



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 06:47 am BST

PDB ID : 5EY7
Title : Crystal structure of Fructokinase from *Vibrio cholerae* O395 in apo form
Authors : Paul, R.; Nath, S.; Sen, U.
Deposited on : 2015-11-24
Resolution : 2.46 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

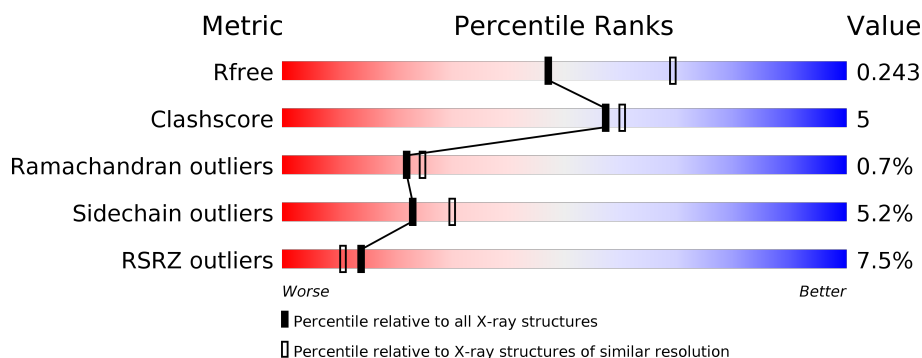
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.46 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	323	<div> <div>5%</div> <div> <div></div> <div>85%</div> <div>10%</div> <div>5%</div> </div> </div>
1	B	323	<div> <div>9%</div> <div> <div></div> <div>72%</div> <div>16%</div> <div>• 10%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4627 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 Fructokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2332	1475	400	447	10			
1	B	291	Total	C	N	O	S	0	0	0
			2211	1396	382	424	9			

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		


- Molecule 3 is water.

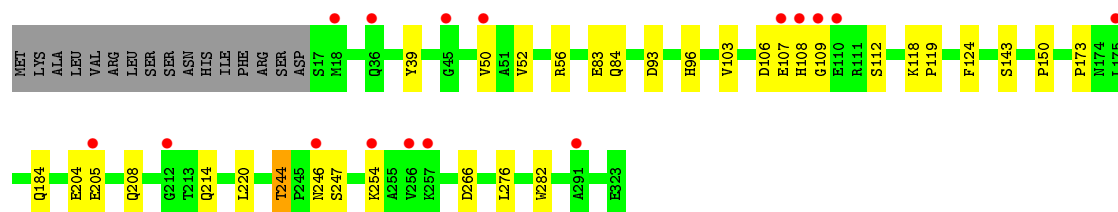
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	47	Total	O	0	0
			47	47		
3	B	36	Total	O	0	0
			36	36		

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

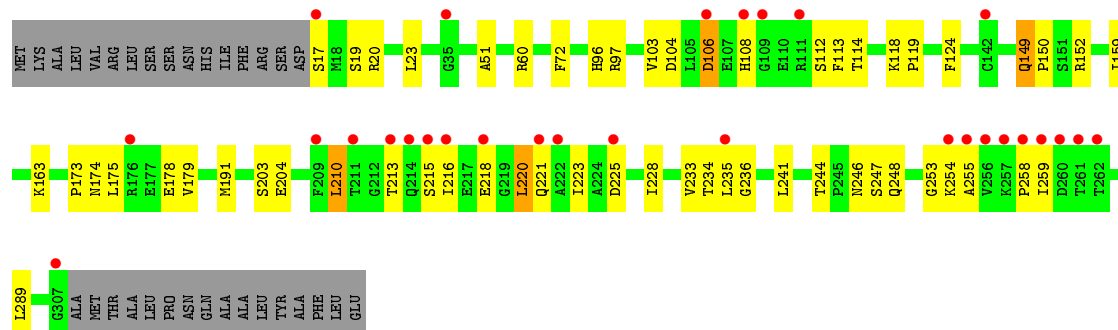
• Molecule 1: Fructokinase

Chain A: 



• Molecule 1: Fructokinase

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	107.12Å 99.86Å 61.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.41 – 2.46 29.41 – 2.46	Depositor EDS
% Data completeness (in resolution range)	95.0 (29.41-2.46) 91.2 (29.41-2.46)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.215 , 0.242 0.224 , 0.243	Depositor DCC
R_{free} test set	1174 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	41.9	Xtriage
Anisotropy	0.967	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4627	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.93% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.26	0/2382	0.43	0/3240
1	B	0.25	0/2258	0.41	0/3071
All	All	0.25	0/4640	0.42	0/6311

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

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	2332	0	2283	18	0
1	B	2211	0	2164	27	0
2	A	1	0	0	0	0
3	A	47	0	0	0	0
3	B	36	0	0	1	0
All	All	4627	0	4447	44	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 5.

All (44) 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:106:ASP:HB2	1:A:112:SER:HB3	1.60	0.83
1:B:213:THR:HG21	1:B:218:GLU:HB2	1.77	0.65
1:A:56:ARG:NH1	1:A:83:GLU:OE2	2.30	0.64
1:B:218:GLU:HA	1:B:221:GLN:HB3	1.78	0.64
1:A:244:THR:HG22	1:A:247:SER:H	1.63	0.63
1:A:93:ASP:OD2	1:A:96:HIS:ND1	2.29	0.62
1:B:244:THR:HG22	1:B:246:ASN:H	1.64	0.61
1:B:223:ILE:HD13	1:B:228:ILE:HD12	1.81	0.61
1:A:276:LEU:HD22	1:A:282:TRP:HB2	1.83	0.60
1:A:83:GLU:N	1:A:84:GLN:HA	2.17	0.60
1:A:143:SER:HB3	1:A:173:PRO:HA	1.84	0.59
1:B:103:VAL:HG12	1:B:113:PHE:HB3	1.84	0.59
1:B:60:ARG:NH1	3:B:402:HOH:O	2.32	0.58
1:B:104:ASP:N	1:B:112:SER:O	2.30	0.54
1:A:83:GLU:H	1:A:84:GLN:HA	1.74	0.53
1:B:149:GLN:HG3	1:B:150:PRO:HA	1.91	0.53
1:A:124:PHE:HA	1:A:150:PRO:HD2	1.91	0.52
1:B:96:HIS:O	1:B:97:ARG:NH1	2.43	0.52
1:A:52:VAL:HG22	1:A:83:GLU:HG2	1.94	0.50
1:A:108:HIS:N	1:A:109:GLY:HA2	2.26	0.50
1:B:235:LEU:HD11	1:B:241:LEU:HB2	1.94	0.49
1:A:107:GLU:O	1:A:108:HIS:HB2	2.13	0.48
1:A:208:GLN:NE2	1:A:214:GLN:O	2.46	0.48
1:B:118:LYS:HA	1:B:119:PRO:HA	1.80	0.47
1:B:124:PHE:HA	1:B:150:PRO:HD2	1.96	0.46
1:B:233:VAL:HB	1:B:241:LEU:HB3	1.97	0.46
1:B:106:ASP:HB3	1:B:108:HIS:H	1.81	0.46
1:B:173:PRO:O	1:B:175:LEU:N	2.49	0.45
1:B:17:SER:HB2	1:B:60:ARG:CZ	2.48	0.44
1:B:253:GLY:O	1:B:255:ALA:N	2.51	0.43
1:A:244:THR:HG23	1:A:246:ASN:H	1.84	0.43
1:A:39:TYR:HE2	1:B:72:PHE:HE1	1.65	0.43
1:B:213:THR:C	1:B:215:SER:H	2.22	0.43
1:B:103:VAL:HA	1:B:113:PHE:HA	2.00	0.43
1:A:50:VAL:HG22	1:A:266:ASP:O	2.20	0.42
1:B:213:THR:CG2	1:B:218:GLU:HB2	2.48	0.41
1:B:216:ILE:HG13	1:B:216:ILE:H	1.67	0.41
1:A:118:LYS:HA	1:A:119:PRO:HA	1.74	0.41
1:B:159:ILE:O	1:B:163:LYS:HG3	2.20	0.41
1:A:52:VAL:HG13	1:A:83:GLU:HG2	2.03	0.41
1:B:220:LEU:O	1:B:223:ILE:HG13	2.20	0.41
1:B:23:LEU:HD13	1:B:51:ALA:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:ILE:O	1:B:220:LEU:HB2	2.20	0.40
1:B:191:MET:SD	1:B:210:LEU:HG	2.62	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	305/323 (94%)	292 (96%)	13 (4%)	0	100	100
1	B	289/323 (90%)	262 (91%)	23 (8%)	4 (1%)	11	9
All	All	594/646 (92%)	554 (93%)	36 (6%)	4 (1%)	22	25

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	254	LYS
1	B	258	PRO
1	B	174	ASN
1	B	236	GLY

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	247/262 (94%)	240 (97%)	7 (3%)	43 56
1	B	236/262 (90%)	218 (92%)	18 (8%)	13 15
All	All	483/524 (92%)	458 (95%)	25 (5%)	23 30

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	VAL
1	A	184	GLN
1	A	204	GLU
1	A	205	GLU
1	A	220	LEU
1	A	244	THR
1	A	254	LYS
1	B	19	SER
1	B	20	ARG
1	B	106	ASP
1	B	114	THR
1	B	149	GLN
1	B	152	ARG
1	B	178	GLU
1	B	179	VAL
1	B	203	SER
1	B	204	GLU
1	B	210	LEU
1	B	220	LEU
1	B	225	ASP
1	B	234	THR
1	B	247	SER
1	B	248	GLN
1	B	259	ILE
1	B	289	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	249	GLN
1	A	285	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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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	307/323 (95%)	0.28	16 (5%) 27 24	36, 60, 112, 178	0
1	B	291/323 (90%)	0.56	29 (9%) 7 4	37, 63, 135, 158	0
All	All	598/646 (92%)	0.42	45 (7%) 14 11	36, 62, 127, 178	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	259	ILE	9.3
1	B	258	PRO	7.3
1	B	261	THR	6.0
1	B	35	GLY	5.7
1	B	262	THR	4.8
1	B	209	PHE	4.4
1	B	17	SER	4.1
1	A	108	HIS	4.1
1	B	214	GLN	3.9
1	B	255	ALA	3.8
1	B	254	LYS	3.8
1	A	18	MET	3.8
1	B	221	GLN	3.7
1	B	213	THR	3.7
1	A	109	GLY	3.7
1	B	218	GLU	3.7
1	B	211	THR	3.6
1	A	256	VAL	3.4
1	B	142	CYS	3.4
1	B	257	LYS	3.3
1	A	107	GLU	3.3
1	A	36	GLN	3.1
1	B	260	ASP	3.1
1	A	257	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	307	GLY	3.0
1	B	225	ASP	2.8
1	B	216	ILE	2.8
1	B	222	ALA	2.7
1	A	110	GLU	2.7
1	B	108	HIS	2.7
1	B	176	ARG	2.7
1	B	256	VAL	2.6
1	B	235	LEU	2.6
1	A	254	LYS	2.5
1	B	215	SER	2.5
1	B	109	GLY	2.5
1	A	246	ASN	2.5
1	A	50	VAL	2.4
1	A	175	LEU	2.4
1	B	106	ASP	2.1
1	A	291	ALA	2.1
1	A	205	GLU	2.1
1	A	45	GLY	2.1
1	A	212	GLY	2.1
1	B	111	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NA	A	401	1/1	0.96	0.16	79,79,79,79	0

6.5 Other polymers [i](#)

There are no such residues in this entry.