



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 21, 2016 – 01:50 PM EST

PDB ID : 5HTK
Title : Human Heart 6-Phosphofructo-2-Kinase/Fructose-2,6-Bisphosphatase (PFKFB2)
Authors : Crochet, R.B.
Deposited on : 2016-01-27
Resolution : 2.01 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
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) : rb-20028442

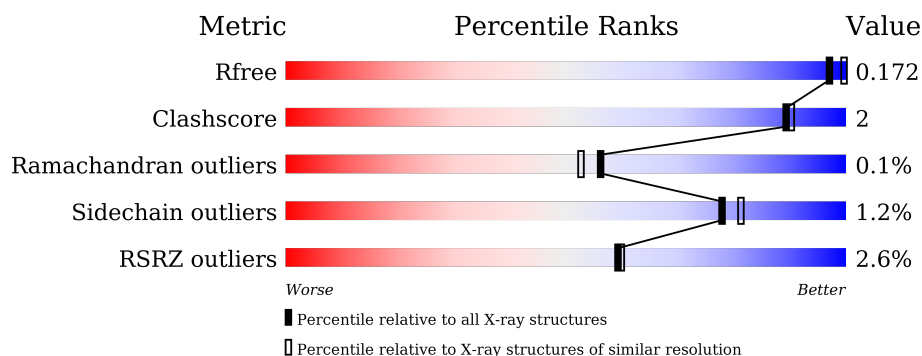
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	505	
1	B	505	

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
6	EDO	B	605	-	-	-	X
6	EDO	B	606	-	-	-	X
7	GOL	A	608	-	-	-	X
7	GOL	B	609	-	-	-	X
7	GOL	B	610	-	-	-	X
7	GOL	B	611	-	-	-	X
7	GOL	B	612	-	-	-	X

2 Entry composition [i](#)

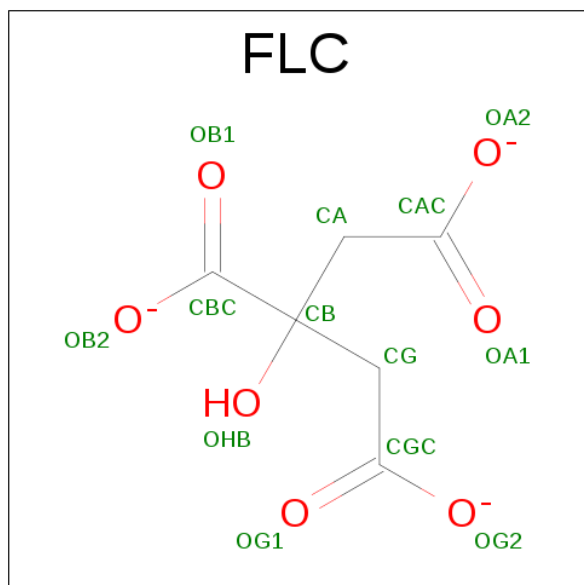
There are 9 unique types of molecules in this entry. The entry contains 14900 atoms, of which 7064 are hydrogens and 0 are deuteriums.

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 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2.

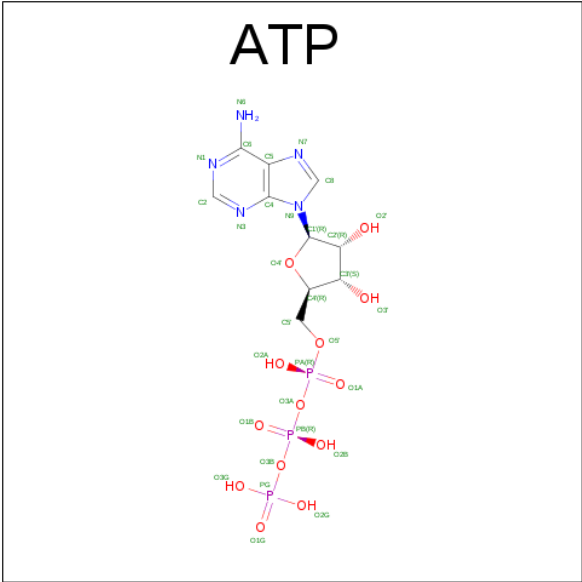
Mol	Chain	Residues	Atoms								ZeroOcc	AltConf	Trace
1	A	425	Total	C	H	N	O	P	S	0	0	0	
			6961	2222	3477	594	650	1	17				
1	B	420	Total	C	H	N	O	P	S	0	0	0	
			6877	2194	3436	586	643	1	17				

- Molecule 2 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			18	6	5	7		
2	B	1	Total	C	H	O	0	0
			18	6	5	7		

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

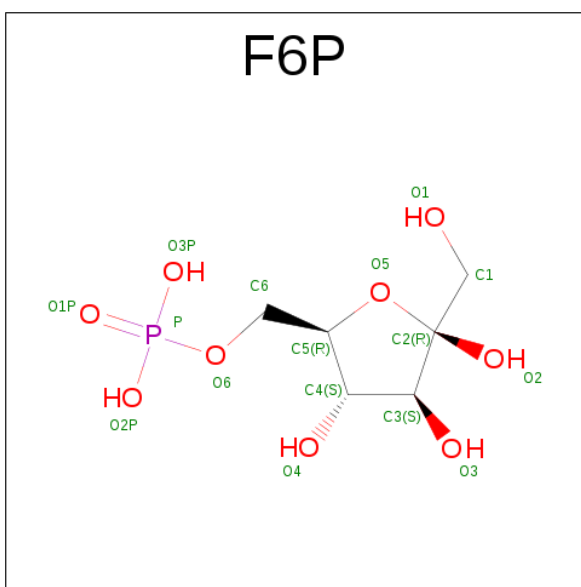


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	A	1	Total	C	H	N	O	P	0	0
			43	10	12	5	13	3		
3	B	1	Total	C	H	N	O	P	0	0
			43	10	12	5	13	3		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

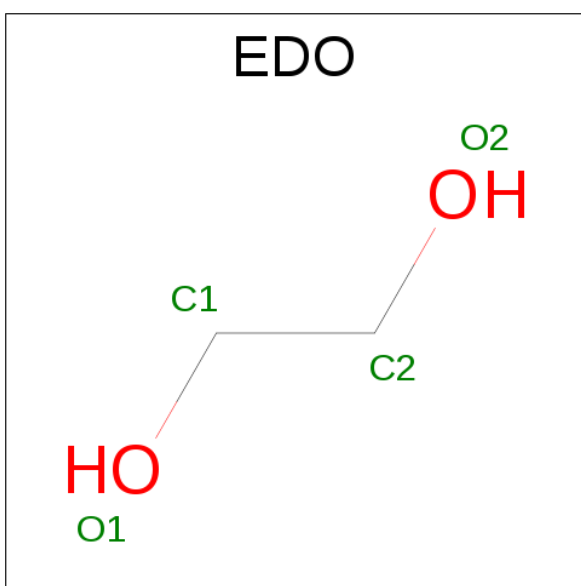
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is FRUCTOSE-6-PHOSPHATE (three-letter code: F6P) (formula: C₆H₁₃O₉P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	H	O	P	0	0
			27	6	11	9	1		
5	B	1	Total	C	H	O	P	0	0
			27	6	11	9	1		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



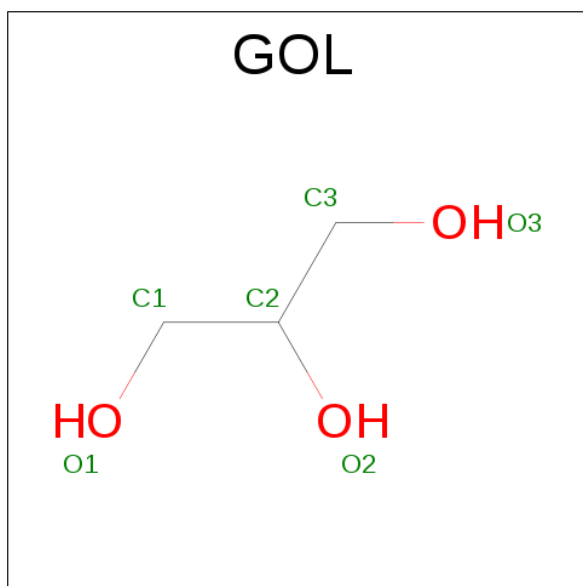
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		

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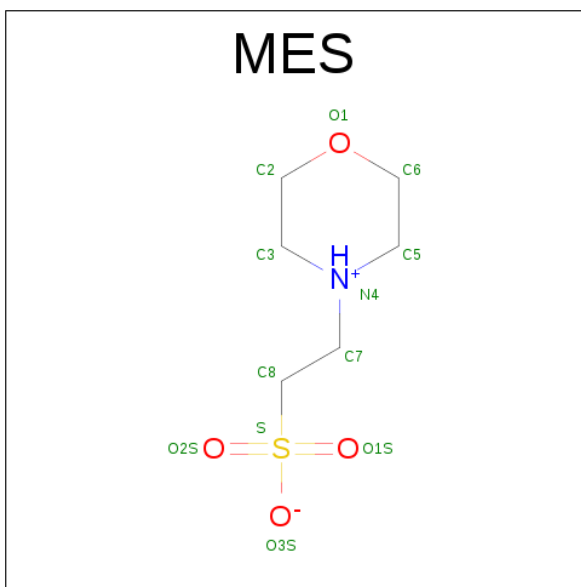
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			14	3	8	3		
7	A	1	Total	C	H	O	0	0
			14	3	8	3		
7	A	1	Total	C	H	O	0	0
			14	3	8	3		
7	B	1	Total	C	H	O	0	0
			14	3	8	3		
7	B	1	Total	C	H	O	0	0
			14	3	8	3		
7	B	1	Total	C	H	O	0	0
			14	3	8	3		
7	B	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 8 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	B	1	Total	C	H	N	O	S	
			25	6	13	1	4	1	
								0	0

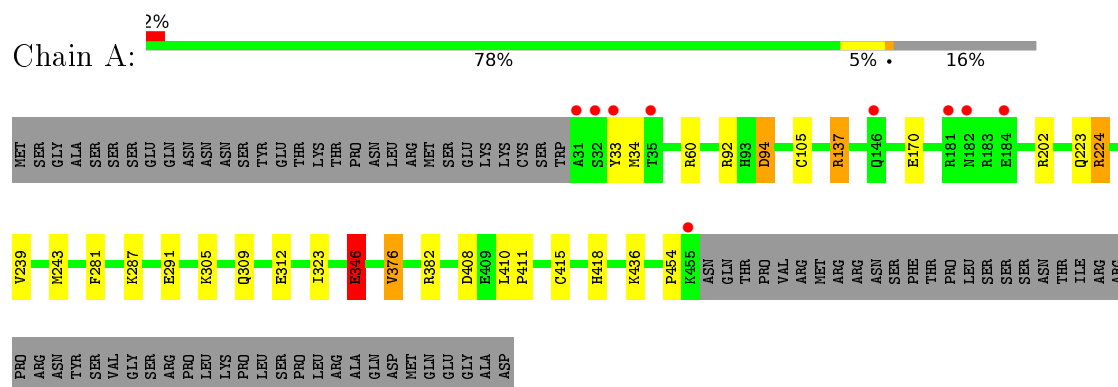
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	323	Total	O		
			323	323	0	0
9	B	394	Total	O		
			394	394	0	0

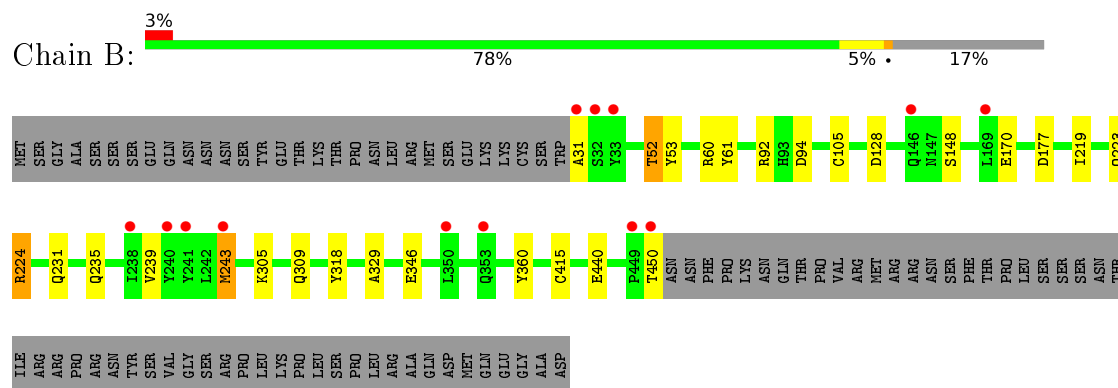
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2



- Molecule 1: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	106.52Å 113.95Å 133.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.55 – 2.01 40.10 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.5 (38.55-2.01) 97.7 (40.10-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.00Å)	Xtriage
Refinement program	PHENIX (dev_2000: ???)	Depositor
R, R_{free}	0.149 , 0.175 0.144 , 0.172	Depositor DCC
R_{free} test set	5308 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	32.4	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 52.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14900	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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: GOL, MG, MES, EDO, ATP, FLC, NEP, 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	0.63	3/3540 (0.1%)	0.72	4/4785 (0.1%)
1	B	0.66	2/3495 (0.1%)	0.72	2/4724 (0.0%)
All	All	0.64	5/7035 (0.1%)	0.72	6/9509 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	415	CYS	CB-SG	-7.59	1.69	1.82
1	B	318	TYR	CD2-CE2	6.36	1.48	1.39
1	A	415	CYS	CB-SG	-6.12	1.71	1.82
1	A	376	VAL	CB-CG2	-5.52	1.41	1.52
1	A	346	GLU	CG-CD	5.35	1.59	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	ARG	NE-CZ-NH2	-8.69	115.95	120.30
1	B	52	THR	CA-CB-CG2	-7.76	101.53	112.40
1	A	224	ARG	NE-CZ-NH2	-6.77	116.91	120.30
1	A	94	ASP	CB-CA-C	-6.70	97.01	110.40
1	A	382	ARG	NE-CZ-NH2	-5.40	117.60	120.30
1	B	243	MET	CA-CB-CG	5.39	122.47	113.30

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	3484	3477	3478	14	0
1	B	3441	3436	3436	17	0
2	A	13	5	5	0	0
2	B	13	5	5	0	0
3	A	31	12	12	0	0
3	B	31	12	12	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	16	11	11	0	0
5	B	16	11	11	0	0
6	A	4	6	6	1	0
6	B	8	12	12	0	0
7	A	18	24	24	0	0
7	B	30	40	40	3	0
8	B	12	13	12	0	0
9	A	323	0	0	5	0
9	B	394	0	0	9	1
All	All	7836	7064	7064	34	1

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 2.

All (34) 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)
7:B:610:GOL:O2	9:B:701:HOH:O	1.94	0.84
1:B:170:GLU:OE2	9:B:702:HOH:O	1.94	0.84
1:B:105:CYS:SG	9:B:1017:HOH:O	2.36	0.82
1:A:223:GLN:OE1	9:A:701:HOH:O	1.97	0.81
1:B:61:TYR:OH	9:B:703:HOH:O	2.01	0.78
1:A:312:GLU:OE2	9:A:702:HOH:O	2.08	0.69
1:A:170:GLU:OE2	9:A:703:HOH:O	2.09	0.69
1:B:440:GLU:OE2	9:B:704:HOH:O	2.11	0.69
1:B:223:GLN:NE2	9:B:708:HOH:O	2.22	0.67
1:A:105:CYS:SG	9:A:975:HOH:O	2.55	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:450:THR:O	9:B:706:HOH:O	2.16	0.60
6:A:605:EDO:H21	9:A:929:HOH:O	2.03	0.58
1:B:305:LYS:HG2	1:B:309:GLN:NE2	2.22	0.54
1:B:305:LYS:NZ	9:B:709:HOH:O	2.36	0.53
1:A:137:ARG:NH2	1:A:202:ARG:O	2.38	0.51
1:B:52:THR:OG1	1:B:128:ASP:OD2	2.29	0.51
1:A:305:LYS:HG2	1:A:309:GLN:NE2	2.26	0.50
1:A:346:GLU:CD	1:A:346:GLU:H	2.15	0.50
1:A:92:ARG:NH1	1:A:94:ASP:HB2	2.26	0.50
1:B:231:GLN:HG2	1:B:235:GLN:NE2	2.28	0.49
7:B:612:GOL:O2	9:B:707:HOH:O	2.19	0.48
1:B:219:ILE:HB	1:B:224:ARG:HG3	1.97	0.47
1:B:239:VAL:O	1:B:243:MET:HG2	2.15	0.47
1:A:281:PHE:CE2	1:A:418:HIS:HA	2.50	0.46
1:A:239:VAL:O	1:A:243:MET:HG2	2.16	0.46
1:B:329:ALA:HA	1:B:360:TYR:CD2	2.54	0.43
1:B:52:THR:HG21	3:B:602:ATP:C8	2.53	0.42
1:A:287:LYS:HE2	1:A:291:GLU:OE2	2.19	0.42
1:B:31:ALA:HB3	1:B:148:SER:HA	2.01	0.42
1:A:323:ILE:HD11	1:A:376:VAL:HG23	2.03	0.41
1:A:410:LEU:HB3	1:A:411:PRO:HD3	2.02	0.41
1:B:92:ARG:HB3	1:B:94:ASP:OD1	2.21	0.41
1:B:53:TYR:CD2	7:B:612:GOL:H2	2.56	0.41
1:A:33:TYR:CG	1:A:34:MET:N	2.88	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:1029:HOH:O	9:B:1047:HOH:O[4_565]	1.86	0.34

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	422/505 (84%)	410 (97%)	11 (3%)	1 (0%)	52	48
1	B	417/505 (83%)	408 (98%)	9 (2%)	0	100	100
All	All	839/1010 (83%)	818 (98%)	20 (2%)	1 (0%)	56	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	454	PRO

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	382/456 (84%)	377 (99%)	5 (1%)	76	79
1	B	377/456 (83%)	373 (99%)	4 (1%)	80	83
All	All	759/912 (83%)	750 (99%)	9 (1%)	78	81

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	ARG
1	A	224	ARG
1	A	346	GLU
1	A	408	ASP
1	A	436	LYS
1	B	60	ARG
1	B	177	ASP
1	B	224	ARG
1	B	346	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	NEP	A	257	1	8,14,15	5.41	3 (37%)	5,20,22	4.11	1 (20%)
1	NEP	B	257	1	8,14,15	1.74	2 (25%)	5,20,22	1.06	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	NEP	A	257	1	-	0/4/12/14	0/1/1/1
1	NEP	B	257	1	-	0/4/12/14	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	257	NEP	P-O2P	-4.77	1.44	1.54
1	B	257	NEP	P-O3P	-3.71	1.44	1.47
1	A	257	NEP	P-O1P	2.20	1.59	1.54
1	B	257	NEP	P-O1P	2.29	1.59	1.54
1	A	257	NEP	P-O3P	14.17	1.59	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	257	NEP	O1P-P-O3P	-9.03	84.01	112.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 2 are monoatomic - leaving 18 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	FLC	A	601	-	3,12,12	1.05	0	3,17,17	2.81	1 (33%)
3	ATP	A	602	4	26,33,33	1.18	4 (15%)	26,52,52	2.16	5 (19%)
5	F6P	A	604	-	15,16,16	1.22	1 (6%)	16,25,25	0.93	1 (6%)
6	EDO	A	605	-	3,3,3	0.43	0	2,2,2	0.32	0
7	GOL	A	606	-	5,5,5	0.57	0	5,5,5	0.25	0
7	GOL	A	607	-	5,5,5	0.32	0	5,5,5	0.65	0
7	GOL	A	608	-	5,5,5	0.55	0	5,5,5	0.30	0
2	FLC	B	601	-	3,12,12	2.39	1 (33%)	3,17,17	1.75	1 (33%)
3	ATP	B	602	4	26,33,33	1.07	2 (7%)	26,52,52	2.08	4 (15%)
5	F6P	B	604	-	15,16,16	1.44	2 (13%)	16,25,25	0.78	0
6	EDO	B	605	-	3,3,3	0.60	0	2,2,2	0.15	0
6	EDO	B	606	-	3,3,3	0.60	0	2,2,2	0.51	0
7	GOL	B	607	-	5,5,5	0.43	0	5,5,5	0.31	0
8	MES	B	608	-	12,12,12	1.71	1 (8%)	16,16,16	1.88	4 (25%)
7	GOL	B	609	-	5,5,5	0.23	0	5,5,5	0.46	0
7	GOL	B	610	-	5,5,5	0.41	0	5,5,5	0.64	0
7	GOL	B	611	-	5,5,5	0.55	0	5,5,5	0.81	0
7	GOL	B	612	-	5,5,5	0.23	0	5,5,5	0.63	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	FLC	A	601	-	-	0/6/16/16	0/0/0/0
3	ATP	A	602	4	-	0/18/38/38	0/3/3/3
5	F6P	A	604	-	-	0/9/28/28	0/1/1/1
6	EDO	A	605	-	-	0/1/1/1	0/0/0/0
7	GOL	A	606	-	-	0/4/4/4	0/0/0/0
7	GOL	A	607	-	-	0/4/4/4	0/0/0/0
7	GOL	A	608	-	-	0/4/4/4	0/0/0/0
2	FLC	B	601	-	-	0/6/16/16	0/0/0/0
3	ATP	B	602	4	-	0/18/38/38	0/3/3/3
5	F6P	B	604	-	-	0/9/28/28	0/1/1/1
6	EDO	B	605	-	-	0/1/1/1	0/0/0/0
6	EDO	B	606	-	-	0/1/1/1	0/0/0/0
7	GOL	B	607	-	-	0/4/4/4	0/0/0/0
8	MES	B	608	-	-	0/6/14/14	0/1/1/1
7	GOL	B	609	-	-	0/4/4/4	0/0/0/0
7	GOL	B	610	-	-	0/4/4/4	0/0/0/0
7	GOL	B	611	-	-	0/4/4/4	0/0/0/0
7	GOL	B	612	-	-	0/4/4/4	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	608	MES	C8-S	-4.83	1.69	1.78
3	A	602	ATP	C2'-C1'	-2.51	1.49	1.53
3	A	602	ATP	PG-O3G	-2.19	1.47	1.54
3	B	602	ATP	C2-N3	2.10	1.35	1.32
3	A	602	ATP	C2-N3	2.25	1.36	1.32
3	B	602	ATP	C5-C4	2.94	1.47	1.40
3	A	602	ATP	C5-C4	2.95	1.47	1.40
5	B	604	F6P	C1-C2	3.04	1.57	1.52
5	A	604	F6P	O2-C2	3.70	1.47	1.40
5	B	604	F6P	O2-C2	3.81	1.47	1.40
2	B	601	FLC	OHB-CB	4.12	1.49	1.43

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	602	ATP	N3-C2-N1	-7.46	123.01	128.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	ATP	N3-C2-N1	-7.41	123.05	128.87
2	A	601	FLC	CB-CG-CGC	-4.33	108.19	114.95
3	A	602	ATP	O2A-PA-O5'	-3.99	89.22	108.24
8	B	608	MES	O3S-S-O2S	-3.37	104.09	112.39
2	B	601	FLC	CG-CB-CA	-2.69	103.17	109.85
3	B	602	ATP	O2B-PB-O1B	2.29	124.48	112.56
3	A	602	ATP	O2A-PA-O1A	2.52	125.66	112.56
5	A	604	F6P	O3P-P-O6	2.67	114.50	106.72
3	A	602	ATP	O3G-PG-O2G	2.78	117.66	107.44
8	B	608	MES	C5-N4-C3	2.87	116.01	109.75
8	B	608	MES	C7-N4-C5	3.11	119.61	111.62
3	B	602	ATP	O2G-PG-O1G	3.14	120.88	110.63
8	B	608	MES	O3S-S-C8	3.15	114.44	105.91
3	A	602	ATP	N6-C6-N1	3.89	125.04	118.52
3	B	602	ATP	N6-C6-N1	4.26	125.66	118.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	605	EDO	1	0
3	B	602	ATP	1	0
7	B	610	GOL	1	0
7	B	612	GOL	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	424/505 (83%)	-0.10	9 (2%) 67 67	24, 36, 67, 98	0
1	B	419/505 (82%)	-0.10	13 (3%) 52 53	23, 33, 58, 97	0
All	All	843/1010 (83%)	-0.10	22 (2%) 59 60	23, 35, 63, 98	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	33	TYR	8.4
1	A	32	SER	6.8
1	B	31	ALA	6.6
1	A	33	TYR	6.3
1	B	32	SER	6.0
1	A	31	ALA	5.9
1	A	181	ARG	5.5
1	A	455	LYS	5.4
1	B	450	THR	4.4
1	A	182	ASN	3.5
1	B	169	LEU	3.1
1	A	35	THR	2.7
1	A	184	GLU	2.5
1	B	240	TYR	2.5
1	B	353	GLN	2.4
1	B	241	TYR	2.4
1	B	238	ILE	2.3
1	B	146	GLN	2.2
1	B	350	LEU	2.2
1	B	449	PRO	2.1
1	B	243	MET	2.1
1	A	146	GLN	2.1

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

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	NEP	B	257	14/15	0.97	0.12	-	20,24,34,38	0
1	NEP	A	257	14/15	0.96	0.10	-	21,25,46,52	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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
6	EDO	B	606	4/4	0.79	0.31	8.44	59,71,78,83	0
7	GOL	B	609	6/6	0.82	0.22	5.81	45,71,86,87	0
6	EDO	B	605	4/4	0.77	0.54	5.79	62,74,85,85	0
7	GOL	B	612	6/6	0.87	0.21	4.99	42,70,87,100	0
7	GOL	A	608	6/6	0.91	0.16	3.80	52,65,74,79	0
7	GOL	B	611	6/6	0.80	0.20	3.58	42,67,77,92	0
7	GOL	B	610	6/6	0.84	0.17	2.27	36,51,69,74	0
2	FLC	B	601	13/13	0.96	0.13	1.20	29,32,41,47	0
7	GOL	A	607	6/6	0.93	0.17	0.82	52,69,80,85	0
2	FLC	A	601	13/13	0.96	0.12	0.44	34,40,51,51	0
6	EDO	A	605	4/4	0.96	0.10	0.43	37,52,63,63	0
3	ATP	B	602	31/31	0.98	0.11	0.29	26,35,54,57	0
3	ATP	A	602	31/31	0.97	0.12	0.27	30,43,57,67	0
8	MES	B	608	12/12	0.93	0.14	0.08	39,63,70,70	0
5	F6P	B	604	16/16	0.98	0.09	-0.33	24,30,40,41	0
5	F6P	A	604	16/16	0.99	0.08	-0.60	26,31,38,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	GOL	A	606	6/6	0.97	0.08	-0.78	35,46,55,55	0
7	GOL	B	607	6/6	0.98	0.07	-1.62	24,32,39,39	0
4	MG	B	603	1/1	0.50	0.17	-	32,32,32,32	0
4	MG	A	603	1/1	0.44	0.17	-	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.