



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 11:44 am BST

PDB ID : 3QPU
Title : PFKFB3 in complex with PPI
Authors : Cavalier, M.C.; Kim, S.G.; Neau, D.; Lee, Y.H.
Deposited on : 2011-02-14
Resolution : 2.30 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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 : 2.11
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) : 2.11

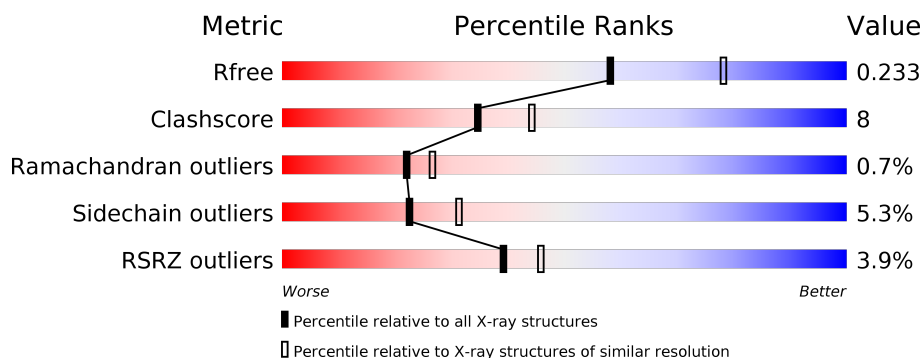
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 ≥ 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	520	<div> <div>3%</div> <div> <div></div> <div>67%</div> <div>15%</div> <div>•</div> <div>16%</div> </div> </div>

2 Entry composition [i](#)

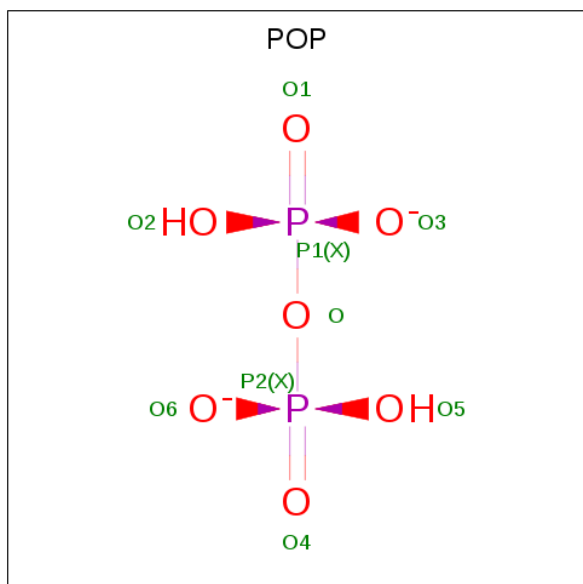
There are 5 unique types of molecules in this entry. The entry contains 3959 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3.

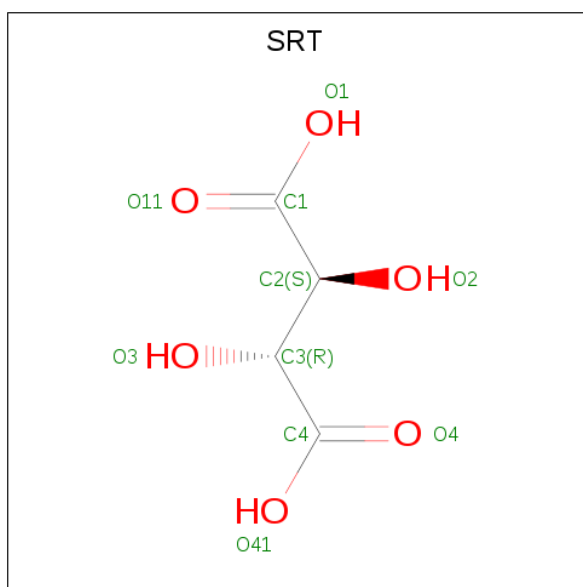
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	439	3584	2263	630	669	22	0	1	0

- Molecule 2 is PYROPHOSPHATE 2- (three-letter code: POP) (formula: $\text{H}_2\text{O}_7\text{P}_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	A	1	9	7	2	0	0
2	A	1	9	7	2	0	0
2	A	1	9	7	2	0	0

- Molecule 3 is S,R MESO-TARTARIC ACID (three-letter code: SRT) (formula: $\text{C}_4\text{H}_6\text{O}_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	4	6		
3	A	1	Total	C	O	0	0
			10	4	6		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		

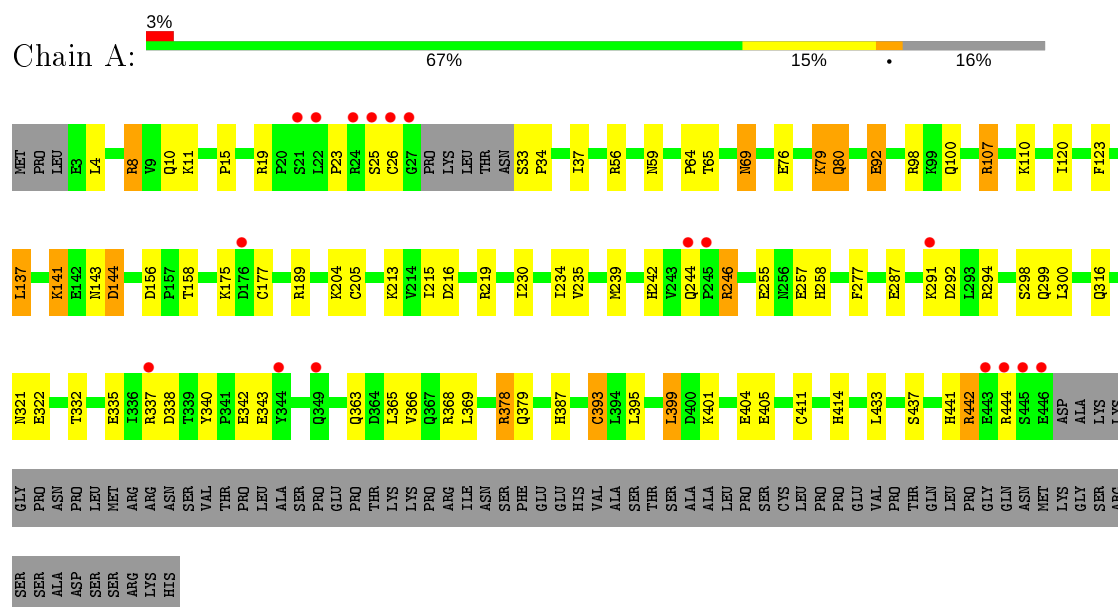
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	320	Total 320	O 320	0	0

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: 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	102.97Å 102.97Å 258.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.00 – 2.30 34.08 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (35.00-2.30) 99.8 (34.08-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.18 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.184 , 0.236 0.180 , 0.233	Depositor DCC
R_{free} test set	1836 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	38.0	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3959	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: SRT, POP, EDO

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	1.16	7/3660 (0.2%)	1.00	12/4946 (0.2%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	322	GLU	CB-CG	5.93	1.63	1.52
1	A	322	GLU	CG-CD	5.91	1.60	1.51
1	A	404	GLU	CG-CD	5.61	1.60	1.51
1	A	123	PHE	CE1-CZ	5.27	1.47	1.37
1	A	92	GLU	CG-CD	5.24	1.59	1.51
1	A	8	ARG	CG-CD	5.11	1.64	1.51
1	A	56	ARG	CG-CD	5.03	1.64	1.51

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	189	ARG	NE-CZ-NH1	7.55	124.08	120.30
1	A	378	ARG	NE-CZ-NH1	7.14	123.87	120.30
1	A	411	CYS	CA-CB-SG	-6.42	102.44	114.00
1	A	98	ARG	NE-CZ-NH2	-6.33	117.14	120.30
1	A	137	LEU	CA-CB-CG	6.15	129.44	115.30
1	A	378	ARG	NE-CZ-NH2	-6.00	117.30	120.30
1	A	338	ASP	CB-CG-OD1	5.81	123.53	118.30
1	A	189	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	A	393	CYS	CB-CA-C	5.44	121.27	110.40
1	A	292	ASP	N-CA-C	-5.36	96.54	111.00
1	A	246	ARG	NE-CZ-NH2	-5.29	117.66	120.30
1	A	98	ARG	NE-CZ-NH1	5.16	122.88	120.30

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	3584	0	3566	59	0
2	A	27	0	0	0	0
3	A	20	0	8	3	0
4	A	8	0	12	0	0
5	A	320	0	0	11	1
All	All	3959	0	3586	60	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 8.

All (60) 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:235:VAL:O	1:A:239:MET:HG3	1.63	0.96
1:A:19:ARG:HH11	1:A:23:PRO:HB3	1.35	0.91
1:A:100:GLN:HG2	5:A:666:HOH:O	1.73	0.88
1:A:255:GLU:H	1:A:414:HIS:HE1	1.25	0.82
1:A:107[A]:ARG:HH11	1:A:107[A]:ARG:HG2	1.50	0.75
1:A:25:SER:HB3	5:A:684:HOH:O	1.85	0.75
1:A:107[A]:ARG:NH1	1:A:107[A]:ARG:HG2	2.02	0.73
1:A:19:ARG:HH11	1:A:23:PRO:CB	2.01	0.72
1:A:299:GLN:H	1:A:321:ASN:ND2	1.88	0.72
1:A:59:ASN:HD21	1:A:65:THR:H	1.38	0.70
1:A:175:LYS:HE3	5:A:829:HOH:O	1.90	0.70
1:A:107[A]:ARG:HH11	1:A:107[A]:ARG:CG	2.05	0.69
1:A:299:GLN:H	1:A:321:ASN:HD21	1.41	0.68
1:A:337:ARG:HD3	5:A:743:HOH:O	1.92	0.67
1:A:366:VAL:HG22	1:A:393:CYS:SG	2.37	0.65
1:A:298:SER:HB2	1:A:321:ASN:HD22	1.60	0.64
1:A:69:ASN:C	1:A:69:ASN:HD22	2.02	0.64
1:A:255:GLU:H	1:A:414:HIS:CE1	2.12	0.62
1:A:215:ILE:HG22	1:A:216:ASP:N	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:HIS:HA	5:A:566:HOH:O	2.01	0.59
1:A:19:ARG:NH1	1:A:23:PRO:CB	2.67	0.57
1:A:401:LYS:HB3	1:A:405:GLU:HG3	1.85	0.57
1:A:332:THR:OG1	1:A:335:GLU:HG3	2.05	0.56
1:A:19:ARG:NH1	1:A:23:PRO:HB3	2.14	0.56
1:A:442:ARG:HB2	1:A:442:ARG:HH11	1.71	0.56
1:A:277:PHE:CE1	1:A:433:LEU:HD12	2.41	0.55
1:A:216:ASP:O	1:A:219:ARG:HB2	2.09	0.53
1:A:340:TYR:HB3	1:A:343:GLU:HB2	1.91	0.53
1:A:395:LEU:HG	1:A:399:LEU:HD22	1.91	0.52
1:A:215:ILE:CG2	1:A:216:ASP:N	2.75	0.49
1:A:287:GLU:HG3	5:A:688:HOH:O	2.13	0.49
1:A:37:ILE:HD11	1:A:234:ILE:HD13	1.96	0.48
1:A:441:HIS:HB3	3:A:650:SRT:H2	1.95	0.48
1:A:378:ARG:NH2	3:A:700:SRT:O4	2.44	0.48
1:A:65:THR:HA	1:A:120:ILE:O	2.14	0.47
1:A:110:LYS:NZ	5:A:740:HOH:O	2.47	0.47
1:A:299:GLN:HG2	1:A:316:GLN:HE21	1.80	0.47
1:A:244:GLN:HB3	5:A:602:HOH:O	2.14	0.46
1:A:65:THR:HG23	1:A:120:ILE:HB	1.98	0.46
1:A:59:ASN:ND2	1:A:65:THR:H	2.12	0.46
1:A:156:ASP:OD1	1:A:158:THR:HB	2.15	0.45
1:A:300:LEU:HD12	1:A:387:HIS:CE1	2.52	0.45
1:A:294:ARG:HG3	1:A:379:GLN:NE2	2.31	0.45
1:A:204:LYS:HE2	5:A:755:HOH:O	2.17	0.44
1:A:213:LYS:NZ	5:A:607:HOH:O	2.51	0.44
1:A:143:ASN:O	1:A:144:ASP:HB2	2.18	0.43
1:A:337:ARG:HD2	5:A:820:HOH:O	2.18	0.43
1:A:10:GLN:O	1:A:11:LYS:HB2	2.19	0.43
1:A:4:LEU:HD23	1:A:15:PRO:HA	2.00	0.43
1:A:19:ARG:NH1	1:A:23:PRO:HB2	2.33	0.42
1:A:294:ARG:HG3	1:A:379:GLN:HE22	1.84	0.42
1:A:365:LEU:HD23	1:A:365:LEU:HA	1.78	0.42
1:A:33:SER:HA	1:A:34:PRO:HD3	1.73	0.41
1:A:141:LYS:HB2	1:A:141:LYS:HE2	1.62	0.41
1:A:10:GLN:NE2	1:A:363:GLN:HE22	2.19	0.41
1:A:414:HIS:CD2	1:A:437:SER:HB3	2.55	0.41
1:A:369:LEU:HD12	1:A:393:CYS:SG	2.62	0.41
1:A:59:ASN:ND2	1:A:64:PRO:HA	2.36	0.41
3:A:650:SRT:O1	3:A:650:SRT:C4	2.69	0.40
1:A:230:ILE:HD12	1:A:230:ILE:HA	1.90	0.40

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)
5:A:718:HOH:O	5:A:731:HOH:O[10_665]	2.07	0.13

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	436/520 (84%)	419 (96%)	14 (3%)	3 (1%)	22 26

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	79	LYS
1	A	80	GLN
1	A	291	LYS

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	397/468 (85%)	375 (94%)	22 (6%)	21 30

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ARG

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Mol	Chain	Res	Type
1	A	26	CYS
1	A	69	ASN
1	A	76	GLU
1	A	79	LYS
1	A	80	GLN
1	A	92	GLU
1	A	107[A]	ARG
1	A	107[B]	ARG
1	A	137	LEU
1	A	141	LYS
1	A	144	ASP
1	A	177	CYS
1	A	205	CYS
1	A	246	ARG
1	A	257	GLU
1	A	258	HIS
1	A	342	GLU
1	A	368	ARG
1	A	399	LEU
1	A	442	ARG
1	A	444	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	59	ASN
1	A	69	ASN
1	A	163	ASN
1	A	224	ASN
1	A	227	GLN
1	A	242	HIS
1	A	316	GLN
1	A	321	ASN
1	A	379	GLN
1	A	388	GLN
1	A	414	HIS

5.3.3 RNA ⓘ

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

7 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	$\# Z > 2$
4	EDO	A	800	-	3,3,3	0.29	0	2,2,2	1.17	0
2	POP	A	520	-	6,8,8	0.60	0	13,13,13	1.06	0
3	SRT	A	700	-	3,9,9	1.52	1 (33%)	6,12,12	3.97	4 (66%)
2	POP	A	600	-	6,8,8	0.64	0	13,13,13	1.62	3 (23%)
3	SRT	A	650	-	3,9,9	0.86	0	6,12,12	4.55	5 (83%)
2	POP	A	550	-	6,8,8	1.29	1 (16%)	13,13,13	0.95	1 (7%)
4	EDO	A	750	-	3,3,3	0.63	0	2,2,2	0.88	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
4	EDO	A	800	-	-	0/1/1/1	-
2	POP	A	520	-	-	5/6/6/6	-
3	SRT	A	700	-	-	4/4/12/12	-
2	POP	A	600	-	-	0/6/6/6	-
3	SRT	A	650	-	-	0/4/12/12	-
2	POP	A	550	-	-	0/6/6/6	-
4	EDO	A	750	-	-	0/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	700	SRT	O3-C3	2.43	1.47	1.42
2	A	550	POP	P2-O4	2.31	1.58	1.50

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	650	SRT	O2-C2-C3	-7.87	82.63	108.90
3	A	700	SRT	C4-C3-C2	-6.18	99.81	113.11
3	A	650	SRT	O3-C3-C2	-5.25	91.37	108.90
3	A	700	SRT	O2-C2-C1	4.70	122.42	111.10
3	A	700	SRT	O2-C2-C3	-4.29	94.58	108.90
3	A	650	SRT	O3-C3-C4	4.15	121.09	111.10
3	A	700	SRT	O3-C3-C4	3.75	120.14	111.10
3	A	650	SRT	O2-C2-C1	3.12	118.61	111.10
2	A	600	POP	O2-P1-O	-3.06	94.37	104.64
3	A	650	SRT	C1-C2-C3	-2.59	107.52	113.11
2	A	600	POP	O5-P2-O4	2.50	120.46	110.68
2	A	550	POP	O6-P2-O	2.22	112.08	104.64
2	A	600	POP	O6-P2-O	2.12	111.75	104.64

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	520	POP	P2-O-P1-O2
2	A	520	POP	P1-O-P2-O5
3	A	700	SRT	C1-C2-C3-C4
3	A	700	SRT	O2-C2-C3-O3
3	A	700	SRT	O2-C2-C3-C4
3	A	700	SRT	C1-C2-C3-O3
2	A	520	POP	P1-O-P2-O6
2	A	520	POP	P2-O-P1-O1
2	A	520	POP	P2-O-P1-O3

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	700	SRT	1	0
3	A	650	SRT	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95th 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 ²)	Q<0.9
1	A	439/520 (84%)	-0.19	17 (3%)	39 46	21, 37, 72, 110	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	26	CYS	9.3
1	A	444	ARG	4.7
1	A	21	SER	4.1
1	A	446	GLU	3.5
1	A	27	GLY	3.2
1	A	22	LEU	3.0
1	A	445	SER	2.9
1	A	244	GLN	2.7
1	A	443	GLU	2.7
1	A	337	ARG	2.6
1	A	344	TYR	2.4
1	A	245	PRO	2.3
1	A	25	SER	2.2
1	A	24	ARG	2.2
1	A	349	GLN	2.1
1	A	291	LYS	2.1
1	A	176	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 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. The B-factors column lists the minimum, median, 95th 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(\AA^2)	Q<0.9
3	SRT	A	700	10/10	0.81	0.18	48,64,69,75	0
3	SRT	A	650	10/10	0.88	0.13	49,58,64,65	0
2	POP	A	600	9/9	0.92	0.15	47,51,58,58	0
4	EDO	A	750	4/4	0.92	0.20	45,46,49,50	0
4	EDO	A	800	4/4	0.98	0.10	34,35,36,38	0
2	POP	A	550	9/9	0.99	0.11	22,26,28,30	0
2	POP	A	520	9/9	0.99	0.09	33,36,40,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.