WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 09:18 pm GMT

PDB ID	:	4GWS
Title	:	Crystal Structure of AMP complexes of Porcine Liver Fructose-1,6-bisphosph atase with Filled Central Cavity
Authors	:	Gao, Y.; Honzatko, R.B.
Deposited on	:	2012-09-03
Resolution	:	2.75 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949
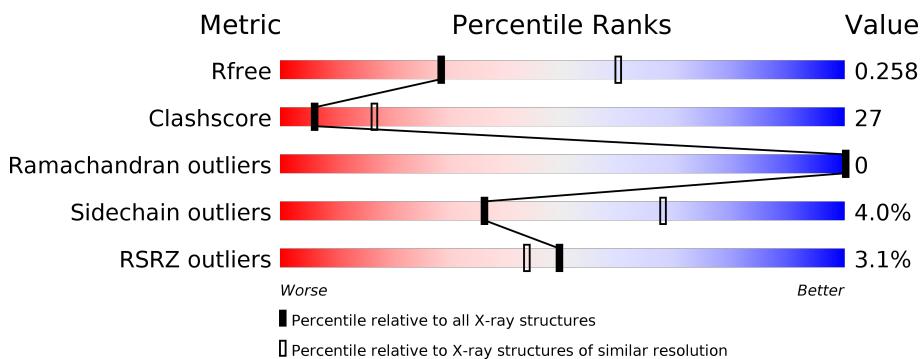
1   Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION
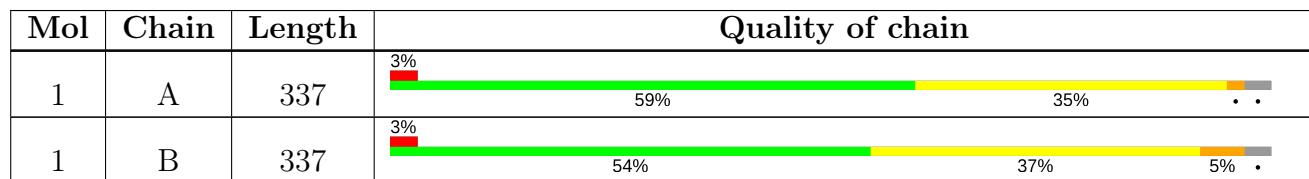
The reported resolution of this entry is 2.75 Å.

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}	100719	3666 (2.80-2.72)
Clashscore	112137	4174 (2.80-2.72)
Ramachandran outliers	110173	4103 (2.80-2.72)
Sidechain outliers	110143	4106 (2.80-2.72)
RSRZ outliers	101464	3697 (2.80-2.72)

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 <=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	337	3% ... 59% ... 35% ... · ·
1	B	337	3% ... 54% ... 37% ... 5% ·

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
4	AMP	B	403	X	-	X	-
5	PO4	A	404	-	-	X	-

2 Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 5376 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.
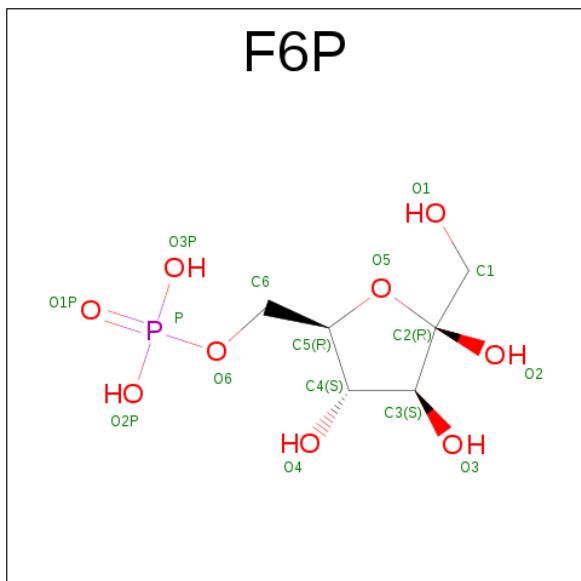
- Molecule 1 is a protein called Fructose-1,6-bisphosphatase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	0	0
			2508	1595	425	473	15			
1	B	327	Total	C	N	O	S	0	0	0
			2508	1595	425	473	15			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	45	HIS	SER	ENGINEERED MUTATION	UNP P00636
A	46	ARG	THR	ENGINEERED MUTATION	UNP P00636
A	186	TYR	LEU	ENGINEERED MUTATION	UNP P00636
B	45	HIS	SER	ENGINEERED MUTATION	UNP P00636
B	46	ARG	THR	ENGINEERED MUTATION	UNP P00636
B	186	TYR	LEU	ENGINEERED MUTATION	UNP P00636

- Molecule 2 is SUGAR (FRUCTOSE-6-PHOSPHATE) (three-letter code: F6P) (formula: $C_6H_{13}O_9P$).
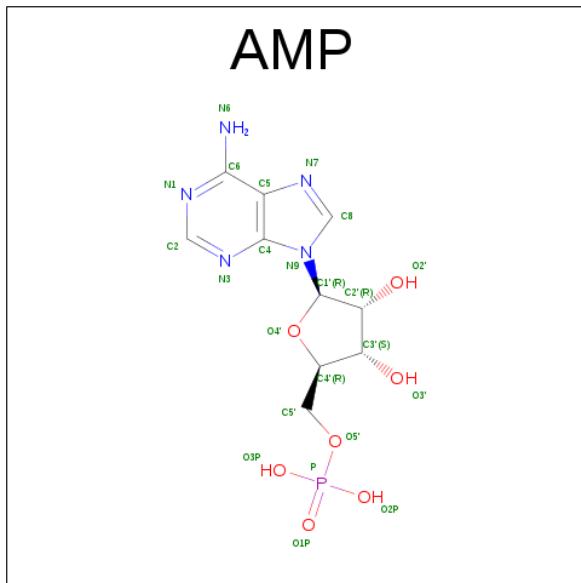
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 16	C 6	O 9	P 1	0	0
2	B	1	Total 16	C 6	O 9	P 1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).
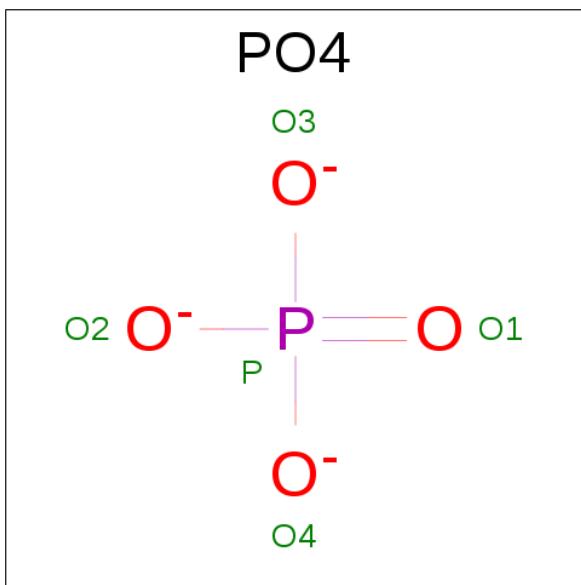
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Mg 1	0	0
3	A	1	Total 1	Mg 1	0	0

- Molecule 4 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 23	C 10	N 5	O 7	P 1	0	0
4	B	1	Total 23	C 10	N 5	O 7	P 1	0	0

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 5	O 4	P 1	0	0
5	B	1	Total 5	O 4	P 1	0	0
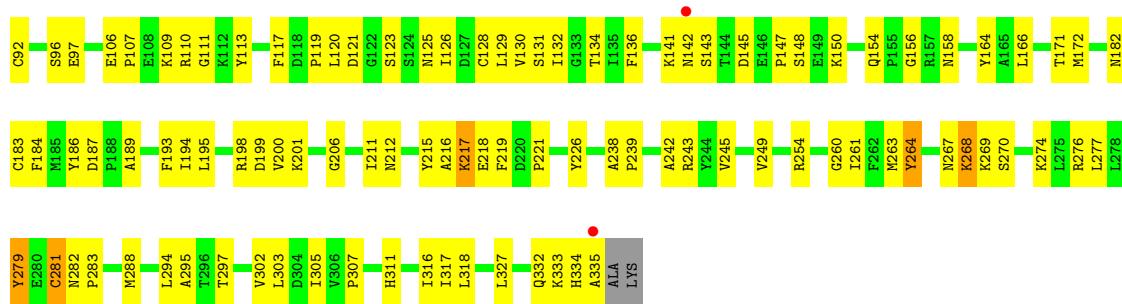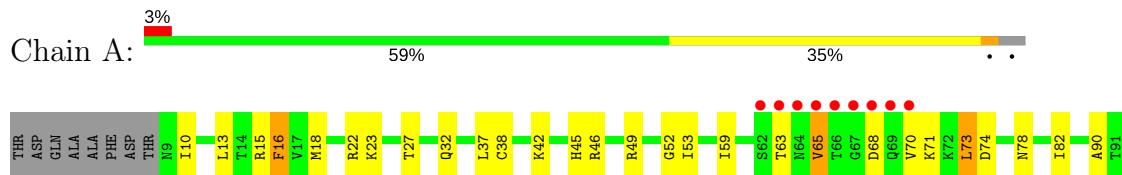
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	112	Total 112	O 112	0	0
6	B	158	Total 158	O 158	0	0
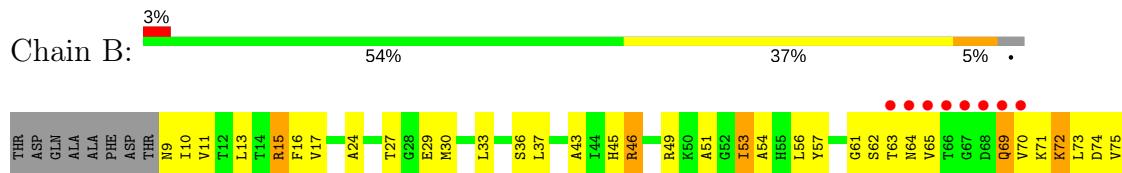
3 Residue-property plots ⓘ

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 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: Fructose-1,6-bisphosphatase 1

- Molecule 1: Fructose-1,6-bisphosphatase 1

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	60.24Å 164.28Å 79.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.19 – 2.75 31.19 – 2.75	Depositor EDS
% Data completeness (in resolution range)	81.9 (31.19-2.75) 81.9 (31.19-2.75)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.01 (at 2.76Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.200 , 0.262 0.198 , 0.258	Depositor DCC
R_{free} test set	896 reflections (5.47%)	DCC
Wilson B-factor (Å^2)	27.4	Xtriage
Anisotropy	0.283	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 45.2	EDS
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	5376	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.32% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: AMP, PO4, MG, 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	1.13	9/2552 (0.4%)	0.80	0/3452
1	B	1.12	17/2552 (0.7%)	0.84	2/3452 (0.1%)
All	All	1.13	26/5104 (0.5%)	0.82	2/6904 (0.0%)

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	281	CYS	CB-SG	-13.62	1.59	1.82
1	B	281	CYS	CB-SG	-12.19	1.61	1.82
1	B	128	CYS	CB-SG	-9.35	1.66	1.82
1	B	264	TYR	CD2-CE2	-7.53	1.28	1.39
1	A	264	TYR	CD2-CE2	-7.29	1.28	1.39
1	B	300	GLU	CG-CD	-6.46	1.42	1.51
1	B	300	GLU	CB-CG	-6.21	1.40	1.52
1	B	279	TYR	CD1-CE1	-5.99	1.30	1.39
1	B	264	TYR	CD1-CE1	-5.96	1.30	1.39
1	A	215	TYR	CD1-CE1	-5.92	1.30	1.39
1	B	279	TYR	CD2-CE2	-5.92	1.30	1.39
1	B	322	GLU	CG-CD	-5.91	1.43	1.51
1	B	192	GLU	CD-OE1	-5.80	1.19	1.25
1	A	16	PHE	CD2-CE2	-5.77	1.27	1.39
1	B	322	GLU	CD-OE1	-5.75	1.19	1.25
1	A	215	TYR	CD2-CE2	-5.56	1.31	1.39
1	B	264	TYR	CE2-CZ	-5.55	1.31	1.38
1	A	264	TYR	CD1-CE1	-5.51	1.31	1.39
1	B	133	GLY	C-O	-5.46	1.15	1.23
1	B	192	GLU	CG-CD	-5.28	1.44	1.51
1	B	130	VAL	CB-CG1	-5.27	1.41	1.52
1	B	237	SER	CB-OG	-5.18	1.35	1.42
1	A	16	PHE	CD1-CE1	-5.12	1.28	1.39
1	B	322	GLU	CB-CG	-5.08	1.42	1.52

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	279	TYR	CD2-CE2	-5.06	1.31	1.39
1	A	264	TYR	CE2-CZ	-5.04	1.31	1.38

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	237	SER	N-CA-CB	-5.38	102.43	110.50
1	B	199	ASP	N-CA-CB	5.00	119.61	110.60

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	2508	0	2558	129	0
1	B	2508	0	2558	162	0
2	A	16	0	11	1	0
2	B	16	0	11	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	23	0	12	1	0
4	B	23	0	10	10	0
5	A	5	0	0	2	0
5	B	5	0	0	1	0
6	A	112	0	0	7	0
6	B	158	0	0	15	0
All	All	5376	0	5160	280	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 27.

All (280) 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:69:GLN:HG2	1:B:69:GLN:O	1.54	1.08
1:A:13:LEU:HD21	1:A:38:CYS:SG	1.99	1.02
1:A:15:ARG:HH11	1:A:15:ARG:HG3	1.24	1.01
1:B:235:ASP:OD1	1:B:237:SER:HB2	1.62	1.00
1:B:218:GLU:HG3	6:B:616:HOH:O	1.63	0.97
1:A:121:ASP:HA	5:A:404:PO4:O2	1.65	0.96
1:B:113:TYR:OH	4:B:403:AMP:H5'2	1.65	0.96
1:B:64:ASN:HD22	1:B:65:VAL:HG23	1.31	0.94
1:B:64:ASN:ND2	1:B:65:VAL:HG23	1.82	0.94
1:B:15:ARG:HD3	6:B:522:HOH:O	1.70	0.91
1:A:218:GLU:OE1	1:A:269:LYS:HD3	1.71	0.90
1:A:13:LEU:CD2	1:A:38:CYS:SG	2.60	0.90
1:B:268:LYS:HG2	1:B:269:LYS:N	1.88	0.89
1:A:97:GLU:HB2	1:A:279:TYR:CE1	2.08	0.88
1:A:123:SER:HA	1:A:126:ILE:HG13	1.55	0.87
1:A:267:ASN:OD1	1:A:270:SER:HB2	1.75	0.86
4:B:403:AMP:O3'	4:B:403:AMP:O5'	1.94	0.85
1:A:110:ARG:HD3	1:A:147:PRO:HG3	1.56	0.85
1:B:144:THR:O	1:B:144:THR:HG22	1.76	0.85
1:B:268:LYS:HG2	1:B:269:LYS:H	1.43	0.84
1:B:29:GLU:OE1	1:B:112:LYS:HG2	1.75	0.83
1:B:202:ILE:HD12	1:B:256:LEU:HA	1.60	0.83
1:B:268:LYS:CG	1:B:269:LYS:N	2.41	0.83
1:B:269:LYS:O	1:B:269:LYS:HD2	1.81	0.81
1:B:106:GLU:CD	1:B:106:GLU:H	1.84	0.81
1:B:121:ASP:HA	5:B:404:PO4:O4	1.82	0.79
1:B:236:ASN:OD1	1:B:236:ASN:O	2.00	0.79
1:A:186:TYR:HB2	1:A:193:PHE:CE1	2.19	0.78
1:B:45:HIS:CE1	1:B:49:ARG:HE	2.01	0.78
1:A:332:GLN:HG3	6:A:603:HOH:O	1.84	0.78
1:B:108:GLU:HG2	6:B:625:HOH:O	1.82	0.78
1:A:217:LYS:HG3	1:B:232:PHE:CD1	2.21	0.75
1:A:123:SER:HA	1:A:126:ILE:CG1	2.17	0.75
1:B:269:LYS:CD	1:B:269:LYS:C	2.55	0.75
1:B:144:THR:O	1:B:144:THR:CG2	2.35	0.73
1:A:276:ARG:NH1	1:A:311:HIS:O	2.21	0.73
1:B:269:LYS:CD	1:B:269:LYS:O	2.37	0.72
1:B:321:PRO:O	1:B:325:THR:HG23	1.90	0.72
1:B:73:LEU:HG	1:B:120:LEU:HD21	1.71	0.72
1:A:282:ASN:HB2	1:A:283:PRO:HD3	1.71	0.71
1:B:69:GLN:CG	1:B:69:GLN:O	2.30	0.71
1:B:267:ASN:O	1:B:270:SER:C	2.29	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:GLU:CD	1:B:268:LYS:HD2	2.11	0.71
1:A:217:LYS:HG3	1:B:232:PHE:CE1	2.25	0.71
1:A:110:ARG:NH1	1:A:147:PRO:HG2	2.07	0.70
1:B:72:LYS:HE2	1:B:74:ASP:OD1	1.91	0.70
1:B:102:ALA:HB2	1:B:149:GLU:HG2	1.74	0.70
1:A:110:ARG:NH1	1:A:147:PRO:CG	2.55	0.69
1:B:269:LYS:C	1:B:269:LYS:HD2	2.13	0.69
1:A:130:VAL:CG1	1:A:131:SER:N	2.56	0.69
1:B:204:LYS:HD3	6:B:546:HOH:O	1.94	0.67
1:A:96:SER:HB2	1:A:117:PHE:CZ	2.30	0.66
1:B:218:GLU:OE1	1:B:268:LYS:HB3	1.95	0.66
1:B:251:ASP:OD1	1:B:254:ARG:NH2	2.25	0.66
1:B:218:GLU:OE1	1:B:268:LYS:HD2	1.96	0.66
1:A:333:LYS:HG2	1:A:333:LYS:O	1.96	0.65
1:B:74:ASP:HB2	6:B:601:HOH:O	1.96	0.65
1:A:110:ARG:HH11	1:A:147:PRO:CG	2.10	0.65
1:B:211:ILE:HD12	1:B:263:MET:HB2	1.79	0.65
1:A:282:ASN:CB	1:A:283:PRO:HD3	2.27	0.64
1:A:130:VAL:HG12	1:A:131:SER:N	2.12	0.64
1:B:123:SER:HA	1:B:126:ILE:HG13	1.78	0.64
1:B:62:SER:HA	1:B:64:ASN:OD1	1.97	0.64
1:A:277:LEU:HA	1:A:281:CYS:HB2	1.79	0.64
1:B:143:SER:OG	1:B:144:THR:N	2.30	0.63
1:B:77:SER:OG	1:B:120:LEU:HD22	1.98	0.63
1:B:268:LYS:O	1:B:271:PRO:HD3	1.99	0.63
1:B:113:TYR:HH	4:B:403:AMP:H5'2	1.62	0.63
1:A:15:ARG:CG	1:A:15:ARG:HH11	2.04	0.63
1:B:140:ARG:HH11	4:B:403:AMP:H5'1	1.62	0.63
1:A:15:ARG:NH1	1:A:15:ARG:HG3	1.99	0.63
1:B:104:ILE:HD13	1:B:104:ILE:N	2.13	0.62
1:B:140:ARG:NH1	4:B:403:AMP:H5'1	2.15	0.62
1:B:13:LEU:HD23	1:B:184:PHE:CG	2.34	0.62
1:A:267:ASN:O	1:A:270:SER:N	2.21	0.62
1:B:72:LYS:NZ	1:B:72:LYS:HB2	2.15	0.62
1:A:128:CYS:O	1:A:129:LEU:HB2	2.00	0.61
1:A:195:LEU:HD21	1:A:198:ARG:HG3	1.82	0.61
1:A:73:LEU:HG	1:A:120:LEU:HD21	1.81	0.61
1:A:123:SER:CA	1:A:126:ILE:HG13	2.30	0.60
1:B:16:PHE:CZ	1:B:182:ASN:ND2	2.68	0.60
1:A:267:ASN:O	1:A:269:LYS:N	2.34	0.60
1:A:63:THR:HG23	1:A:63:THR:O	2.01	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:LEU:HD21	1:A:136:PHE:CD2	2.36	0.60
1:B:11:VAL:HG13	1:B:15:ARG:HG2	1.84	0.58
1:A:37:LEU:HD21	1:A:136:PHE:CE2	2.37	0.58
1:A:45:HIS:CE1	1:A:171:THR:OG1	2.57	0.58
1:B:229:ARG:NH1	1:B:330:ILE:HD11	2.17	0.58
1:B:16:PHE:CE2	1:B:182:ASN:ND2	2.72	0.58
1:B:78:ASN:O	1:B:82:ILE:HG13	2.03	0.58
1:B:27:THR:N	4:B:403:AMP:O1P	2.33	0.57
1:A:73:LEU:HG	1:A:120:LEU:CD2	2.33	0.57
1:B:9:ASN:HA	6:B:502:HOH:O	2.04	0.57
1:A:156:GLY:HA3	1:A:303:LEU:HD22	1.86	0.57
1:A:221:PRO:HB2	1:A:334:HIS:CE1	2.40	0.56
1:A:45:HIS:CE1	1:A:49:ARG:HE	2.22	0.56
1:A:141:LYS:NZ	1:A:145:ASP:O	2.36	0.56
1:B:37:LEU:HD21	1:B:136:PHE:CZ	2.40	0.56
1:A:189:ALA:HB2	1:B:51:ALA:HB1	1.87	0.56
1:A:15:ARG:CG	1:A:15:ARG:NH1	2.62	0.56
1:A:16:PHE:CZ	1:A:182:ASN:ND2	2.74	0.56
1:A:53:ILE:HG22	1:B:187:ASP:HB2	1.87	0.56
1:B:316:ILE:HD11	1:B:318:LEU:HD23	1.86	0.56
1:A:154:GLN:HE21	1:A:158:ASN:HD22	1.54	0.56
1:B:130:VAL:HG12	1:B:131:SER:N	2.21	0.56
1:A:70:VAL:HG22	1:A:71:LYS:N	2.21	0.55
1:B:63:THR:HG22	1:B:63:THR:O	2.05	0.55
1:A:106:GLU:CD	1:A:106:GLU:H	2.06	0.55
1:B:173:LEU:HD23	1:B:173:LEU:C	2.27	0.55
1:B:194:ILE:O	1:B:196:VAL:HG13	2.06	0.55
1:A:261:ILE:HD11	1:A:317:ILE:HG23	1.89	0.55
1:A:123:SER:HA	1:A:126:ILE:CD1	2.36	0.55
1:A:274:LYS:HE2	2:A:401:F6P:H12	1.88	0.54
1:B:142:ASN:HB2	6:B:598:HOH:O	2.07	0.54
1:B:318:LEU:HD12	1:B:318:LEU:C	2.28	0.54
1:A:49:ARG:NH1	1:B:169:SER:HA	2.23	0.54
1:A:166:LEU:HD13	1:A:249:VAL:HG12	1.88	0.54
1:B:130:VAL:CG1	1:B:131:SER:N	2.70	0.54
1:A:13:LEU:HD23	1:A:38:CYS:SG	2.43	0.54
1:B:223:ILE:O	1:B:227:ILE:HG12	2.07	0.54
1:B:282:ASN:HB2	1:B:283:PRO:HD3	1.89	0.54
1:A:218:GLU:HB2	1:A:267:ASN:HB2	1.89	0.54
1:B:146:GLU:HG2	6:B:614:HOH:O	2.07	0.53
1:B:276:ARG:HG2	1:B:279:TYR:CE1	2.43	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:ILE:HD12	1:B:57:TYR:O	2.08	0.53
1:A:334:HIS:O	1:A:335:ALA:C	2.45	0.53
1:B:70:VAL:HG22	1:B:71:LYS:H	1.72	0.53
1:A:120:LEU:HD11	1:A:132:ILE:HD12	1.91	0.53
1:B:128:CYS:O	1:B:129:LEU:HB2	2.08	0.52
1:A:194:ILE:HD11	1:B:54:ALA:HB2	1.91	0.52
1:B:82:ILE:HD13	1:B:103:ILE:HD13	1.91	0.52
1:A:254:ARG:HD2	6:A:516:HOH:O	2.09	0.52
1:B:150:LYS:HB2	6:B:584:HOH:O	2.08	0.52
1:A:129:LEU:HD11	1:B:172:MET:HB2	1.92	0.52
1:B:103:ILE:C	1:B:104:ILE:HD13	2.31	0.52
1:B:246:GLY:O	2:B:401:F6P:H4	2.09	0.52
1:A:45:HIS:ND1	1:A:171:THR:OG1	2.41	0.52
1:A:23:LYS:NZ	6:A:584:HOH:O	2.43	0.51
1:A:216:ALA:HA	1:A:219:PHE:CD2	2.45	0.51
1:A:242:ALA:O	1:A:243:ARG:HG2	2.10	0.51
1:B:13:LEU:HD23	1:B:184:PHE:CD2	2.45	0.51
1:A:90:ALA:O	1:A:113:TYR:HB2	2.11	0.51
1:A:45:HIS:CE1	1:A:171:THR:HG1	2.27	0.51
1:A:18:MET:O	1:A:22:ARG:HG3	2.11	0.51
1:A:68:ASP:HA	6:A:607:HOH:O	2.11	0.51
1:B:316:ILE:CD1	1:B:318:LEU:HD23	2.41	0.51
1:B:73:LEU:HG	1:B:120:LEU:CD2	2.40	0.51
1:A:226:TYR:CG	1:A:327:LEU:HD13	2.46	0.50
1:B:197:ASP:OD1	1:B:200:VAL:HG22	2.11	0.50
1:A:276:ARG:NH1	1:A:311:HIS:HB3	2.26	0.50
1:A:110:ARG:HH11	1:A:147:PRO:CD	2.24	0.50
1:B:70:VAL:HA	6:B:624:HOH:O	2.11	0.50
1:B:102:ALA:CB	1:B:149:GLU:HG2	2.41	0.50
1:B:218:GLU:CD	1:B:268:LYS:CD	2.81	0.50
1:B:70:VAL:HG22	1:B:71:LYS:N	2.27	0.50
1:B:125:ASN:HB3	1:B:130:VAL:HB	1.94	0.49
1:A:211:ILE:HB	1:A:263:MET:HB2	1.94	0.49
1:B:198:ARG:HD2	6:B:526:HOH:O	2.11	0.49
1:B:37:LEU:HD21	1:B:136:PHE:CE2	2.48	0.49
1:B:146:GLU:OE2	1:B:147:PRO:HD2	2.13	0.49
1:A:42:LYS:O	1:A:45:HIS:HB3	2.12	0.49
1:B:267:ASN:O	1:B:268:LYS:C	2.47	0.48
1:A:211:ILE:HG12	1:A:212:ASN:N	2.28	0.48
1:A:78:ASN:ND2	1:A:82:ILE:HD11	2.28	0.48
1:A:27:THR:HG23	6:A:554:HOH:O	2.12	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:VAL:CG1	1:A:131:SER:H	2.25	0.48
1:A:282:ASN:CB	1:A:283:PRO:CD	2.90	0.48
1:A:113:TYR:OH	4:A:403:AMP:H5'2	2.14	0.48
1:A:148:SER:OG	1:A:150:LYS:HG2	2.13	0.48
1:A:52:GLY:HA2	6:B:510:HOH:O	2.12	0.48
1:A:117:PHE:CE2	1:A:119:PRO:HG3	2.49	0.47
1:A:200:VAL:O	1:A:201:LYS:HD3	2.14	0.47
1:B:130:VAL:CG1	1:B:131:SER:H	2.27	0.47
1:B:13:LEU:HD23	1:B:184:PHE:CD1	2.49	0.47
1:B:24:ALA:HB1	4:B:403:AMP:O2'	2.13	0.47
1:B:33:LEU:O	1:B:36:SER:HB2	2.14	0.47
1:A:277:LEU:HD23	1:A:307:PRO:HB3	1.97	0.47
1:B:143:SER:OG	1:B:145:ASP:N	2.35	0.47
1:B:220:ASP:HB2	1:B:221:PRO:HD2	1.97	0.47
1:A:97:GLU:HG2	1:A:97:GLU:O	2.14	0.47
1:A:172:MET:SD	1:A:183:CYS:HB3	2.54	0.47
1:A:129:LEU:CD1	1:B:172:MET:HB2	2.45	0.46
1:A:187:ASP:OD1	1:A:189:ALA:HB3	2.15	0.46
1:A:267:ASN:OD1	1:A:267:ASN:O	2.34	0.46
1:B:276:ARG:HG2	1:B:279:TYR:CZ	2.51	0.46
1:B:106:GLU:OE2	1:B:106:GLU:N	2.38	0.46
1:A:206:GLY:HA3	1:A:260:GLY:N	2.31	0.46
1:B:123:SER:HA	1:B:126:ILE:CG1	2.46	0.46
1:A:32:GLN:HA	1:A:32:GLN:OE1	2.15	0.46
1:B:123:SER:HA	1:B:126:ILE:CD1	2.46	0.46
1:B:195:LEU:CD2	1:B:198:ARG:NH1	2.79	0.46
1:B:74:ASP:OD1	1:B:75:VAL:N	2.49	0.46
1:A:134:THR:O	1:A:164:TYR:HA	2.16	0.46
1:A:269:LYS:HD2	1:A:269:LYS:N	2.31	0.46
1:A:65:VAL:O	1:A:65:VAL:HG12	2.16	0.46
1:A:217:LYS:HB3	1:A:218:GLU:OE2	2.17	0.45
1:A:117:PHE:HE2	1:A:119:PRO:HG3	1.80	0.45
1:A:130:VAL:HG13	1:A:131:SER:H	1.80	0.45
1:B:282:ASN:ND2	6:B:517:HOH:O	2.37	0.45
1:B:328:LEU:HA	1:B:328:LEU:HD23	1.71	0.45
1:B:263:MET:HB3	1:B:317:ILE:CD1	2.47	0.45
1:A:267:ASN:O	1:A:268:LYS:C	2.54	0.45
1:B:85:LEU:HD23	1:B:85:LEU:HA	1.68	0.45
1:B:227:ILE:HG22	1:B:231:LYS:HE3	1.99	0.45
1:B:267:ASN:OD1	1:B:267:ASN:C	2.55	0.45
1:A:107:PRO:HG3	1:A:110:ARG:NH2	2.31	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:140:ARG:HH12	4:B:403:AMP:C4'	2.28	0.45
1:A:70:VAL:CG2	1:A:71:LYS:N	2.80	0.45
1:B:195:LEU:HD21	1:B:198:ARG:HG3	1.99	0.45
1:A:318:LEU:C	1:A:318:LEU:HD12	2.36	0.45
1:B:133:GLY:CA	1:B:165:ALA:O	2.65	0.44
1:B:46:ARG:HE	1:B:46:ARG:HB3	1.48	0.44
1:A:142:ASN:OD1	1:A:143:SER:N	2.49	0.44
1:A:226:TYR:HB2	1:A:327:LEU:CD1	2.47	0.44
1:B:203:LYS:HE3	1:B:258:TYR:O	2.17	0.44
1:B:317:ILE:HG21	1:B:327:LEU:HD23	1.98	0.44
1:A:218:GLU:HB3	1:A:268:LYS:H	1.83	0.44
1:A:282:ASN:OD1	6:A:507:HOH:O	2.21	0.44
1:A:106:GLU:OE1	1:A:109:LYS:HD2	2.18	0.44
1:A:288:MET:HG3	1:A:318:LEU:HB2	1.99	0.44
1:B:200:VAL:O	1:B:201:LYS:HD3	2.18	0.44
1:A:245:VAL:HG13	1:B:245:VAL:HG22	1.99	0.44
1:B:77:SER:HG	1:B:120:LEU:HD22	1.83	0.44
1:B:206:GLY:HA3	1:B:260:GLY:N	2.33	0.44
1:A:186:TYR:HB2	1:A:193:PHE:HE1	1.77	0.43
1:B:276:ARG:HG2	1:B:279:TYR:OH	2.17	0.43
1:A:123:SER:HA	1:A:126:ILE:HD11	1.99	0.43
1:A:154:GLN:HE21	1:A:158:ASN:ND2	2.17	0.43
1:B:97:GLU:OE1	1:B:118:ASP:OD2	2.37	0.43
1:B:43:ALA:HB1	1:B:80:LEU:HD13	2.01	0.43
1:B:45:HIS:O	1:B:49:ARG:HD3	2.18	0.43
1:A:295:ALA:HB3	6:A:530:HOH:O	2.19	0.43
1:A:297:THR:HG21	1:A:305:ILE:HD11	2.00	0.42
1:B:142:ASN:HB2	1:B:154:GLN:NE2	2.33	0.42
1:B:220:ASP:HB2	1:B:221:PRO:CD	2.49	0.42
1:B:267:ASN:O	1:B:270:SER:O	2.37	0.42
1:B:198:ARG:HH11	1:B:198:ARG:HD2	1.69	0.42
1:B:267:ASN:O	1:B:270:SER:N	2.53	0.42
1:B:320:SER:HA	1:B:321:PRO:HD3	1.93	0.42
1:B:63:THR:CG2	1:B:63:THR:O	2.68	0.42
1:B:269:LYS:O	1:B:269:LYS:HD3	2.19	0.42
1:A:110:ARG:NH1	1:A:147:PRO:HD2	2.35	0.42
1:A:184:PHE:HB3	1:A:193:PHE:HB3	2.01	0.42
1:A:238:ALA:HA	1:A:239:PRO:HD3	1.65	0.42
1:B:312:GLN:NE2	6:B:590:HOH:O	2.20	0.42
1:B:157:ARG:NH2	1:B:289:GLU:OE2	2.53	0.42
1:B:184:PHE:CD1	1:B:184:PHE:N	2.87	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43:ALA:CB	1:B:80:LEU:HD13	2.49	0.42
1:A:110:ARG:NH1	1:A:147:PRO:CD	2.83	0.42
1:A:125:ASN:HB3	1:A:130:VAL:HB	2.02	0.41
1:B:202:ILE:HD11	1:B:255:THR:O	2.20	0.41
1:B:203:LYS:CE	1:B:258:TYR:O	2.68	0.41
1:B:235:ASP:O	1:B:236:ASN:HB3	2.19	0.41
1:B:140:ARG:NH1	4:B:403:AMP:C5'	2.82	0.41
1:A:294:LEU:O	1:A:318:LEU:HA	2.20	0.41
1:B:53:ILE:HA	1:B:56:LEU:HD13	2.02	0.41
1:B:282:ASN:CB	1:B:283:PRO:HD3	2.51	0.41
1:B:61:GLY:O	1:B:64:ASN:OD1	2.38	0.41
1:A:302:VAL:HG21	1:A:316:ILE:HD12	2.01	0.41
1:B:173:LEU:HD23	1:B:174:VAL:N	2.34	0.41
1:B:37:LEU:HD21	1:B:136:PHE:CE1	2.55	0.41
1:B:71:LYS:N	6:B:624:HOH:O	2.53	0.41
1:B:156:GLY:HA3	1:B:303:LEU:HD22	2.02	0.41
1:A:10:ILE:HD12	1:B:57:TYR:C	2.41	0.41
1:A:59:ILE:HB	1:B:10:ILE:HD13	2.03	0.41
1:A:68:ASP:O	1:A:68:ASP:OD1	2.38	0.41
1:A:97:GLU:OE1	5:A:404:PO4:O3	2.38	0.41
1:A:92:CYS:HB3	1:A:111:GLY:O	2.20	0.40
1:A:123:SER:O	1:A:126:ILE:HG13	2.21	0.40
1:B:255:THR:O	1:B:259:GLY:HA2	2.20	0.40
1:B:30:MET:O	1:B:30:MET:HG2	2.20	0.40
1:B:113:TYR:OH	4:B:403:AMP:C5'	2.52	0.40
1:B:13:LEU:HB2	1:B:193:PHE:HB2	2.03	0.40
1:B:309:ASP:O	1:B:312:GLN:HB2	2.21	0.40
1:B:187:ASP:OD1	1:B:187:ASP:C	2.59	0.40
1:B:257:VAL:HG12	1:B:258:TYR:CD2	2.56	0.40
1:A:277:LEU:O	1:A:282:ASN:N	2.51	0.40
1:B:13:LEU:O	1:B:17:VAL:HG22	2.21	0.40
1:B:229:ARG:NH2	1:B:330:ILE:HD12	2.36	0.40
1:B:227:ILE:CG2	1:B:231:LYS:HE3	2.51	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	325/337 (96%)	316 (97%)	9 (3%)	0	100	100
1	B	325/337 (96%)	320 (98%)	5 (2%)	0	100	100
All	All	650/674 (96%)	636 (98%)	14 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	272/279 (98%)	264 (97%)	8 (3%)	48	78
1	B	272/279 (98%)	258 (95%)	14 (5%)	28	58
All	All	544/558 (98%)	522 (96%)	22 (4%)	36	68

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	ARG
1	A	65	VAL
1	A	73	LEU
1	A	74	ASP
1	A	199	ASP
1	A	217	LYS
1	A	264	TYR
1	A	268	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	15	ARG
1	B	46	ARG
1	B	53	ILE
1	B	69	GLN
1	B	72	LYS
1	B	106	GLU
1	B	146	GLU
1	B	157	ARG
1	B	197	ASP
1	B	205	LYS
1	B	264	TYR
1	B	268	LYS
1	B	269	LYS
1	B	276	ARG

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	154	GLN
1	B	154	GLN

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 ⓘ

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	F6P	A	401	3	15,16,16	0.92	1 (6%)	17,25,25	0.87	0
4	AMP	A	403	-	22,25,25	1.07	2 (9%)	24,38,38	1.42	3 (12%)
5	PO4	A	404	3	4,4,4	1.14	0	6,6,6	0.70	0
2	F6P	B	401	3	15,16,16	0.69	0	17,25,25	0.95	1 (5%)
4	AMP	B	403	-	22,25,25	1.20	1 (4%)	24,38,38	4.86	7 (29%)
5	PO4	B	404	3	4,4,4	1.02	0	6,6,6	0.55	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	F6P	A	401	3	-	0/9/28/28	0/1/1/1
4	AMP	A	403	-	-	0/6/26/26	0/3/3/3
5	PO4	A	404	3	-	0/0/0/0	0/0/0/0
2	F6P	B	401	3	-	0/9/28/28	0/1/1/1
4	AMP	B	403	-	2/2/5/5	0/6/26/26	0/3/3/3
5	PO4	B	404	3	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	F6P	O2-C2	2.22	1.44	1.40
4	A	403	AMP	O4'-C1'	2.23	1.44	1.41
4	A	403	AMP	C5-C4	2.88	1.47	1.40
4	B	403	AMP	C5-C4	2.91	1.47	1.40

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	403	AMP	C4'-O4'-C1'	-21.01	87.40	109.77
4	A	403	AMP	N3-C2-N1	-4.43	125.00	128.86
4	B	403	AMP	O3'-C3'-C4'	-4.40	98.24	111.09
4	B	403	AMP	N3-C2-N1	-3.56	125.76	128.86

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	401	F6P	O2-C2-O5	-2.34	104.78	109.45
4	A	403	AMP	O3P-P-O2P	2.18	116.39	107.61
4	A	403	AMP	C2-N1-C6	2.55	123.23	118.77
4	B	403	AMP	P-O5'-C5'	2.98	126.50	118.30
4	B	403	AMP	C1'-N9-C4	3.08	131.95	126.64
4	B	403	AMP	O4'-C4'-C3'	3.17	111.48	105.17
4	B	403	AMP	O4'-C4'-C5'	6.37	130.91	109.40

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	403	AMP	C4'
4	B	403	AMP	C1'

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	F6P	1	0
4	A	403	AMP	1	0
5	A	404	PO4	2	0
2	B	401	F6P	1	0
4	B	403	AMP	10	0
5	B	404	PO4	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	327/337 (97%)	-0.31	11 (3%)	46	40	8, 19, 41, 83	0
1	B	327/337 (97%)	-0.36	9 (2%)	53	48	4, 18, 43, 81	0
All	All	654/674 (97%)	-0.33	20 (3%)	49	44	4, 18, 43, 83	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	68	ASP	7.5
1	A	67	GLY	7.3
1	B	66	THR	6.6
1	A	66	THR	6.6
1	A	69	GLN	5.7
1	B	67	GLY	5.6
1	B	69	GLN	5.2
1	A	65	VAL	4.6
1	A	70	VAL	4.6
1	B	65	VAL	4.3
1	B	70	VAL	3.6
1	B	63	THR	3.5
1	A	64	ASN	3.0
1	B	68	ASP	3.0
1	B	64	ASN	2.9
1	B	142	ASN	2.7
1	A	62	SER	2.7
1	A	63	THR	2.6
1	A	335	ALA	2.3
1	A	142	ASN	2.1

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

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

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
5	PO4	A	404	5/5	0.93	0.18	1.25	34,37,38,41	0
4	AMP	B	403	23/23	0.90	0.20	0.92	22,29,40,46	0
5	PO4	B	404	5/5	0.98	0.12	-0.38	41,42,44,45	0
4	AMP	A	403	23/23	0.97	0.13	-0.71	10,21,25,29	0
2	F6P	B	401	16/16	0.98	0.11	-0.90	11,15,19,23	0
3	MG	A	402	1/1	0.94	0.12	-1.27	20,20,20,20	0
2	F6P	A	401	16/16	0.98	0.09	-2.01	14,17,20,20	0
3	MG	B	402	1/1	0.93	0.08	-2.56	19,19,19,19	0

6.5 Other polymers ⓘ

There are no such residues in this entry.