



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 19, 2023 – 03:37 AM EST

PDB ID : 2P5W  
Title : Crystal structures of high affinity human T-cell receptors bound to pMHC reveal native diagonal binding geometry  
Authors : Sami, M.; Rizkallah, P.J.; Dunn, S.; Li, Y.; Moysey, R.; Vuidepot, A.; Baston, E.; Todorov, P.; Molloy, P.; Gao, F.; Boulter, J.M.; Jakobsen, B.K.  
Deposited on : 2007-03-16  
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

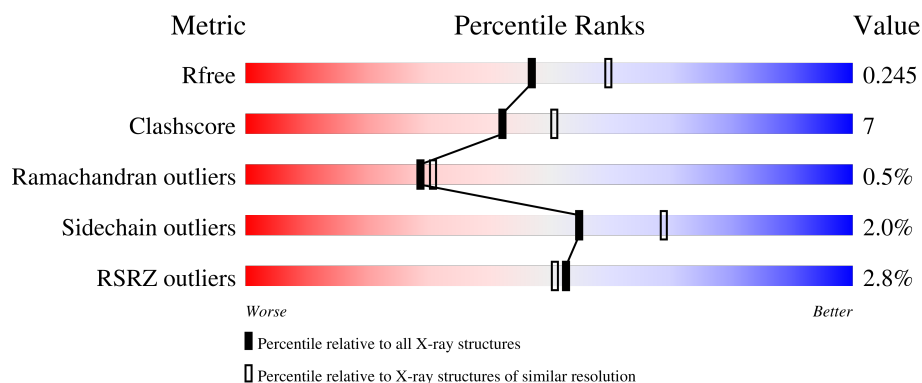
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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))
$R_{free}$	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	276	<div> <div>3%</div> <div>85%</div> <div>13%</div> <div>.</div> </div>
2	B	100	<div> <div>%</div> <div>90%</div> <div>8%</div> <div>..</div> </div>
3	C	9	<div> <div>67%</div> <div>33%</div> </div>
4	D	192	<div> <div>7%</div> <div>84%</div> <div>14%</div> <div>.</div> </div>
5	E	243	<div> <div>85%</div> <div>13%</div> <div>.</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
6	SO4	B	806	-	-	-	X

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 7417 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 class I histocompatibility antigen, A-2 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	2	0
			2267	1417	413	428	9			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	1	0
			845	536	144	160	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	insertion	UNP P61769
B	91	CYS	LYS	conflict	UNP P61769

- Molecule 3 is a protein called Cancer/testis antigen 1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	S	0	0	0
			75	49	11	13	2			

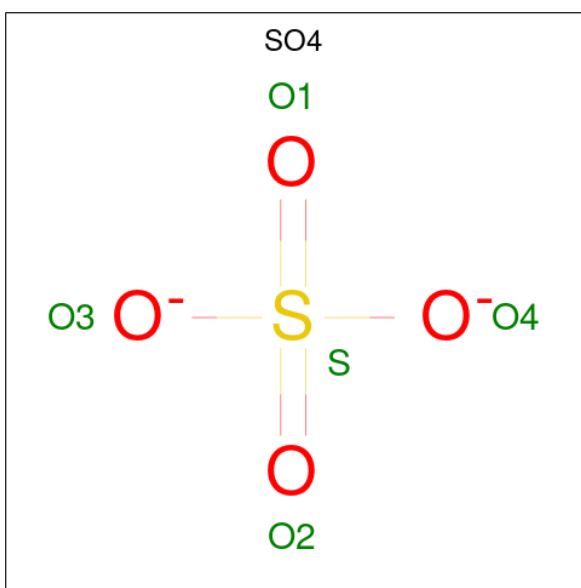
- Molecule 4 is a protein called T-CELL RECEPTOR, ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	192	Total	C	N	O	S	0	3	0
			1497	934	252	302	9			

- Molecule 5 is a protein called Hypothetical protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	242	Total	C	N	O	S	0	4	0
			1945	1222	334	377	12			

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	D	1	Total	C	O	0	0
			6	3	3		
7	D	1	Total	C	O	0	0
			6	3	3		
7	D	1	Total	C	O	0	0
			6	3	3		
7	D	1	Total	C	O	0	0
			6	3	3		
7	E	1	Total	C	O	0	0
			6	3	3		

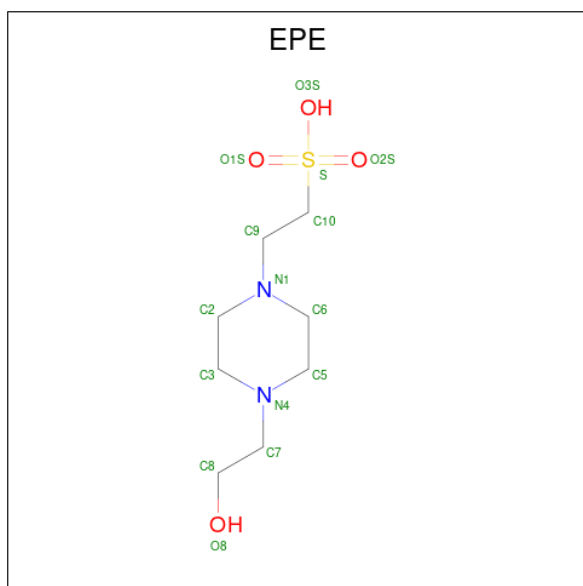
- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Ca	0	0
			1	1		

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	Mg	0	0
			1	1		

- Molecule 10 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S).



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

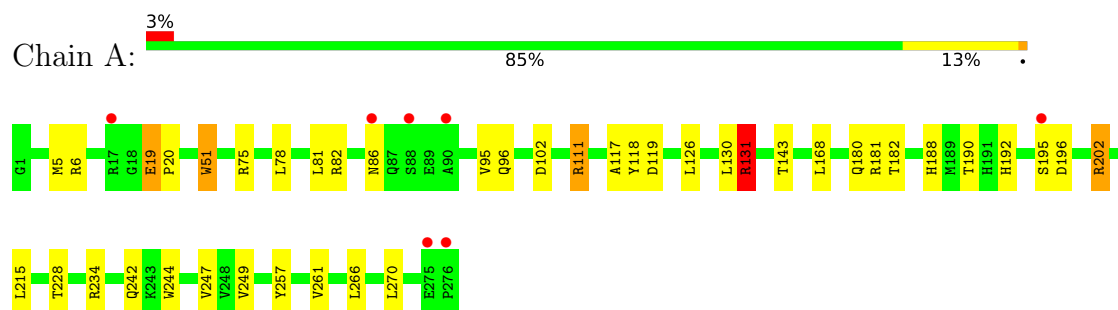
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	224	Total	O	0	0
			224	224		
11	B	104	Total	O	0	0
			104	104		
11	C	10	Total	O	0	0
			10	10		
11	D	115	Total	O	0	0
			115	115		
11	E	222	Total	O	0	0
			222	222		

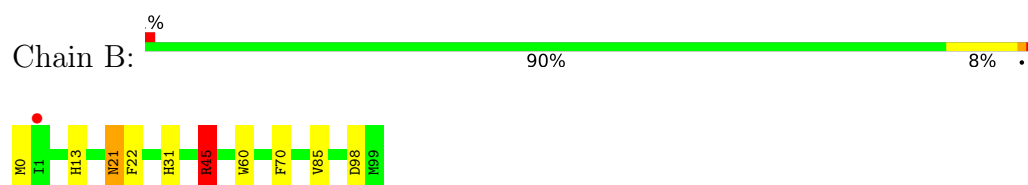
### 3 Residue-property plots [i](#)

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.

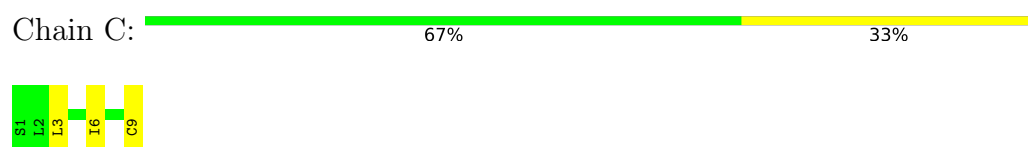
- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain



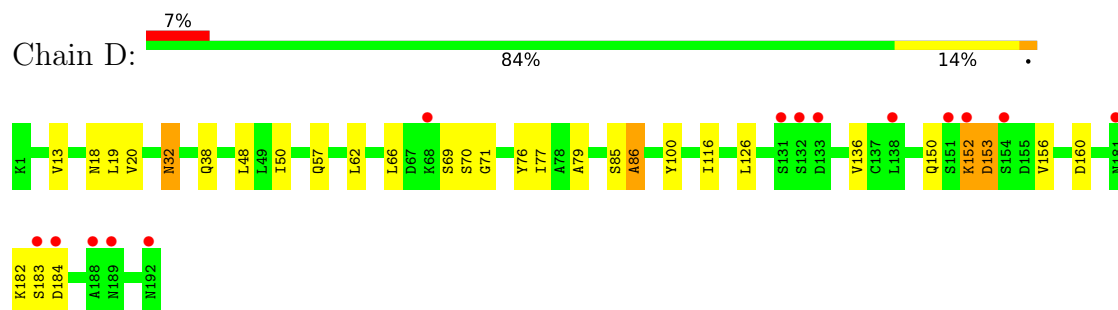
- Molecule 2: Beta-2-microglobulin



- Molecule 3: Cancer/testis antigen 1B



- Molecule 4: T-CELL RECEPTOR, ALPHA CHAIN



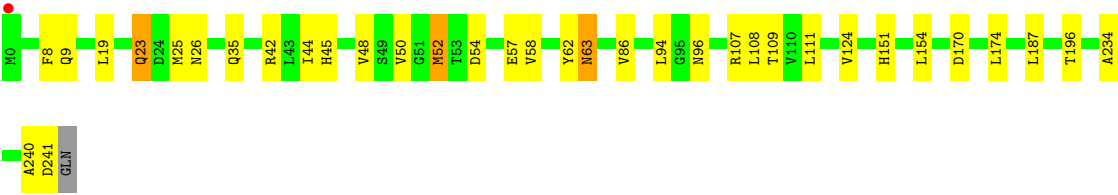
- Molecule 5: Hypothetical protein



Chain E: 

85%

13%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.59Å 52.33Å 118.93Å 90.00° 98.13° 90.00°	Depositor
Resolution (Å)	24.80 – 2.20 24.81 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.3 (24.80-2.20) 99.3 (24.81-2.20)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.42 (at 2.19Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.165 , 0.245 0.169 , 0.245	Depositor DCC
$R_{free}$ test set	2334 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.5	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 46.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7417	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.44% 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: SO4, EPE, CA, MG, GOL

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	0.80	1/2339 (0.0%)	0.80	1/3175 (0.0%)
2	B	0.76	0/868	0.84	1/1173 (0.1%)
3	C	0.70	0/76	1.00	0/101
4	D	0.71	0/1528	0.84	0/2079
5	E	0.81	0/1999	0.84	1/2720 (0.0%)
All	All	0.78	1/6810 (0.0%)	0.83	3/9248 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	19	GLU	CB-CG	5.51	1.62	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	45	ARG	NE-CZ-NH1	7.06	123.83	120.30
1	A	131	ARG	NE-CZ-NH1	6.04	123.32	120.30
5	E	174	LEU	CA-CB-CG	5.06	126.94	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2267	0	2122	32	0
2	B	845	0	807	10	0
3	C	75	0	79	3	0
4	D	1497	0	1441	22	0
5	E	1945	0	1840	32	0
6	A	15	0	0	0	0
6	B	5	0	0	0	0
6	D	5	0	0	0	0
6	E	5	0	0	0	0
7	A	24	0	32	1	0
7	B	12	0	16	0	0
7	D	24	0	32	3	0
7	E	6	0	8	0	0
8	B	1	0	0	0	0
9	B	1	0	0	0	0
10	E	15	0	17	0	0
11	A	224	0	0	3	1
11	B	104	0	0	1	1
11	C	10	0	0	0	0
11	D	115	0	0	0	0
11	E	222	0	0	4	0
All	All	7417	0	6394	91	1

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 91 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)
5:E:109:THR:HG22	5:E:111:LEU:CD1	1.91	1.01
5:E:42:ARG:NH1	5:E:58:VAL:HG11	1.84	0.92
5:E:109:THR:HG22	5:E:111:LEU:HD11	1.53	0.86
2:B:21:ASN:HD22	2:B:22:PHE:H	1.18	0.86
4:D:32:ASN:C	4:D:32:ASN:HD22	1.83	0.82

All (1) 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)
11:A:1054:HOH:O	11:B:1085:HOH:O[2_556]	2.14	0.06

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	276/276 (100%)	268 (97%)	8 (3%)	0	100	100
2	B	99/100 (99%)	96 (97%)	3 (3%)	0	100	100
3	C	7/9 (78%)	7 (100%)	0	0	100	100
4	D	193/192 (100%)	179 (93%)	10 (5%)	4 (2%)	7	4
5	E	244/243 (100%)	236 (97%)	8 (3%)	0	100	100
All	All	819/820 (100%)	786 (96%)	29 (4%)	4 (0%)	29	31

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	70	SER
4	D	153	ASP
4	D	86	ALA
4	D	152	LYS

### 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	
1	A	234/232 (101%)	229 (98%)	5 (2%)	53	67
2	B	96/95 (101%)	93 (97%)	3 (3%)	40	51
3	C	9/9 (100%)	9 (100%)	0	100	100
4	D	172/169 (102%)	170 (99%)	2 (1%)	71	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	215/212 (101%)	211 (98%)	4 (2%)	57	71
All	All	726/717 (101%)	712 (98%)	14 (2%)	55	71

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	70	PHE
4	D	32	ASN
5	E	96	ASN
5	E	52	MET
5	E	63	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	189	ASN
5	E	55	GLN
4	D	192	ASN
5	E	26	ASN
5	E	63	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 2 are monoatomic - leaving 18 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
10	EPE	E	901	-	15,15,15	0.75	1 (6%)	18,20,20	1.11	1 (5%)
6	SO4	D	801	-	4,4,4	0.20	0	6,6,6	0.17	0
7	GOL	B	1001	-	5,5,5	0.37	0	5,5,5	0.37	0
6	SO4	A	803	-	4,4,4	0.20	0	6,6,6	0.13	0
7	GOL	A	1006	-	5,5,5	0.43	0	5,5,5	0.14	0
7	GOL	A	1009	-	5,5,5	0.58	0	5,5,5	0.70	0
6	SO4	E	804	-	4,4,4	0.12	0	6,6,6	0.16	0
7	GOL	A	1008	-	5,5,5	0.66	0	5,5,5	0.84	0
7	GOL	E	1002	-	5,5,5	0.43	0	5,5,5	0.42	0
7	GOL	B	1010	-	5,5,5	0.57	0	5,5,5	0.47	0
7	GOL	A	1005	-	5,5,5	0.44	0	5,5,5	0.35	0
7	GOL	D	1004	-	5,5,5	0.33	0	5,5,5	0.26	0
6	SO4	A	805	-	4,4,4	0.14	0	6,6,6	0.14	0
7	GOL	D	1011	-	5,5,5	0.60	0	5,5,5	0.30	0
6	SO4	B	806	-	4,4,4	0.19	0	6,6,6	0.08	0
7	GOL	D	1003	-	5,5,5	0.58	0	5,5,5	0.90	0
6	SO4	A	802	-	4,4,4	0.15	0	6,6,6	0.06	0
7	GOL	D	1007	-	5,5,5	0.41	0	5,5,5	0.21	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
10	EPE	E	901	-	-	2/9/19/19	0/1/1/1
7	GOL	B	1001	-	-	4/4/4/4	-
7	GOL	A	1006	-	-	4/4/4/4	-
7	GOL	A	1009	-	-	2/4/4/4	-
7	GOL	A	1008	-	-	2/4/4/4	-
7	GOL	E	1002	-	-	3/4/4/4	-
7	GOL	B	1010	-	-	2/4/4/4	-
7	GOL	A	1005	-	-	0/4/4/4	-
7	GOL	D	1004	-	-	4/4/4/4	-
7	GOL	D	1011	-	-	4/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	GOL	D	1003	-	-	2/4/4/4	-
7	GOL	D	1007	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	E	901	EPE	C10-S	2.56	1.81	1.77

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	E	901	EPE	O3S-S-C10	2.72	110.17	105.77

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1006	GOL	O1-C1-C2-C3
7	A	1009	GOL	O1-C1-C2-C3
7	B	1001	GOL	C1-C2-C3-O3
7	D	1007	GOL	O1-C1-C2-C3
7	B	1010	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1008	GOL	1	0
7	D	1004	GOL	2	0
7	D	1003	GOL	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	276/276 (100%)	-0.28	7 (2%) 57 55	5, 15, 34, 70	0
2	B	100/100 (100%)	-0.37	1 (1%) 82 81	6, 14, 32, 61	0
3	C	9/9 (100%)	0.37	0 100 100	3, 5, 9, 11	0
4	D	192/192 (100%)	0.09	14 (7%) 15 14	7, 18, 55, 68	0
5	E	242/243 (99%)	-0.41	1 (0%) 92 91	5, 12, 27, 45	0
All	All	819/820 (99%)	-0.23	23 (2%) 53 51	3, 15, 37, 70	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1	ILE	5.8
4	D	183	SER	4.3
4	D	132	SER	4.3
4	D	184	ASP	3.8
5	E	0	MET	3.7

### 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	SO4	B	806	5/5	0.71	0.47	100,100,100,100	0
7	GOL	B	1010	6/6	0.71	0.24	38,44,48,50	0
7	GOL	D	1003	6/6	0.79	0.30	21,25,31,39	0
7	GOL	A	1006	6/6	0.82	0.24	30,40,51,54	0
7	GOL	A	1009	6/6	0.86	0.30	22,27,35,39	0
7	GOL	D	1004	6/6	0.86	0.30	26,28,37,59	0
7	GOL	A	1008	6/6	0.87	0.34	9,27,35,51	0
7	GOL	A	1005	6/6	0.88	0.15	28,37,40,48	0
6	SO4	A	805	5/5	0.89	0.29	65,77,80,90	0
7	GOL	B	1001	6/6	0.91	0.19	22,26,38,49	0
6	SO4	A	802	5/5	0.91	0.18	90,91,95,97	0
7	GOL	D	1007	6/6	0.92	0.18	42,44,54,56	0
6	SO4	D	801	5/5	0.93	0.30	52,55,64,72	0
6	SO4	A	803	5/5	0.93	0.35	51,60,72,78	0
7	GOL	E	1002	6/6	0.93	0.12	22,27,30,50	0
6	SO4	E	804	5/5	0.95	0.25	38,50,61,63	0
7	GOL	D	1011	6/6	0.96	0.23	17,32,47,49	0
8	CA	B	701	1/1	0.97	0.12	44,44,44,44	0
9	MG	B	702	1/1	0.97	0.07	23,23,23,23	0
10	EPE	E	901	15/15	0.97	0.22	35,54,75,76	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.