



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2020 – 06:09 pm BST

PDB ID : 2V4M
Title : The isomerase domain of human glutamine-fructose-6-phosphate transaminase 1 (GFPT1) in complex with fructose 6-phosphate
Authors : Moche, M.; Lehtio, L.; Andersson, J.; Arrowsmith, C.H.; Berglund, H.; Collins, R.; Dahlgren, L.G.; Edwards, A.M.; Flodin, S.; Flores, A.; Graslund, S.; Hammarstrom, M.; Johansson, A.; Johansson, I.; Karlberg, T.; Kotenyova, T.; Nilsson, M.E.; Nyman, T.; Persson, C.; Sagemark, J.; Svensson, S.; Schueler, H.; Thorsell, A.G.; Tresaugues, L.; Uppenberg, J.; Van Den Berg, S.; Welin, M.; Wisniewska, M.; Weigelt, J.; Nordlund, P.; Wikstrom, M.
Deposited on : 2008-09-26
Resolution : 2.29 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](#) ①) 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
buster-report	:	1.1.7 (2018)
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

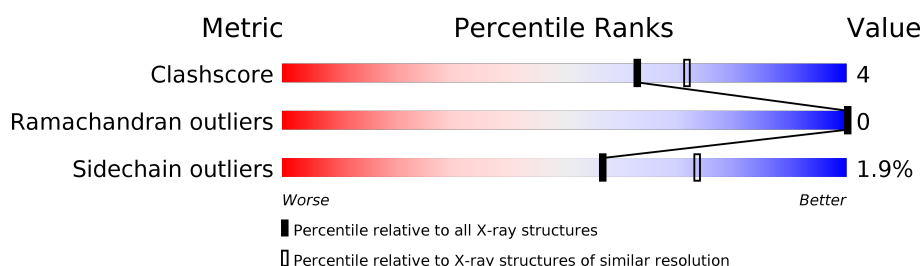
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	376	
1	B	376	
1	C	376	
1	D	376	

2 Entry composition [i](#)

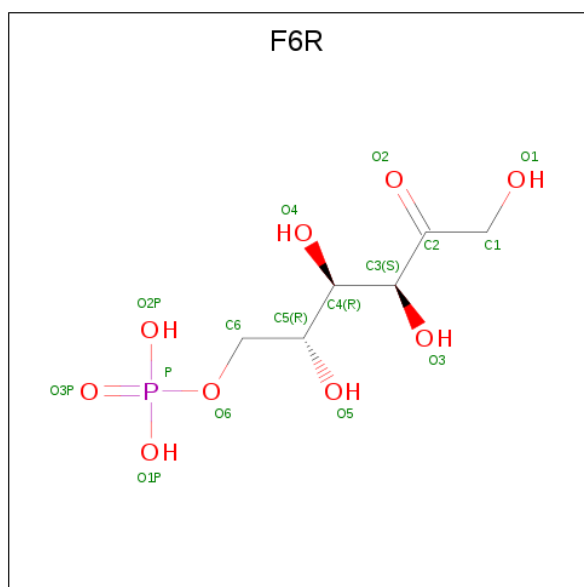
There are 4 unique types of molecules in this entry. The entry contains 11333 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINO-TRANSFERASE [ISOMERIZING] 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	3	0
			2775	1747	482	518	28			
1	B	351	Total	C	N	O	S	0	2	0
			2762	1739	481	516	26			
1	C	352	Total	C	N	O	S	0	4	0
			2794	1760	488	519	27			
1	D	350	Total	C	N	O	S	0	4	0
			2773	1745	483	518	27			

- Molecule 2 is FRUCTOSE -6-PHOSPHATE (three-letter code: F6R) (formula: C₆H₁₃O₉P).



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

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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total	Cl	0	0
			1	1		

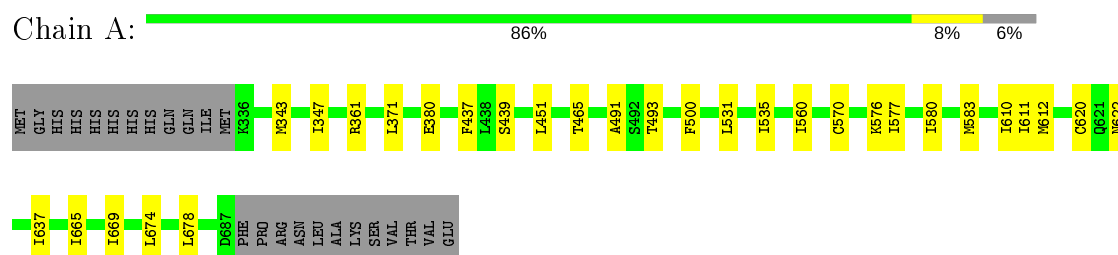
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	35	Total	O	0	0
			35	35		
4	B	14	Total	O	0	0
			14	14		
4	C	50	Total	O	0	0
			50	50		
4	D	65	Total	O	0	0
			65	65		

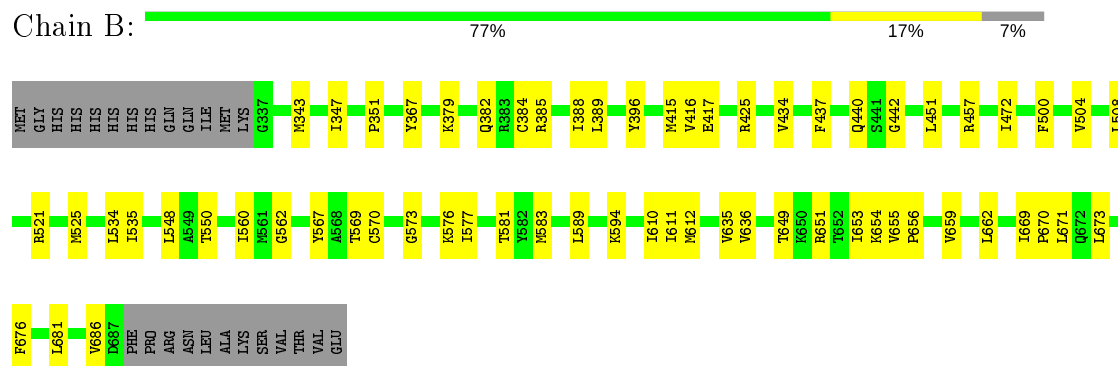
3 Residue-property plots

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. 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.

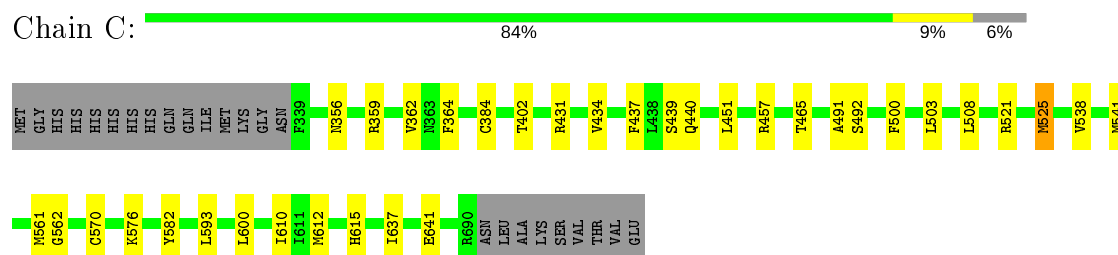
- Molecule 1: GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] 1



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- Molecule 1: GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] 1



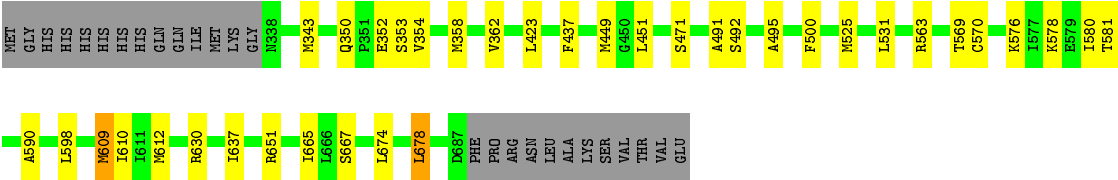
- Molecule 1: GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] 1

Chain D:

83%

9%

• 7%



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	178.82Å 178.82Å 157.11Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	54.89 – 2.29 54.85 – 2.29	Depositor EDS
% Data completeness (in resolution range)	99.2 (54.89-2.29) 96.8 (54.85-2.29)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.17 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0035	Depositor
R, R_{free}	0.167 , 0.185 0.218 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	40.7	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtriage
Estimated twinning fraction	0.000 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.679 for H, K, L 0.321 for -H-K, K, -L	Depositor
Outliers	0 of 81887 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11333	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% 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: F6R, CL

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	0.41	0/2815	0.56	0/3794
1	B	0.37	0/2803	0.52	0/3780
1	C	0.45	0/2836	0.59	0/3824
1	D	0.47	0/2813	0.60	0/3792
All	All	0.43	0/11267	0.57	0/15190

There are no bond length outliers.

There are no bond angle outliers.

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	2775	0	2833	19	0
1	B	2762	0	2814	41	0
1	C	2794	0	2849	19	0
1	D	2773	0	2829	20	0
2	A	16	0	11	0	0
2	B	16	0	11	1	0
2	C	16	0	11	0	0
2	D	16	0	11	0	0
3	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	35	0	0	0	0
4	B	14	0	0	0	0
4	C	50	0	0	0	0
4	D	65	0	0	0	0
All	All	11333	0	11369	97	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 (97) 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:D:563:ARG:HG3	1:D:590:ALA:HB3	1.40	1.01
1:B:548:LEU:HD22	1:B:653:ILE:HD11	1.63	0.81
1:D:612:MET:CE	1:D:637:ILE:HG22	2.17	0.74
1:D:491:ALA:HB1	1:D:576:LYS:HE3	1.71	0.73
1:C:508:LEU:O	1:C:521[A]:ARG:NH1	2.23	0.71
1:D:612:MET:HE1	1:D:637:ILE:HG22	1.72	0.70
1:B:576:LYS:NZ	2:B:800:F6R:O1	2.23	0.67
1:B:550:THR:HG22	1:B:681:LEU:HD21	1.76	0.67
1:A:570[B]:CYS:SG	1:A:610:ILE:HD12	2.38	0.63
1:B:389:LEU:HD12	1:B:416:VAL:HG22	1.81	0.62
1:D:362:VAL:HG13	1:D:525:MET:HE3	1.82	0.61
1:D:570[B]:CYS:SG	1:D:610:ILE:HD12	2.42	0.60
1:B:396:TYR:CE1	1:B:416:VAL:HG12	2.37	0.60
1:A:611:ILE:HD12	1:A:620:CYS:HB3	1.85	0.59
1:B:384:CYS:SG	1:B:434:VAL:HG23	2.43	0.59
1:B:417:GLU:OE1	1:B:425:ARG:NH2	2.35	0.58
1:B:569:THR:HG21	1:B:610:ILE:HD13	1.85	0.58
1:B:343:MET:CE	1:B:347:ILE:HD11	2.36	0.55
1:D:343:MET:SD	1:D:580:ILE:HD13	2.47	0.54
1:B:548:LEU:HD21	1:B:635:VAL:HG11	1.89	0.54
1:C:491:ALA:HB1	1:C:576:LYS:HE3	1.90	0.54
1:B:573:GLY:HA3	1:B:671:LEU:HD13	1.91	0.53
1:B:655:VAL:HG13	1:B:656:PRO:HD2	1.91	0.52
1:C:362:VAL:HG13	1:C:525:MET:CE	2.40	0.52
1:B:659:VAL:HG12	1:B:662:LEU:HD12	1.91	0.52
1:D:598:LEU:O	1:D:630:ARG:NH1	2.42	0.52
1:B:569:THR:CG2	1:B:610:ILE:HD13	2.39	0.52
1:B:611:ILE:HD12	1:B:636:VAL:HG13	1.92	0.52
1:D:354:VAL:HG12	1:D:358:MET:HE2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:612:MET:HE2	1:A:637:ILE:HG22	1.93	0.51
1:C:570[B]:CYS:SG	1:C:610:ILE:HD12	2.51	0.51
1:A:531:LEU:HD21	1:A:665:ILE:HD13	1.93	0.51
1:B:388:ILE:HD13	1:B:415:MET:HE2	1.92	0.51
1:B:442:GLY:HA2	1:B:472:ILE:HD12	1.93	0.51
1:A:437:PHE:CZ	1:A:451:LEU:HA	2.46	0.50
1:B:343:MET:HE2	1:B:347:ILE:HD11	1.93	0.50
1:C:561:MET:SD	1:C:593:LEU:HD11	2.51	0.50
1:C:362:VAL:HG11	1:C:364:PHE:CE1	2.47	0.50
1:B:635:VAL:HG22	1:B:651:ARG:HD2	1.94	0.50
1:A:361:ARG:HG2	1:A:371:LEU:HD23	1.93	0.49
1:A:583:MET:CE	1:A:678:LEU:HD21	2.43	0.49
1:A:560:ILE:HD11	1:A:577:ILE:HD12	1.95	0.49
1:C:437:PHE:CZ	1:C:451:LEU:HA	2.49	0.48
1:C:356:ASN:OD1	1:C:359:ARG:NH1	2.46	0.48
1:B:567:TYR:CD1	1:B:589:LEU:HD13	2.49	0.48
1:D:569:THR:HG21	1:D:667[A]:SER:OG	2.14	0.48
1:B:611:ILE:HD12	1:B:636:VAL:CG1	2.44	0.48
1:C:439:SER:O	1:C:465:THR:HA	2.14	0.48
1:B:577:ILE:CG2	1:B:583:MET:HE3	2.43	0.47
1:D:437:PHE:CZ	1:D:451:LEU:HA	2.48	0.47
1:D:531:LEU:HD21	1:D:665:ILE:HD13	1.95	0.47
1:B:562:GLY:HA3	1:B:570[B]:CYS:SG	2.54	0.47
1:A:610:ILE:O	1:A:611:ILE:HD13	2.15	0.47
1:C:612:MET:CE	1:C:637:ILE:HG22	2.44	0.47
1:D:674:LEU:HG	1:D:678:LEU:HD22	1.97	0.46
1:A:535:ILE:HG23	1:A:669:ILE:CD1	2.45	0.46
1:B:379:LYS:HA	1:B:382:GLN:HE21	1.81	0.46
1:D:354:VAL:CG1	1:D:358:MET:HE2	2.45	0.46
1:B:550:THR:CG2	1:B:681:LEU:HD11	2.46	0.46
1:B:508:LEU:HD22	1:B:521:ARG:HB2	1.97	0.45
1:B:550:THR:HG22	1:B:681:LEU:HD11	1.99	0.45
1:B:534:LEU:HD22	1:B:656:PRO:HB2	1.99	0.45
1:B:351:PRO:HG3	1:B:535:ILE:HG22	1.99	0.45
1:B:347:ILE:HG21	1:B:673:LEU:CD2	2.47	0.44
1:B:437:PHE:CZ	1:B:451:LEU:HA	2.51	0.44
1:A:674:LEU:O	1:A:678:LEU:HB2	2.17	0.44
1:A:491:ALA:HB1	1:A:576:LYS:HE3	1.99	0.44
1:B:500:PHE:O	1:B:504:VAL:HG23	2.17	0.44
1:A:439:SER:O	1:A:465:THR:HA	2.18	0.43
1:A:535:ILE:HG23	1:A:669:ILE:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:577:ILE:HG21	1:B:583:MET:HE3	1.99	0.43
1:D:492:SER:OG	1:D:495:ALA:HB3	2.18	0.43
1:A:343:MET:SD	1:A:580:ILE:HD13	2.59	0.43
1:A:380:GLU:HG2	1:C:431:ARG:HD2	2.00	0.43
1:D:354:VAL:HG12	1:D:358:MET:CE	2.48	0.42
1:B:548:LEU:CD2	1:B:653:ILE:HD11	2.43	0.42
1:C:562:GLY:N	1:C:570[B]:CYS:SG	2.92	0.42
1:D:350:GLN:HA	1:D:353:SER:OG	2.19	0.42
1:B:636:VAL:HG23	1:B:649:THR:HG21	2.02	0.42
1:A:612:MET:CE	1:A:637:ILE:HG22	2.50	0.42
1:C:612:MET:HE1	1:C:637:ILE:HG22	2.02	0.42
1:D:609:MET:HE2	1:D:609:MET:HB2	1.98	0.42
1:A:347:ILE:HG13	1:A:493:THR:HG21	2.02	0.42
1:B:384:CYS:SG	1:B:434:VAL:CG2	3.07	0.41
1:C:402:THR:HG21	1:C:503:LEU:HB2	2.03	0.41
1:C:362:VAL:HG13	1:C:525:MET:HE1	2.02	0.41
1:B:560:ILE:HG22	1:B:570[B]:CYS:SG	2.61	0.41
1:C:384[A]:CYS:CB	1:C:434:VAL:HG23	2.50	0.41
1:C:492:SER:O	1:C:576:LYS:HE2	2.21	0.41
1:A:531:LEU:HD21	1:A:665:ILE:CD1	2.51	0.40
1:B:569:THR:CG2	1:B:610:ILE:CD1	2.99	0.40
1:B:669:ILE:HB	1:B:670:PRO:HD3	2.04	0.40
1:B:676:PHE:CD1	1:B:686:VAL:HG21	2.56	0.40
1:C:538:VAL:O	1:C:541:MET:HG2	2.21	0.40
1:D:423:LEU:HD11	1:D:449[B]:MET:HB2	2.04	0.40
1:B:367:TYR:HD2	1:B:525:MET:HE3	1.86	0.40
1:C:600:LEU:HD22	1:D:578:LYS:HG2	2.04	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	353/376 (94%)	342 (97%)	11 (3%)	0	100	100
1	B	351/376 (93%)	344 (98%)	7 (2%)	0	100	100
1	C	354/376 (94%)	349 (99%)	5 (1%)	0	100	100
1	D	352/376 (94%)	346 (98%)	6 (2%)	0	100	100
All	All	1410/1504 (94%)	1381 (98%)	29 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	311/330 (94%)	309 (99%)	2 (1%)	86	94
1	B	309/330 (94%)	302 (98%)	7 (2%)	50	67
1	C	313/330 (95%)	306 (98%)	7 (2%)	52	69
1	D	311/330 (94%)	304 (98%)	7 (2%)	50	67
All	All	1244/1320 (94%)	1221 (98%)	23 (2%)	57	75

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	500	PHE
1	A	622	ASN
1	B	385	ARG
1	B	440	GLN
1	B	457	ARG
1	B	581	THR
1	B	594	LYS
1	B	612	MET
1	B	654	LYS
1	C	440	GLN
1	C	457	ARG
1	C	500	PHE
1	C	525	MET

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Mol	Chain	Res	Type
1	C	582	TYR
1	C	615	HIS
1	C	641	GLU
1	D	352	GLU
1	D	471	SER
1	D	500	PHE
1	D	581	THR
1	D	609	MET
1	D	651	ARG
1	D	678	LEU

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

Mol	Chain	Res	Type
1	A	622	ASN
1	B	382	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 1 is 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
2	F6R	D	800	-	14,15,15	0.69	0	16,21,21	0.97	0
2	F6R	B	800	-	14,15,15	0.51	0	16,21,21	0.89	1 (6%)
2	F6R	C	800	-	14,15,15	0.56	0	16,21,21	1.07	0
2	F6R	A	800	-	14,15,15	0.64	0	16,21,21	0.84	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
2	F6R	D	800	-	-	0/20/20/20	-
2	F6R	B	800	-	-	0/20/20/20	-
2	F6R	C	800	-	-	0/20/20/20	-
2	F6R	A	800	-	-	0/20/20/20	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	800	F6R	O1P-P-O6	-2.14	101.03	106.73

There are no chirality outliers.

There are no torsion outliers.

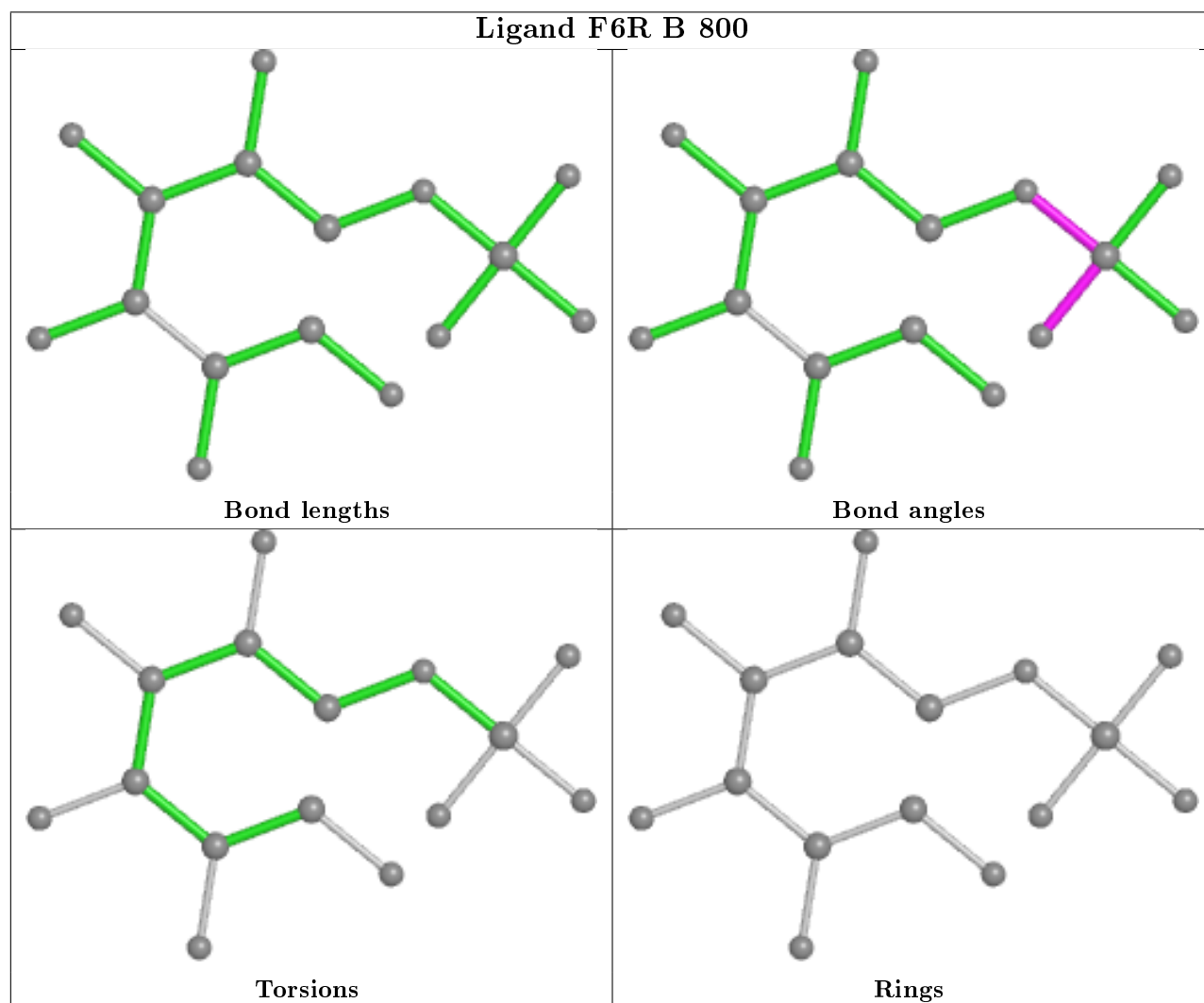
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	800	F6R	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

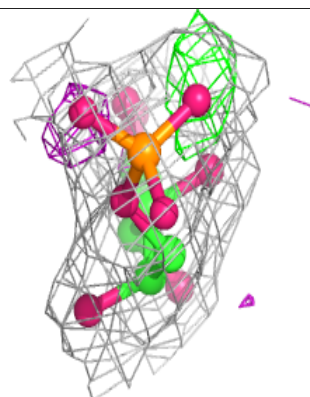
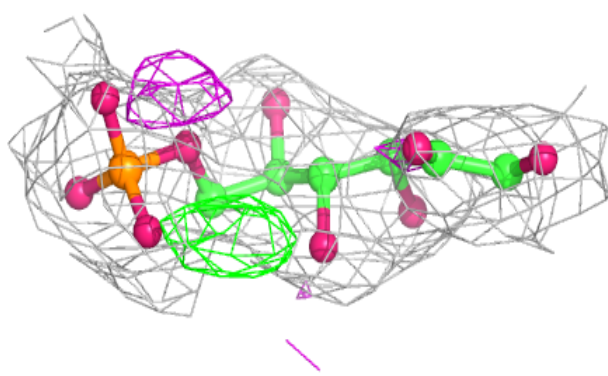
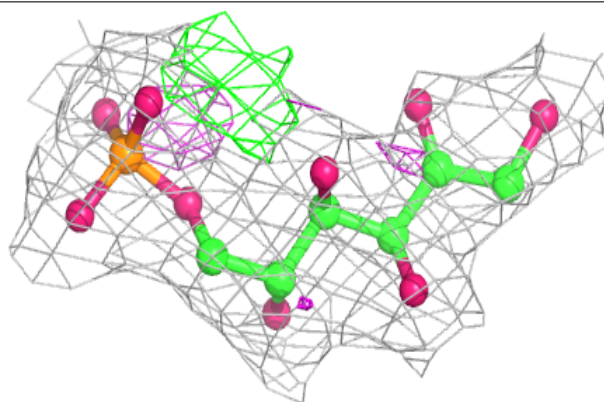
6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around F6R B 800:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.