



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 3, 2024 – 12:45 pm GMT

PDB ID : 5CKV  
Title : DAHP synthase from Mycobacterium tuberculosis, fully inhibited by tyrosine, phenylalanine, and tryptophan  
Authors : Munack, S.; Kregel, U.  
Deposited on : 2015-07-15  
Resolution : 2.79 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 : 1.8.4, 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

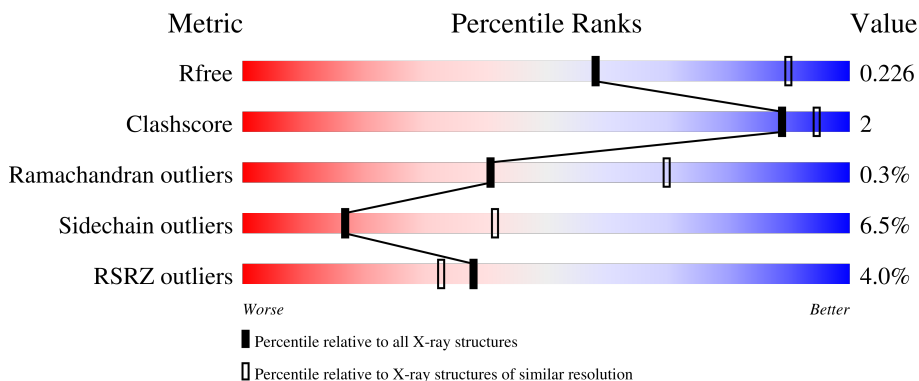
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.79 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	4107 (2.80-2.76)
Clashscore	141614	4575 (2.80-2.76)
Ramachandran outliers	138981	4487 (2.80-2.76)
Sidechain outliers	138945	4489 (2.80-2.76)
RSRZ outliers	127900	4027 (2.80-2.76)

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	472	 4% 85% 10% . .
1	B	472	 3% 88% 8% .

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 13997 atoms, of which 6914 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 Phospho-2-dehydro-3-deoxyheptonate aldolase AroG.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	451	6868	2160	3420	632	639	17	0	0	0
1	B	454	6874	2171	3406	631	649	17	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	MET	-	initiating methionine	UNP O53512
A	-8	HIS	-	expression tag	UNP O53512
A	-7	HIS	-	expression tag	UNP O53512
A	-6	HIS	-	expression tag	UNP O53512
A	-5	HIS	-	expression tag	UNP O53512
A	-4	HIS	-	expression tag	UNP O53512
A	-3	HIS	-	expression tag	UNP O53512
A	-2	SER	-	expression tag	UNP O53512
A	-1	SER	-	expression tag	UNP O53512
A	0	GLY	-	expression tag	UNP O53512
B	-9	MET	-	initiating methionine	UNP O53512
B	-8	HIS	-	expression tag	UNP O53512
B	-7	HIS	-	expression tag	UNP O53512
B	-6	HIS	-	expression tag	UNP O53512
B	-5	HIS	-	expression tag	UNP O53512
B	-4	HIS	-	expression tag	UNP O53512
B	-3	HIS	-	expression tag	UNP O53512
B	-2	SER	-	expression tag	UNP O53512
B	-1	SER	-	expression tag	UNP O53512
B	0	GLY	-	expression tag	UNP O53512

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0
2	B	1	Total Cl 1 1	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



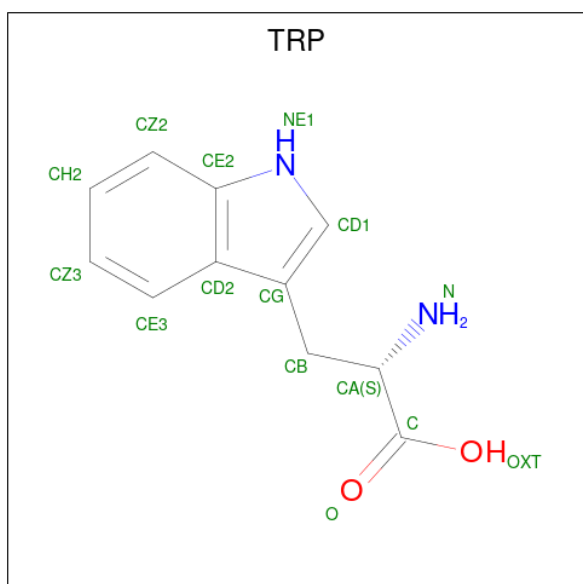
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0

- Molecule 4 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
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	B	1	Total	C	H	O	0	0
			14	3	8	3		
4	B	1	Total	C	H	O	0	0
			14	3	8	3		
4	B	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 5 is TRYPTOPHAN (three-letter code: TRP) (formula:  $C_{11}H_{12}N_2O_2$ ).

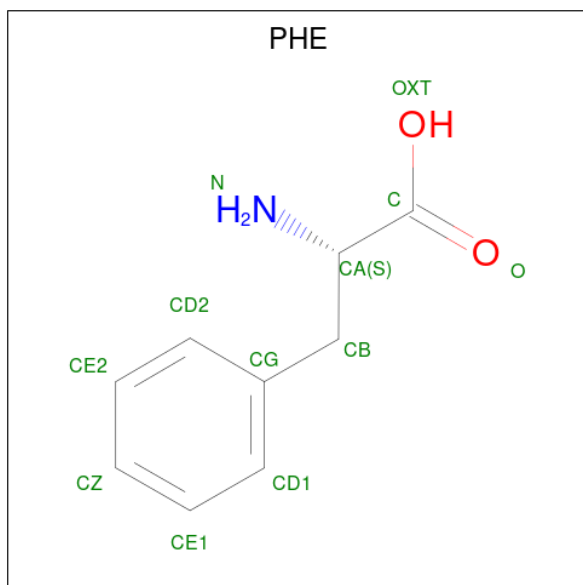


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	0	0
			27	11	12	2	2		
5	B	1	Total	C	H	N	O	0	0
			24	11	9	2	2		

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

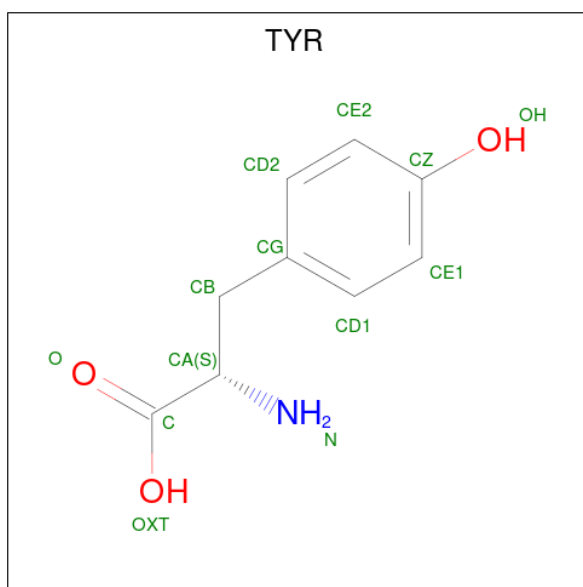
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mn	0	0
			1	1		
6	B	1	Total	Mn	0	0
			1	1		

- Molecule 7 is PHENYLALANINE (three-letter code: PHE) (formula: C<sub>9</sub>H<sub>11</sub>NO<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	H	N	O	0	0
			20	9	8	1	2		
7	B	1	Total	C	H	N	O	0	0
			20	9	8	1	2		

- Molecule 8 is TYROSINE (three-letter code: TYR) (formula: C<sub>9</sub>H<sub>11</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
8	B	1	24	9	11	1	3	0	0

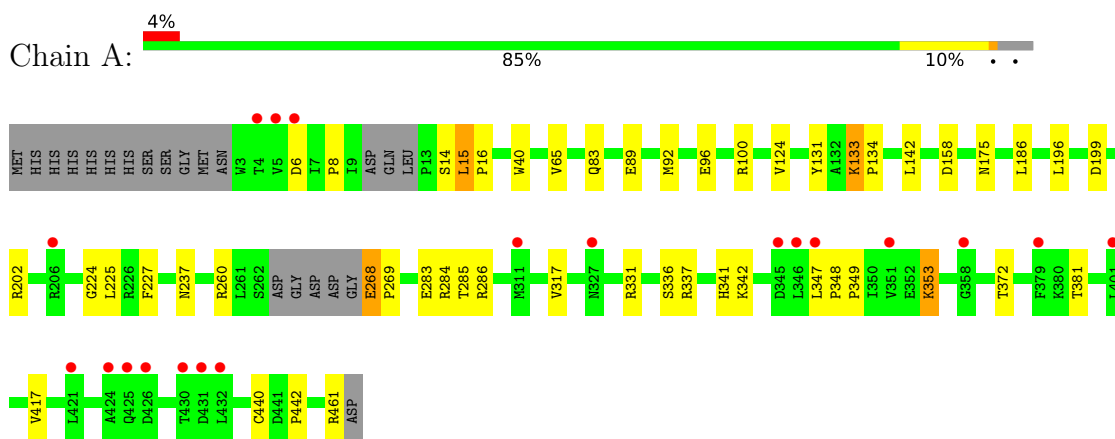
- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	18	Total O 18 18	0	0
9	B	23	Total O 23 23	0	0

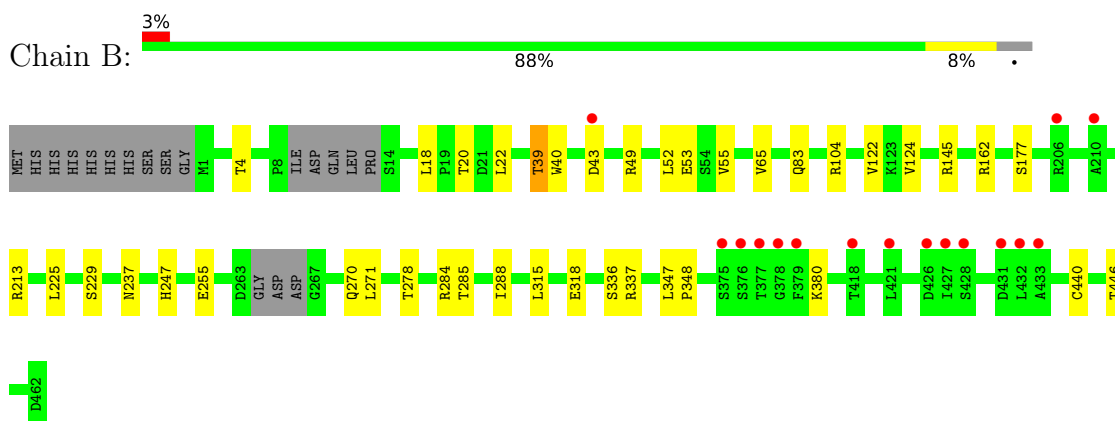
### 3 Residue-property plots [i](#)

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: Phospho-2-dehydro-3-deoxyheptonate aldolase AroG



- Molecule 1: Phospho-2-dehydro-3-deoxyheptonate aldolase AroG





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	204.76Å 204.76Å 66.77Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.30 – 2.79 47.30 – 2.79	Depositor EDS
% Data completeness (in resolution range)	99.4 (47.30-2.79) 99.4 (47.30-2.79)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.94 (at 2.77Å)	Xtrriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, $R_{free}$	0.175 , 0.226 0.175 , 0.226	Depositor DCC
$R_{free}$ test set	2009 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	55.7	Xtrriage
Anisotropy	0.075	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 51.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.033 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	13997	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% 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: CL, SO4, MN, 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	0.33	0/3518	0.52	0/4786
1	B	0.33	0/3539	0.52	0/4818
All	All	0.33	0/7057	0.52	0/9604

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	3448	3420	3418	17	0
1	B	3468	3406	3407	9	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	15	0	0	0	0
3	B	10	0	0	0	0
4	A	12	16	16	0	0
4	B	18	24	24	0	0
5	A	15	12	9	0	0
5	B	15	9	9	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	1	0	0	0	0
7	A	12	8	8	1	0
7	B	12	8	8	0	0
8	B	13	11	8	0	0
9	A	18	0	0	0	0
9	B	23	0	0	0	0
All	All	7083	6914	6907	26	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 2.

All (26) 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:133:LYS:NZ	1:A:440:CYS:SG	2.46	0.88
1:A:96:GLU:OE2	1:A:100:ARG:NH1	2.35	0.59
1:A:15:LEU:HB3	1:A:16:PRO:HD2	1.95	0.49
1:B:315:LEU:O	1:B:318:GLU:N	2.46	0.48
1:A:15:LEU:HB3	1:A:16:PRO:CD	2.44	0.48
1:B:83:GLN:HA	1:B:124:VAL:O	2.15	0.46
1:A:196:LEU:O	1:A:199:ASP:HB2	2.16	0.46
1:A:134:PRO:HB2	1:A:284:ARG:HD2	1.97	0.46
1:A:317:VAL:HG21	1:A:353:LYS:HD3	1.98	0.46
1:B:18:LEU:HD21	1:B:271:LEU:HD21	1.97	0.46
1:B:39:THR:O	1:B:39:THR:OG1	2.31	0.45
1:A:283:GLU:OE2	1:A:286:ARG:NH2	2.48	0.45
1:B:52:LEU:O	1:B:55:VAL:HG22	2.17	0.45
1:A:83:GLN:HA	1:A:124:VAL:O	2.16	0.45
1:A:175:ASN:HD21	7:A:509:PHE:N	2.15	0.45
1:B:347:LEU:N	1:B:348:PRO:CD	2.80	0.44
1:A:199:ASP:OD1	1:A:202:ARG:NH2	2.51	0.44
1:A:89:GLU:HB3	1:A:131:TYR:CE1	2.54	0.43
1:A:268:GLU:N	1:A:268:GLU:OE1	2.52	0.43
1:A:224:GLY:O	1:A:227:PHE:HB3	2.19	0.43
1:A:348:PRO:N	1:A:349:PRO:HD2	2.34	0.43
1:B:145:ARG:O	1:B:162:ARG:NH1	2.44	0.43
1:A:347:LEU:N	1:A:348:PRO:CD	2.82	0.41
1:B:49:ARG:O	1:B:53:GLU:HG3	2.21	0.41
1:B:247:HIS:HE1	1:B:255:GLU:OE1	2.03	0.40
1:A:381:THR:HA	1:A:442:PRO:HG3	2.02	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	445/472 (94%)	418 (94%)	25 (6%)	2 (0%)	34	64
1	B	448/472 (95%)	425 (95%)	22 (5%)	1 (0%)	47	76
All	All	893/944 (95%)	843 (94%)	47 (5%)	3 (0%)	41	70

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	440	CYS
1	A	269	PRO
1	A	8	PRO

### 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	360/385 (94%)	336 (93%)	24 (7%)	16	40
1	B	360/385 (94%)	337 (94%)	23 (6%)	17	42
All	All	720/770 (94%)	673 (94%)	47 (6%)	17	41

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASP
1	A	14	SER
1	A	15	LEU
1	A	40	TRP
1	A	65	VAL
1	A	92	MET
1	A	133	LYS
1	A	142	LEU
1	A	158	ASP
1	A	186	LEU
1	A	225	LEU
1	A	237	ASN
1	A	260	ARG
1	A	268	GLU
1	A	285	THR
1	A	331	ARG
1	A	336	SER
1	A	337	ARG
1	A	341	HIS
1	A	342	LYS
1	A	353	LYS
1	A	372	THR
1	A	417	VAL
1	A	461	ARG
1	B	4	THR
1	B	20	THR
1	B	22	LEU
1	B	39	THR
1	B	40	TRP
1	B	43	ASP
1	B	65	VAL
1	B	104	ARG
1	B	122	VAL
1	B	177	SER
1	B	213	ARG
1	B	225	LEU
1	B	229	SER
1	B	237	ASN
1	B	270	GLN
1	B	278	THR
1	B	284	ARG
1	B	285	THR
1	B	288	ILE

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Mol	Chain	Res	Type
1	B	336	SER
1	B	337	ARG
1	B	380	LYS
1	B	446	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 19 ligands modelled in this entry, 4 are monoatomic - leaving 15 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	GOL	B	506	-	5,5,5	0.34	0	5,5,5	0.14	0
4	GOL	B	505	-	5,5,5	0.37	0	5,5,5	0.15	0
4	GOL	A	506	-	5,5,5	0.36	0	5,5,5	0.24	0
3	SO4	B	503	-	4,4,4	0.13	0	6,6,6	0.16	0
3	SO4	A	504	-	4,4,4	0.18	0	6,6,6	0.12	0
3	SO4	B	504	-	4,4,4	0.11	0	6,6,6	0.12	0
4	GOL	A	505	-	5,5,5	0.39	0	5,5,5	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	TYR	B	508	-	12,13,13	0.70	0	16,17,17	0.96	2 (12%)
5	TRP	A	507	-	14,16,16	0.87	1 (7%)	16,22,22	1.09	1 (6%)
3	SO4	A	502	-	4,4,4	0.11	0	6,6,6	0.13	0
3	SO4	A	503	-	4,4,4	0.14	0	6,6,6	0.08	0
4	GOL	B	507	-	5,5,5	0.41	0	5,5,5	0.33	0
7	PHE	B	510	-	11,12,12	0.71	1 (9%)	14,15,15	0.80	1 (7%)
5	TRP	B	509	-	14,16,16	0.85	0	16,22,22	1.17	2 (12%)
7	PHE	A	509	-	11,12,12	0.72	1 (9%)	14,15,15	1.01	2 (14%)

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	GOL	B	506	-	-	4/4/4/4	-
4	GOL	B	505	-	-	0/4/4/4	-
4	GOL	A	506	-	-	2/4/4/4	-
4	GOL	A	505	-	-	0/4/4/4	-
8	TYR	B	508	-	-	0/8/8/8	0/1/1/1
5	TRP	A	507	-	-	0/7/8/8	0/2/2/2
4	GOL	B	507	-	-	4/4/4/4	-
7	PHE	B	510	-	-	0/8/8/8	0/1/1/1
5	TRP	B	509	-	-	0/7/8/8	0/2/2/2
7	PHE	A	509	-	-	0/8/8/8	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	509	PHE	OXT-C	-2.10	1.23	1.30
7	B	510	PHE	OXT-C	-2.08	1.23	1.30
5	A	507	TRP	OXT-C	-2.07	1.23	1.30

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	508	TYR	OXT-C-O	-2.85	117.61	124.09
7	A	509	PHE	OXT-C-O	-2.68	118.01	124.09
7	A	509	PHE	OXT-C-CA	2.46	121.78	113.38
5	B	509	TRP	OXT-C-CA	2.45	121.72	113.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	507	TRP	OXT-C-O	-2.40	118.63	124.09
5	B	509	TRP	OXT-C-O	-2.34	118.79	124.09
8	B	508	TYR	OXT-C-CA	2.32	121.28	113.38
7	B	510	PHE	OXT-C-O	-2.22	119.06	124.09

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	506	GOL	O1-C1-C2-C3
4	B	506	GOL	C1-C2-C3-O3
4	B	507	GOL	C1-C2-C3-O3
4	B	507	GOL	O1-C1-C2-C3
4	B	506	GOL	O2-C2-C3-O3
4	B	507	GOL	O1-C1-C2-O2
4	A	506	GOL	O1-C1-C2-O2
4	B	507	GOL	O2-C2-C3-O3
4	B	506	GOL	O1-C1-C2-C3
4	B	506	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	509	PHE	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

### 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	451/472 (95%)	0.31	20 (4%) 34 28	27, 51, 80, 116	0
1	B	454/472 (96%)	0.19	16 (3%) 44 38	24, 44, 74, 105	0
All	All	905/944 (95%)	0.25	36 (3%) 38 33	24, 48, 77, 116	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	376	SER	4.8
1	A	351	VAL	3.7
1	B	375	SER	3.6
1	B	432	LEU	3.4
1	A	346	LEU	3.2
1	A	206	ARG	3.1
1	A	311	MET	3.1
1	A	430	THR	3.1
1	B	426	ASP	3.0
1	A	347	LEU	2.9
1	B	377	THR	2.9
1	B	379	PHE	2.9
1	A	6	ASP	2.9
1	A	432	LEU	2.7
1	B	210	ALA	2.7
1	A	358	GLY	2.6
1	A	5	VAL	2.6
1	A	327	ASN	2.6
1	A	426	ASP	2.6
1	A	401	LEU	2.5
1	A	379	PHE	2.5
1	B	421	LEU	2.4
1	B	206	ARG	2.4
1	A	425	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	421	LEU	2.4
1	B	43	ASP	2.3
1	B	418	THR	2.3
1	A	431	ASP	2.3
1	A	4	THR	2.2
1	B	427	ILE	2.2
1	B	428	SER	2.1
1	B	378	GLY	2.1
1	B	433	ALA	2.1
1	A	424	ALA	2.1
1	B	431	ASP	2.1
1	A	345	ASP	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
3	SO4	A	502	5/5	0.75	0.29	88,107,123,153	0
4	GOL	B	505	6/6	0.75	0.23	55,81,107,107	0
4	GOL	B	506	6/6	0.84	0.41	65,80,96,99	0
4	GOL	A	505	6/6	0.88	0.30	53,63,73,74	0
4	GOL	A	506	6/6	0.90	0.26	51,68,79,84	0
3	SO4	A	503	5/5	0.91	0.18	81,84,89,109	0
4	GOL	B	507	6/6	0.92	0.27	45,66,79,82	0
7	PHE	A	509	12/12	0.93	0.24	37,50,61,61	0
2	CL	A	501	1/1	0.94	0.23	67,67,67,67	0
6	MN	B	502	1/1	0.94	0.11	59,59,59,59	1
3	SO4	B	504	5/5	0.94	0.12	84,86,98,131	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
7	PHE	B	510	12/12	0.94	0.29	31,54,74,76	20
5	TRP	A	507	15/15	0.96	0.19	35,47,60,62	0
2	CL	B	501	1/1	0.96	0.10	54,54,54,54	0
8	TYR	B	508	13/13	0.96	0.19	33,45,61,72	0
3	SO4	A	504	5/5	0.97	0.17	51,56,63,77	0
5	TRP	B	509	15/15	0.97	0.15	30,40,46,54	0
3	SO4	B	503	5/5	0.97	0.19	47,49,56,64	0
6	MN	A	508	1/1	0.98	0.12	65,65,65,65	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.