



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:46 PM GMT

PDB ID : 1QKC  
Title : ESCHERICHIA COLI FERRIC HYDROXAMATE UPTAKE RECEPTOR (FHUA) IN COMPLEX DELTA TWO-ALBOMYCIN  
Authors : Ferguson, A.D.; Braun, V.; Fiedler, H.-P.; Coulton, J.W.; Diederichs, K.; Welte, W.  
Deposited on : 1999-07-18  
Resolution : 3.10 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

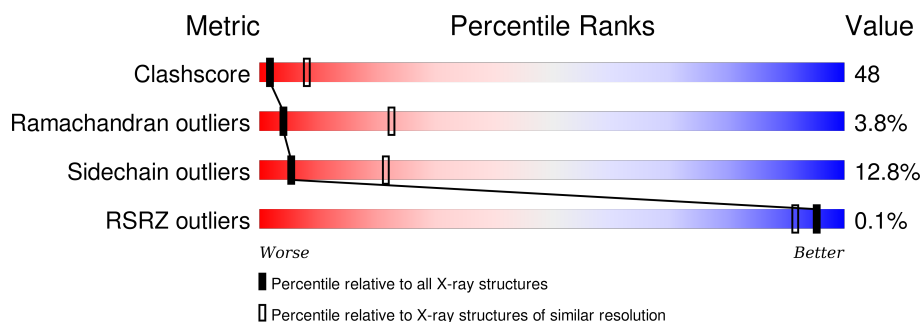
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


The reported resolution of this entry is 3.10 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))
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

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	725	

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
2	GCN	A	1001	X	-	-	-
2	GMH	A	1011	X	-	-	-
2	GMH	A	1012	X	-	-	-
3	FTT	A	1002	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	FTT	A	1004	-	-	-	X
3	FTT	A	1005	-	-	-	X
3	FTT	A	1006	X	-	-	-
3	FTT	A	1007	-	-	-	X
5	PO4	A	1014	-	-	X	-
7	ALB	A	1022[A]	-	-	-	X
7	ALB	A	1022[B]	X	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6195 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 FERRIC HYDROXAMATE RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	707	Total	C	N	O	S	0	0	0
			5523	3475	944	1090	14			

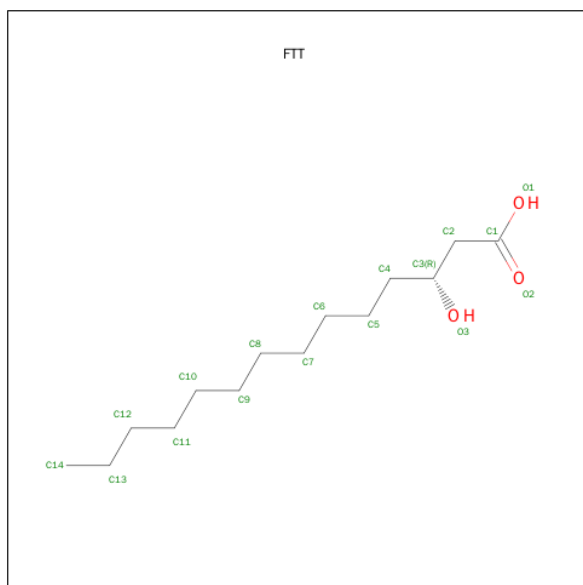
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	406	SER	-	INSERTION (LINKER RES	UNP P06971
A	407	SER	-	INSERTION (LINKER RES	UNP P06971
A	408	HIS	-	INSERTION (AFFINITY T	UNP P06971
A	409	HIS	-	INSERTION (AFFINITY T	UNP P06971
A	410	HIS	-	INSERTION (AFFINITY T	UNP P06971
A	411	HIS	-	INSERTION (AFFINITY T	UNP P06971
A	412	HIS	-	INSERTION (AFFINITY T	UNP P06971
A	413	HIS	-	INSERTION (AFFINITY T	UNP P06971
A	414	GLY	-	INSERTION (LINKER RES	UNP P06971
A	415	SER	-	INSERTION (LINKER RES	UNP P06971
A	416	SER	-	INSERTION (LINKER RES	UNP P06971

- Molecule 2 is a polymer of unknown type called SUGAR (11-MER).

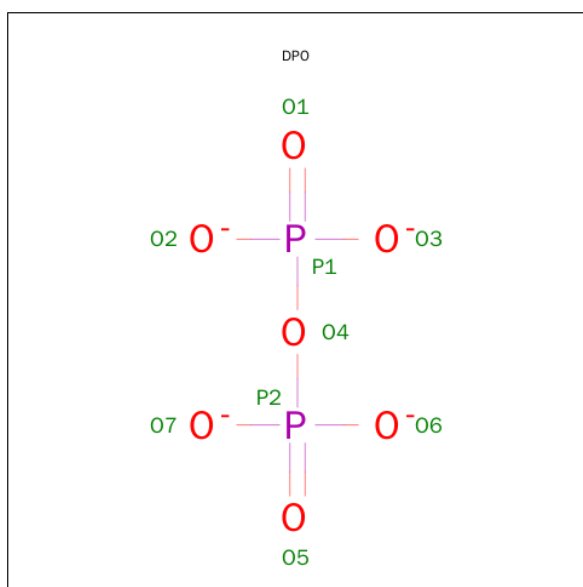
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	11	Total	C	N	O	0	0
			134	73	2	59		

- Molecule 3 is 3-HYDROXY-TETRADECANOIC ACID (three-letter code: FTT) (formula: C<sub>14</sub>H<sub>28</sub>O<sub>3</sub>).



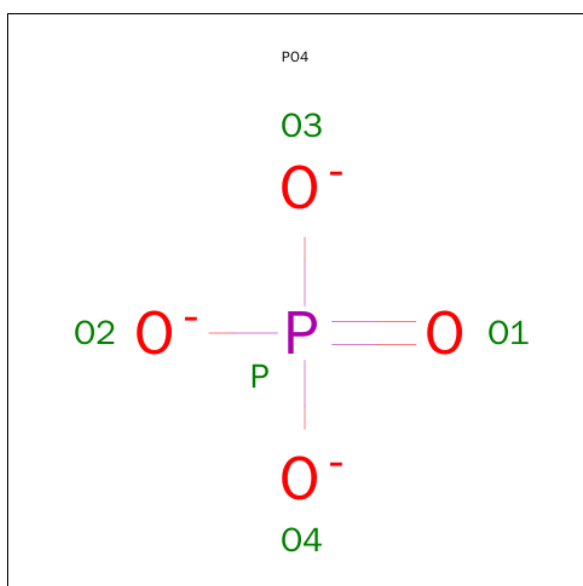
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			16	14	2		
3	A	1	Total	C	O	0	0
			7	4	3		
3	A	1	Total	C	O	0	0
			16	14	2		
3	A	1	Total	C	O	0	0
			13	12	1		
3	A	1	Total	C	O	0	0
			17	14	3		
3	A	1	Total	C	O	0	0
			15	14	1		

- Molecule 4 is DIPHOSPHATE (three-letter code: DPO) (formula:  $O_7P_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			8	6	2		
4	A	1	Total	O	P	0	0
			8	6	2		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula:  $O_4P$ ).

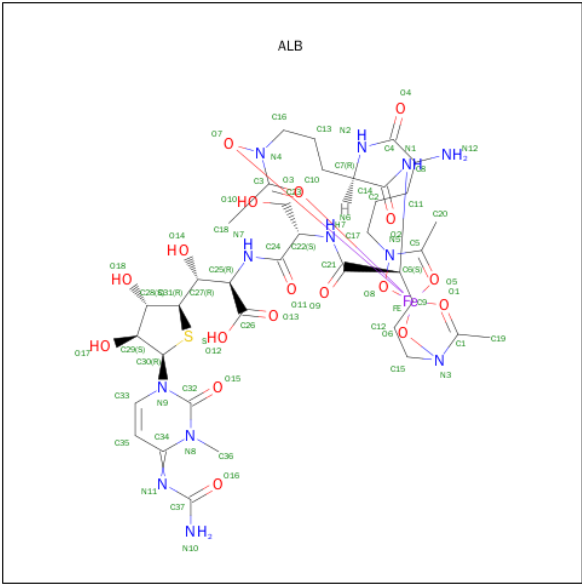


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			4	3	1		
5	A	1	Total	O	P	0	0
			4	3	1		

- Molecule 6 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Ni 1 1	0	0

- Molecule 7 is DELTA-2-ALBOMYCIN A1 (three-letter code: ALB) (formula: C<sub>37</sub>H<sub>57</sub>FeN<sub>12</sub>O<sub>18</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C Fe N O S 97 51 1 17 26 2	0	1

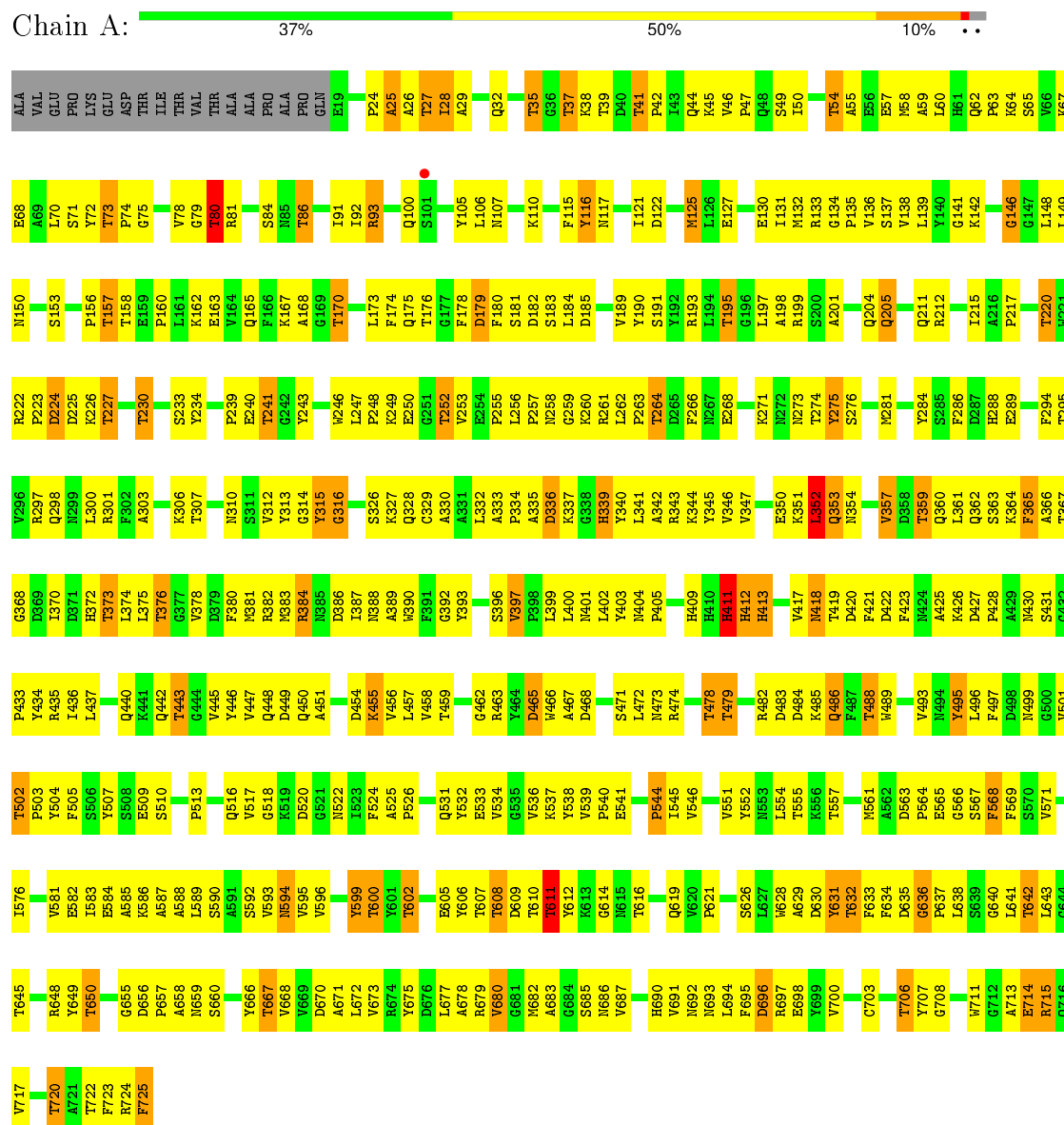
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	332	Total O 332 332	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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: FERRIC HYDROXAMATE RECEPTOR





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	171.80 Å 171.80 Å 86.35 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 3.10 47.12 – 2.70	Depositor EDS
% Data completeness (in resolution range)	94.3 (50.00-3.10) 92.8 (47.12-2.70)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.16 (at 2.69 Å)	Xtriage
Refinement program	CNS 0.4	Depositor
R, $R_{free}$	0.222 , 0.283 0.220 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	71.3	Xtriage
Anisotropy	0.327	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 62.4	EDS
Estimated twinning fraction	0.029 for h,-h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 38001 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6195	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NI, GMH, FTT, PA1, GLA, PO4, GLC, ALB, GCN, KDO, DPO

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	0.92	0/5663	0.87	2/7696 (0.0%)

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	0	1
2	A	4	0
All	All	4	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	179	ASP	CB-CG-OD2	-7.08	111.93	118.30
1	A	352	LEU	CA-CB-CG	5.02	126.85	115.30

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1001	GCN	C1,C2
2	A	1011	GMH	C6
2	A	1012	GMH	C6

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	599	TYR	Sidechain

## 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	5523	0	5223	516	0
2	A	134	0	102	11	0
3	A	84	0	126	8	0
4	A	16	0	0	1	0
5	A	8	0	0	2	0
6	A	1	0	0	0	0
7	A	97	0	36	13	0
8	A	332	0	0	67	0
All	All	6195	0	5487	542	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 48.

The worst 5 of 542 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:220:THR:HG23	1:A:230:THR:HG23	1.26	1.17
1:A:378:VAL:HG12	1:A:445:VAL:HG12	1.39	1.04
1:A:632:THR:HG23	1:A:642:THR:HG23	1.41	1.03
1:A:380:PHE:HD1	1:A:443:THR:HG23	1.22	1.02
7:A:1022[B]:ALB:H27	7:A:1022[B]:ALB:O11	1.54	1.02

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	705/725 (97%)	601 (85%)	77 (11%)	27 (4%)	4	22

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	24	PRO
1	A	224	ASP
1	A	412	HIS
1	A	696	ASP
1	A	25	ALA

### 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	587/601 (98%)	512 (87%)	75 (13%)	5	21

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	357	VAL
1	A	397	VAL
1	A	650	THR
1	A	359	THR
1	A	376	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	360	GLN
1	A	362	GLN
1	A	440	GLN
1	A	328	GLN

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Mol	Chain	Res	Type
1	A	354	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

11 carbohydrates 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$
2	PA1	A	1000	3,2,4	11,11,12	2.78	4 (36%)	11,15,17	1.67	3 (27%)
2	GCN	A	1001	3,2,5	10,10,11	2.36	5 (50%)	10,13,15	5.95	4 (40%)
2	KDO	A	1008	2	12,15,16	0.81	0	12,21,24	0.95	0
2	KDO	A	1009	2	12,15,16	0.87	1 (8%)	12,21,24	1.15	1 (8%)
2	GMH	A	1010	2,4	13,13,14	0.89	1 (7%)	17,18,20	0.95	1 (5%)
2	GMH	A	1011	2,5	13,13,14	0.75	0	17,18,20	1.05	1 (5%)
2	GMH	A	1012	2	13,13,14	1.35	3 (23%)	17,18,20	1.06	1 (5%)
2	GLC	A	1017	2	11,11,12	0.42	0	14,15,17	1.12	1 (7%)
2	GLC	A	1018	2	11,11,12	0.74	0	14,15,17	0.71	0
2	GLA	A	1019	2	11,11,12	0.71	0	14,15,17	0.72	0
2	GLC	A	1020	2	11,11,12	1.61	3 (27%)	14,15,17	1.29	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
2	PA1	A	1000	3,2,4	-	0/2/18/22	0/1/1/1
2	GCN	A	1001	3,2,5	2/2/3/4	0/2/15/18	0/1/1/1
2	KDO	A	1008	2	-	0/6/26/30	0/1/1/1
2	KDO	A	1009	2	-	0/6/26/30	0/1/1/1
2	GMH	A	1010	2,4	-	0/6/23/26	0/1/1/1
2	GMH	A	1011	2,5	1/1/5/6	0/6/23/26	1/1/1/1
2	GMH	A	1012	2	1/1/5/6	0/6/23/26	0/1/1/1
2	GLC	A	1017	2	-	0/2/19/22	0/1/1/1
2	GLC	A	1018	2	-	0/2/19/22	0/1/1/1
2	GLA	A	1019	2	-	0/2/19/22	0/1/1/1
2	GLC	A	1020	2	-	0/2/19/22	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	GCN	C1-C2	-3.30	1.48	1.52
2	A	1000	PA1	C3-C4	-3.04	1.47	1.52
2	A	1001	GCN	C3-C2	-2.99	1.46	1.53
2	A	1000	PA1	O1-C1	-2.21	1.31	1.39
2	A	1012	GMH	C1-C2	2.09	1.57	1.52

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1000	PA1	C3-C2-N2	-3.88	98.66	110.94
2	A	1009	KDO	C3-C4-C5	-3.12	106.31	110.56
2	A	1000	PA1	O1-C1-O5	-2.12	104.44	110.25
2	A	1010	GMH	C1-O5-C5	2.35	115.33	111.52
2	A	1000	PA1	C3-C2-C1	2.46	115.98	109.54

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1001	GCN	C1
2	A	1001	GCN	C2
2	A	1012	GMH	C6
2	A	1011	GMH	C6

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1011	GMH	C1-C2-C3-C4-C5-O5

8 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1000	PA1	1	0
2	A	1001	GCN	4	0
2	A	1009	KDO	2	0
2	A	1010	GMH	1	0
2	A	1012	GMH	1	0
2	A	1017	GLC	1	0
2	A	1018	GLC	2	0
2	A	1020	GLC	2	0

## 5.6 Ligand geometry ⓘ

Of 13 ligands modelled in this entry, 1 is monoatomic - leaving 12 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	$\# Z  > 2$
3	FTT	A	1002	2	14,15,16	1.76	2 (14%)	15,15,17	2.33	1 (6%)
3	FTT	A	1003	2	3,6,16	0.27	0	3,7,17	1.51	1 (33%)
3	FTT	A	1004	3,2	14,15,16	1.01	1 (7%)	15,15,17	2.60	3 (20%)
3	FTT	A	1005	3	12,12,16	0.35	0	10,11,17	0.54	0
3	FTT	A	1006	3,2	13,16,16	0.66	1 (7%)	13,17,17	0.68	0
3	FTT	A	1007	3	14,14,16	0.45	0	12,13,17	0.59	0
4	DPO	A	1013	2	4,7,8	2.42	2 (50%)	6,10,13	1.73	2 (33%)
5	PO4	A	1014	2	0,3,4	0.00	-	0,3,6	0.00	-
4	DPO	A	1015	2	4,7,8	1.81	1 (25%)	6,10,13	1.51	1 (16%)
5	PO4	A	1016	2,6	0,3,4	0.00	-	0,3,6	0.00	-
7	ALB	A	1022[A]	-	63,75,75	2.20	15 (23%)	63,117,117	2.99	20 (31%)
7	ALB	A	1022[B]	-	63,75,75	2.40	11 (17%)	63,117,117	3.42	20 (31%)

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	FTT	A	1002	2	-	0/14/14/15	0/0/0/0
3	FTT	A	1003	2	-	0/2/4/15	0/0/0/0
3	FTT	A	1004	3,2	-	0/14/14/15	0/0/0/0
3	FTT	A	1005	3	-	0/9/10/15	0/0/0/0
3	FTT	A	1006	3,2	1/1/2/2	0/13/15/15	0/0/0/0
3	FTT	A	1007	3	-	0/11/12/15	0/0/0/0
4	DPO	A	1013	2	-	0/3/5/6	0/0/0/0
5	PO4	A	1014	2	-	0/0/0/0	0/0/0/0
4	DPO	A	1015	2	-	0/3/5/6	0/0/0/0
5	PO4	A	1016	2,6	-	0/0/0/0	0/0/0/0
7	ALB	A	1022[A]	-	-	1/59/142/142	0/2/7/7
7	ALB	A	1022[B]	-	2/2/23/27	1/59/142/142	0/2/7/7

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1022[B]	ALB	C35-C34	-6.65	1.31	1.40
7	A	1022[A]	ALB	C36-N8	-6.53	1.33	1.47
7	A	1022[A]	ALB	C33-N9	-4.60	1.29	1.35
7	A	1022[B]	ALB	C33-N9	-3.93	1.30	1.35
4	A	1013	DPO	P2-O4	-3.68	1.51	1.62

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1022[B]	ALB	C36-N8-C32	-13.68	90.13	119.51
7	A	1022[A]	ALB	O11-C24-N7	-10.32	102.71	122.93
7	A	1022[B]	ALB	O11-C24-N7	-9.27	104.78	122.93
7	A	1022[A]	ALB	C36-N8-C32	-9.23	99.69	119.51
7	A	1022[B]	ALB	O11-C24-C22	-9.23	99.95	120.36

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1006	FTT	C3
7	A	1022[B]	ALB	C27
7	A	1022[B]	ALB	C25

All (2) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
7	A	1022[A]	ALB	O4-C4-C8-C11
7	A	1022[B]	ALB	O4-C4-C8-C11

There are no ring outliers.

9 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1003	FTT	1	0
3	A	1004	FTT	4	0
3	A	1005	FTT	1	0
3	A	1006	FTT	6	0
3	A	1007	FTT	2	0
5	A	1014	PO4	2	0
4	A	1015	DPO	1	0
7	A	1022[A]	ALB	5	0
7	A	1022[B]	ALB	8	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	707/725 (97%)	-0.54	1 (0%) 95 91	44, 80, 113, 117	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	101	SER	2.1

### 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](#)

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
2	GMH	A	1010	13/14	0.95	0.10	-2.53	72,78,83,87	0
2	KDO	A	1008	15/16	0.97	0.08	-2.99	67,74,78,84	0
2	GLC	A	1020	11/12	0.80	0.40	-	116,116,117,118	0
2	GLC	A	1017	11/12	0.93	0.17	-	93,101,110,113	0
2	GLA	A	1019	11/12	0.93	0.10	-	110,112,113,113	0
2	GCN	A	1001	10/11	0.95	0.07	-	46,54,63,71	0
2	GMH	A	1012	13/14	0.82	0.19	-	115,116,117,118	0
2	PA1	A	1000	11/12	0.96	0.08	-	53,64,78,81	0
2	GMH	A	1011	13/14	0.94	0.10	-	89,98,111,116	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	KDO	A	1009	15/16	0.94	0.10	-	80,84,88,90	0
2	GLC	A	1018	11/12	0.92	0.25	-	111,114,116,117	0

## 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	FTT	A	1007	15/17	0.90	0.66	14.61	79,99,107,110	0
3	FTT	A	1005	13/17	0.91	0.43	7.58	77,80,89,90	0
3	FTT	A	1002	16/17	0.90	0.36	5.74	80,91,96,96	0
3	FTT	A	1004	16/17	0.93	0.32	4.43	70,73,77,78	0
7	ALB	A	1022[B]	69/69	0.93	0.35	2.67	69,87,115,120	28
7	ALB	A	1022[A]	69/69	0.93	0.35	2.67	69,88,114,120	28
6	NI	A	1021	1/1	0.94	0.07	-	119,119,119,119	0
4	DPO	A	1013	8/9	0.97	0.10	-	84,86,90,92	4
5	PO4	A	1014	4/5	0.96	0.13	-	76,77,78,84	0
3	FTT	A	1003	7/17	0.89	0.14	-	88,103,108,109	0
5	PO4	A	1016	4/5	0.96	0.07	-	112,113,114,114	0
3	FTT	A	1006	17/17	0.94	0.34	-	67,91,100,100	0
4	DPO	A	1015	8/9	0.96	0.09	-	86,89,93,94	4

## 6.5 Other polymers [i](#)

There are no such residues in this entry.