



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:18 PM GMT

PDB ID : 1T10
Title : Phosphoglucose isomerase from *Leishmania mexicana* in complex with substrate D-fructose-6-phosphate
Authors : Cordeiro, A.T.; Thiemann, O.T.
Deposited on : 2004-04-14
Resolution : 2.35 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

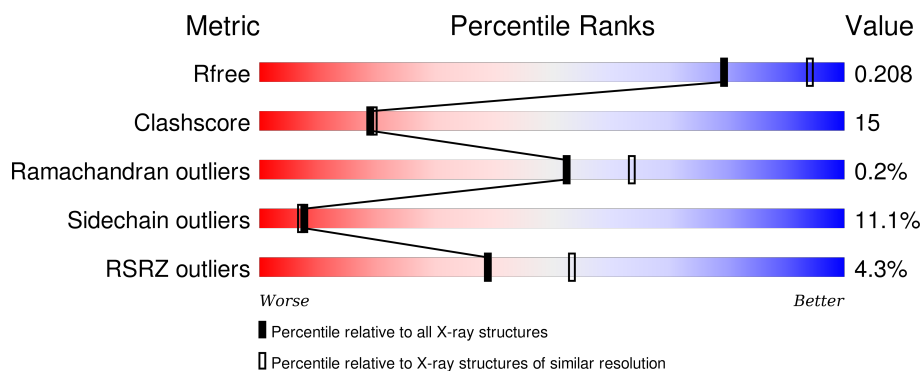
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

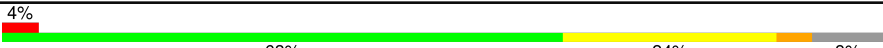
The reported resolution of this entry is 2.35 Å.

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	1352 (2.38-2.34)
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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	605	

2 Entry composition [i](#)

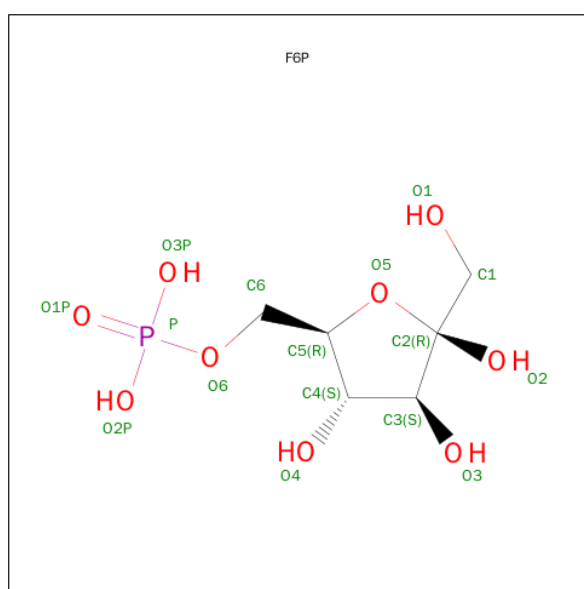
There are 3 unique types of molecules in this entry. The entry contains 4551 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glucose-6-phosphate isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	556	Total	C	N	O	S	0	0	0
			4355	2756	758	819	22			

- Molecule 2 is SUGAR (FRUCTOSE-6-PHOSPHATE) (three-letter code: F6P) (formula: $C_6H_{13}O_9P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			16	6	9	1		

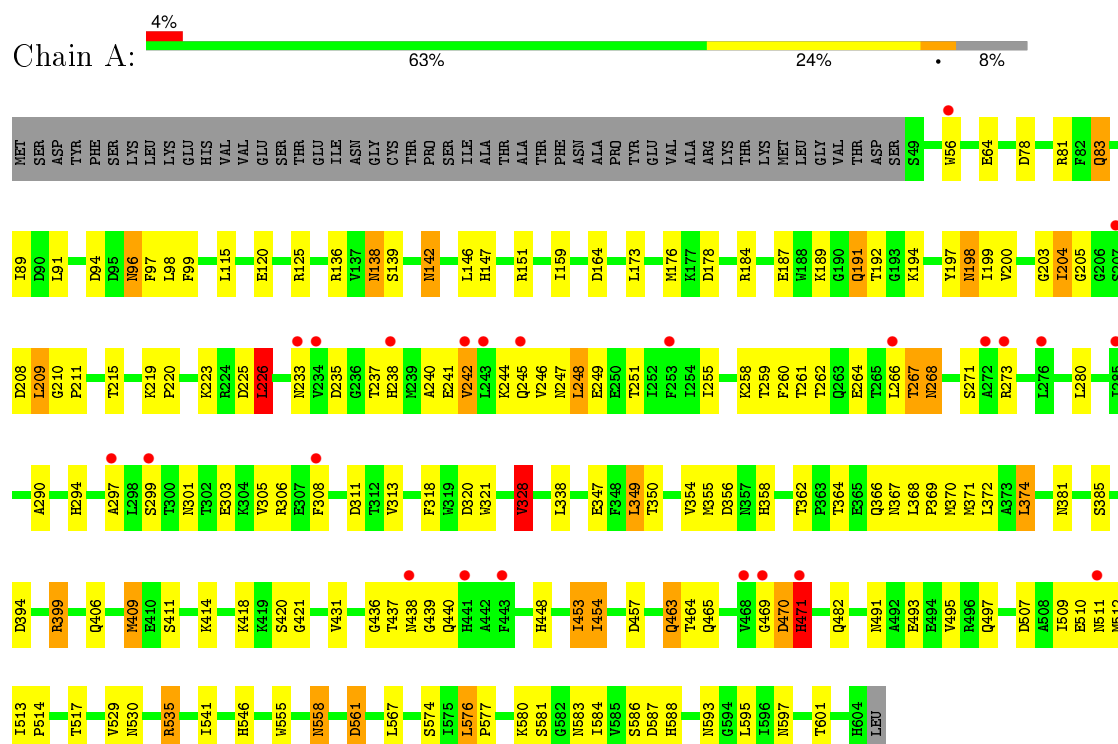
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	180	Total	O	0	0
			180	180		

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 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 ($RSRZ > 2$). 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: Glucose-6-phosphate isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	85.13Å 85.13Å 350.09Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	74.53 – 2.35 73.72 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.9 (74.53-2.35) 99.9 (73.72-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.51 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.1.09	Depositor
R, R_{free}	0.220 , 0.260 0.226 , 0.208	Depositor DCC
R_{free} test set	1648 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	53.1	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 47.9	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	0 of 32521 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4551	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: F6P

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	0.75	1/4447 (0.0%)	0.94	17/6020 (0.3%)

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	409	MET	SD-CE	-8.03	1.32	1.77

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	164	ASP	CB-CG-OD2	7.89	125.41	118.30
1	A	235	ASP	CB-CG-OD2	7.89	125.41	118.30
1	A	561	ASP	CB-CG-OD2	7.36	124.93	118.30
1	A	587	ASP	CB-CG-OD2	6.99	124.59	118.30
1	A	470	ASP	CB-CG-OD2	6.48	124.13	118.30
1	A	226	LEU	CA-CB-CG	5.86	128.77	115.30
1	A	311	ASP	CB-CG-OD2	5.80	123.52	118.30
1	A	349	LEU	CA-CB-CG	5.78	128.59	115.30
1	A	178	ASP	CB-CG-OD2	5.52	123.27	118.30
1	A	225	ASP	CB-CG-OD2	5.42	123.17	118.30
1	A	535	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	A	394	ASP	CB-CG-OD2	5.25	123.02	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	208	ASP	CB-CG-OD2	5.15	122.94	118.30
1	A	328	VAL	CB-CA-C	-5.13	101.64	111.40
1	A	94	ASP	CB-CG-OD2	5.13	122.92	118.30
1	A	507	ASP	CB-CG-OD2	5.03	122.83	118.30
1	A	457	ASP	CB-CG-OD2	5.01	122.81	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	436	GLY	Peptide

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	4355	0	4274	130	0
2	A	16	0	11	2	0
3	A	180	0	0	41	0
All	All	4551	0	4285	132	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 15.

All (132) 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:454:ILE:HG21	3:A:1004:HOH:O	1.33	1.29
1:A:355:MET:SD	3:A:1062:HOH:O	1.95	1.22
1:A:597:ASN:O	1:A:601:THR:HG23	1.57	1.02
1:A:199:ILE:HD13	1:A:338:LEU:HD13	1.46	0.97
1:A:96:ASN:HD22	1:A:97:PHE:H	1.16	0.94
1:A:409:MET:HE2	1:A:431:VAL:H	1.32	0.92
1:A:198:ASN:CG	3:A:1124:HOH:O	2.08	0.92
1:A:233:ASN:HD21	1:A:238:HIS:H	1.19	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:ASN:ND2	3:A:1124:HOH:O	2.08	0.85
1:A:409:MET:CE	1:A:431:VAL:H	1.91	0.83
1:A:96:ASN:HD22	1:A:97:PHE:N	1.78	0.80
1:A:355:MET:HG3	3:A:1062:HOH:O	1.80	0.79
1:A:299:SER:HA	3:A:1132:HOH:O	1.82	0.79
1:A:125:ARG:NH2	1:A:362:THR:O	2.16	0.79
1:A:513:ILE:HB	1:A:514:PRO:HD3	1.65	0.77
1:A:247:ASN:O	1:A:251:THR:HG23	1.83	0.77
1:A:173:LEU:HD23	1:A:176:MET:HE3	1.67	0.76
1:A:199:ILE:HD12	1:A:226:LEU:HD23	1.66	0.76
1:A:469:GLY:HA3	1:A:471:HIS:NE2	2.03	0.73
1:A:437:THR:HA	3:A:1150:HOH:O	1.88	0.73
1:A:246:VAL:HG21	3:A:1173:HOH:O	1.88	0.72
1:A:204:ILE:HG12	1:A:205:GLY:N	2.04	0.72
1:A:260:PHE:HE2	3:A:1176:HOH:O	1.74	0.71
1:A:463:GLN:HE22	1:A:530:ASN:ND2	1.90	0.68
1:A:463:GLN:HE22	1:A:530:ASN:CG	1.97	0.67
1:A:297:ALA:HA	3:A:1176:HOH:O	1.93	0.67
1:A:355:MET:CG	3:A:1062:HOH:O	2.21	0.67
1:A:258:LYS:HA	3:A:1132:HOH:O	1.94	0.67
1:A:453:ILE:HD12	1:A:453:ILE:H	1.59	0.67
1:A:267:THR:HG22	1:A:268:ASN:HD22	1.59	0.66
1:A:493:GLU:HG3	3:A:1171:HOH:O	1.94	0.66
1:A:209:LEU:HD23	1:A:406:GLN:HE21	1.62	0.65
1:A:262:THR:HG22	3:A:1161:HOH:O	1.94	0.65
1:A:255:ILE:O	3:A:1176:HOH:O	2.14	0.64
1:A:197:TYR:O	3:A:1124:HOH:O	2.15	0.64
1:A:203:GLY:HA3	3:A:1170:HOH:O	1.98	0.63
1:A:453:ILE:CD1	1:A:453:ILE:H	2.12	0.62
1:A:593:ASN:OD1	3:A:1138:HOH:O	2.16	0.61
1:A:454:ILE:O	1:A:454:ILE:HG13	2.00	0.61
1:A:308:PHE:CD1	3:A:1175:HOH:O	2.52	0.60
1:A:247:ASN:O	1:A:251:THR:CG2	2.50	0.60
1:A:240:ALA:O	1:A:244:LYS:HG2	2.02	0.60
1:A:347:GLU:OE2	1:A:535:ARG:HD2	2.00	0.59
1:A:320:ASP:HB2	3:A:1110:HOH:O	2.00	0.59
1:A:264:GLU:O	1:A:267:THR:HB	2.03	0.58
1:A:367:ASN:CG	1:A:370:MET:HG3	2.24	0.58
1:A:308:PHE:HD1	3:A:1175:HOH:O	1.85	0.58
1:A:588:HIS:H	1:A:593:ASN:HD21	1.52	0.57
1:A:448:HIS:HE1	1:A:482:GLN:OE1	1.89	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:GLY:HA3	3:A:1009:HOH:O	2.05	0.56
1:A:454:ILE:CG2	3:A:1004:HOH:O	2.15	0.56
1:A:381:ASN:HD21	1:A:555:TRP:HE1	1.51	0.55
1:A:368:LEU:HB3	1:A:369:PRO:HD3	1.89	0.54
1:A:89:ILE:HG12	1:A:358:HIS:CD2	2.43	0.54
1:A:318:PHE:CE1	3:A:1132:HOH:O	2.54	0.53
1:A:437:THR:HG22	3:A:1168:HOH:O	2.08	0.52
1:A:194:LYS:NZ	1:A:249:GLU:OE2	2.38	0.52
1:A:356:ASP:OD1	1:A:546:HIS:HE1	1.92	0.51
1:A:199:ILE:CD1	1:A:226:LEU:HD23	2.40	0.51
1:A:192:THR:HG21	1:A:249:GLU:OE1	2.10	0.51
1:A:509:ILE:O	1:A:513:ILE:HG12	2.11	0.51
1:A:493:GLU:O	1:A:497:GLN:HG2	2.11	0.51
1:A:358:HIS:C	1:A:358:HIS:ND1	2.64	0.51
1:A:414:LYS:HE2	3:A:1010:HOH:O	2.11	0.50
1:A:303:GLU:OE1	1:A:306:ARG:HD3	2.11	0.50
1:A:199:ILE:HD12	1:A:226:LEU:CD2	2.37	0.50
1:A:259:THR:O	1:A:301:ASN:ND2	2.41	0.50
1:A:264:GLU:HB2	3:A:1161:HOH:O	2.11	0.50
1:A:184:ARG:HD2	1:A:338:LEU:O	2.12	0.50
1:A:147:HIS:HE1	3:A:1019:HOH:O	1.95	0.49
1:A:297:ALA:CA	3:A:1176:HOH:O	2.58	0.49
1:A:255:ILE:HB	3:A:1176:HOH:O	2.13	0.49
1:A:260:PHE:CD2	1:A:305:VAL:HG22	2.48	0.49
1:A:414:LYS:HE2	1:A:561:ASP:OD2	2.13	0.49
1:A:146:LEU:HB2	1:A:321:TRP:CE3	2.48	0.49
1:A:233:ASN:ND2	1:A:237:THR:OG1	2.46	0.49
1:A:350:THR:O	1:A:354:VAL:HG23	2.13	0.49
1:A:204:ILE:CG1	1:A:205:GLY:N	2.73	0.49
1:A:576:LEU:HB3	1:A:577:PRO:HD3	1.94	0.49
1:A:453:ILE:N	1:A:453:ILE:CD1	2.75	0.48
1:A:371:MET:HE1	1:A:374:LEU:HD23	1.95	0.48
1:A:385:SER:OG	1:A:453:ILE:HG12	2.13	0.48
1:A:576:LEU:HB3	1:A:577:PRO:CD	2.44	0.47
1:A:191:GLN:N	1:A:294:HIS:NE2	2.61	0.47
1:A:381:ASN:ND2	1:A:555:TRP:HE1	2.11	0.47
1:A:238:HIS:O	1:A:242:VAL:HG12	2.15	0.47
1:A:223:LYS:HG2	1:A:226:LEU:HD12	1.95	0.47
1:A:138:ASN:ND2	1:A:558:ASN:OD1	2.48	0.47
1:A:136:ARG:HD2	1:A:142:ASN:ND2	2.31	0.46
2:A:1001:F6P:H4	3:A:1169:HOH:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:GLN:NE2	1:A:530:ASN:ND2	2.62	0.46
1:A:209:LEU:HD23	1:A:406:GLN:NE2	2.29	0.46
1:A:219:LYS:N	1:A:220:PRO:CD	2.79	0.46
1:A:358:HIS:CE1	1:A:368:LEU:H	2.35	0.45
1:A:210:GLY:HA3	1:A:328:VAL:HG13	1.97	0.45
1:A:273:ARG:HD2	3:A:1159:HOH:O	2.15	0.45
1:A:268:ASN:HD22	1:A:268:ASN:N	2.13	0.45
1:A:495:VAL:HG12	1:A:513:ILE:HD13	1.99	0.45
1:A:358:HIS:HE1	1:A:367:ASN:HA	1.82	0.45
1:A:115:LEU:HB3	1:A:374:LEU:HG	1.99	0.45
1:A:268:ASN:O	1:A:271:SER:HB2	2.17	0.45
1:A:509:ILE:HG23	1:A:510:GLU:N	2.33	0.44
1:A:264:GLU:HG2	3:A:1005:HOH:O	2.17	0.44
1:A:159:ILE:HD12	1:A:159:ILE:N	2.32	0.44
1:A:197:TYR:O	1:A:226:LEU:HA	2.17	0.44
1:A:233:ASN:ND2	1:A:238:HIS:H	2.01	0.44
1:A:418:LYS:C	1:A:420:SER:H	2.21	0.44
1:A:98:LEU:HD23	1:A:99:PHE:N	2.33	0.43
1:A:248:LEU:CD2	1:A:248:LEU:N	2.81	0.43
1:A:580:LYS:HG3	1:A:583:ASN:HB2	1.99	0.43
2:A:1001:F6P:C4	3:A:1169:HOH:O	2.67	0.43
1:A:399:ARG:NH2	3:A:1098:HOH:O	2.51	0.43
1:A:438:ASN:HA	3:A:1168:HOH:O	2.17	0.43
1:A:411:SER:O	1:A:414:LYS:NZ	2.48	0.43
1:A:409:MET:CE	1:A:431:VAL:N	2.72	0.42
1:A:437:THR:O	1:A:440:GLN:HB2	2.20	0.42
1:A:463:GLN:HB2	1:A:463:GLN:HE21	1.54	0.42
1:A:120:GLU:OE2	1:A:364:THR:HG21	2.20	0.42
1:A:83:GLN:NE2	1:A:83:GLN:H	2.18	0.42
1:A:497:GLN:NE2	3:A:1171:HOH:O	2.53	0.41
1:A:191:GLN:NE2	1:A:290:ALA:HA	2.34	0.41
1:A:83:GLN:HE21	1:A:83:GLN:H	1.67	0.41
1:A:513:ILE:O	1:A:517:THR:HG23	2.20	0.41
1:A:513:ILE:HB	1:A:514:PRO:CD	2.42	0.41
1:A:541:ILE:N	1:A:541:ILE:HD13	2.34	0.41
1:A:418:LYS:C	1:A:420:SER:N	2.72	0.41
1:A:211:PRO:O	1:A:215:THR:HG23	2.21	0.41
1:A:297:ALA:CB	3:A:1176:HOH:O	2.69	0.41
1:A:439:GLY:N	3:A:1143:HOH:O	2.54	0.41
1:A:81:ARG:HA	3:A:1047:HOH:O	2.20	0.41
1:A:448:HIS:HD2	3:A:1061:HOH:O	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:PHE:O	1:A:529:VAL:HA	2.20	0.41

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	554/605 (92%)	528 (95%)	25 (4%)	1 (0%)	52 63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	471	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	470/514 (91%)	418 (89%)	52 (11%)	8 7

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	TRP
1	A	64	GLU

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Mol	Chain	Res	Type
1	A	78	ASP
1	A	83	GLN
1	A	91	LEU
1	A	96	ASN
1	A	138	ASN
1	A	139	SER
1	A	142	ASN
1	A	151	ARG
1	A	187	GLU
1	A	189	LYS
1	A	191	GLN
1	A	198	ASN
1	A	200	VAL
1	A	204	ILE
1	A	209	LEU
1	A	226	LEU
1	A	241	GLU
1	A	242	VAL
1	A	245	GLN
1	A	248	LEU
1	A	261	THR
1	A	266	LEU
1	A	267	THR
1	A	268	ASN
1	A	280	LEU
1	A	313	VAL
1	A	328	VAL
1	A	349	LEU
1	A	366	GLN
1	A	372	LEU
1	A	374	LEU
1	A	399	ARG
1	A	453	ILE
1	A	454	ILE
1	A	463	GLN
1	A	464	THR
1	A	465	GLN
1	A	470	ASP
1	A	471	HIS
1	A	491	ASN
1	A	511	ASN
1	A	512	MET

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Mol	Chain	Res	Type
1	A	558	ASN
1	A	567	LEU
1	A	574	SER
1	A	576	LEU
1	A	581	SER
1	A	584	ILE
1	A	586	SER
1	A	595	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	96	ASN
1	A	106	HIS
1	A	138	ASN
1	A	142	ASN
1	A	147	HIS
1	A	175	GLN
1	A	191	GLN
1	A	201	ASN
1	A	233	ASN
1	A	245	GLN
1	A	263	GLN
1	A	268	ASN
1	A	314	ASN
1	A	344	ASN
1	A	357	ASN
1	A	358	HIS
1	A	380	ASN
1	A	381	ASN
1	A	405	GLN
1	A	406	GLN
1	A	448	HIS
1	A	463	GLN
1	A	472	HIS
1	A	491	ASN
1	A	511	ASN
1	A	546	HIS
1	A	551	GLN
1	A	558	ASN
1	A	593	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	F6P	A	1001	-	15,16,16	0.88	1 (6%)	16,25,25	1.13	1 (6%)

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	F6P	A	1001	-	-	0/9/28/28	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	F6P	O2-C2	2.51	1.45	1.41

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	1001	F6P	O3P-P-O6	2.81	114.64	106.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	F6P	2	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	556/605 (91%)	0.41	24 (4%)	39 53	22, 33, 54, 72	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	266	LEU	5.8
1	A	468	VAL	5.7
1	A	272	ALA	5.3
1	A	234	VAL	5.2
1	A	238	HIS	5.0
1	A	469	GLY	4.7
1	A	471	HIS	3.9
1	A	441	HIS	3.4
1	A	243	LEU	3.4
1	A	276	LEU	3.0
1	A	273	ARG	2.7
1	A	443	PHE	2.6
1	A	56	TRP	2.5
1	A	438	ASN	2.5
1	A	207	SER	2.3
1	A	511	ASN	2.3
1	A	253	PHE	2.3
1	A	299	SER	2.2
1	A	308	PHE	2.2
1	A	242	VAL	2.1
1	A	297	ALA	2.1
1	A	233	ASN	2.1
1	A	245	GLN	2.0
1	A	285	ILE	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. 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(\AA^2)	Q<0.9
2	F6P	A	1001	16/16	0.80	0.22	0.74	74,79,81,82	0

6.5 Other polymers [i](#)

There are no such residues in this entry.