35:ARG:NH1	2:B:54:MET:HE1	2.22	0.55
1:A:97:TRP:HH2	1:A:114:TRP:CD2	2.25	0.55
3:P:1:ARG:HG3	3:P:1:ARG:NH1	2.20	0.54
3:P:1:ARG:HB2	3:P:1:ARG:NH1	2.24	0.53
2:B:13:HIS:HD2	6:B:157:HOH:O	1.92	0.52
1:A:104:GLU:OE2	1:A:110:LEU:HD11	2.09	0.52
1:A:74:PHE:HZ	1:A:97:TRP:CD1	2.28	0.52
1:A:115:GLN:OE1	2:B:58:LYS:HD2	2.10	0.52
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.45	0.52
1:A:74:PHE:CZ	1:A:97:TRP:CD1	3.00	0.49
1:A:9:VAL:HB	1:A:97:TRP:CD1	2.48	0.49
1:A:238:ASP:CB	2:B:12:ARG:HD2	2.40	0.48
2:B:58:LYS:HG2	2:B:60:TRP:CE2	2.49	0.48
1:A:19:GLU:HG3	1:A:75:ARG:HD2	1.97	0.47
1:A:217:TRP:H	1:A:228:MET:HE1	1.79	0.47
2:B:13:HIS:CD2	6:B:157:HOH:O	2.68	0.47
1:A:9:VAL:HG11	1:A:97:TRP:HD1	1.80	0.46
1:A:147:TRP:CZ2	4:A:280:EDO:H11	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ARG:HH12	4:A:279:EDO:C2	2.28	0.46
2:B:58:LYS:CA	2:B:60:TRP:N	2.50	0.45
1:A:99:ALA:HB3	3:P:3:PRO:HG3	1.99	0.45
1:A:194:ARG:HD3	1:A:198:ASP:OD1	2.15	0.45
2:B:36:GLU:HB3	2:B:83:LYS:HG2	2.00	0.44
3:P:1:ARG:CG	3:P:1:ARG:NH1	2.67	0.44
2:B:54:MET:HA	2:B:63:TYR:O	2.17	0.44
1:A:9:VAL:HB	1:A:97:TRP:HB3	1.99	0.44
1:A:104:GLU:HG2	1:A:110:LEU:HG	1.98	0.44
2:B:1:ILE:HG22	2:B:86:SER:CA	2.48	0.43
1:A:19:GLU:HG2	6:A:313:HOH:O	2.18	0.42
1:A:98:MET:HG3	2:B:58:LYS:HE3	2.01	0.42
2:B:1:ILE:HG22	2:B:86:SER:CB	2.50	0.41
2:B:99:MET:HE3	2:B:99:MET:HB3	1.87	0.41
1:A:138:MET:HE2	1:A:138:MET:CA	2.49	0.41
2:B:1:ILE:HG21	2:B:85:ALA:HB3	2.02	0.41
2:B:59:ASP:HB2	6:B:167:HOH:O	2.21	0.41
1:A:12:VAL:HG11	4:A:281:EDO:H12	2.04	0.40

All (5) 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)
1:A:181:ARG:NH1	6:A:488:HOH:O[4_455]	0.25	1.95
1:A:181:ARG:NH2	6:A:408:HOH:O[4_455]	0.51	1.69
1:A:181:ARG:CZ	6:A:488:HOH:O[4_455]	1.40	0.80
1:A:181:ARG:CZ	6:A:408:HOH:O[4_455]	1.55	0.65
1:A:181:ARG:NH2	6:A:309:HOH:O[4_455]	2.08	0.12

## 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	271/277 (98%)	264 (97%)	7 (3%)	0	100	100
2	B	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
3	P	8/10 (80%)	8 (100%)	0	0	100	100
All	All	376/387 (97%)	365 (97%)	11 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	229/232 (99%)	223 (97%)	6 (3%)	40	23
2	B	93/94 (99%)	89 (96%)	4 (4%)	26	10
3	P	7/7 (100%)	6 (86%)	1 (14%)	3	0
All	All	329/333 (99%)	318 (97%)	11 (3%)	33	17

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	VAL
1	A	41	GLU
1	A	45	TYR
1	A	88	SER
1	A	149	GLN
1	A	181	ARG
2	B	1	ILE
2	B	56	PHE
2	B	97	ARG
2	B	99	MET
3	P	1	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	29	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 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	B	101	-	3,3,3	0.42	0	2,2,2	0.49	0
4	EDO	A	281	-	3,3,3	0.44	0	2,2,2	0.35	0
4	EDO	A	280	-	3,3,3	0.45	0	2,2,2	0.32	0
4	EDO	A	279	-	3,3,3	0.38	0	2,2,2	0.61	0
4	EDO	A	278	-	3,3,3	0.38	0	2,2,2	0.46	0
4	EDO	B	100	-	3,3,3	0.47	0	2,2,2	0.66	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	101	-	-	0/1/1/1	-
4	EDO	A	281	-	-	0/1/1/1	-
4	EDO	A	280	-	-	0/1/1/1	-
4	EDO	A	279	-	-	1/1/1/1	-
4	EDO	A	278	-	-	1/1/1/1	-
4	EDO	B	100	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	278	EDO	O1-C1-C2-O2
4	A	279	EDO	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	281	EDO	1	0
4	A	280	EDO	1	0
4	A	279	EDO	1	0
4	B	100	EDO	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

### 6.1 Protein, DNA and RNA chains

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	273/277 (98%)	0.26	12 (4%) 39 42	20, 29, 47, 70	0
2	B	99/100 (99%)	0.64	9 (9%) 15 15	21, 34, 55, 65	0
3	P	10/10 (100%)	0.24	1 (10%) 12 13	25, 27, 31, 42	0
All	All	382/387 (98%)	0.36	22 (5%) 29 32	20, 31, 49, 70	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1	ILE	8.9
1	A	181	ARG	4.2
2	B	58	LYS	3.7
1	A	97	TRP	3.7
2	B	59	ASP	3.7
2	B	54	MET	3.4
1	A	42	ASN	3.4
1	A	19	GLU	3.2
2	B	48	LYS	3.0
2	B	18	GLY	2.9
1	A	274	TRP	2.8
2	B	63	TYR	2.5
1	A	212	ASP	2.4
1	A	149	GLN	2.3
2	B	2	GLN	2.3
1	A	41	GLU	2.2
2	B	88	ALA	2.2
1	A	150	ALA	2.1
1	A	255	GLN	2.1
1	A	75	ARG	2.0
3	P	1	ARG	2.0
1	A	43	PRO	2.0

## 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 oligosaccharides 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(Å <sup>2</sup> )	Q<0.9
4	EDO	A	278	4/4	0.75	0.20	32,42,48,59	0
4	EDO	A	281	4/4	0.86	0.20	50,58,66,80	0
4	EDO	B	101	4/4	0.88	0.13	31,35,35,47	0
4	EDO	A	280	4/4	0.90	0.14	32,33,36,40	0
5	MG	A	282	1/1	0.90	0.15	45,45,45,45	0
4	EDO	A	279	4/4	0.91	0.20	36,37,49,69	0
4	EDO	B	100	4/4	0.91	0.21	22,28,37,99	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.