



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:30 PM GMT

PDB ID : 4LRE
Title : Phosphopentomutase soaked with 2,3-dideoxyribose 5-phosphate
Authors : Birmingham, W.A.; Starbird, C.A.; Panosian, T.D.; Nannemann, D.P.; Iversen, T.M.; Bachmann, B.O.
Deposited on : 2013-07-19
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/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 : 1.7 (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

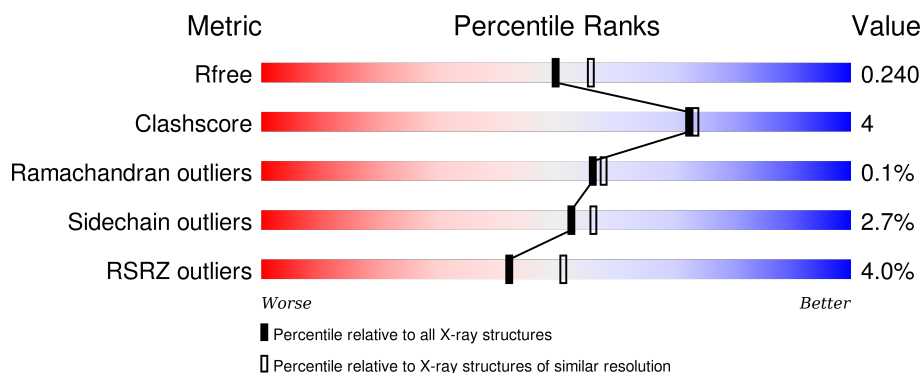
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
R_{free}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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. 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	416	 2% 83% 11% 6%
1	B	416	 2% 84% 10% 6%
1	C	416	 7% 82% 11% 6%

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	MN	B	402	-	-	-	X
3	1X4	A	404	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9898 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 Phosphopentomutase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	391	Total	C	N	O	P	S	14	0	0
			3068	1939	505	606	1	17			
1	B	391	Total	C	N	O	P	S	7	0	0
			3068	1939	505	606	1	17			
1	C	390	Total	C	N	O	P	S	47	0	0
			3060	1935	503	604	1	17			

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	EXPRESSION TAG	UNP Q818Z9
A	-20	GLY	-	EXPRESSION TAG	UNP Q818Z9
A	-19	SER	-	EXPRESSION TAG	UNP Q818Z9
A	-18	SER	-	EXPRESSION TAG	UNP Q818Z9
A	-17	HIS	-	EXPRESSION TAG	UNP Q818Z9
A	-16	HIS	-	EXPRESSION TAG	UNP Q818Z9
A	-15	HIS	-	EXPRESSION TAG	UNP Q818Z9
A	-14	HIS	-	EXPRESSION TAG	UNP Q818Z9
A	-13	HIS	-	EXPRESSION TAG	UNP Q818Z9
A	-12	HIS	-	EXPRESSION TAG	UNP Q818Z9
A	-11	SER	-	EXPRESSION TAG	UNP Q818Z9
A	-10	SER	-	EXPRESSION TAG	UNP Q818Z9
A	-9	GLY	-	EXPRESSION TAG	UNP Q818Z9
A	-8	LEU	-	EXPRESSION TAG	UNP Q818Z9
A	-7	VAL	-	EXPRESSION TAG	UNP Q818Z9
A	-6	PRO	-	EXPRESSION TAG	UNP Q818Z9
A	-5	ARG	-	EXPRESSION TAG	UNP Q818Z9
A	-4	GLY	-	EXPRESSION TAG	UNP Q818Z9
A	-3	SER	-	EXPRESSION TAG	UNP Q818Z9
A	-2	HIS	-	EXPRESSION TAG	UNP Q818Z9
A	-1	MET	-	EXPRESSION TAG	UNP Q818Z9
A	0	ALA	-	EXPRESSION TAG	UNP Q818Z9
A	1	SER	-	EXPRESSION TAG	UNP Q818Z9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-21	MET	-	EXPRESSION TAG	UNP Q818Z9
B	-20	GLY	-	EXPRESSION TAG	UNP Q818Z9
B	-19	SER	-	EXPRESSION TAG	UNP Q818Z9
B	-18	SER	-	EXPRESSION TAG	UNP Q818Z9
B	-17	HIS	-	EXPRESSION TAG	UNP Q818Z9
B	-16	HIS	-	EXPRESSION TAG	UNP Q818Z9
B	-15	HIS	-	EXPRESSION TAG	UNP Q818Z9
B	-14	HIS	-	EXPRESSION TAG	UNP Q818Z9
B	-13	HIS	-	EXPRESSION TAG	UNP Q818Z9
B	-12	HIS	-	EXPRESSION TAG	UNP Q818Z9
B	-11	SER	-	EXPRESSION TAG	UNP Q818Z9
B	-10	SER	-	EXPRESSION TAG	UNP Q818Z9
B	-9	GLY	-	EXPRESSION TAG	UNP Q818Z9
B	-8	LEU	-	EXPRESSION TAG	UNP Q818Z9
B	-7	VAL	-	EXPRESSION TAG	UNP Q818Z9
B	-6	PRO	-	EXPRESSION TAG	UNP Q818Z9
B	-5	ARG	-	EXPRESSION TAG	UNP Q818Z9
B	-4	GLY	-	EXPRESSION TAG	UNP Q818Z9
B	-3	SER	-	EXPRESSION TAG	UNP Q818Z9
B	-2	HIS	-	EXPRESSION TAG	UNP Q818Z9
B	-1	MET	-	EXPRESSION TAG	UNP Q818Z9
B	0	ALA	-	EXPRESSION TAG	UNP Q818Z9
B	1	SER	-	EXPRESSION TAG	UNP Q818Z9
C	-21	MET	-	EXPRESSION TAG	UNP Q818Z9
C	-20	GLY	-	EXPRESSION TAG	UNP Q818Z9
C	-19	SER	-	EXPRESSION TAG	UNP Q818Z9
C	-18	SER	-	EXPRESSION TAG	UNP Q818Z9
C	-17	HIS	-	EXPRESSION TAG	UNP Q818Z9
C	-16	HIS	-	EXPRESSION TAG	UNP Q818Z9
C	-15	HIS	-	EXPRESSION TAG	UNP Q818Z9
C	-14	HIS	-	EXPRESSION TAG	UNP Q818Z9
C	-13	HIS	-	EXPRESSION TAG	UNP Q818Z9
C	-12	HIS	-	EXPRESSION TAG	UNP Q818Z9
C	-11	SER	-	EXPRESSION TAG	UNP Q818Z9
C	-10	SER	-	EXPRESSION TAG	UNP Q818Z9
C	-9	GLY	-	EXPRESSION TAG	UNP Q818Z9
C	-8	LEU	-	EXPRESSION TAG	UNP Q818Z9
C	-7	VAL	-	EXPRESSION TAG	UNP Q818Z9
C	-6	PRO	-	EXPRESSION TAG	UNP Q818Z9
C	-5	ARG	-	EXPRESSION TAG	UNP Q818Z9
C	-4	GLY	-	EXPRESSION TAG	UNP Q818Z9
C	-3	SER	-	EXPRESSION TAG	UNP Q818Z9

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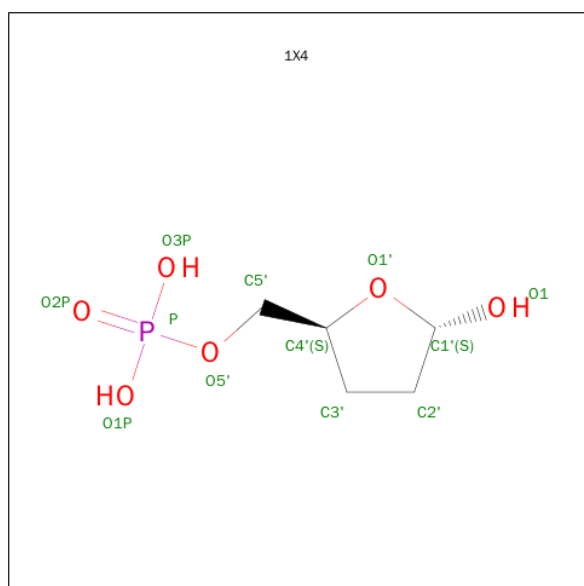
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	HIS	-	EXPRESSION TAG	UNP Q818Z9
C	-1	MET	-	EXPRESSION TAG	UNP Q818Z9
C	0	ALA	-	EXPRESSION TAG	UNP Q818Z9
C	1	SER	-	EXPRESSION TAG	UNP Q818Z9

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	4	Total Mn 4 4	0	0
2	A	3	Total Mn 3 3	0	0
2	C	3	Total Mn 3 3	0	0

- Molecule 3 is 2,3-DIDEOXYRIBOSE-5-PHOSPHATE (three-letter code: 1X4) (formula: C₅H₁₁O₆P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O P 12 5 6 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	246	Total 246	O 246	0	0
4	B	294	Total 294	O 294	0	0
4	C	140	Total 140	O 140	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.50 Å 76.52 Å 107.29 Å 90.00° 108.76° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 19.99 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.5 (20.00-2.10) 96.5 (19.99-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 2.09 Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.193 , 0.239 0.194 , 0.240	Depositor DCC
R_{free} test set	4048 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	23.5	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 47.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 79129 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9898	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, MN, 1X4

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	0.48	1/3117 (0.0%)	0.60	0/4208
1	B	0.48	0/3117	0.63	1/4208 (0.0%)
1	C	0.70	3/3109 (0.1%)	0.72	8/4197 (0.2%)
All	All	0.56	4/9343 (0.0%)	0.65	9/12613 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	118	GLU	CB-CG	19.64	1.89	1.52
1	C	187	GLU	CA-CB	-15.69	1.19	1.53
1	C	110	LYS	CB-CG	11.50	1.83	1.52
1	A	257	LYS	CB-CG	-8.28	1.30	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	187	GLU	CB-CA-C	-11.32	87.75	110.40
1	C	187	GLU	N-CA-CB	10.48	129.46	110.60
1	C	110	LYS	CA-CB-CG	-8.85	93.94	113.40
1	C	111	GLU	CB-CG-CD	-7.97	92.68	114.20
1	C	187	GLU	CA-CB-CG	-6.68	98.69	113.40
1	C	182	GLU	CG-CD-OE1	-6.16	105.98	118.30
1	C	182	GLU	CG-CD-OE2	6.11	130.51	118.30
1	B	362	LEU	CA-CB-CG	5.68	128.37	115.30
1	C	362	LEU	CA-CB-CG	5.55	128.07	115.30

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	3068	0	3007	30	0
1	B	3068	0	3007	25	0
1	C	3060	0	3001	25	0
2	A	3	0	0	0	0
2	B	4	0	0	0	0
2	C	3	0	0	0	0
3	A	12	0	11	0	0
4	A	246	0	0	2	0
4	B	294	0	0	3	0
4	C	140	0	0	1	0
All	All	9898	0	9026	76	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 4.

All (76) 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:B:4:TYR:H	1:B:376:ASN:HD21	1.10	0.99
1:A:4:TYR:H	1:A:376:ASN:HD21	1.07	0.93
1:A:164:HIS:HD2	1:A:166:GLU:H	1.16	0.93
1:C:4:TYR:H	1:C:376:ASN:HD21	1.17	0.92
1:B:164:HIS:HD2	1:B:166:GLU:H	1.27	0.81
1:C:164:HIS:HD2	1:C:166:GLU:H	1.33	0.74
1:B:227:GLU:OE2	4:B:767:HOH:O	2.07	0.72
1:A:164:HIS:CD2	1:A:166:GLU:H	2.08	0.64
1:B:45:GLN:H	1:B:303:GLN:HE21	1.45	0.63
1:A:45:GLN:H	1:A:303:GLN:HE21	1.46	0.63
1:B:56:ASN:HD21	1:B:66:VAL:H	1.46	0.62
1:A:4:TYR:N	1:A:376:ASN:HD21	1.88	0.62
1:B:164:HIS:CD2	1:B:166:GLU:H	2.15	0.62
1:B:28:ASP:OD1	4:B:736:HOH:O	2.16	0.61
1:B:227:GLU:HG3	1:B:379:VAL:HB	1.83	0.60
1:A:36:HIS:HD2	1:A:331:ASP:OD2	1.86	0.58
1:B:232:ASP:OD1	1:C:213:HIS:HE1	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:GLU:HB2	1:A:203:PRO:HD2	1.85	0.57
1:A:56:ASN:HD21	1:A:66:VAL:H	1.53	0.57
1:C:101:PHE:HE2	1:C:217:LEU:HD23	1.69	0.57
1:C:14:SER:HB2	1:C:330:ASN:HB2	1.86	0.57
1:A:202:GLU:HB2	1:A:203:PRO:CD	2.35	0.56
1:A:85:TPO:O1P	1:A:339:HIS:HE1	1.89	0.56
1:C:164:HIS:HE1	1:C:201:GLY:O	1.88	0.56
1:B:164:HIS:HE1	1:B:201:GLY:O	1.88	0.56
1:A:14:SER:HB2	1:A:330:ASN:HB2	1.88	0.56
1:B:213:HIS:HD2	1:C:234:ASP:OD1	1.88	0.56
1:A:85:TPO:O1P	1:A:339:HIS:CE1	2.59	0.55
1:B:4:TYR:H	1:B:376:ASN:ND2	1.93	0.54
1:A:333:ILE:HG22	1:A:333:ILE:O	2.07	0.54
1:A:36:HIS:CD2	1:A:331:ASP:OD2	2.61	0.53
1:C:56:ASN:HD21	1:C:66:VAL:H	1.55	0.53
1:C:40:HIS:HB2	4:C:512:HOH:O	2.09	0.53
1:C:158:VAL:HG12	1:C:193:ARG:HB3	1.91	0.52
1:A:164:HIS:HE1	1:A:201:GLY:O	1.93	0.51
1:B:119:LYS:HE3	1:B:183:LEU:HD21	1.92	0.51
1:A:212:ARG:HD3	1:A:214:ASP:OD1	2.10	0.51
1:A:256:THR:HG21	1:A:262:GLY:HA2	1.94	0.50
1:A:158:VAL:HG12	1:A:193:ARG:HB3	1.92	0.50
1:C:143:GLN:HG2	1:C:148:SER:O	2.12	0.49
1:A:45:GLN:H	1:A:303:GLN:NE2	2.10	0.49
1:B:222:ARG:NH2	1:B:230:ASP:OD1	2.38	0.48
1:B:14:SER:HB2	1:B:330:ASN:HB2	1.93	0.48
1:C:85:TPO:O	1:C:89:HIS:HD2	1.97	0.47
1:C:256:THR:HG21	1:C:262:GLY:HA2	1.96	0.47
1:B:143:GLN:HG2	1:B:148:SER:O	2.15	0.47
1:C:45:GLN:H	1:C:303:GLN:HE21	1.64	0.46
1:B:21:PRO:HD3	1:B:343:TYR:CZ	2.51	0.46
1:A:143:GLN:HG2	1:A:148:SER:O	2.15	0.46
1:A:141:GLN:HG3	1:A:203:PRO:HG3	1.99	0.45
1:B:22:ASP:O	1:B:25:GLN:HG2	2.17	0.45
1:A:6:ARG:HD2	1:A:274:PHE:CE1	2.51	0.45
1:C:331:ASP:HB3	1:C:334:HIS:HB2	1.99	0.45
1:A:14:SER:HB2	1:A:330:ASN:CB	2.48	0.44
1:B:234:ASP:OD1	1:C:213:HIS:HD2	2.01	0.43
1:C:363:ARG:NE	1:C:368:ASP:OD1	2.51	0.43
1:A:36:HIS:HB3	1:A:333:ILE:HD12	2.00	0.43
1:A:128:LYS:HE2	4:A:746:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:56:ASN:HD21	1:C:66:VAL:HG22	1.84	0.42
1:B:32:ASP:OD2	1:B:58:ARG:NH2	2.42	0.42
1:C:14:SER:HB2	1:C:330:ASN:CB	2.47	0.42
1:B:133:THR:OG1	1:B:208:ARG:NH1	2.52	0.42
1:B:16:GLY:O	1:B:34:ILE:HG13	2.18	0.42
1:B:68:LYS:HE2	4:B:688:HOH:O	2.20	0.42
1:A:56:ASN:HB3	1:A:73:TYR:CE2	2.55	0.42
1:C:45:GLN:H	1:C:303:GLN:NE2	2.17	0.42
1:B:232:ASP:OD1	1:C:213:HIS:CE1	2.71	0.41
1:C:90:TRP:HB3	1:C:95:LEU:HD12	2.02	0.41
1:C:50:VAL:HG22	1:C:63:ILE:HG23	2.01	0.41
1:C:238:ILE:HD11	1:C:269:THR:HG21	2.02	0.41
1:A:85:TPO:O2P	1:A:286:ASP:OD1	2.38	0.41
1:C:181:ARG:O	1:C:185:LEU:HD13	2.21	0.41
1:B:56:ASN:HD22	1:B:56:ASN:H	1.69	0.41
1:A:52:LEU:HA	1:A:70:LEU:HB2	2.03	0.41
1:A:202:GLU:HB3	4:A:651:HOH:O	2.21	0.40
1:A:79:LYS:HD2	1:A:365:THR:HB	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	388/416 (93%)	374 (96%)	13 (3%)	1 (0%)	46	45
1	B	388/416 (93%)	375 (97%)	13 (3%)	0	100	100
1	C	387/416 (93%)	369 (95%)	18 (5%)	0	100	100
All	All	1163/1248 (93%)	1118 (96%)	44 (4%)	1 (0%)	56	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	328	HIS

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	332/353 (94%)	324 (98%)	8 (2%)	57	61
1	B	332/353 (94%)	324 (98%)	8 (2%)	57	61
1	C	331/353 (94%)	320 (97%)	11 (3%)	45	47
All	All	995/1059 (94%)	968 (97%)	27 (3%)	52	56

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	135	ILE
1	A	136	LEU
1	A	189	TYR
1	A	212	ARG
1	A	279	PHE
1	A	281	ASN
1	A	298	TYR
1	A	360	LEU
1	B	67	GLU
1	B	110	LYS
1	B	189	TYR
1	B	279	PHE
1	B	281	ASN
1	B	298	TYR
1	B	362	LEU
1	B	391	GLU
1	C	65	LYS
1	C	110	LYS
1	C	185	LEU
1	C	189	TYR
1	C	191	VAL
1	C	217	LEU

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Mol	Chain	Res	Type
1	C	279	PHE
1	C	298	TYR
1	C	316	LEU
1	C	360	LEU
1	C	362	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	HIS
1	A	48	ASN
1	A	56	ASN
1	A	89	HIS
1	A	164	HIS
1	A	205	ASN
1	A	259	ASN
1	A	281	ASN
1	A	303	GLN
1	A	358	GLN
1	A	376	ASN
1	A	390	ASN
1	B	56	ASN
1	B	89	HIS
1	B	102	GLN
1	B	164	HIS
1	B	205	ASN
1	B	211	ASN
1	B	213	HIS
1	B	259	ASN
1	B	281	ASN
1	B	303	GLN
1	B	376	ASN
1	C	45	GLN
1	C	56	ASN
1	C	77	GLN
1	C	89	HIS
1	C	164	HIS
1	C	213	HIS
1	C	259	ASN
1	C	281	ASN
1	C	303	GLN
1	C	376	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 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	85	1,2	8,10,11	0.46	0	7,14,16	1.59	1 (14%)
1	TPO	B	85	1,2	8,10,11	0.74	0	7,14,16	1.21	0
1	TPO	C	85	1,2	8,10,11	0.71	0	7,14,16	1.12	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
1	TPO	A	85	1,2	-	0/8/11/13	0/0/0/0
1	TPO	B	85	1,2	-	0/8/11/13	0/0/0/0
1	TPO	C	85	1,2	-	0/8/11/13	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	85	TPO	O2P-P-O1P	2.14	117.46	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	85	TPO	3	0
1	C	85	TPO	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 10 are monoatomic - leaving 1 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	1X4	A	404	-	12,12,12	1.37	1 (8%)	10,17,17	1.37	1 (10%)

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	1X4	A	404	-	-	0/6/15/15	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	404	1X4	P-O2P	3.49	1.62	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	404	1X4	O3P-P-O5'	2.64	114.17	106.56

There are no chirality outliers.

There are no torsion outliers.

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

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, 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	390/416 (93%)	0.03	8 (2%) 67 72	15, 21, 31, 36	17 (4%)
1	B	390/416 (93%)	0.15	10 (2%) 59 66	15, 21, 30, 43	13 (3%)
1	C	389/416 (93%)	0.49	29 (7%) 17 23	18, 27, 39, 46	23 (5%)
All	All	1169/1248 (93%)	0.23	47 (4%) 42 51	15, 23, 35, 46	53 (4%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	ASN	5.1
1	C	355	GLU	4.8
1	C	105	PRO	4.6
1	B	222	ARG	4.3
1	C	204	GLY	4.1
1	C	189	TYR	3.7
1	C	42	ASN	3.4
1	C	64	SER	3.3
1	C	318	GLU	3.3
1	C	161	ILE	3.1
1	B	212	ARG	3.0
1	C	110	LYS	2.9
1	C	364	GLN	2.8
1	C	212	ARG	2.8
1	A	202	GLU	2.7
1	B	355	GLU	2.7
1	C	390	ASN	2.7
1	B	67	GLU	2.7
1	C	133	THR	2.6
1	C	67	GLU	2.6
1	C	114	ASP	2.5
1	C	66	VAL	2.5
1	C	104	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	154	SER	2.4
1	C	155	ALA	2.4
1	A	161	ILE	2.3
1	C	99	THR	2.3
1	C	383	GLU	2.3
1	B	162	ALA	2.3
1	A	150	ILE	2.3
1	C	203	PRO	2.2
1	B	106	GLU	2.2
1	C	132	GLY	2.2
1	C	186	ASP	2.2
1	A	203	PRO	2.2
1	A	133	THR	2.2
1	C	292	ARG	2.2
1	A	204	GLY	2.2
1	A	106	GLU	2.1
1	C	102	GLN	2.1
1	B	118	GLU	2.1
1	C	61	LYS	2.1
1	A	205	ASN	2.1
1	B	390	ASN	2.0
1	B	236	ILE	2.0
1	C	129	PRO	2.0
1	C	202	GLU	2.0

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, 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	LLDF	B-factors(Å ²)	Q<0.9
1	TPO	A	85	11/12	0.96	0.16	-	18,19,20,20	4
1	TPO	B	85	11/12	0.96	0.16	-	20,22,24,24	4
1	TPO	C	85	11/12	0.94	0.16	-	25,26,28,28	4

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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	1X4	A	404	12/12	0.79	0.26	10.32	35,35,36,36	12
2	MN	B	402	1/1	1.00	0.13	2.44	22,22,22,22	0
2	MN	B	401	1/1	1.00	0.13	1.31	21,21,21,21	0
2	MN	C	402	1/1	0.99	0.12	0.19	27,27,27,27	0
2	MN	A	402	1/1	0.99	0.12	0.02	22,22,22,22	0
2	MN	A	401	1/1	1.00	0.12	-0.11	19,19,19,19	0
2	MN	C	401	1/1	0.99	0.10	-0.69	29,29,29,29	0
2	MN	B	403	1/1	0.94	0.10	-1.18	49,49,49,49	1
2	MN	C	403	1/1	0.98	0.05	-3.13	46,46,46,46	0
2	MN	A	403	1/1	0.98	0.04	-3.64	33,33,33,33	1
2	MN	B	404	1/1	0.80	0.09	-	54,54,54,54	1

6.5 Other polymers [i](#)

There are no such residues in this entry.