



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 01:20 AM UTC

PDB ID : 2FLI / pdb_00002fli
Title : The crystal structure of D-ribulose 5-phosphate 3-epimerase from *Streptococcus pyogenes* complexed with D-xylitol 5-phosphate
Authors : Fedorov, A.A.; Fedorov, E.V.; Akana, J.; Gerlt, J.A.; Almo, S.C.
Deposited on : 2006-01-06
Resolution : 1.80 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

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

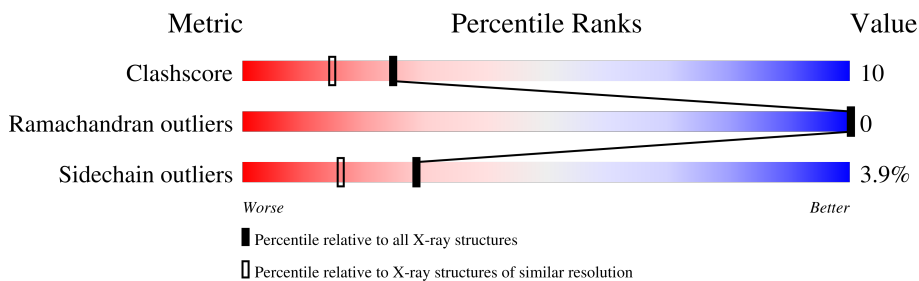
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)





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 ≥ 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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	220	81% 18% .
1	B	220	75% 24% .
1	C	220	83% 16%
1	D	220	78% 20% .
1	E	220	82% 16% .
1	F	220	80% 17% .
1	G	220	81% 17% ..
1	H	220	76% 19% . .

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Mol	Chain	Length	Quality of chain
1	I	220	 77% 20% ..
1	J	220	 80% 17% ..
1	K	220	 75% 22% ..
1	L	220	 80% 16% ..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 20886 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 ribulose-phosphate 3-epimerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	217	Total 1645	C 1046	N 276	O 314	S 9	0	0	0
1	B	217	Total 1643	C 1045	N 275	O 314	S 9	0	0	0
1	C	219	Total 1659	C 1054	N 278	O 318	S 9	0	0	0
1	D	217	Total 1643	C 1045	N 275	O 314	S 9	0	0	0
1	E	216	Total 1637	C 1042	N 274	O 312	S 9	0	0	0
1	F	216	Total 1637	C 1042	N 274	O 312	S 9	0	0	0
1	G	218	Total 1651	C 1049	N 277	O 316	S 9	0	0	0
1	H	216	Total 1637	C 1042	N 274	O 312	S 9	0	0	0
1	I	217	Total 1645	C 1046	N 276	O 314	S 9	0	0	0
1	J	218	Total 1651	C 1049	N 277	O 316	S 9	0	0	0
1	K	216	Total 1637	C 1042	N 274	O 312	S 9	0	0	0
1	L	218	Total 1653	C 1051	N 277	O 316	S 9	0	0	0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

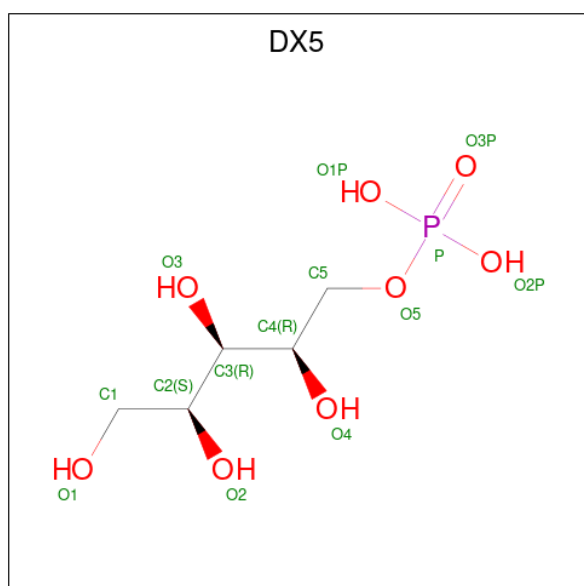
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Zn 1	0	0
2	B	1	Total 1	Zn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		
2	F	1	Total	Zn	0	0
			1	1		
2	G	1	Total	Zn	0	0
			1	1		
2	H	1	Total	Zn	0	0
			1	1		
2	I	1	Total	Zn	0	0
			1	1		
2	J	1	Total	Zn	0	0
			1	1		
2	K	1	Total	Zn	0	0
			1	1		
2	L	1	Total	Zn	0	0
			1	1		

- Molecule 3 is D-XYLITOL-5-PHOSPHATE (CCD ID: DX5) (formula: C₅H₁₃O₈P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			14	5	8	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	O	P	0	0
			14	5	8	1		
3	C	1	Total	C	O	P	0	0
			14	5	8	1		
3	D	1	Total	C	O	P	0	0
			14	5	8	1		
3	E	1	Total	C	O	P	0	0
			14	5	8	1		
3	F	1	Total	C	O	P	0	0
			14	5	8	1		
3	G	1	Total	C	O	P	0	0
			14	5	8	1		
3	H	1	Total	C	O	P	0	0
			14	5	8	1		
3	I	1	Total	C	O	P	0	0
			14	5	8	1		
3	J	1	Total	C	O	P	0	0
			14	5	8	1		
3	K	1	Total	C	O	P	0	0
			14	5	8	1		
3	L	1	Total	C	O	P	0	0
			14	5	8	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	97	Total	O	0	0
			97	97		
4	B	86	Total	O	0	0
			86	86		
4	C	102	Total	O	0	0
			102	102		
4	D	85	Total	O	0	0
			85	85		
4	E	89	Total	O	0	0
			89	89		
4	F	69	Total	O	0	0
			69	69		
4	G	55	Total	O	0	0
			55	55		
4	H	104	Total	O	0	0
			104	104		

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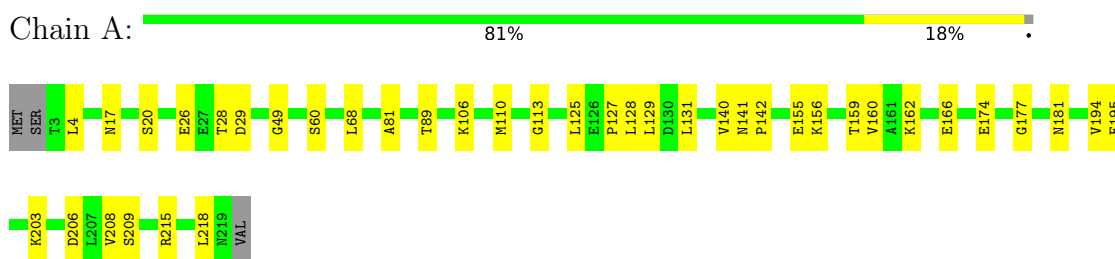
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	I	53	Total O 53 53	0	0
4	J	94	Total O 94 94	0	0
4	K	62	Total O 62 62	0	0
4	L	72	Total O 72 72	0	0

3 Residue-property plots [i](#)

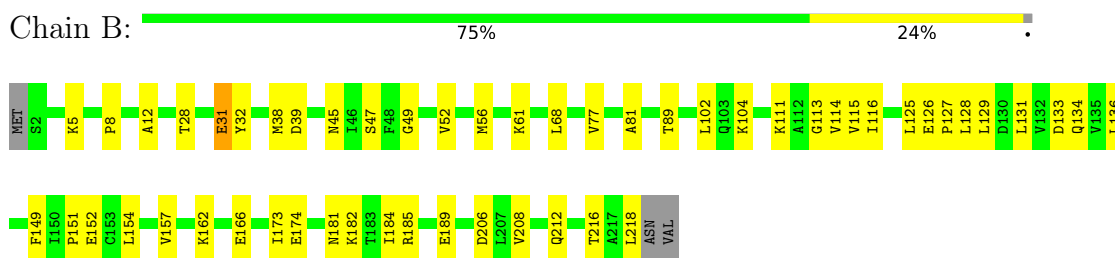
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

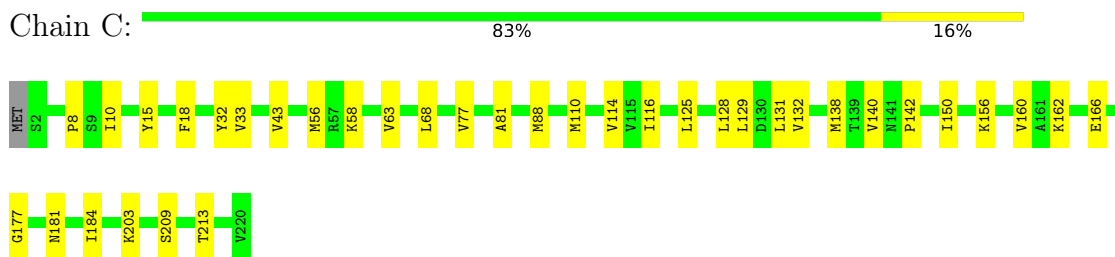
- Molecule 1: ribulose-phosphate 3-epimerase



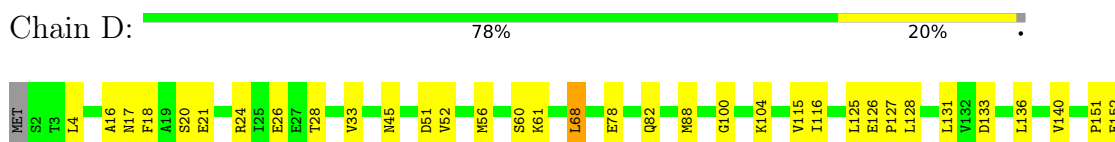
- Molecule 1: ribulose-phosphate 3-epimerase



- Molecule 1: ribulose-phosphate 3-epimerase



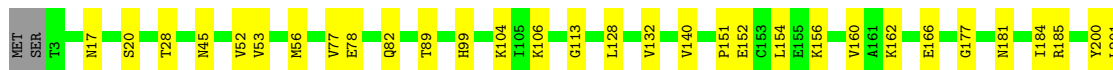
- Molecule 1: ribulose-phosphate 3-epimerase





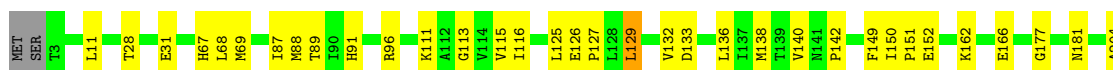
- Molecule 1: ribulose-phosphate 3-epimerase

Chain E: 82% 16%



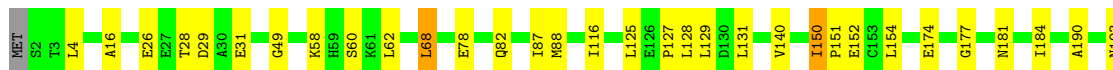
- Molecule 1: ribulose-phosphate 3-epimerase

Chain F: 80% 17%



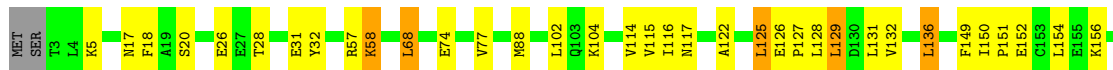
- Molecule 1: ribulose-phosphate 3-epimerase

Chain G: 81% 17%



- Molecule 1: ribulose-phosphate 3-epimerase

Chain H: 76% 19%



- Molecule 1: ribulose-phosphate 3-epimerase

Chain I: 77% 20%





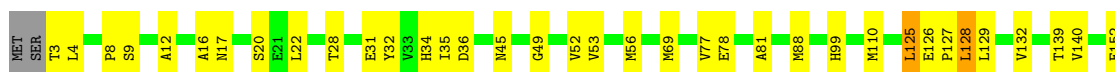
- Molecule 1: ribulose-phosphate 3-epimerase

Chain J: 80% 17% ..



- Molecule 1: ribulose-phosphate 3-epimerase

Chain K: 75% 22% ..



- Molecule 1: ribulose-phosphate 3-epimerase

Chain L: 80% 16% ..



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	80.02Å 199.45Å 87.62Å 90.00° 109.76° 90.00°	Depositor
Resolution (Å)	24.99 – 1.80	Depositor
% Data completeness (in resolution range)	(Not available) (24.99-1.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.224 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	20886	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

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: ZN, DX5

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	0.39	0/1675	0.92	4/2274 (0.2%)
1	B	0.37	0/1673	0.91	6/2271 (0.3%)
1	C	0.40	0/1689	0.95	8/2292 (0.3%)
1	D	0.39	0/1673	0.91	4/2271 (0.2%)
1	E	0.38	0/1667	0.92	2/2263 (0.1%)
1	F	0.38	0/1667	0.94	6/2263 (0.3%)
1	G	0.36	0/1681	0.89	4/2282 (0.2%)
1	H	0.39	0/1667	0.91	4/2263 (0.2%)
1	I	0.37	0/1675	0.87	1/2274 (0.0%)
1	J	0.39	0/1681	0.92	3/2282 (0.1%)
1	K	0.37	0/1667	0.88	3/2263 (0.1%)
1	L	0.38	0/1683	0.92	5/2284 (0.2%)
All	All	0.38	0/20098	0.91	50/27282 (0.2%)

There are no bond length outliers.

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	132	VAL	N-CA-C	8.52	119.34	110.05
1	L	129	LEU	N-CA-C	8.25	121.32	111.33
1	L	132	VAL	N-CA-C	7.00	119.18	109.45
1	K	132	VAL	N-CA-C	6.85	119.72	109.17
1	F	129	LEU	N-CA-C	6.64	118.52	111.28

There are no chirality outliers.

There are no planarity outliers.

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	1645	0	1641	33	0
1	B	1643	0	1640	46	0
1	C	1659	0	1655	23	0
1	D	1643	0	1640	40	0
1	E	1637	0	1635	22	0
1	F	1637	0	1635	25	0
1	G	1651	0	1646	36	0
1	H	1637	0	1635	38	0
1	I	1645	0	1641	35	0
1	J	1651	0	1646	29	0
1	K	1637	0	1635	37	0
1	L	1653	0	1650	33	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	14	0	11	0	0
3	B	14	0	11	0	0
3	C	14	0	11	0	0
3	D	14	0	11	0	0
3	E	14	0	11	0	0
3	F	14	0	11	0	0
3	G	14	0	11	0	0
3	H	14	0	11	0	0
3	I	14	0	11	0	0
3	J	14	0	11	0	0
3	K	14	0	11	0	0
3	L	14	0	11	0	0
4	A	97	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	86	0	0	2	0
4	C	102	0	0	0	0
4	D	85	0	0	1	0
4	E	89	0	0	1	0
4	F	69	0	0	0	0
4	G	55	0	0	2	0
4	H	104	0	0	4	0
4	I	53	0	0	0	0
4	J	94	0	0	2	0
4	K	62	0	0	3	0
4	L	72	0	0	0	0
All	All	20886	0	19831	389	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 10.

The worst 5 of 389 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:J:53:VAL:HA	1:J:56:MET:HE3	1.34	1.06
1:J:52:VAL:HG12	1:J:56:MET:HE2	1.37	1.04
1:K:53:VAL:HA	1:K:56:MET:HE2	1.42	1.01
1:E:53:VAL:HA	1:E:56:MET:HE3	1.40	0.99
1:L:116:ILE:HD13	1:L:125:LEU:HD21	1.45	0.97

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	215/220 (98%)	208 (97%)	7 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	215/220 (98%)	208 (97%)	7 (3%)	0	100	100
1	C	217/220 (99%)	210 (97%)	7 (3%)	0	100	100
1	D	215/220 (98%)	208 (97%)	7 (3%)	0	100	100
1	E	214/220 (97%)	208 (97%)	6 (3%)	0	100	100
1	F	214/220 (97%)	207 (97%)	7 (3%)	0	100	100
1	G	216/220 (98%)	209 (97%)	7 (3%)	0	100	100
1	H	214/220 (97%)	209 (98%)	5 (2%)	0	100	100
1	I	215/220 (98%)	208 (97%)	7 (3%)	0	100	100
1	J	216/220 (98%)	210 (97%)	6 (3%)	0	100	100
1	K	214/220 (97%)	206 (96%)	8 (4%)	0	100	100
1	L	216/220 (98%)	208 (96%)	8 (4%)	0	100	100
All	All	2581/2640 (98%)	2499 (97%)	82 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	B	21/177 (12%)	20 (95%)	1 (5%)	23	11
1	G	48/177 (27%)	47 (98%)	1 (2%)	47	36
1	H	173/177 (98%)	163 (94%)	10 (6%)	18	7
1	I	174/177 (98%)	167 (96%)	7 (4%)	28	15
1	J	175/177 (99%)	169 (97%)	6 (3%)	32	20
1	K	173/177 (98%)	169 (98%)	4 (2%)	44	33
1	L	175/177 (99%)	167 (95%)	8 (5%)	24	12
All	All	939/1239 (76%)	902 (96%)	37 (4%)	28	16

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	181	ASN
1	L	181	ASN
1	L	31	GLU
1	L	128	LEU
1	I	48	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	181	ASN
1	L	82	GLN
1	L	219	ASN
1	L	134	GLN
1	L	41	GLN

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 24 ligands modelled in this entry, 12 are 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	DX5	E	1905	2	13,13,13	1.58	2 (15%)	17,18,18	1.45	1 (5%)
3	DX5	J	1914	2	13,13,13	1.64	3 (23%)	17,18,18	1.45	1 (5%)
3	DX5	H	1912	2	13,13,13	1.68	3 (23%)	17,18,18	1.41	1 (5%)
3	DX5	B	1902	2	13,13,13	1.64	2 (15%)	17,18,18	1.49	1 (5%)
3	DX5	G	1911	2	13,13,13	1.72	2 (15%)	17,18,18	1.51	1 (5%)
3	DX5	F	1906	-	13,13,13	1.59	2 (15%)	17,18,18	1.53	1 (5%)
3	DX5	L	1916	2	13,13,13	1.70	2 (15%)	17,18,18	1.56	1 (5%)
3	DX5	I	1913	2	13,13,13	1.61	2 (15%)	17,18,18	1.54	1 (5%)
3	DX5	D	1904	2	13,13,13	1.59	2 (15%)	17,18,18	1.54	1 (5%)
3	DX5	K	1915	2	13,13,13	1.57	2 (15%)	17,18,18	1.54	1 (5%)
3	DX5	A	1901	2	13,13,13	1.70	2 (15%)	17,18,18	1.47	1 (5%)
3	DX5	C	1903	2	13,13,13	1.65	2 (15%)	17,18,18	1.43	1 (5%)

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	DX5	E	1905	2	-	9/16/16/16	-
3	DX5	J	1914	2	-	5/16/16/16	-
3	DX5	H	1912	2	-	9/16/16/16	-
3	DX5	B	1902	2	-	5/16/16/16	-
3	DX5	G	1911	2	-	11/16/16/16	-
3	DX5	F	1906	-	-	0/16/16/16	-
3	DX5	L	1916	2	-	4/16/16/16	-
3	DX5	I	1913	2	-	8/16/16/16	-
3	DX5	D	1904	2	-	7/16/16/16	-
3	DX5	K	1915	2	-	6/16/16/16	-
3	DX5	A	1901	2	-	5/16/16/16	-
3	DX5	C	1903	2	-	7/16/16/16	-

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	1911	DX5	P-O3P	4.09	1.63	1.50
3	L	1916	DX5	P-O3P	4.07	1.63	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	1913	DX5	P-O3P	4.07	1.63	1.50
3	C	1903	DX5	P-O5	-3.94	1.47	1.60
3	H	1912	DX5	P-O5	-3.85	1.48	1.60

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	1916	DX5	O5-C5-C4	4.68	121.85	109.36
3	K	1915	DX5	O5-C5-C4	4.64	121.75	109.36
3	F	1906	DX5	O5-C5-C4	4.64	121.74	109.36
3	G	1911	DX5	O5-C5-C4	4.63	121.72	109.36
3	I	1913	DX5	O5-C5-C4	4.52	121.44	109.36

There are no chirality outliers.

5 of 76 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1902	DX5	C3-C4-C5-O5
3	C	1903	DX5	C3-C4-C5-O5
3	C	1903	DX5	O4-C4-C5-O5
3	C	1903	DX5	C5-O5-P-O2P
3	E	1905	DX5	C2-C3-C4-C5

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.