



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 08:37 pm GMT

PDB ID : 2NRU  
Title : Crystal structure of IRAK-4  
Authors : Wang, Z.; Liu, J.; Walker, N.P.C.  
Deposited on : 2006-11-02  
Resolution : 2.00 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

<http://wwpdb.org/validation/2016/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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

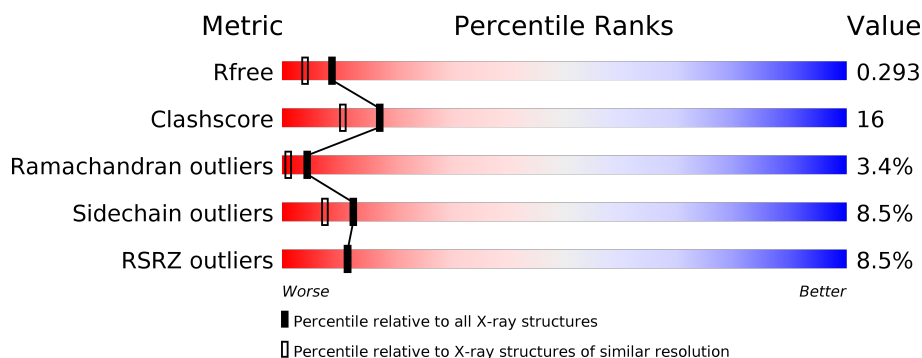
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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  $\leq 5\%$ . 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	307	<div> <div>7%</div> <div> <div></div> <div>70%</div> <div>21%</div> <div>• •</div> </div> </div>
1	B	307	<div> <div>6%</div> <div> <div></div> <div>70%</div> <div>19%</div> <div>6% • •</div> </div> </div>
1	C	307	<div> <div>10%</div> <div> <div></div> <div>62%</div> <div>27%</div> <div>7% •</div> </div> </div>
1	D	307	<div> <div>9%</div> <div> <div></div> <div>63%</div> <div>27%</div> <div>5% • •</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	TPO	A	345	X	-	-	-
1	TPO	B	345	X	-	-	-
1	TPO	C	345	X	-	-	-
1	TPO	D	345	X	-	-	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9949 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 Interleukin-1 receptor-associated kinase 4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	P	S	0	0	0
			2329	1462	391	459	2	15			
1	B	296	Total	C	N	O	P	S	0	1	0
			2339	1468	392	461	2	16			
1	C	295	Total	C	N	O	P	S	0	1	0
			2330	1462	391	460	2	15			
1	D	295	Total	C	N	O	P	S	0	1	0
			2330	1462	391	460	2	15			

There are 8 discrepancies between the modelled and reference sequences:

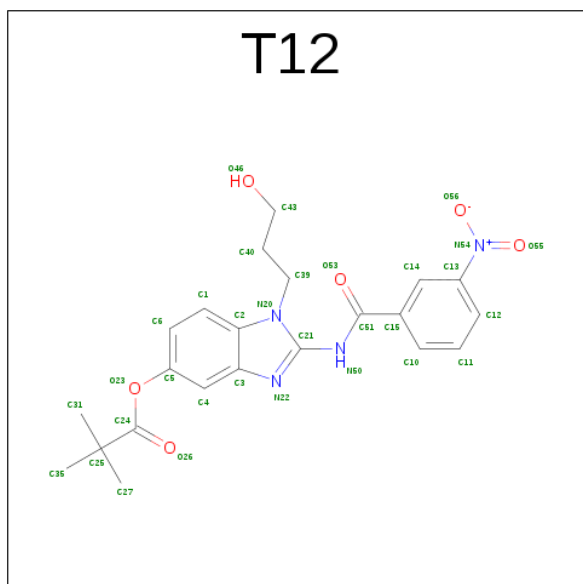
Chain	Residue	Modelled	Actual	Comment	Reference
A	345	TPO	THR	MODIFIED RESIDUE	UNP Q9NWZ3
A	346	SEP	SER	MODIFIED RESIDUE	UNP Q9NWZ3
B	345	TPO	THR	MODIFIED RESIDUE	UNP Q9NWZ3
B	346	SEP	SER	MODIFIED RESIDUE	UNP Q9NWZ3
C	345	TPO	THR	MODIFIED RESIDUE	UNP Q9NWZ3
C	346	SEP	SER	MODIFIED RESIDUE	UNP Q9NWZ3
D	345	TPO	THR	MODIFIED RESIDUE	UNP Q9NWZ3
D	346	SEP	SER	MODIFIED RESIDUE	UNP Q9NWZ3

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is 1-(3-HYDROXYPROPYL)-2-[(3-NITROBENZOYL)AMINO]-1H-BENZIMIDAZOL-5-YL PIVALATE (three-letter code: T12) (formula: C<sub>22</sub>H<sub>24</sub>N<sub>4</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			32	22	4	6		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			32	22	4	6		
3	C	1	Total	C	N	O	0	0
			32	22	4	6		
3	D	1	Total	C	N	O	0	0
			32	22	4	6		

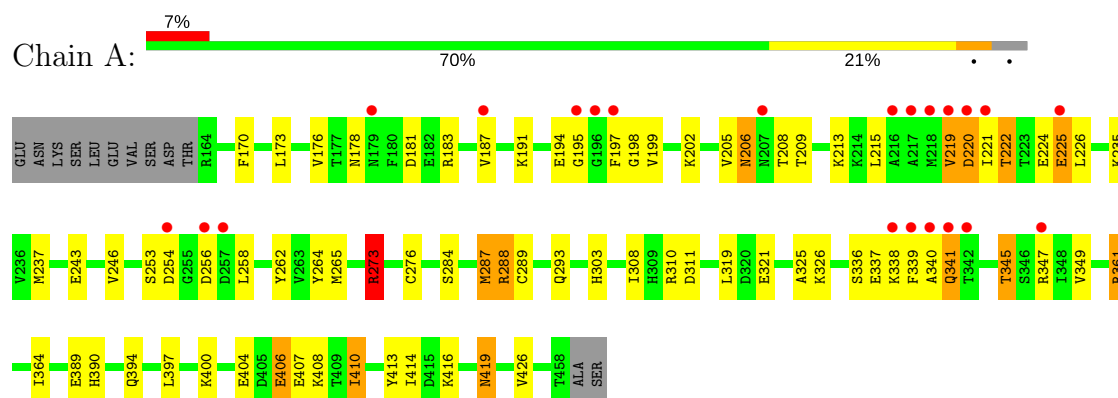
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	114	Total	O	0	0
			114	114		
4	B	121	Total	O	0	0
			121	121		
4	C	126	Total	O	0	0
			126	126		
4	D	122	Total	O	0	0
			122	122		

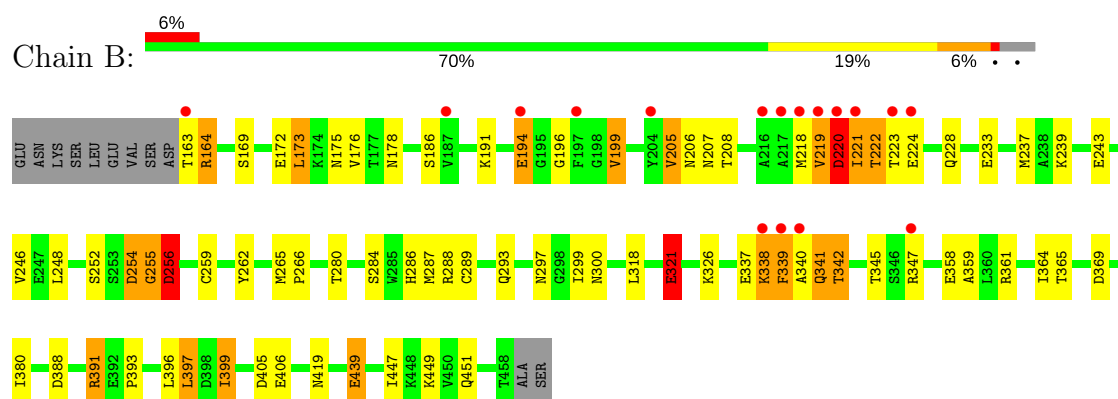
### 3 Residue-property plots [i](#)

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 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.

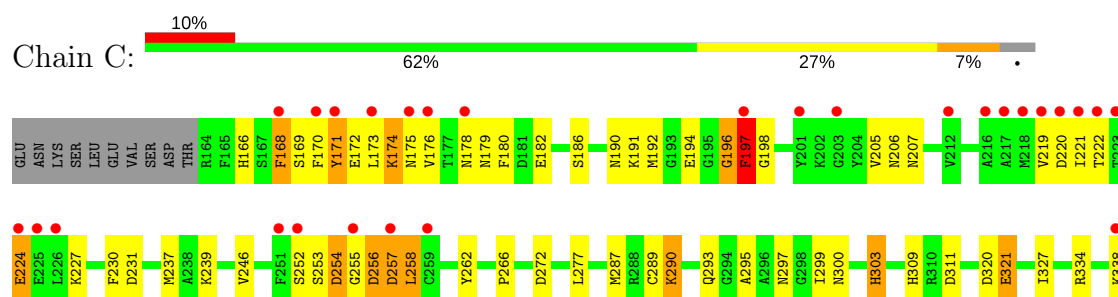
- Molecule 1: Interleukin-1 receptor-associated kinase 4



- Molecule 1: Interleukin-1 receptor-associated kinase 4

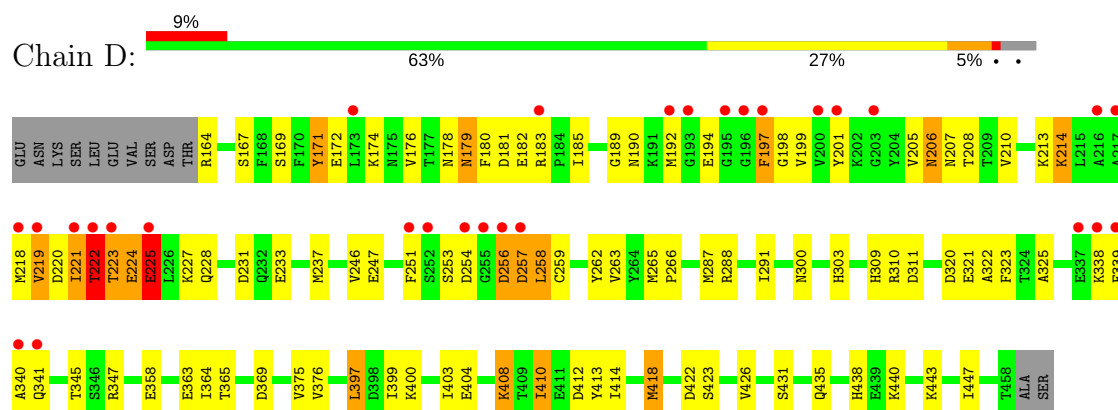


- Molecule 1: Interleukin-1 receptor-associated kinase 4





• Molecule 1: Interleukin-1 receptor-associated kinase 4





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	145.30Å 141.29Å 88.42Å 90.00° 125.80° 90.00°	Depositor
Resolution (Å)	90.29 – 2.00 43.73 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.2 (90.29-2.00) 87.7 (43.73-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.65 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.233 , 0.299 0.229 , 0.293	Depositor DCC
$R_{free}$ test set	4644 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.7	Xtriage
Anisotropy	0.586	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 35.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.187 for -h-2*k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	9949	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.38% 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: TPO, SO4, T12, SEP

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	0.90	2/2347 (0.1%)	0.99	8/3164 (0.3%)
1	B	0.96	3/2362 (0.1%)	0.92	4/3184 (0.1%)
1	C	0.98	1/2353 (0.0%)	0.94	4/3172 (0.1%)
1	D	1.01	1/2353 (0.0%)	0.95	1/3172 (0.0%)
All	All	0.96	7/9415 (0.1%)	0.95	17/12692 (0.1%)

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
1	A	2	0
1	B	1	2
1	C	2	0
1	D	1	1
All	All	6	3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	376	VAL	CB-CG1	6.47	1.66	1.52
1	D	376	VAL	CB-CG1	6.01	1.65	1.52
1	B	280	THR	CA-CB	5.49	1.67	1.53
1	B	246	VAL	CB-CG1	5.32	1.64	1.52
1	A	321	GLU	CD-OE1	5.21	1.31	1.25

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	273	ARG	NE-CZ-NH2	-16.54	112.03	120.30
1	A	273	ARG	NE-CZ-NH1	13.88	127.24	120.30
1	C	355	MET	CG-SD-CE	7.50	112.20	100.20
1	A	288	ARG	NE-CZ-NH1	-7.27	116.67	120.30
1	D	418	MET	CG-SD-CE	-6.30	90.12	100.20

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	345	TPO	CB,CA
1	B	345	TPO	CB
1	C	345	TPO	CB,CA
1	D	345	TPO	CB

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	255	GLY	Peptide
1	B	256	ASP	Peptide
1	D	222	THR	Peptide

## 5.2 Too-close contacts

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	2329	0	2293	58	0
1	B	2339	0	2306	52	0
1	C	2330	0	2295	83	0
1	D	2330	0	2295	99	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
3	A	32	0	24	0	0
3	B	32	0	24	0	0
3	C	32	0	24	2	0
3	D	32	0	24	3	0
4	A	114	0	0	6	0
4	B	121	0	0	4	0
4	C	126	0	0	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	122	0	0	11	0
All	All	9949	0	9285	291	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 16.

The worst 5 of 291 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:D:323:PHE:HB2	4:D:615:HOH:O	1.13	1.26
1:B:191:LYS:HE3	1:B:194:GLU:HB2	1.30	1.14
1:B:284:SER:N	1:B:287[A]:MET:HE3	1.68	1.09
1:D:288:ARG:CZ	1:D:418:MET:HE1	1.85	1.06
1:D:287:MET:HE1	4:D:615:HOH:O	0.86	1.04

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	291/307 (95%)	268 (92%)	16 (6%)	7 (2%)	7	2
1	B	293/307 (95%)	268 (92%)	13 (4%)	12 (4%)	3	1
1	C	292/307 (95%)	266 (91%)	16 (6%)	10 (3%)	4	1
1	D	292/307 (95%)	257 (88%)	24 (8%)	11 (4%)	4	1
All	All	1168/1228 (95%)	1059 (91%)	69 (6%)	40 (3%)	4	1

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	220	ASP

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Mol	Chain	Res	Type
1	A	406	GLU
1	B	219	VAL
1	B	220	ASP
1	B	221	ILE

### 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	255/266 (96%)	241 (94%)	14 (6%)	25	20
1	B	257/266 (97%)	232 (90%)	25 (10%)	9	5
1	C	256/266 (96%)	224 (88%)	32 (12%)	5	3
1	D	256/266 (96%)	240 (94%)	16 (6%)	21	15
All	All	1024/1064 (96%)	937 (92%)	87 (8%)	12	7

5 of 87 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	168	PHE
1	C	227	LYS
1	D	347	ARG
1	C	171	TYR
1	C	197	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	394	GLN
1	C	303	HIS
1	D	394	GLN
1	B	419	ASN
1	C	190	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	TPO	A	345	1	9,10,11	2.16	2 (22%)	10,14,16	2.39	3 (30%)
1	SEP	A	346	1	9,9,10	1.87	2 (22%)	9,12,14	1.65	2 (22%)
1	TPO	B	345	1	9,10,11	2.70	2 (22%)	10,14,16	1.93	3 (30%)
1	SEP	B	346	1	9,9,10	1.55	1 (11%)	9,12,14	1.43	1 (11%)
1	TPO	C	345	1	9,10,11	1.38	1 (11%)	10,14,16	2.48	3 (30%)
1	SEP	C	346	1	9,9,10	1.78	2 (22%)	9,12,14	2.39	3 (33%)
1	TPO	D	345	1	9,10,11	1.88	1 (11%)	10,14,16	2.09	3 (30%)
1	SEP	D	346	1	9,9,10	1.73	2 (22%)	9,12,14	1.80	2 (22%)

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
1	TPO	A	345	1	2/2/3/4	1/8/11/13	0/0/0/0
1	SEP	A	346	1	-	0/5/8/10	0/0/0/0
1	TPO	B	345	1	1/1/3/4	0/8/11/13	0/0/0/0
1	SEP	B	346	1	-	0/5/8/10	0/0/0/0
1	TPO	C	345	1	2/2/3/4	0/8/11/13	0/0/0/0
1	SEP	C	346	1	-	0/5/8/10	0/0/0/0
1	TPO	D	345	1	1/1/3/4	0/8/11/13	0/0/0/0
1	SEP	D	346	1	-	0/5/8/10	0/0/0/0

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	345	TPO	CA-C	-7.14	1.40	1.50
1	D	345	TPO	P-OG1	-4.84	1.51	1.59
1	A	345	TPO	P-OG1	-4.55	1.51	1.59
1	A	345	TPO	CA-C	-4.46	1.44	1.50
1	B	345	TPO	P-OG1	-3.35	1.53	1.59

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	345	TPO	CG2-CB-CA	-4.56	104.75	113.22
1	D	346	SEP	P-OG-CB	-3.77	107.91	118.30
1	B	345	TPO	O-C-CA	-3.52	116.94	125.15
1	D	345	TPO	O-C-CA	-3.33	117.39	125.15
1	A	346	SEP	P-OG-CB	-3.27	109.29	118.30

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	C	345	TPO	CB
1	C	345	TPO	CA
1	A	345	TPO	CB
1	A	345	TPO	CA
1	B	345	TPO	CB

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	345	TPO	P-OG1-CB-CA

There are no ring outliers.

4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	345	TPO	3	0
1	B	345	TPO	4	0
1	C	345	TPO	3	0
1	D	345	TPO	3	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

6 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	T12	A	600	-	30,34,34	2.86	10 (33%)	37,49,49	1.71	11 (29%)
2	SO4	A	612	-	4,4,4	0.23	0	6,6,6	1.15	0
3	T12	B	601	-	30,34,34	2.85	7 (23%)	37,49,49	1.63	6 (16%)
2	SO4	B	611	-	4,4,4	0.27	0	6,6,6	0.55	0
3	T12	C	602	-	30,34,34	2.66	9 (30%)	37,49,49	2.23	10 (27%)
3	T12	D	603	-	30,34,34	2.84	10 (33%)	37,49,49	1.89	7 (18%)

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	T12	A	600	-	-	0/22/26/26	0/3/3/3
2	SO4	A	612	-	-	0/0/0/0	0/0/0/0
3	T12	B	601	-	-	0/22/26/26	0/3/3/3
2	SO4	B	611	-	-	0/0/0/0	0/0/0/0
3	T12	C	602	-	-	0/22/26/26	0/3/3/3
3	T12	D	603	-	-	0/22/26/26	0/3/3/3

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	601	T12	O23-C5	-7.86	1.24	1.41
3	A	600	T12	O23-C5	-7.72	1.24	1.41
3	C	602	T12	O23-C5	-6.89	1.26	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	603	T12	O23-C5	-6.51	1.27	1.41
3	D	603	T12	C13-N54	-2.92	1.39	1.45

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	602	T12	C4-C3-C2	-4.43	116.57	121.10
3	A	600	T12	O23-C24-O26	-4.32	115.40	123.31
3	C	602	T12	O53-C51-C15	-3.82	114.16	120.94
3	B	601	T12	C4-C3-C2	-3.81	117.20	121.10
3	B	601	T12	O23-C24-O26	-3.71	116.53	123.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	612	SO4	1	0
3	C	602	T12	2	0
3	D	603	T12	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 [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	293/307 (95%)	0.32	22 (7%) 15 15	22, 39, 74, 89	0
1	B	294/307 (95%)	0.32	17 (5%) 24 24	20, 38, 70, 87	0
1	C	293/307 (95%)	0.51	32 (10%) 6 6	21, 39, 73, 95	0
1	D	293/307 (95%)	0.43	29 (9%) 8 8	20, 39, 69, 88	0
All	All	1173/1228 (95%)	0.40	100 (8%) 11 11	20, 39, 73, 95	0

The worst 5 of 100 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	340	ALA	12.4
1	A	219	VAL	9.3
1	C	221	ILE	7.8
1	D	216	ALA	7.5
1	C	219	VAL	7.3

### 6.2 Non-standard residues in protein, DNA, RNA chains [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, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	TPO	C	345	11/12	0.94	0.15	-	57,60,61,62	0
1	TPO	A	345	11/12	0.89	0.19	-	55,56,56,58	0
1	SEP	D	346	10/11	0.89	0.09	-	47,51,63,64	0
1	SEP	B	346	10/11	0.85	0.10	-	53,55,62,64	0
1	SEP	C	346	10/11	0.77	0.15	-	56,60,65,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	SEP	A	346	10/11	0.88	0.10	-	55,56,65,65	0
1	TPO	B	345	11/12	0.94	0.13	-	50,54,56,56	0
1	TPO	D	345	11/12	0.95	0.13	-	42,47,48,48	0

### 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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	T12	B	601	32/32	0.96	0.12	0.41	22,26,38,40	0
2	SO4	A	612	5/5	0.88	0.15	0.07	50,51,56,58	0
3	T12	D	603	32/32	0.92	0.14	-0.07	34,38,45,49	0
3	T12	C	602	32/32	0.94	0.12	-0.37	27,33,38,45	0
3	T12	A	600	32/32	0.95	0.10	-0.65	22,28,39,48	0
2	SO4	B	611	5/5	0.97	0.08	-1.50	42,43,47,51	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.