



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:46 AM GMT

PDB ID : 2BIF  
Title : 6-PHOSPHOFRUCTO-2-KINASE/FRUCTOSE-2,6-BISPHOSPHATASE  
H256A MUTANT WITH F6P IN PHOSPHATASE ACTIVE SITE  
Authors : Yuen, M.H.; Hasemann, C.A.  
Deposited on : 1998-10-26  
Resolution : 2.40 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](mailto: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.

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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

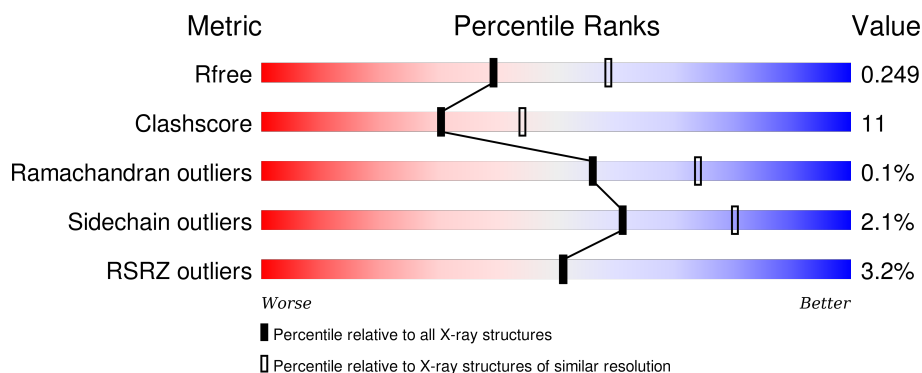
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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  $\geq 3$ , 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	469	
1	B	469	

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
2	BOG	A	555	-	-	-	X
2	BOG	B	525	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7444 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.

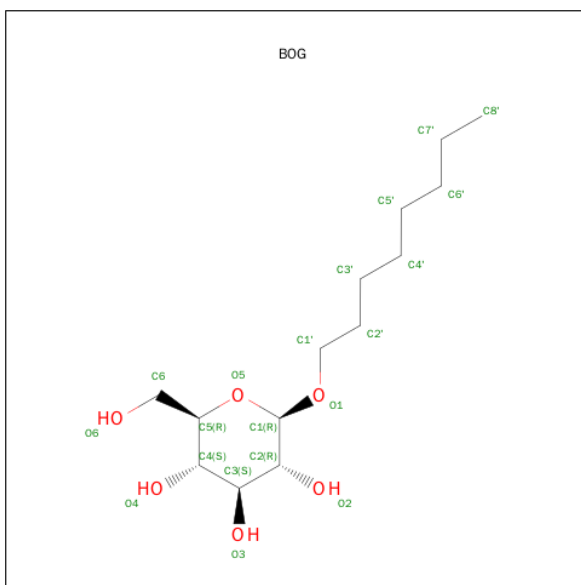
- Molecule 1 is a protein called PROTEIN (6-PHOSPHOFRUCTO-2-KINASE/FRUCTOSE-2,6-BISPHOSPHATASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	432	Total	C	N	O	S	0	1	0
			3508	2218	607	663	20			
1	B	432	Total	C	N	O	S	0	1	0
			3506	2217	604	665	20			

There are 12 discrepancies between the modelled and reference sequences:

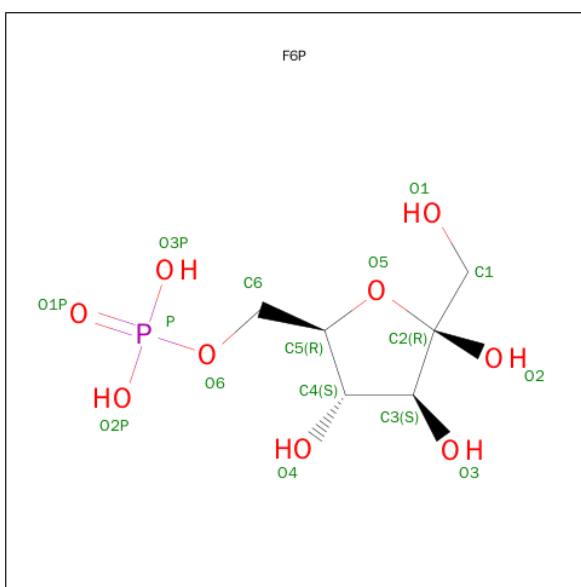
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	SEE REMARK 999	UNP P25114
B	0	MET	-	SEE REMARK 999	UNP P25114
A	15	PHE	TRP	ENGINEERED	UNP P25114
B	15	PHE	TRP	ENGINEERED	UNP P25114
A	64	PHE	TRP	ENGINEERED	UNP P25114
B	64	PHE	TRP	ENGINEERED	UNP P25114
A	256	ALA	HIS	ENGINEERED	UNP P25114
B	256	ALA	HIS	ENGINEERED	UNP P25114
A	299	PHE	TRP	ENGINEERED	UNP P25114
B	299	PHE	TRP	ENGINEERED	UNP P25114
A	320	PHE	TRP	ENGINEERED	UNP P25114
B	320	PHE	TRP	ENGINEERED	UNP P25114

- Molecule 2 is B-OCTYLGLUCOSIDE (three-letter code: BOG) (formula: C<sub>14</sub>H<sub>28</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			20	14	6		
2	B	1	Total	C	O	0	0
			20	14	6		
2	A	1	Total	C	O	0	0
			20	14	6		

- Molecule 3 is FRUCTOSE-6-PHOSPHATE (three-letter code: F6P) (formula:  $C_6H_{13}O_9P$ ).



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

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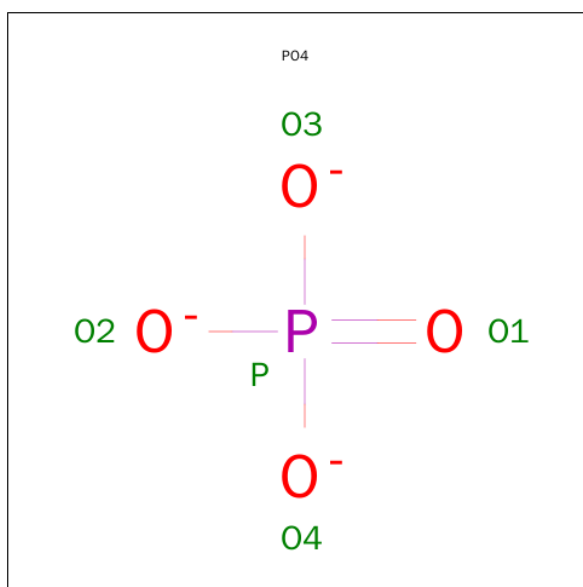
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	O	P	0	0
			16	6	9	1		

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

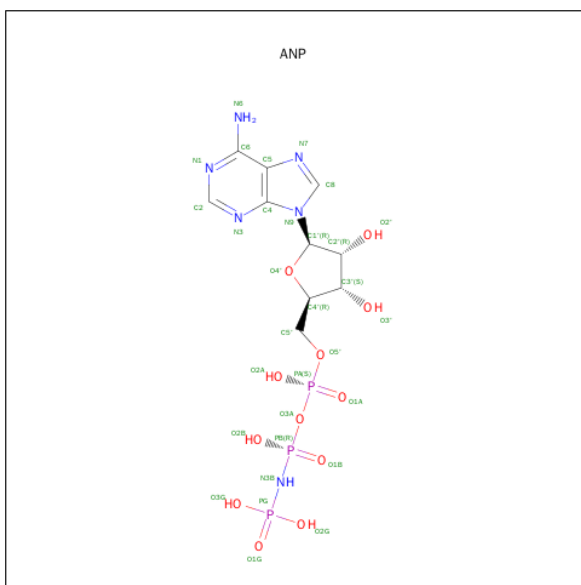
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



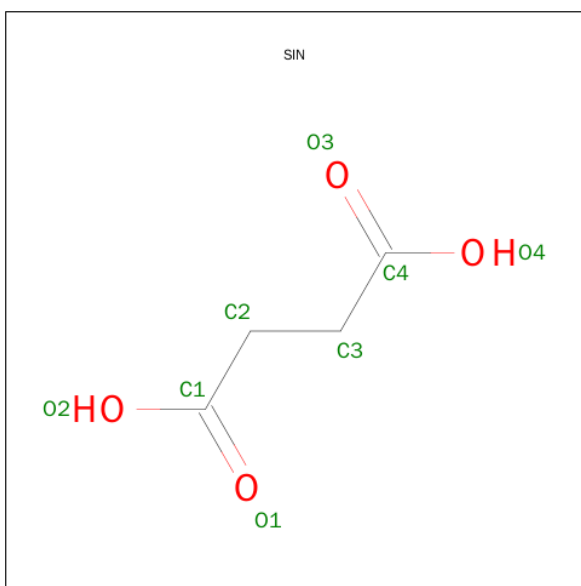
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 7 is SUCCINIC ACID (three-letter code: SIN) (formula:  $C_4H_6O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total 8	C 4	O 4	0	0
7	B	1	Total 8	C 4	O 4	0	0

- Molecule 8 is water.

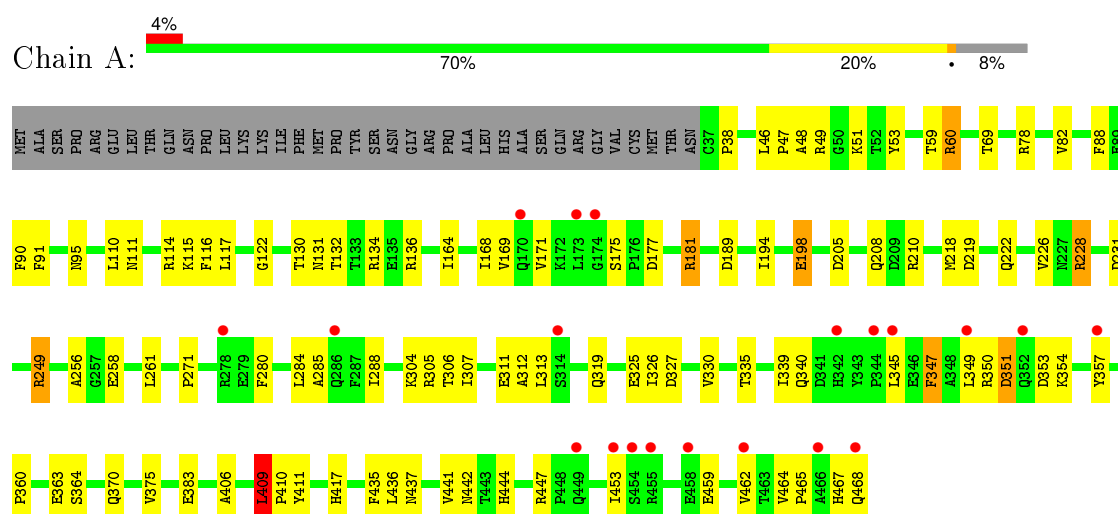
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	122	Total 122	O 122	0	0
8	B	153	Total 153	O 153	0	0



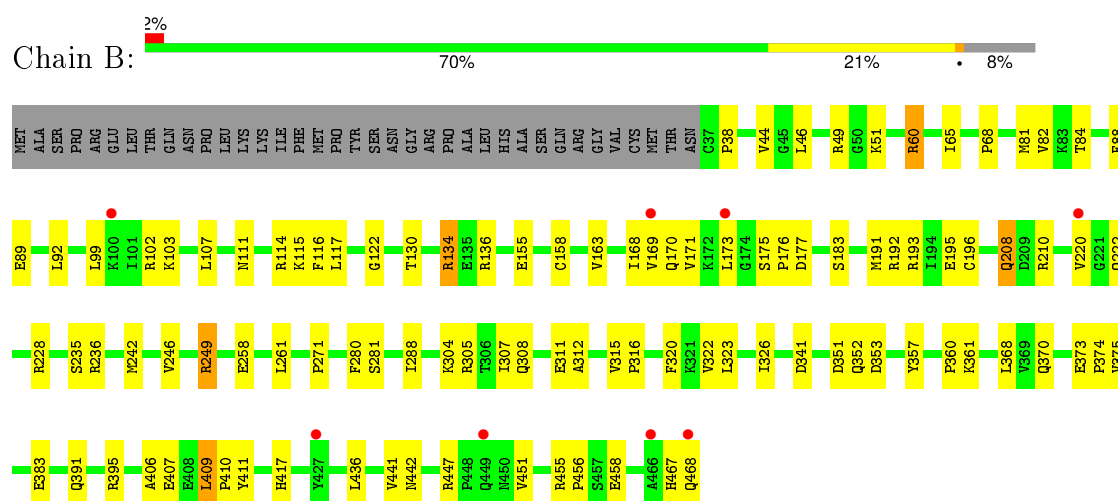
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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: PROTEIN (6-PHOSPHOFRUCTO-2-KINASE/FRUCTOSE-2,6-BISPHOSPHATASE)



- Molecule 1: PROTEIN (6-PHOSPHOFRUCTO-2-KINASE/FRUCTOSE-2,6-BISPHOSPHATASE)



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.74Å 73.51Å 76.70Å 116.90° 99.31° 105.20°	Depositor
Resolution (Å)	30.00 – 2.40 29.59 – 2.42	Depositor EDS
% Data completeness (in resolution range)	86.5 (30.00-2.40) 74.0 (29.59-2.42)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.03	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.70 (at 2.42Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.200 , 0.244 0.209 , 0.249	Depositor DCC
$R_{free}$ test set	3887 reflections (10.23%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.6	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 48.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 38618 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7444	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PO4, ANP, F6P, SIN, BOG

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	0.58	0/3581	0.75	4/4839 (0.1%)
1	B	0.56	0/3579	0.76	3/4838 (0.1%)
All	All	0.57	0/7160	0.76	7/9677 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	134	ARG	NE-CZ-NH1	-7.55	116.53	120.30
1	B	134	ARG	NE-CZ-NH2	6.93	123.77	120.30
1	A	409	LEU	CA-CB-CG	6.66	130.61	115.30
1	A	347	PHE	CB-CG-CD2	-6.50	116.25	120.80
1	B	409	LEU	CA-CB-CG	6.27	129.73	115.30
1	A	181	ARG	NE-CZ-NH1	5.21	122.90	120.30
1	A	210	ARG	NE-CZ-NH1	5.20	122.90	120.30

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	3508	0	3472	81	0
1	B	3506	0	3465	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	40	0	56	4	0
2	B	20	0	28	7	0
3	A	16	0	11	0	0
3	B	16	0	11	0	0
4	A	1	0	0	0	0
5	A	5	0	0	0	0
5	B	10	0	0	0	0
6	A	31	0	13	2	0
7	A	8	0	4	0	0
7	B	8	0	4	0	0
8	A	122	0	0	10	0
8	B	153	0	0	7	0
All	All	7444	0	7064	156	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 11.

All (156) 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:220:VAL:HG11	1:B:246:VAL:HG22	1.59	0.83
1:A:375:VAL:HG13	2:B:525:BOG:H8'3	1.61	0.82
1:B:92:LEU:HD23	1:B:196:CYS:SG	2.19	0.81
1:A:375:VAL:HG13	2:B:525:BOG:C8'	2.11	0.81
1:A:370:GLN:HG2	8:A:709:HOH:O	1.81	0.80
1:A:181:ARG:HD2	8:A:637:HOH:O	1.84	0.77
1:A:134:ARG:NH2	1:A:208:GLN:HG3	2.01	0.76
1:B:171:VAL:O	1:B:175:SER:HB3	1.86	0.75
1:A:134:ARG:HH22	1:A:208:GLN:HG3	1.51	0.74
1:A:219:ASP:HB2	1:A:222:GLN:HB3	1.70	0.73
1:A:285:ALA:HA	1:A:313:LEU:HD23	1.71	0.73
1:B:220:VAL:HG11	1:B:246:VAL:CG2	2.19	0.72
1:B:370:GLN:HG2	8:B:899:HOH:O	1.88	0.72
1:B:193:ARG:HD2	8:B:905:HOH:O	1.91	0.70
1:B:351:ASP:HB3	1:B:451:VAL:HG13	1.75	0.69
1:A:90:PHE:HA	1:A:95:ASN:ND2	2.08	0.69
1:B:353:ASP:HB3	1:B:357:TYR:CD1	2.28	0.68
1:B:447:ARG:HE	1:B:451:VAL:HG21	1.60	0.65
1:B:352:GLN:HG2	1:B:451:VAL:HG12	1.79	0.65
1:A:345:LEU:CD1	1:A:453:ILE:HD11	2.26	0.65
1:B:169:VAL:O	1:B:173:LEU:HG	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:PHE:HA	1:A:95:ASN:HD22	1.61	0.65
1:A:285:ALA:HA	1:A:313:LEU:CD2	2.27	0.64
1:B:353:ASP:HB3	1:B:357:TYR:HD1	1.63	0.64
1:B:38:PRO:HB3	1:B:117:LEU:HD22	1.79	0.63
1:A:340:GLN:OE1	1:A:340:GLN:HA	1.98	0.63
1:B:65:ILE:HD12	2:B:525:BOG:HO4	1.64	0.62
1:A:305:ARG:HG2	8:A:638:HOH:O	1.98	0.62
1:B:280:PHE:CE1	1:B:436:LEU:HD12	2.35	0.61
1:A:110:LEU:HD11	2:A:510:BOG:H8'3	1.83	0.61
1:A:48:ALA:H	6:A:500:ANP:HNB1	1.48	0.60
1:A:78:ARG:HB2	8:A:711:HOH:O	2.01	0.60
1:B:220:VAL:O	1:B:220:VAL:HG12	2.02	0.60
1:A:467:HIS:O	1:A:468:GLN:HB2	1.99	0.60
1:A:134:ARG:HD3	8:A:704:HOH:O	2.00	0.60
1:A:319:GLN:HG2	8:A:663:HOH:O	2.00	0.59
1:A:38:PRO:HB2	1:A:117:LEU:HD13	1.83	0.59
1:A:171:VAL:O	1:A:175:SER:HB3	2.02	0.59
1:A:228:ARG:NH1	1:B:222:GLN:OE1	2.36	0.58
1:A:280:PHE:CE1	1:A:417:HIS:HA	2.39	0.57
1:A:53:TYR:CD2	6:A:500:ANP:H8	2.39	0.57
1:A:78:ARG:O	1:A:82:VAL:HG22	2.05	0.57
1:B:65:ILE:HD12	2:B:525:BOG:O4	2.05	0.56
1:A:280:PHE:CE1	1:A:436:LEU:HD12	2.40	0.56
1:B:451:VAL:HG12	1:B:451:VAL:O	2.04	0.56
1:B:183:SER:HA	8:B:947:HOH:O	2.05	0.56
1:A:205:ASP:HB3	1:A:208:GLN:HB2	1.86	0.56
1:B:456:PRO:HB2	1:B:458:GLU:OE1	2.06	0.56
1:A:256:ALA:HB2	1:A:306:THR:HG22	1.88	0.56
1:A:375:VAL:HG13	2:B:525:BOG:H8'2	1.88	0.55
1:A:411:TYR:CE1	1:A:447:ARG:HB2	2.41	0.55
1:A:164:ILE:O	1:A:168:ILE:HG13	2.06	0.55
1:A:110:LEU:CD1	2:A:510:BOG:H8'3	2.36	0.55
1:B:210:ARG:HH11	1:B:210:ARG:HG2	1.71	0.55
1:A:130:THR:HB	1:A:132:THR:HG23	1.88	0.55
1:B:451:VAL:HA	1:B:455:ARG:NH1	2.21	0.55
1:A:350:ARG:HA	1:A:357:TYR:HB2	1.89	0.55
1:A:88:PHE:HB3	1:A:189:ASP:OD1	2.06	0.54
1:A:307:ILE:O	1:A:311:GLU:HG2	2.08	0.54
1:A:285:ALA:CA	1:A:313:LEU:HD23	2.36	0.54
1:A:349:LEU:O	1:A:357:TYR:HD2	1.91	0.53
1:A:258:GLU:OE2	1:A:441:VAL:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:258:GLU:OE2	1:B:441:VAL:HG23	2.08	0.53
1:B:134:ARG:HH12	1:B:208:GLN:CD	2.12	0.53
1:B:89:GLU:HA	1:B:92:LEU:HG	1.91	0.53
1:A:46:LEU:O	1:A:49:ARG:HB2	2.09	0.53
1:B:341:ASP:HA	8:B:917:HOH:O	2.09	0.53
1:B:111:ASN:OD1	1:B:114:ARG:NH1	2.42	0.52
1:B:280:PHE:HE1	1:B:436:LEU:HD12	1.75	0.52
1:B:103:LYS:HG2	1:B:136:ARG:HH22	1.75	0.52
1:A:375:VAL:CG1	2:B:525:BOG:H8'3	2.37	0.51
1:A:111:ASN:ND2	1:A:115:LYS:HE3	2.25	0.51
1:B:169:VAL:O	1:B:169:VAL:HG12	2.11	0.51
1:B:305:ARG:HG2	8:B:822:HOH:O	2.11	0.51
1:A:345:LEU:HD12	1:A:453:ILE:HD11	1.92	0.51
2:A:555:BOG:H7'2	1:B:375:VAL:HG22	1.92	0.51
1:B:352:GLN:CG	1:B:451:VAL:HG12	2.40	0.50
1:A:406:ALA:O	1:A:410:PRO:HD3	2.11	0.50
1:B:249:ARG:HG2	1:B:383:GLU:HA	1.94	0.50
1:B:441:VAL:HG12	1:B:442:ASN:N	2.27	0.50
1:A:364:SER:HA	8:A:646:HOH:O	2.12	0.49
1:A:353:ASP:HB3	1:A:357:TYR:CD2	2.47	0.49
1:A:51:LYS:HE3	1:A:130:THR:HA	1.93	0.49
1:A:330:VAL:CG2	1:A:360:PRO:HD2	2.43	0.49
1:B:81:MET:HB2	8:B:933:HOH:O	2.12	0.49
1:B:220:VAL:CG1	1:B:246:VAL:HG22	2.39	0.49
1:B:175:SER:OG	1:B:177:ASP:HB2	2.13	0.48
1:B:307:ILE:O	1:B:311:GLU:HG2	2.14	0.48
1:A:325:GLU:HG3	1:A:326:ILE:N	2.29	0.48
1:A:169:VAL:HG12	1:A:169:VAL:O	2.14	0.47
1:A:116:PHE:CZ	1:A:122:GLY:HA3	2.49	0.47
1:B:60:ARG:C	1:B:60:ARG:HD3	2.35	0.47
1:A:435:PHE:CE2	1:A:437:ASN:HA	2.50	0.47
1:B:210:ARG:HG2	1:B:210:ARG:NH1	2.29	0.47
1:B:281:SER:HB3	1:B:312:ALA:HB2	1.97	0.46
1:A:60:ARG:C	1:A:60:ARG:HD3	2.36	0.46
1:B:406:ALA:O	1:B:410:PRO:HD3	2.15	0.46
1:B:88:PHE:CE2	1:B:192:ARG:HD2	2.51	0.46
1:B:373[B]:GLU:HB2	1:B:374:PRO:HD3	1.96	0.46
1:B:280:PHE:CE1	1:B:417:HIS:HA	2.50	0.46
1:B:353:ASP:HB3	1:B:357:TYR:CE1	2.50	0.46
1:A:345:LEU:O	1:A:349:LEU:HG	2.15	0.46
1:A:441:VAL:HG12	1:A:442:ASN:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:GLN:OE1	1:B:228:ARG:NH1	2.48	0.46
1:A:131:ASN:HA	1:A:136:ARG:HD3	1.97	0.46
1:B:467:HIS:O	1:B:468:GLN:CB	2.64	0.46
1:A:285:ALA:HB2	1:A:312:ALA:O	2.15	0.45
1:B:99:LEU:HD23	1:B:102:ARG:HH21	1.80	0.45
1:A:330:VAL:HG22	1:A:360:PRO:HD2	1.99	0.45
2:A:555:BOG:H8'2	1:B:323:LEU:HD11	1.98	0.45
1:A:261:LEU:HG	1:A:271:PRO:HB3	1.99	0.45
1:B:320:PHE:HB3	1:B:322:VAL:HG12	1.97	0.45
1:B:49:ARG:HG3	1:B:158:CYS:H	1.82	0.45
1:A:249:ARG:HG2	1:A:383:GLU:HA	1.99	0.44
1:B:467:HIS:O	1:B:468:GLN:HB2	2.16	0.44
1:B:411:TYR:CE1	1:B:447:ARG:HB2	2.52	0.44
1:A:231:ASP:HB2	8:A:622:HOH:O	2.18	0.44
1:A:409:LEU:C	1:A:409:LEU:HD12	2.38	0.44
1:B:261:LEU:HG	1:B:271:PRO:HB3	2.00	0.43
1:B:391:GLN:O	1:B:395:ARG:HG3	2.18	0.43
1:B:158:CYS:SG	1:B:163:VAL:HG11	2.58	0.43
1:B:315:VAL:HG13	1:B:316:PRO:HD2	2.01	0.43
1:B:38:PRO:HB2	1:B:117:LEU:HD13	2.00	0.43
1:A:327:ASP:HB3	1:A:363:GLU:HG3	2.00	0.43
1:B:373[A]:GLU:HB3	1:B:374:PRO:HD3	1.99	0.43
1:B:407:GLU:HB2	8:B:948:HOH:O	2.18	0.43
1:A:171:VAL:HG22	8:A:645:HOH:O	2.18	0.43
1:A:59:THR:HG23	1:A:69:THR:HG22	2.01	0.43
1:A:175:SER:OG	1:A:177:ASP:HB2	2.19	0.42
1:B:44:VAL:O	1:B:155:GLU:HA	2.18	0.42
1:A:47:PRO:HB2	1:A:194:ILE:HG12	2.01	0.42
1:B:360:PRO:O	1:B:361:LYS:HB2	2.20	0.42
1:A:46:LEU:HD11	1:A:198:GLU:HG3	2.01	0.42
1:A:459:GLU:O	1:A:462:VAL:HG12	2.19	0.42
1:B:175:SER:HA	1:B:176:PRO:HD3	1.84	0.42
1:B:111:ASN:HD21	1:B:115:LYS:HE3	1.85	0.42
1:A:444:HIS:O	1:A:465:PRO:HG3	2.20	0.42
1:B:46:LEU:O	1:B:49:ARG:HB2	2.20	0.41
1:B:51:LYS:HE3	1:B:130:THR:HA	2.02	0.41
1:B:373[B]:GLU:OE1	2:B:525:BOG:H61	2.20	0.41
1:A:354:LYS:HB2	8:A:628:HOH:O	2.20	0.41
1:B:168:ILE:C	1:B:170:GLN:H	2.24	0.41
1:A:226:VAL:HG21	1:B:242:MET:HE1	2.02	0.41
1:B:116:PHE:CZ	1:B:122:GLY:HA3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:VAL:O	1:A:175:SER:CB	2.68	0.41
1:A:284:LEU:HA	1:A:436:LEU:HD13	2.03	0.41
1:A:464:VAL:HA	1:A:465:PRO:HD3	1.96	0.41
1:A:347:PHE:O	1:A:351:ASP:HB2	2.20	0.41
1:B:304:LYS:O	1:B:308:GLN:HG3	2.21	0.41
1:B:288:ILE:HD13	1:B:288:ILE:HA	1.90	0.40
1:B:326:ILE:HB	1:B:368:LEU:HD22	2.02	0.40
1:B:191:MET:O	1:B:195:GLU:HG3	2.21	0.40
1:A:288:ILE:HA	1:A:288:ILE:HD13	1.88	0.40
1:A:90:PHE:HD2	1:A:91:PHE:CE1	2.39	0.40
1:A:335:THR:O	1:A:339:ILE:HG13	2.21	0.40
1:B:82:VAL:C	1:B:84:THR:H	2.25	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	431/469 (92%)	409 (95%)	22 (5%)	0	100	100
1	B	431/469 (92%)	406 (94%)	24 (6%)	1 (0%)	52	69
All	All	862/938 (92%)	815 (94%)	46 (5%)	1 (0%)	56	74

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	68	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	387/418 (93%)	378 (98%)	9 (2%)	58	78
1	B	387/418 (93%)	380 (98%)	7 (2%)	66	84
All	All	774/836 (93%)	758 (98%)	16 (2%)	61	80

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

Mol	Chain	Res	Type
1	A	60	ARG
1	A	114	ARG
1	A	198	GLU
1	A	218	MET
1	A	228	ARG
1	A	249	ARG
1	A	304	LYS
1	A	351	ASP
1	A	409	LEU
1	B	60	ARG
1	B	107	LEU
1	B	208	GLN
1	B	235	SER
1	B	236	ARG
1	B	249	ARG
1	B	409	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	ASN
1	A	167	ASN
1	A	199	ASN
1	A	232	HIS
1	A	342	HIS
1	B	208	GLN

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Mol	Chain	Res	Type
1	B	302	GLN
1	B	342	HIS
1	B	467	HIS

### 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 12 ligands modelled in this entry, 1 is monoatomic - leaving 11 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	$\# Z  > 2$
6	ANP	A	500	4	27,33,33	2.26	11 (40%)	30,52,52	2.02	8 (26%)
7	SIN	A	505	-	1,7,7	0.12	0	2,8,8	2.40	2 (100%)
2	BOG	A	510	-	20,20,20	0.86	1 (5%)	25,25,25	0.89	1 (4%)
5	PO4	A	515	-	4,4,4	0.85	0	6,6,6	0.27	0
3	F6P	A	520	-	15,16,16	0.81	1 (6%)	16,25,25	1.25	3 (18%)
2	BOG	A	555	-	20,20,20	0.73	0	25,25,25	0.75	0
2	BOG	B	525	-	20,20,20	0.93	1 (5%)	25,25,25	0.73	0
5	PO4	B	530	-	4,4,4	0.20	0	6,6,6	0.29	0
7	SIN	B	535	-	1,7,7	0.02	0	2,8,8	2.96	1 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	PO4	B	545	-	4,4,4	2.47	3 (75%)	6,6,6	0.29	0
3	F6P	B	550	-	15,16,16	0.98	1 (6%)	16,25,25	1.25	3 (18%)

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
6	ANP	A	500	4	-	0/12/38/38	0/3/3/3
7	SIN	A	505	-	-	0/1/5/5	0/0/0/0
2	BOG	A	510	-	-	0/11/31/31	0/1/1/1
5	PO4	A	515	-	-	0/0/0/0	0/0/0/0
3	F6P	A	520	-	-	0/9/28/28	0/1/1/1
2	BOG	A	555	-	-	0/11/31/31	0/1/1/1
2	BOG	B	525	-	-	0/11/31/31	0/1/1/1
5	PO4	B	530	-	-	0/0/0/0	0/0/0/0
7	SIN	B	535	-	-	0/1/5/5	0/0/0/0
5	PO4	B	545	-	-	0/0/0/0	0/0/0/0
3	F6P	B	550	-	-	0/9/28/28	0/1/1/1

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	500	ANP	PG-O3G	-4.25	1.44	1.56
5	B	545	PO4	P-O3	-3.02	1.42	1.53
6	A	500	ANP	PG-O2G	-3.00	1.48	1.56
5	B	545	PO4	P-O4	-2.75	1.43	1.53
5	B	545	PO4	P-O2	-2.71	1.43	1.53
6	A	500	ANP	PB-O2B	-2.47	1.49	1.56
3	B	550	F6P	P-O2P	-2.17	1.46	1.54
3	A	520	F6P	P-O2P	-2.09	1.47	1.54
6	A	500	ANP	O2'-C2'	2.00	1.47	1.43
6	A	500	ANP	C5'-C4'	2.37	1.59	1.51
2	B	525	BOG	O1-C1	2.46	1.44	1.40
6	A	500	ANP	C4-N3	2.73	1.39	1.35
6	A	500	ANP	PB-O3A	2.79	1.62	1.59
2	A	510	BOG	O1-C1	3.11	1.45	1.40
6	A	500	ANP	C3'-C4'	3.16	1.61	1.53
6	A	500	ANP	PB-O1B	3.91	1.50	1.46
6	A	500	ANP	PG-O1G	4.00	1.50	1.46
6	A	500	ANP	C6-N6	4.61	1.49	1.34

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	500	ANP	O1B-PB-N3B	-5.79	103.01	111.90
7	B	535	SIN	C2-C3-C4	-3.75	105.87	112.75
6	A	500	ANP	C4'-O4'-C1'	-3.53	105.84	109.72
6	A	500	ANP	N3-C2-N1	-3.36	126.32	128.89
3	A	520	F6P	O6-P-O1P	-3.07	99.32	107.14
3	B	550	F6P	O6-P-O1P	-2.78	100.07	107.14
7	A	505	SIN	C3-C2-C1	-2.71	107.77	112.75
6	A	500	ANP	C2'-C1'-N9	-2.29	110.79	114.29
3	B	550	F6P	O2-C2-O5	-2.08	105.08	109.37
7	A	505	SIN	C2-C3-C4	-2.04	109.01	112.75
3	A	520	F6P	O4-C4-C5	2.00	117.06	111.05
3	A	520	F6P	O2P-P-O1P	2.12	117.39	110.58
6	A	500	ANP	O3A-PA-O5'	2.20	108.77	102.94
6	A	500	ANP	C4-C5-N7	2.29	111.58	109.48
6	A	500	ANP	O3G-PG-O2G	2.64	115.42	107.58
2	A	510	BOG	O1-C1-C2	2.67	111.42	108.04
3	B	550	F6P	O3P-P-O1P	2.76	119.45	110.58
6	A	500	ANP	O2B-PB-O1B	4.51	119.42	110.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	500	ANP	2	0
2	A	510	BOG	2	0
2	A	555	BOG	2	0
2	B	525	BOG	7	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	432/469 (92%)	-0.02	20 (4%) 36 37	6, 35, 70, 85	0
1	B	432/469 (92%)	-0.34	8 (1%) 70 69	9, 29, 57, 75	0
All	All	864/938 (92%)	-0.18	28 (3%) 51 51	6, 32, 65, 85	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	466	ALA	7.6
1	A	357	TYR	7.4
1	A	468	GLN	6.5
1	A	453	ILE	5.5
1	B	173	LEU	4.3
1	A	173	LEU	4.0
1	B	169	VAL	3.7
1	B	427	TYR	3.4
1	A	314	SER	3.4
1	B	220	VAL	3.2
1	A	345	LEU	3.1
1	A	455	ARG	2.9
1	B	468	GLN	2.9
1	A	286	GLN	2.8
1	A	462	VAL	2.8
1	A	344	PRO	2.8
1	A	458	GLU	2.6
1	A	174	GLY	2.6
1	A	454	SER	2.5
1	A	449	GLN	2.5
1	B	100	LYS	2.4
1	B	466	ALA	2.4
1	A	352	GLN	2.2
1	B	449	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	342	HIS	2.1
1	A	278	ARG	2.1
1	A	170	GLN	2.1
1	A	349	LEU	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	BOG	B	525	20/20	0.62	0.37	14.66	47,84,92,96	0
2	BOG	A	555	20/20	0.76	0.23	3.72	37,63,66,67	0
2	BOG	A	510	20/20	0.91	0.17	1.58	28,37,65,69	0
5	PO4	B	530	5/5	0.93	0.22	1.12	65,66,68,68	0
3	F6P	A	520	16/16	0.95	0.22	0.77	36,41,46,51	0
3	F6P	B	550	16/16	0.99	0.16	0.35	15,24,33,34	0
7	SIN	B	535	8/8	0.96	0.13	-0.10	29,34,35,38	0
5	PO4	A	515	5/5	0.94	0.17	-0.10	44,48,49,53	0
5	PO4	B	545	5/5	0.98	0.16	-0.18	24,25,35,36	0
7	SIN	A	505	8/8	0.94	0.12	-0.40	21,25,27,32	0
6	ANP	A	500	31/31	0.95	0.12	-0.47	19,41,45,46	3
4	MG	A	501	1/1	0.53	0.22	-	39,39,39,39	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.