



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 9, 2024 – 02:04 PM EST

PDB ID : 8V51  
Title : Crystal structure of a HLA-B\*35:01-NP10 with D1 TCR  
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Deposited on : 2023-11-30  
Resolution : 2.10 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 : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.21  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.004 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

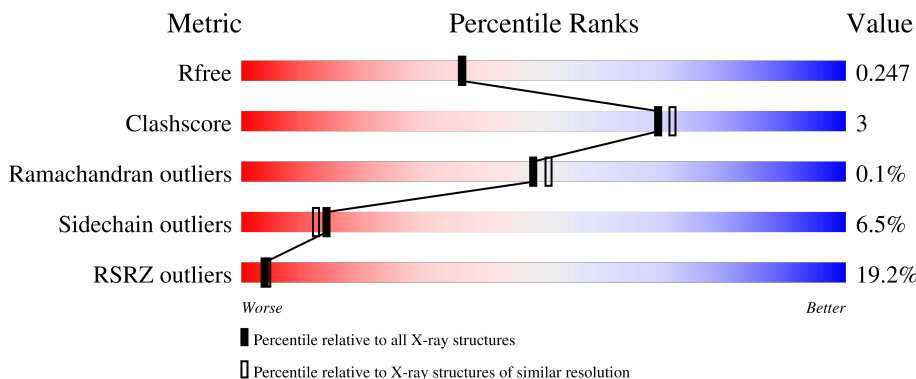
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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))
$R_{free}$	164625	6234 (2.10-2.10)
Clashscore	180529	6893 (2.10-2.10)
Ramachandran outliers	177936	6839 (2.10-2.10)
Sidechain outliers	177891	6840 (2.10-2.10)
RSRZ outliers	164620	6234 (2.10-2.10)

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	273	
2	B	99	
3	C	9	
4	D	198	
5	E	242	

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 7107 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 HLA-B35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	273	2231	1388	408	428	7	0	1	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	99	825	525	139	158	3	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	75	ALA	LYS	conflict	UNP P61769

- Molecule 3 is a protein called LEU-PRO-PHE-GLU-LYS-SER-THR-VAL-MET.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	9	73	48	10	14	1	0	0	0

- Molecule 4 is a protein called D1 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	198	1554	974	251	318	11	0	3	0

- Molecule 5 is a protein called D1 TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	242	1949	1225	340	377	7	0	4	0

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

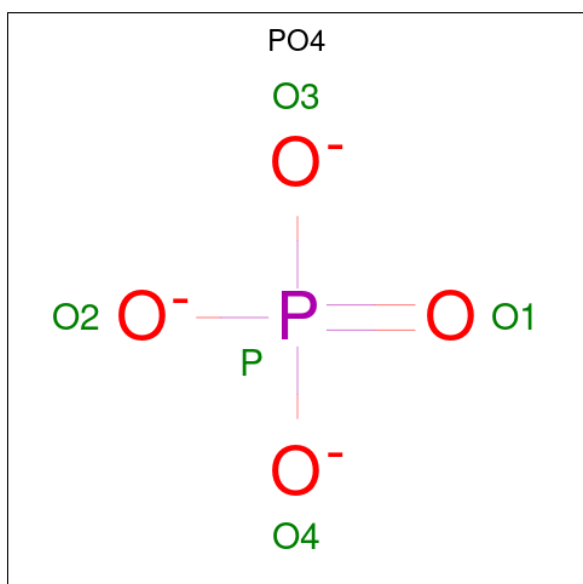


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O	0	0
			4 2 2		

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Na	0	0
			1 1		

- Molecule 8 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	P	0	0
			5	4	1		
8	D	1	Total	O	P	0	0
			5	4	1		
8	D	1	Total	O	P	0	0
			5	4	1		
8	E	1	Total	O	P	0	0
			5	4	1		
8	E	1	Total	O	P	0	0
			5	4	1		

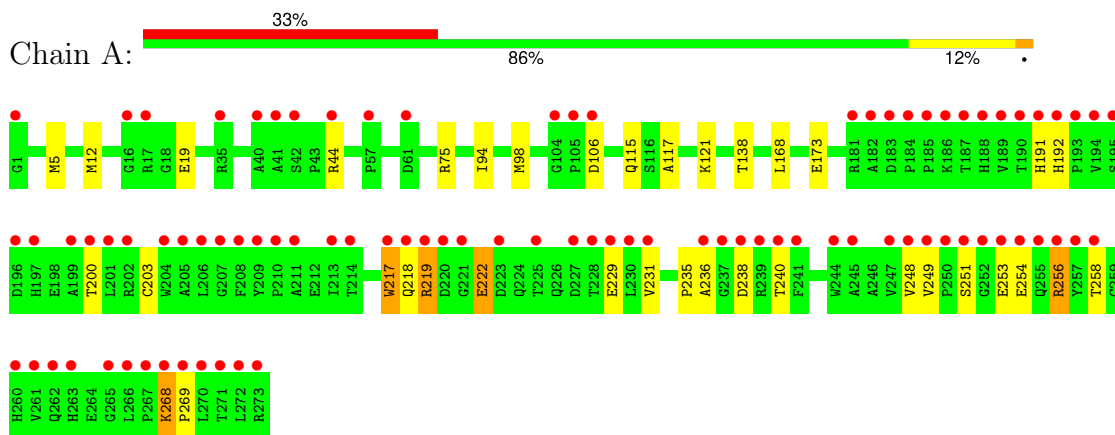
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	122	Total	O	0	0
			122	122		
9	B	31	Total	O	0	0
			31	31		
9	C	7	Total	O	0	0
			7	7		
9	D	117	Total	O	0	0
			117	117		
9	E	168	Total	O	0	0
			168	168		

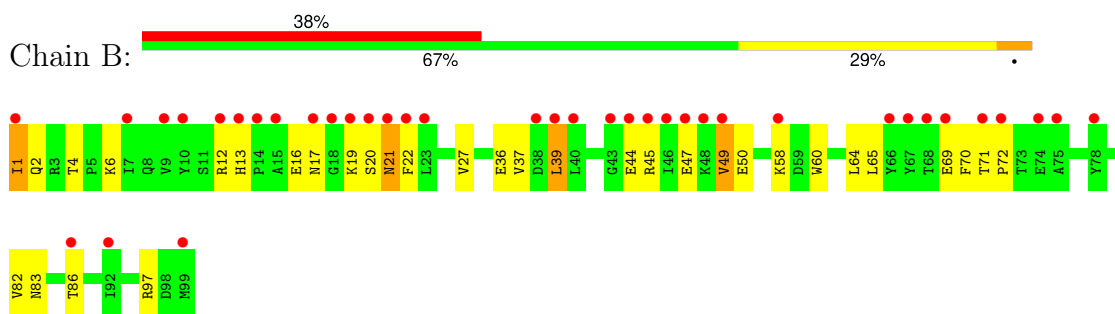
### 3 Residue-property plots [i](#)

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: HLA-B35



- Molecule 2: Beta-2-microglobulin

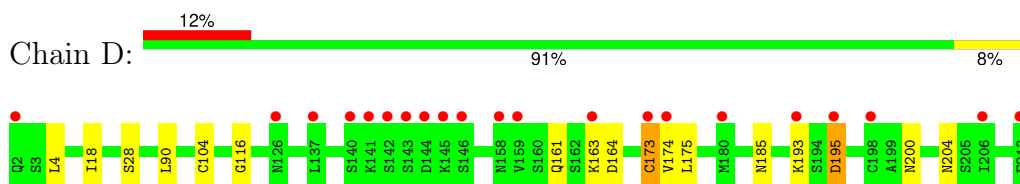


- Molecule 3: LEU-PRO-PHE-GLU-LYS-SER-THR-VAL-MET

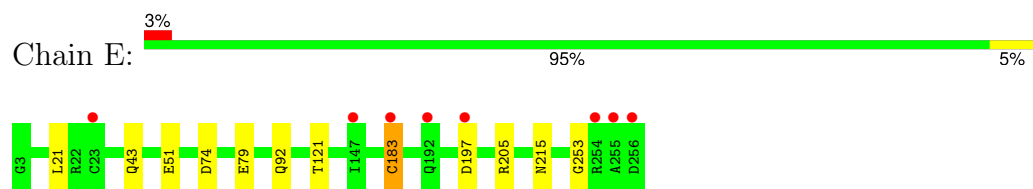


There are no outlier residues recorded for this chain.

- Molecule 4: D1 TCR alpha chain



## ● Molecule 5: D1 TCR beta chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	149.27Å 46.16Å 161.96Å 90.00° 101.40° 90.00°	Depositor
Resolution (Å)	39.50 – 2.10 39.50 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.50-2.10) 91.8 (39.50-2.10)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.27 (at 2.10Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, $R_{free}$	0.210 , 0.244 0.213 , 0.247	Depositor DCC
$R_{free}$ test set	3198 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.5	Xtrriage
Anisotropy	0.024	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 59.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7107	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.26% 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: NA, EDO, PO4

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	0.40	0/2291	0.65	0/3114
2	B	0.41	0/848	0.82	0/1148
3	C	0.38	0/74	0.60	0/97
4	D	0.37	0/1587	0.59	0/2149
5	E	0.35	0/2001	0.62	0/2722
All	All	0.38	0/6801	0.65	0/9230

There are no bond length outliers.

There are no bond angle outliers.

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	2231	0	2097	17	0
2	B	825	0	786	18	0
3	C	73	0	78	0	0
4	D	1554	0	1445	8	0
5	E	1949	0	1845	5	0
6	A	4	0	6	3	0
7	A	1	0	0	0	0
8	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	D	10	0	0	0	0
8	E	10	0	0	0	0
9	A	122	0	0	0	0
9	B	31	0	0	0	0
9	C	7	0	0	0	0
9	D	117	0	0	0	0
9	E	168	0	0	0	0
All	All	7107	0	6257	44	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 3.

All (44) 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:A:236:ALA:HB3	1:A:240:THR:HG23	1.32	1.09
1:A:236:ALA:CB	1:A:240:THR:HG23	1.86	1.05
2:B:4:THR:HA	2:B:86:THR:HG21	1.59	0.83
1:A:218:GLN:HG2	1:A:222:GLU:HA	1.77	0.65
1:A:268:LYS:HG3	1:A:269:PRO:HD2	1.82	0.62
5:E:21:LEU:HD22	5:E:121:THR:HG21	1.81	0.61
4:D:4:LEU:HD11	4:D:116:GLY:CA	2.33	0.58
1:A:12:MET:HG3	1:A:94:ILE:HG12	1.86	0.57
1:A:19:GLU:HB3	6:A:301:EDO:H12	1.85	0.56
4:D:4:LEU:HD13	4:D:104[A]:CYS:SG	2.45	0.56
1:A:236:ALA:HB1	1:A:240:THR:HG23	1.83	0.55
1:A:219:ARG:HG3	1:A:258:THR:OG1	2.06	0.53
4:D:175:LEU:HB3	5:E:183[A]:CYS:HB2	1.90	0.53
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.94	0.50
4:D:18:ILE:HD12	4:D:90:LEU:HD11	1.93	0.49
5:E:43:GLN:O	5:E:51[A]:GLU:HG2	2.14	0.47
4:D:4:LEU:HD11	4:D:116:GLY:HA3	1.97	0.46
2:B:19:LYS:CG	2:B:20:SER:H	2.28	0.46
1:A:75:ARG:HD2	6:A:301:EDO:H21	1.97	0.45
2:B:1:ILE:HD12	2:B:2:GLN:HG3	1.97	0.45
2:B:21:ASN:N	2:B:21:ASN:HD22	2.14	0.45
1:A:200:THR:HG22	1:A:248:VAL:HA	1.97	0.45
1:A:235:PRO:HG2	2:B:65:LEU:HD13	1.99	0.44
5:E:215:ASN:O	5:E:253:GLY:HA3	2.18	0.44
4:D:173[A]:CYS:HB3	5:E:183[A]:CYS:SG	2.58	0.43
2:B:12:ARG:CD	2:B:22:PHE:HB2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:71:THR:OG1	2:B:72:PRO:HD3	2.19	0.43
2:B:37:VAL:HG22	2:B:82:VAL:HG22	1.99	0.43
1:A:75:ARG:HB2	6:A:301:EDO:O1	2.18	0.42
1:A:191:HIS:CE1	1:A:200:THR:H	2.36	0.42
2:B:39:LEU:HD22	2:B:49:VAL:HG21	2.02	0.42
2:B:27:VAL:HG11	2:B:82:VAL:HG21	2.01	0.42
2:B:19:LYS:CG	2:B:20:SER:N	2.83	0.41
4:D:193:LYS:HG3	4:D:195:ASP:H	1.84	0.41
1:A:203:CYS:HB2	1:A:217:TRP:CZ3	2.55	0.41
2:B:69:GLU:OE2	2:B:71:THR:HG23	2.19	0.41
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.55	0.41
4:D:174:VAL:HG22	4:D:185:ASN:OD1	2.20	0.41
2:B:13:HIS:O	2:B:21:ASN:OD1	2.39	0.41
2:B:69:GLU:OE2	2:B:71:THR:CG2	2.69	0.41
2:B:71:THR:N	2:B:72:PRO:CD	2.84	0.41
1:A:219:ARG:HD3	1:A:256:ARG:O	2.21	0.41
2:B:36:GLU:HB2	2:B:83:ASN:HB3	2.02	0.41
2:B:44:GLU:HG3	2:B:45:ARG:HB2	2.04	0.40

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	272/273 (100%)	254 (93%)	18 (7%)	0	100	100
2	B	97/99 (98%)	88 (91%)	8 (8%)	1 (1%)	13	9
3	C	7/9 (78%)	7 (100%)	0	0	100	100
4	D	199/198 (100%)	195 (98%)	4 (2%)	0	100	100
5	E	244/242 (101%)	239 (98%)	5 (2%)	0	100	100
All	All	819/821 (100%)	783 (96%)	35 (4%)	1 (0%)	48	51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	47	GLU

### 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	232/231 (100%)	212 (91%)	20 (9%)	8 6
2	B	93/93 (100%)	81 (87%)	12 (13%)	3 2
3	C	9/9 (100%)	9 (100%)	0	100 100
4	D	173/170 (102%)	164 (95%)	9 (5%)	19 18
5	E	212/208 (102%)	205 (97%)	7 (3%)	33 36
All	All	719/711 (101%)	671 (93%)	48 (7%)	14 11

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ARG
1	A	98	MET
1	A	106	ASP
1	A	115	GLN
1	A	121	LYS
1	A	138	THR
1	A	173	GLU
1	A	192	HIS
1	A	217	TRP
1	A	219	ARG
1	A	222	GLU
1	A	229	GLU
1	A	231	VAL
1	A	238	ASP
1	A	249	VAL
1	A	251	SER
1	A	253	GLU

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Mol	Chain	Res	Type
1	A	254	GLU
1	A	256	ARG
1	A	268	LYS
2	B	1	ILE
2	B	6	LYS
2	B	16	GLU
2	B	17	ASN
2	B	21	ASN
2	B	39	LEU
2	B	49	VAL
2	B	50	GLU
2	B	58	LYS
2	B	64	LEU
2	B	70	PHE
2	B	97	ARG
4	D	28	SER
4	D	161	GLN
4	D	163	LYS
4	D	164	ASP
4	D	173[A]	CYS
4	D	173[B]	CYS
4	D	195	ASP
4	D	200	ASN
4	D	204	ASN
5	E	74	ASP
5	E	79	GLU
5	E	92	GLN
5	E	183[A]	CYS
5	E	183[B]	CYS
5	E	197	ASP
5	E	205	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	GLN
1	A	188	HIS
1	A	191	HIS
2	B	21	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 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
6	EDO	A	301	-	3,3,3	0.40	0	2,2,2	0.37	0
8	PO4	E	301	-	4,4,4	2.57	1 (25%)	6,6,6	0.48	0
8	PO4	E	302	-	4,4,4	2.52	1 (25%)	6,6,6	0.47	0
8	PO4	D	301	-	4,4,4	2.57	3 (75%)	6,6,6	0.48	0
8	PO4	A	303	7	4,4,4	2.57	2 (50%)	6,6,6	0.47	0
8	PO4	D	302	-	4,4,4	2.06	3 (75%)	6,6,6	0.39	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	A	301	-	-	0/1/1/1	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	303	PO4	P-O1	4.28	1.60	1.50
8	E	301	PO4	P-O1	4.27	1.60	1.50
8	D	301	PO4	P-O1	4.27	1.60	1.50
8	E	302	PO4	P-O1	4.20	1.60	1.50
8	D	302	PO4	P-O1	2.18	1.55	1.50
8	D	302	PO4	P-O3	2.06	1.60	1.54
8	D	302	PO4	P-O4	2.02	1.60	1.54
8	A	303	PO4	P-O4	2.02	1.60	1.54
8	D	301	PO4	P-O2	2.02	1.60	1.54
8	D	301	PO4	P-O4	2.00	1.60	1.54

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	301	EDO	3	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	273/273 (100%)	1.21	89 (32%) <b>1</b> <b>1</b>	19, 45, 139, 173	1 (0%)
2	B	99/99 (100%)	1.64	38 (38%) <b>1</b> <b>1</b>	28, 60, 116, 130	3 (3%)
3	C	9/9 (100%)	-0.56	0 <b>100</b> <b>100</b>	19, 21, 28, 30	0
4	D	198/198 (100%)	0.58	23 (11%) <b>11</b> <b>11</b>	12, 44, 94, 136	3 (1%)
5	E	242/242 (100%)	0.12	8 (3%) 49 51	10, 36, 63, 130	4 (1%)
All	All	821/821 (100%)	0.77	158 (19%) <b>4</b> <b>4</b>	10, 42, 117, 173	11 (1%)

All (158) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	72	PRO	7.6
1	A	249	VAL	7.0
1	A	199	ALA	6.6
1	A	230	LEU	6.5
1	A	236	ALA	6.2
1	A	217	TRP	6.2
1	A	239	ARG	5.8
1	A	189	VAL	5.6
1	A	252	GLY	5.6
1	A	194	VAL	5.5
2	B	47	GLU	5.4
1	A	187	THR	5.3
1	A	1	GLY	5.3
1	A	206	LEU	5.2
4	D	215	ALA	5.0
1	A	270	LEU	4.7
1	A	240	THR	4.6
1	A	193	PRO	4.4
2	B	49	VAL	4.3
1	A	209	TYR	4.3

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Mol	Chain	Res	Type	RSRZ
2	B	75	ALA	4.3
1	A	225	THR	4.3
1	A	261	VAL	4.2
4	D	146	SER	4.2
1	A	238	ASP	4.2
2	B	15	ALA	4.1
1	A	200	THR	4.1
2	B	14	PRO	4.0
2	B	22	PHE	4.0
1	A	40	ALA	4.0
1	A	190	THR	4.0
1	A	105	PRO	4.0
1	A	192	HIS	4.0
4	D	140	SER	3.9
1	A	251	SER	3.9
1	A	207	GLY	3.9
2	B	17	ASN	3.9
1	A	257	TYR	3.8
1	A	250	PRO	3.8
1	A	253	GLU	3.8
1	A	237	GLY	3.7
1	A	254	GLU	3.7
4	D	143	SER	3.6
1	A	273	ARG	3.6
1	A	201	LEU	3.6
2	B	48	LYS	3.6
1	A	266	LEU	3.5
1	A	196	ASP	3.5
1	A	61[A]	ASP	3.5
1	A	195	SER	3.4
1	A	221	GLY	3.4
2	B	45	ARG	3.4
1	A	219	ARG	3.3
1	A	185	PRO	3.2
2	B	43	GLY	3.2
2	B	1	ILE	3.2
1	A	41	ALA	3.2
2	B	40	LEU	3.2
4	D	145	LYS	3.2
1	A	191	HIS	3.2
4	D	214	ALA	3.1
1	A	271	THR	3.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	241	PHE	3.1
4	D	173[A]	CYS	3.1
5	E	23	CYS	3.1
4	D	144	ASP	3.1
1	A	208	PHE	3.1
2	B	66	TYR	3.1
4	D	195	ASP	3.1
2	B	23	LEU	3.0
1	A	205	ALA	3.0
2	B	86	THR	3.0
2	B	71	THR	3.0
1	A	247	VAL	3.0
1	A	213	ILE	2.9
1	A	256	ARG	2.9
4	D	158	ASN	2.8
1	A	211	ALA	2.8
1	A	181	ARG	2.8
1	A	267	PRO	2.8
2	B	74	GLU	2.8
1	A	186	LYS	2.8
1	A	223	ASP	2.8
2	B	19	LYS	2.7
1	A	229	GLU	2.7
2	B	67	TYR	2.7
1	A	248	VAL	2.7
1	A	197	HIS	2.7
2	B	39	LEU	2.7
1	A	182	ALA	2.7
5	E	197	ASP	2.7
1	A	210	PRO	2.6
2	B	58	LYS	2.6
4	D	163	LYS	2.6
2	B	20	SER	2.6
1	A	214	THR	2.6
1	A	204	TRP	2.6
1	A	255	GLN	2.6
2	B	38	ASP	2.5
2	B	10	TYR	2.5
2	B	99	MET	2.5
1	A	245	ALA	2.5
2	B	9	VAL	2.5
1	A	218	GLN	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	262	GLN	2.5
1	A	269	PRO	2.5
2	B	92	ILE	2.5
2	B	44	GLU	2.5
1	A	188	HIS	2.5
1	A	260	HIS	2.5
2	B	21	ASN	2.5
1	A	228	THR	2.5
2	B	7	ILE	2.4
1	A	202	ARG	2.4
5	E	192	GLN	2.4
2	B	12	ARG	2.4
4	D	193	LYS	2.4
1	A	265	GLY	2.4
5	E	255	ALA	2.4
1	A	272	LEU	2.3
4	D	141	LYS	2.3
2	B	68	THR	2.3
4	D	198	CYS	2.3
4	D	159	VAL	2.3
2	B	78	TYR	2.3
4	D	180	MET	2.3
4	D	174	VAL	2.3
2	B	13	HIS	2.3
4	D	142	SER	2.3
1	A	44	ARG	2.2
4	D	206	ILE	2.2
1	A	183	ASP	2.2
1	A	220	ASP	2.2
4	D	126	ASN	2.2
1	A	42	SER	2.2
1	A	16	GLY	2.2
5	E	183[A]	CYS	2.2
1	A	17	ARG	2.2
4	D	2	GLN	2.2
4	D	213	PHE	2.2
2	B	46	ILE	2.2
4	D	137	LEU	2.2
1	A	106	ASP	2.2
1	A	184	PRO	2.2
5	E	147	ILE	2.1
1	A	268	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	35	ARG	2.1
1	A	244	TRP	2.1
1	A	263	HIS	2.1
1	A	57	PRO	2.1
1	A	104	GLY	2.1
2	B	18	GLY	2.1
1	A	231	VAL	2.1
5	E	254	ARG	2.1
1	A	258	THR	2.1
5	E	256	ASP	2.1
1	A	227	ASP	2.1
2	B	69	GLU	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 monosaccharides 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
6	EDO	A	301	4/4	0.76	0.21	53,54,57,58	0
8	PO4	D	301	5/5	0.82	0.11	86,90,93,97	0
8	PO4	E	301	5/5	0.85	0.11	71,77,81,85	0
8	PO4	D	302	5/5	0.89	0.11	62,63,70,73	0
8	PO4	A	303	5/5	0.91	0.13	70,72,81,83	0
7	NA	A	302	1/1	0.92	0.15	66,66,66,66	0
8	PO4	E	302	5/5	0.92	0.09	67,71,73,77	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.