



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 11, 2023 – 05:52 PM EDT

PDB ID : 4LRC
Title : Phosphopentomutase V158L variant
Authors : Birmingham, W.A.; Starbird, C.A.; Panosian, T.D.; Nannemann, D.P.; Iverson, T.M.; Bachmann, B.O.
Deposited on : 2013-07-19
Resolution : 1.89 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 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

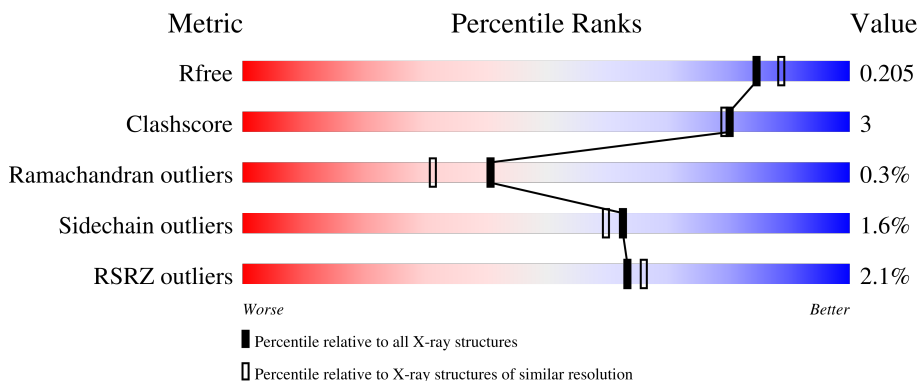
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 $\leq 5\%$. 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	 5% 88% 6% 6%
1	B	416	 87% 7% 6%
1	C	416	 5% 82% 11% 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9965 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
			Total	C	N	O	P	S			
1	A	391	Total 3069	C 1940	N 505	O 606	P 1	S 17	0	0	0
1	B	390	Total 3053	C 1932	N 503	O 600	P 1	S 17	0	0	0
1	C	390	Total 3067	C 1941	N 504	O 603	P 1	S 18	2	2	0

There are 72 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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	158	LEU	VAL	engineered mutation	UNP Q818Z9
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
B	158	LEU	VAL	engineered mutation	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

Continued on next page...

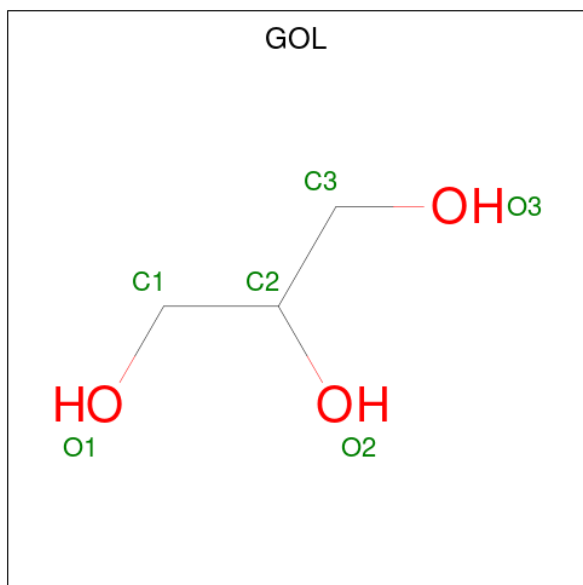
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	GLY	-	expression tag	UNP Q818Z9
C	-3	SER	-	expression tag	UNP Q818Z9
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
C	158	LEU	VAL	engineered mutation	UNP Q818Z9

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

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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	B	1	6	3	3	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

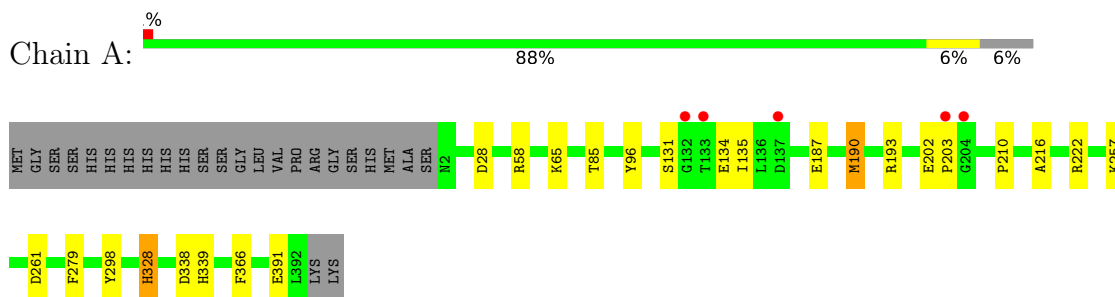
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	283	283	283	0	0
5	B	308	308	308	0	0
5	C	155	155	155	0	0

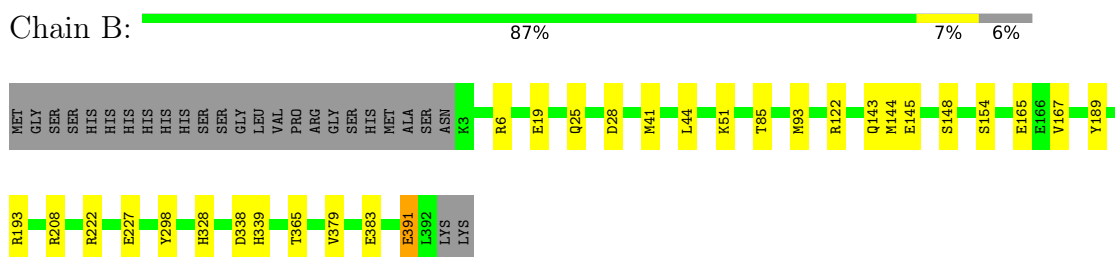
3 Residue-property plots [i](#)

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.

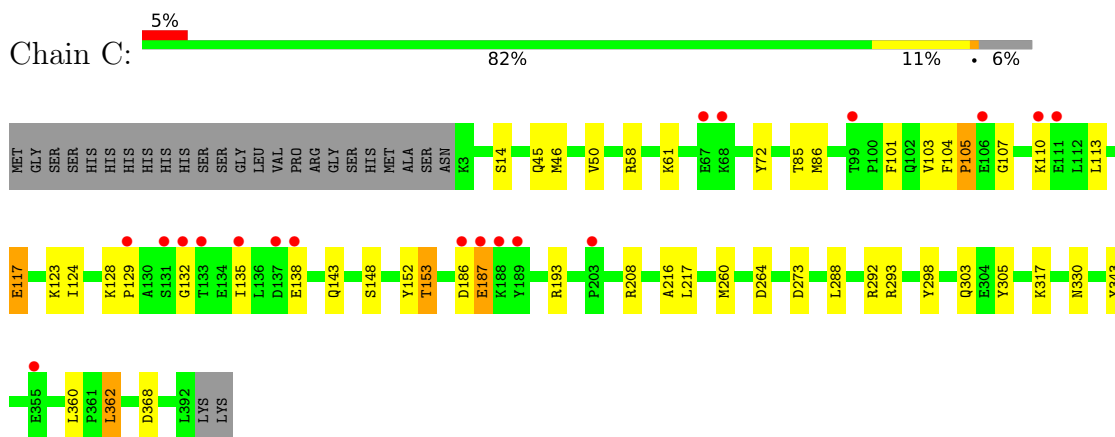
• Molecule 1: Phosphopentomutase



• Molecule 1: Phosphopentomutase



• Molecule 1: Phosphopentomutase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.72Å 76.80Å 107.17Å 90.00° 108.70° 90.00°	Depositor
Resolution (Å)	38.78 – 1.89 38.75 – 1.89	Depositor EDS
% Data completeness (in resolution range)	91.3 (38.78-1.89) 91.4 (38.75-1.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.45 (at 1.89Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.155 , 0.197 0.167 , 0.205	Depositor DCC
R_{free} test set	4956 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	19.6	Xtrriage
Anisotropy	0.644	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 54.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9965	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, MN, GOL, ACT

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	1.03	0/3118	1.04	10/4209 (0.2%)
1	B	1.00	2/3102 (0.1%)	1.02	8/4188 (0.2%)
1	C	1.37	9/3119 (0.3%)	0.96	6/4210 (0.1%)
All	All	1.15	11/9339 (0.1%)	1.01	24/12607 (0.2%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	117[A]	GLU	CD-OE1	-33.66	0.88	1.25
1	C	117[B]	GLU	CD-OE1	-33.66	0.88	1.25
1	C	117[A]	GLU	CD-OE2	-16.82	1.07	1.25
1	C	117[B]	GLU	CD-OE2	-16.82	1.07	1.25
1	C	186	ASP	CG-OD2	14.87	1.59	1.25
1	C	117[A]	GLU	CG-CD	-9.72	1.37	1.51
1	C	117[B]	GLU	CG-CD	-9.72	1.37	1.51
1	C	186	ASP	CG-OD1	5.95	1.39	1.25
1	B	391	GLU	CD-OE2	5.52	1.31	1.25
1	C	305	TYR	CG-CD1	5.24	1.46	1.39
1	B	19	GLU	CD-OE2	-5.00	1.20	1.25

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	186	ASP	CB-CG-OD1	-11.60	107.86	118.30
1	A	190	MET	CG-SD-CE	-11.28	82.15	100.20
1	B	222	ARG	NE-CZ-NH2	-9.21	115.69	120.30
1	B	338	ASP	CB-CG-OD1	7.33	124.90	118.30
1	A	338	ASP	CB-CG-OD1	6.92	124.53	118.30
1	C	368	ASP	CB-CG-OD2	6.90	124.51	118.30
1	A	261	ASP	CB-CG-OD1	6.50	124.15	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	222	ARG	NE-CZ-NH1	-6.37	117.11	120.30
1	B	122	ARG	NE-CZ-NH1	6.35	123.47	120.30
1	B	222	ARG	NE-CZ-NH1	6.31	123.45	120.30
1	C	293	ARG	NE-CZ-NH2	-6.22	117.19	120.30
1	B	93	MET	CG-SD-CE	6.03	109.84	100.20
1	A	338	ASP	CB-CG-OD2	-5.89	113.00	118.30
1	C	186	ASP	OD1-CG-OD2	5.63	134.00	123.30
1	A	28	ASP	CB-CG-OD2	5.37	123.13	118.30
1	C	58	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	A	58	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	C	260	MET	CG-SD-CE	5.27	108.63	100.20
1	B	122	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	B	6	ARG	NE-CZ-NH2	5.22	122.91	120.30
1	B	338	ASP	CB-CG-OD2	-5.19	113.62	118.30
1	A	193	ARG	NE-CZ-NH2	-5.18	117.71	120.30
1	A	366	PHE	CB-CG-CD1	5.14	124.40	120.80
1	A	58	ARG	CG-CD-NE	-5.06	101.18	111.80

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	3069	0	3009	11	0
1	B	3053	0	2995	17	0
1	C	3067	0	3009	24	0
2	A	3	0	0	0	0
2	B	2	0	0	0	0
2	C	3	0	0	0	0
3	A	12	0	16	1	0
3	B	6	0	8	0	0
4	A	4	0	3	0	0
5	A	283	0	0	1	0
5	B	308	0	0	8	0
5	C	155	0	0	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	9965	0	9040	49	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 3.

All (49) 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:51:LYS:NZ	5:B:746:HOH:O	2.11	0.84
1:C:117[B]:GLU:HG2	1:C:123:LYS:HA	1.73	0.70
1:B:28:ASP:OD1	5:B:542:HOH:O	2.10	0.70
1:C:264:ASP:OD1	5:C:655:HOH:O	2.12	0.68
1:C:187:GLU:H	1:C:187:GLU:CD	1.98	0.67
1:A:187:GLU:HA	1:A:190:MET:HE3	1.78	0.66
1:B:383:GLU:OE1	5:B:807:HOH:O	2.14	0.64
1:C:72:TYR:HB3	1:C:360:LEU:HD21	1.82	0.62
1:A:216:ALA:HB1	5:A:729:HOH:O	2.01	0.58
1:C:193:ARG:NH1	1:C:216:ALA:HB2	2.17	0.58
1:C:86[A]:MET:HE1	5:C:564:HOH:O	2.04	0.58
1:C:45:GLN:H	1:C:303:GLN:HE21	1.52	0.57
1:A:131:SER:OG	1:A:134:GLU:HG3	2.09	0.52
1:C:113:LEU:HD13	1:C:124:ILE:HG21	1.90	0.52
1:C:288:LEU:O	1:C:292:ARG:HD2	2.09	0.52
1:B:143:GLN:HG2	1:B:148:SER:O	2.11	0.50
1:C:143:GLN:HG2	1:C:148:SER:O	2.11	0.50
1:C:72:TYR:HB3	1:C:360:LEU:CD2	2.43	0.49
1:A:190:MET:HE3	1:A:190:MET:HB2	1.69	0.48
1:A:257:LYS:HD2	1:B:145:GLU:OE1	2.13	0.48
1:C:187:GLU:CD	1:C:187:GLU:N	2.65	0.48
1:B:227:GLU:OE2	5:B:808:HOH:O	2.19	0.48
1:B:193:ARG:NH1	5:B:724:HOH:O	2.38	0.47
1:C:101:PHE:HE2	1:C:217:LEU:HD12	1.79	0.46
1:A:328:HIS:CE1	1:A:339:HIS:CE1	3.03	0.46
1:C:46:MET:O	1:C:50:VAL:HG23	2.16	0.46
1:C:86[B]:MET:CE	1:C:193:ARG:HH21	2.28	0.46
1:C:343:TYR:CE1	1:C:362:LEU:HD11	2.52	0.45
1:C:14:SER:HB2	1:C:330:ASN:HB2	1.98	0.44
1:A:202:GLU:HB2	1:A:203:PRO:HD2	1.99	0.44
1:C:128:LYS:NZ	1:C:138:GLU:OE1	2.36	0.44
1:C:129:PRO:CA	1:C:153:THR:HG22	2.48	0.44
1:C:103:VAL:HG23	1:C:105:PRO:HD2	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:208:ARG:NH1	5:B:804:HOH:O	2.50	0.43
1:A:202:GLU:HB2	1:A:203:PRO:CD	2.49	0.43
1:C:132:GLY:HA2	1:C:135:ILE:HG22	2.01	0.42
1:B:154:SER:HB2	5:B:760:HOH:O	2.19	0.42
1:A:135:ILE:HD12	1:A:135:ILE:HA	1.87	0.42
1:A:210:PRO:HG2	1:B:167:VAL:HG13	2.01	0.42
1:B:144:MET:HA	1:B:167:VAL:HG21	2.02	0.42
1:B:41:MET:HG3	1:B:44:LEU:HD13	2.02	0.42
1:B:165:GLU:OE2	1:C:273:ASP:OD2	2.37	0.42
1:B:227:GLU:HG3	1:B:379:VAL:HB	2.02	0.42
1:B:227:GLU:CG	1:B:379:VAL:HB	2.49	0.41
1:C:152:TYR:OH	1:C:208:ARG:NH2	2.47	0.41
1:A:96:TYR:CE1	3:A:404:GOL:H12	2.55	0.41
1:B:25:GLN:NE2	5:B:709:HOH:O	2.53	0.40
1:B:208:ARG:HH11	1:B:208:ARG:HG3	1.86	0.40
1:C:104:PHE:HB3	1:C:107:GLY:O	2.22	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%)	372 (96%)	15 (4%)	1 (0%)	41	31
1	B	387/416 (93%)	371 (96%)	14 (4%)	2 (0%)	29	18
1	C	389/416 (94%)	365 (94%)	24 (6%)	0	100	100
All	All	1164/1248 (93%)	1108 (95%)	53 (5%)	3 (0%)	41	31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	328	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	328	HIS
1	B	339	HIS

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	332/353 (94%)	328 (99%)	4 (1%)	71	70
1	B	329/353 (93%)	325 (99%)	4 (1%)	71	70
1	C	331/353 (94%)	323 (98%)	8 (2%)	49	43
All	All	992/1059 (94%)	976 (98%)	16 (2%)	62	60

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	LYS
1	A	279	PHE
1	A	298	TYR
1	A	391	GLU
1	B	189	TYR
1	B	298	TYR
1	B	365	THR
1	B	391	GLU
1	C	61	LYS
1	C	105	PRO
1	C	110	LYS
1	C	153	THR
1	C	187	GLU
1	C	298	TYR
1	C	317	LYS
1	C	362	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	205	ASN
1	C	303	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](#)

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	1.02	1 (12%)	10,14,16	0.97	1 (10%)
1	TPO	C	85	1,2	8,10,11	0.99	0	10,14,16	1.23	1 (10%)
1	TPO	B	85	1,2	8,10,11	1.92	1 (12%)	10,14,16	1.18	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	-	1/9/11/13	-
1	TPO	C	85	1,2	-	1/9/11/13	-
1	TPO	B	85	1,2	-	4/9/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	85	TPO	P-OG1	5.04	1.68	1.59
1	A	85	TPO	P-OG1	2.58	1.64	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	85	TPO	OG1-P-O1P	-2.24	100.74	109.39
1	A	85	TPO	O-C-CA	-2.09	119.29	124.78

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	85	TPO	O-C-CA-CB
1	B	85	TPO	O-C-CA-CB
1	B	85	TPO	C-CA-CB-CG2
1	B	85	TPO	CB-OG1-P-O1P
1	B	85	TPO	CB-OG1-P-O3P
1	C	85	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	ACT	A	406	-	3,3,3	0.60	0	3,3,3	1.14	0
3	GOL	A	405	-	5,5,5	0.62	0	5,5,5	0.40	0
3	GOL	A	404	-	5,5,5	0.86	0	5,5,5	1.43	1 (20%)
3	GOL	B	403	-	5,5,5	0.20	0	5,5,5	0.77	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
3	GOL	A	405	-	-	2/4/4/4	-
3	GOL	A	404	-	-	2/4/4/4	-
3	GOL	B	403	-	-	0/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	404	GOL	C3-C2-C1	2.58	121.73	111.70

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	405	GOL	O1-C1-C2-C3
3	A	405	GOL	O1-C1-C2-O2
3	A	404	GOL	O2-C2-C3-O3
3	A	404	GOL	C1-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	404	GOL	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, 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%)	-0.42	5 (1%) 77 79	10, 18, 39, 60	14 (3%)
1	B	389/416 (93%)	-0.48	0 100 100	10, 19, 36, 51	10 (2%)
1	C	389/416 (93%)	-0.08	19 (4%) 29 33	14, 30, 56, 86	9 (2%)
All	All	1168/1248 (93%)	-0.33	24 (2%) 63 66	10, 22, 46, 86	33 (2%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	133	THR	4.9
1	C	189	TYR	4.4
1	C	132	GLY	4.1
1	C	106	GLU	3.7
1	C	188	LYS	3.6
1	C	110	LYS	3.5
1	A	133	THR	3.1
1	A	137	ASP	3.1
1	C	131	SER	3.0
1	C	137	ASP	3.0
1	C	67	GLU	2.8
1	C	187	GLU	2.8
1	C	186	ASP	2.6
1	C	355	GLU	2.6
1	C	129	PRO	2.5
1	C	68	LYS	2.4
1	A	204	GLY	2.4
1	C	138	GLU	2.3
1	A	132	GLY	2.3
1	C	135	ILE	2.3
1	C	111	GLU	2.1
1	C	203	PRO	2.1
1	C	99	THR	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	203	PRO	2.1

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. 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(Å ²)	Q<0.9
1	TPO	C	85	11/12	0.91	0.13	18,27,67,71	0
1	TPO	B	85	11/12	0.94	0.12	12,18,61,67	0
1	TPO	A	85	11/12	0.95	0.11	12,15,55,58	0

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, 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(Å ²)	Q<0.9
4	ACT	A	406	4/4	0.74	0.20	46,55,56,61	0
3	GOL	A	404	6/6	0.92	0.13	33,35,41,42	0
3	GOL	A	405	6/6	0.94	0.15	19,42,45,46	0
3	GOL	B	403	6/6	0.95	0.09	26,31,36,36	0
2	MN	C	401	1/1	0.99	0.06	19,19,19,19	0
2	MN	C	402	1/1	0.99	0.09	22,22,22,22	0
2	MN	A	403	1/1	0.99	0.03	38,38,38,38	0
2	MN	C	403	1/1	1.00	0.02	41,41,41,41	0
2	MN	B	401	1/1	1.00	0.09	14,14,14,14	0
2	MN	B	402	1/1	1.00	0.09	13,13,13,13	0
2	MN	A	402	1/1	1.00	0.09	12,12,12,12	0
2	MN	A	401	1/1	1.00	0.10	12,12,12,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.