Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 07:31 AM GMT

PDB ID	:	3B1R
Title	:	Structure of Burkholderia thailandensis nucleoside kinase (BthNK) in complex with AMP-Mg-AMP
Authors	:	Yasutake, Y.; Ota, H.; Hino, E.; Sakasegawa, S.; Tamura, T.
Deposited on	:	2011-07-05
Resolution	:	2.00 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

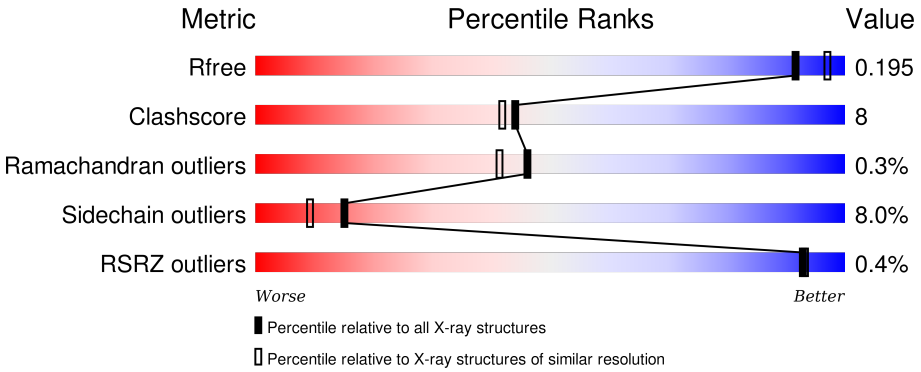
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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 <=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	320	% 79% 16%
1	B	320	76% 18%
1	C	320	78% 17%
1	D	320	82% 13%
1	E	320	% 76% 18%

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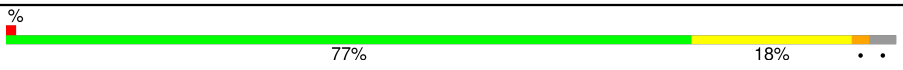
Mol	Chain	Length	Quality of chain
1	F	320	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15572 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 Ribokinase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	1	0
			2377	1495	421	446	15			
1	B	310	Total	C	N	O	S	0	2	0
			2382	1500	421	446	15			
1	C	310	Total	C	N	O	S	0	1	0
			2377	1495	421	446	15			
1	D	310	Total	C	N	O	S	0	0	0
			2372	1491	421	446	14			
1	E	310	Total	C	N	O	S	0	2	0
			2383	1499	422	447	15			
1	F	310	Total	C	N	O	S	0	1	0
			2377	1495	421	446	15			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	EXPRESSION TAG	UNP Q2SZE4
A	-6	GLY	-	EXPRESSION TAG	UNP Q2SZE4
A	-5	HIS	-	EXPRESSION TAG	UNP Q2SZE4
A	-4	HIS	-	EXPRESSION TAG	UNP Q2SZE4
A	-3	HIS	-	EXPRESSION TAG	UNP Q2SZE4
A	-2	HIS	-	EXPRESSION TAG	UNP Q2SZE4
A	-1	HIS	-	EXPRESSION TAG	UNP Q2SZE4
A	0	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	-7	MET	-	EXPRESSION TAG	UNP Q2SZE4
B	-6	GLY	-	EXPRESSION TAG	UNP Q2SZE4
B	-5	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	-4	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	-3	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	-2	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	-1	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	0	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	-7	MET	-	EXPRESSION TAG	UNP Q2SZE4

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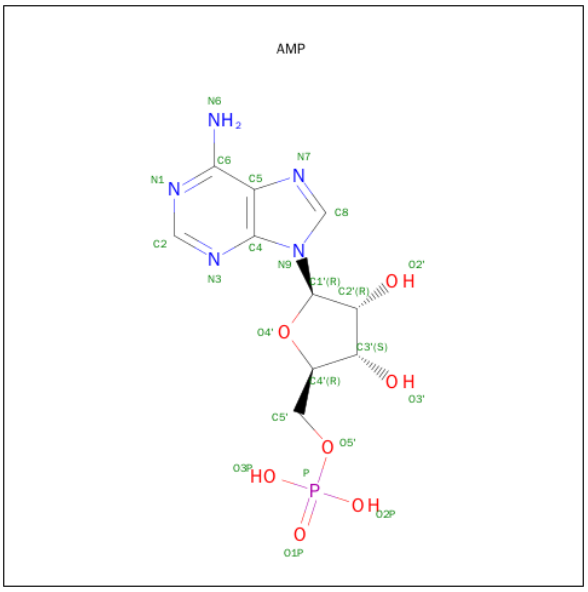
Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	GLY	-	EXPRESSION TAG	UNP Q2SZE4
C	-5	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	-4	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	-3	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	-2	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	-1	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	0	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	-7	MET	-	EXPRESSION TAG	UNP Q2SZE4
D	-6	GLY	-	EXPRESSION TAG	UNP Q2SZE4
D	-5	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	-4	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	-3	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	-2	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	-1	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	0	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	-7	MET	-	EXPRESSION TAG	UNP Q2SZE4
E	-6	GLY	-	EXPRESSION TAG	UNP Q2SZE4
E	-5	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	-4	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	-3	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	-2	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	-1	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	0	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	-7	MET	-	EXPRESSION TAG	UNP Q2SZE4
F	-6	GLY	-	EXPRESSION TAG	UNP Q2SZE4
F	-5	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	-4	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	-3	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	-2	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	-1	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	0	HIS	-	EXPRESSION TAG	UNP Q2SZE4

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	E	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	E	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	F	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	F	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	2	Total Mg 2 2	0	0
3	E	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0
3	F	1	Total Mg 1 1	0	0

- Molecule 4 is water.

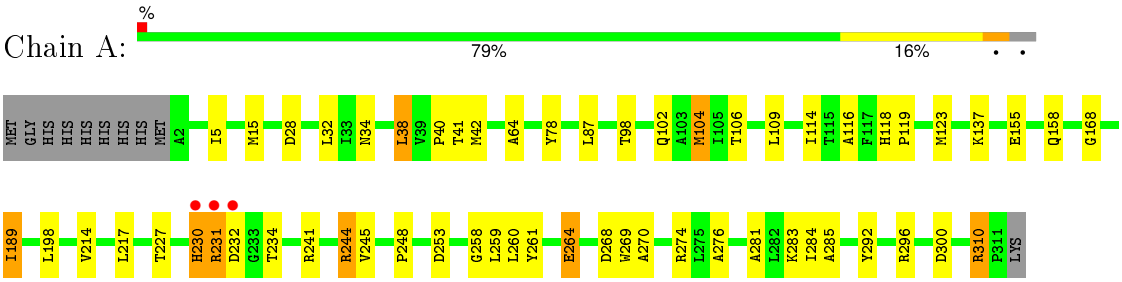
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	150	Total O 150 150	0	0
4	B	202	Total O 202 202	0	0
4	C	160	Total O 160 160	0	0
4	D	164	Total O 164 164	0	0
4	E	201	Total O 201 201	0	0
4	F	144	Total O 144 144	0	0

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.

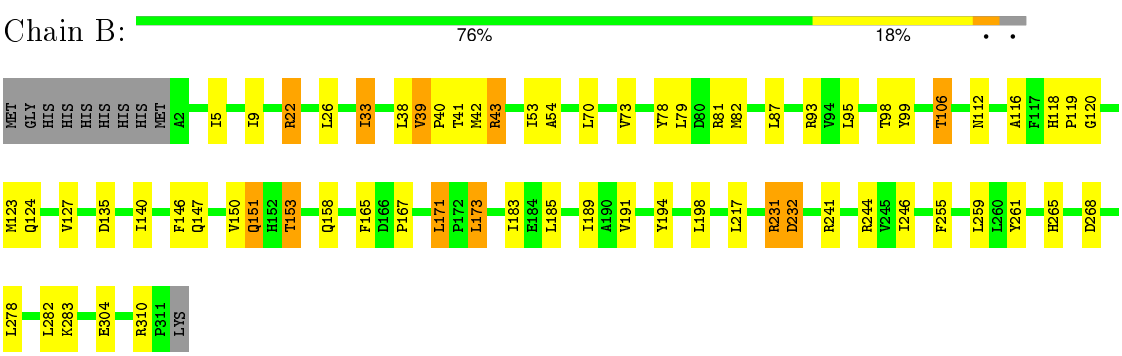
- Molecule 1: Ribokinase, putative

Chain A:



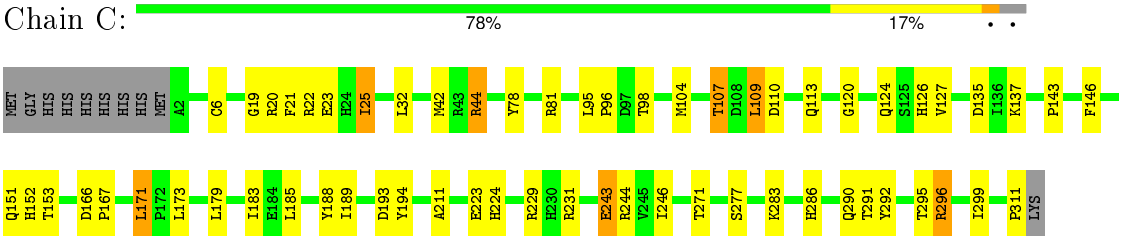
- Molecule 1: Ribokinase, putative

Chain B:



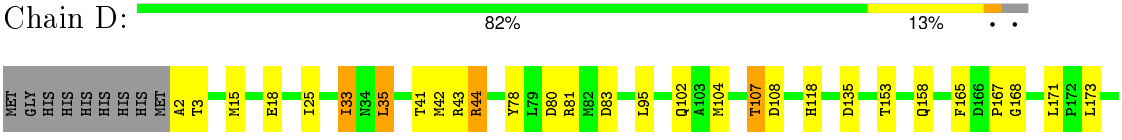
- Molecule 1: Ribokinase, putative

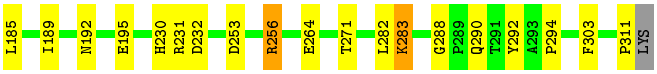
Chain C:



- Molecule 1: Ribokinase, putative

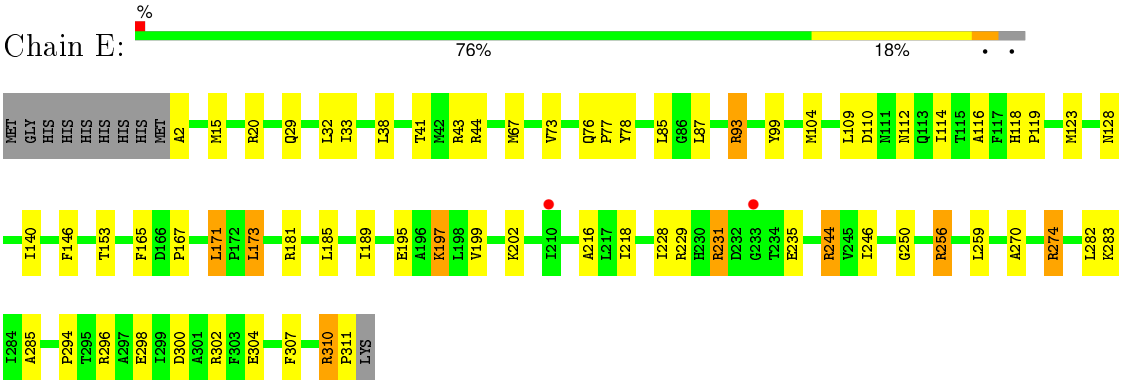
Chain D:





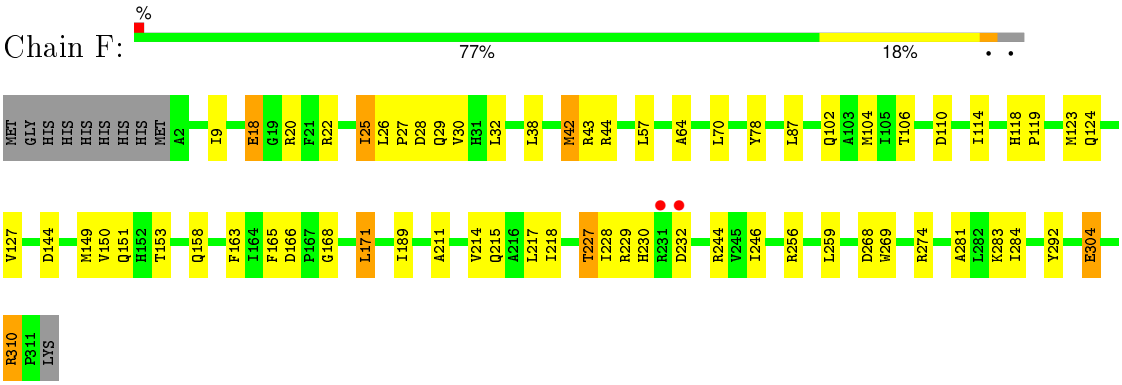
• Molecule 1: Ribokinase, putative

Chain E:



• Molecule 1: Ribokinase, putative

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	125.22Å 125.22Å 115.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.35 – 2.00 42.35 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (42.35-2.00) 99.9 (42.35-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.50 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.167 , 0.204 0.163 , 0.195	Depositor DCC
R_{free} test set	7059 reflections (5.47%)	DCC
Wilson B-factor (Å^2)	21.9	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 48.4	EDS
Estimated twinning fraction	0.501 for H, K, L 0.499 for -H, H+K, -L 0.000 for -h,-k,l 0.022 for h,-h-k,-l 0.156 for -k,-h,-l	Xtriage
Reported twinning fraction	0.501 for H, K, L 0.499 for -H, H+K, -L	Depositor
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 136199 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	15572	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 58.27 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.0959e-05.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: AMP, MG

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	0.45	0/2430	0.63	0/3294
1	B	0.51	0/2438	0.64	0/3305
1	C	0.45	0/2430	0.64	0/3294
1	D	0.45	0/2422	0.63	0/3284
1	E	0.51	0/2439	0.65	0/3306
1	F	0.46	0/2430	0.61	0/3294
All	All	0.47	0/14589	0.64	0/19777

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	2377	0	2323	41	0
1	B	2382	0	2334	45	0
1	C	2377	0	2323	37	0
1	D	2372	0	2314	34	0
1	E	2383	0	2331	52	0
1	F	2377	0	2323	44	0
2	A	46	0	24	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	46	0	24	0	0
2	C	46	0	24	0	0
2	D	46	0	24	1	0
2	E	46	0	24	1	0
2	F	46	0	24	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	2	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	150	0	0	3	0
4	B	202	0	0	5	0
4	C	160	0	0	2	0
4	D	164	0	0	2	0
4	E	201	0	0	5	0
4	F	144	0	0	5	0
All	All	15572	0	14092	228	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 8.

All (228) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:44:ARG:HH11	1:D:44:ARG:HG2	1.08	1.11
1:C:296:ARG:HH11	1:C:296:ARG:HG3	1.22	0.99
1:E:274:ARG:HG3	1:E:274:ARG:HH11	1.27	0.97
1:C:44:ARG:HH11	1:C:44:ARG:CB	1.79	0.95
1:B:33:ILE:HD12	1:E:112:ASN:HB3	1.49	0.93
1:D:44:ARG:HG2	1:D:44:ARG:NH1	1.77	0.92
1:B:39:VAL:HG21	1:E:116:ALA:HB1	1.56	0.88
1:A:244:ARG:CG	1:A:244:ARG:HH21	1.89	0.85
1:A:38:LEU:H	1:A:38:LEU:HD23	1.40	0.85
1:D:256:ARG:HG2	1:D:256:ARG:HH11	1.43	0.84
1:C:44:ARG:HH11	1:C:44:ARG:HB3	1.40	0.84
1:B:231:ARG:HG2	1:B:232:ASP:H	1.42	0.84
1:C:296:ARG:NH1	1:C:296:ARG:HG3	1.92	0.82
1:E:274:ARG:HH11	1:E:274:ARG:CG	1.93	0.82
1:D:44:ARG:HH11	1:D:44:ARG:CG	1.91	0.78
1:A:38:LEU:H	1:A:38:LEU:CD2	1.97	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:ALA:CB	1:E:15[A]:MET:HG2	2.15	0.77
1:A:244:ARG:HG2	1:A:244:ARG:HH21	1.49	0.76
1:F:22:ARG:HD2	4:F:710:HOH:O	1.86	0.75
1:E:310:ARG:HD2	4:E:782:HOH:O	1.86	0.75
1:B:231:ARG:HG2	1:B:232:ASP:N	2.00	0.74
1:F:230:HIS:CE1	1:F:269:TRP:CD1	2.78	0.71
1:D:107:THR:HG22	1:D:108:ASP:H	1.54	0.71
1:A:261:TYR:OH	1:A:296:ARG:NH2	2.24	0.70
1:B:231:ARG:HD3	4:B:363:HOH:O	1.92	0.69
1:E:85:LEU:HB2	1:E:87:LEU:HD13	1.73	0.69
1:C:295:THR:O	1:C:299:ILE:HG13	1.93	0.69
1:A:244:ARG:HH22	1:A:285:ALA:HB1	1.59	0.68
1:B:146:PHE:HB2	1:B:173:LEU:HG	1.75	0.67
1:B:106:THR:HG23	4:B:677:HOH:O	1.94	0.67
1:C:107:THR:HG23	1:C:113:GLN:HA	1.78	0.66
1:A:104:MET:HB3	1:D:15:MET:HE3	1.76	0.66
1:C:21:PHE:CZ	1:F:114:ILE:HD11	2.31	0.66
1:E:231:ARG:HH11	1:E:231:ARG:HB2	1.62	0.65
1:E:231:ARG:NH1	1:E:231:ARG:HB2	2.11	0.64
1:D:271:THR:CG2	1:D:311:PRO:HB3	2.27	0.64
1:C:25:ILE:HG23	1:C:32:LEU:HD11	1.78	0.64
1:B:165:PHE:O	1:B:189[A]:ILE:HD12	1.99	0.63
1:B:95:LEU:HD11	1:B:124:GLN:HB2	1.81	0.63
1:D:230:HIS:O	1:D:232:ASP:N	2.32	0.62
1:A:244:ARG:NH2	1:A:285:ALA:HB1	2.14	0.62
1:F:144:ASP:HB3	1:F:149:MET:HG3	1.82	0.62
1:C:44:ARG:HH11	1:C:44:ARG:CG	2.13	0.61
1:F:57:LEU:HD23	1:F:64:ALA:HB2	1.82	0.61
1:A:15:MET:HB2	1:A:106:THR:HG22	1.83	0.61
1:C:20:ARG:NH1	1:C:110:ASP:OD1	2.34	0.60
1:C:167:PRO:HB2	1:C:171:LEU:HD13	1.83	0.60
1:A:296:ARG:NH1	1:A:300:ASP:OD1	2.33	0.60
1:B:183:ILE:HG23	1:B:189[B]:ILE:HD11	1.82	0.60
1:C:19:GLY:H	1:C:109:LEU:HD22	1.66	0.60
1:E:250:GLY:HA2	2:E:501:AMP:O2P	2.01	0.59
1:B:191:VAL:HG12	4:B:878:HOH:O	2.01	0.59
1:E:2:ALA:N	4:E:521:HOH:O	2.35	0.58
1:C:81:ARG:NH2	1:C:290:GLN:OE1	2.36	0.58
1:D:80:ASP:O	1:D:83:ASP:HB2	2.03	0.58
1:A:104:MET:HB3	1:D:15:MET:CE	2.34	0.57
1:C:124:GLN:O	1:C:127:VAL:HG22	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:256:ARG:HH11	1:D:256:ARG:CG	2.16	0.57
1:A:189:ILE:HG22	1:A:214:VAL:HG21	1.86	0.57
1:F:106:THR:O	1:F:114:ILE:HG22	2.04	0.57
1:E:167:PRO:HB2	1:E:171:LEU:HD13	1.87	0.57
1:E:119:PRO:HD2	4:E:348:HOH:O	2.05	0.57
1:E:165:PHE:HB3	1:E:189:ILE:HD13	1.86	0.56
1:C:179:LEU:O	1:C:183:ILE:HG13	2.04	0.56
1:B:150:VAL:O	1:B:153:THR:HG22	2.04	0.56
1:B:153:THR:HG23	1:B:185:LEU:HD12	1.87	0.56
1:A:102:GLN:HG2	1:A:118:HIS:HB2	1.88	0.56
1:F:218:ILE:HG12	1:F:228:ILE:HG12	1.88	0.56
1:A:310:ARG:HB3	4:A:659:HOH:O	2.06	0.56
4:B:971:HOH:O	1:E:118:HIS:HB3	2.05	0.56
1:F:102:GLN:HB2	1:F:118:HIS:HB2	1.88	0.55
1:B:112:ASN:HD21	1:E:32:LEU:N	2.03	0.55
1:A:109:LEU:HD22	1:A:245:VAL:HG12	1.88	0.55
1:C:193:ASP:OD2	1:F:30:VAL:HG12	2.07	0.54
1:A:230:HIS:NE2	1:A:269:TRP:CD1	2.75	0.54
1:E:218:ILE:HD13	1:E:259:LEU:HD21	1.88	0.54
1:F:166:ASP:OD2	1:F:256:ARG:NE	2.40	0.54
1:E:20:ARG:NH1	1:E:110:ASP:OD1	2.41	0.54
1:B:147:GLN:O	1:B:151:GLN:HB2	2.08	0.53
1:B:146:PHE:CD1	1:B:173:LEU:HB3	2.44	0.53
1:B:26:LEU:HD13	1:E:197:LYS:HG2	1.90	0.53
1:C:296:ARG:HH11	1:C:296:ARG:CG	2.08	0.53
1:B:112:ASN:HD21	1:E:32:LEU:H	1.56	0.53
1:C:223:GLU:HG3	1:C:224:HIS:HD2	1.72	0.53
1:B:147:GLN:HE21	1:B:151:GLN:HE22	1.56	0.53
1:D:153:THR:HG22	1:D:185:LEU:HD12	1.90	0.53
1:A:260:LEU:O	1:A:264:GLU:HG2	2.08	0.52
1:B:73:VAL:HG22	1:B:98:THR:O	2.09	0.52
1:C:146:PHE:HB2	1:C:173:LEU:HD23	1.92	0.52
1:C:286:HIS:HB3	1:C:291:THR:HG22	1.91	0.52
1:F:215:GLN:HG2	4:F:348:HOH:O	2.08	0.52
1:F:230:HIS:HE1	1:F:269:TRP:CD1	2.26	0.51
1:F:274:ARG:NH1	4:F:358:HOH:O	2.44	0.51
1:B:244:ARG:HG3	1:B:246:ILE:HG12	1.92	0.51
1:F:230:HIS:C	1:F:232:ASP:H	2.13	0.51
1:A:114:ILE:HG12	1:D:33:ILE:HD12	1.92	0.51
1:C:211:ALA:CB	1:C:229:ARG:HD3	2.41	0.51
1:E:218:ILE:HG12	1:E:228:ILE:HG12	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ARG:HG3	1:A:244:ARG:HH21	1.74	0.51
1:A:116:ALA:HB3	1:D:15:MET:HE3	1.93	0.51
1:B:112:ASN:ND2	1:E:33:ILE:H	2.08	0.51
1:C:21:PHE:CE1	1:F:114:ILE:HD11	2.45	0.51
1:A:34:ASN:ND2	1:D:192:ASN:HD21	2.09	0.51
1:C:32:LEU:HD22	1:F:22:ARG:HG3	1.93	0.50
1:D:3:THR:OG1	1:D:264:GLU:OE1	2.29	0.50
1:E:195:GLU:O	1:E:199:VAL:HG23	2.10	0.50
1:C:153:THR:HG22	1:C:185:LEU:HD12	1.92	0.50
1:F:304:GLU:CG	1:F:310:ARG:HG3	2.42	0.50
1:B:33:ILE:HD13	1:E:114:ILE:HD11	1.94	0.49
1:D:303:PHE:CE2	1:D:311:PRO:HD3	2.46	0.49
1:A:244:ARG:CG	1:A:244:ARG:NH2	2.59	0.49
1:B:79:LEU:HA	1:B:82:MET:HE3	1.94	0.49
1:F:25:ILE:HG12	1:F:32:LEU:HD11	1.93	0.49
1:D:2:ALA:HB3	1:D:135:ASP:O	2.11	0.49
1:A:231:ARG:HD2	1:A:231:ARG:H	1.78	0.49
1:C:137:LYS:HD3	4:C:608:HOH:O	2.12	0.49
1:F:168:GLY:O	1:F:171:LEU:HD22	2.12	0.49
1:D:271:THR:HG21	1:D:311:PRO:HB3	1.94	0.48
1:B:194:TYR:O	1:B:198:LEU:HD13	2.13	0.48
1:F:43:ARG:NH1	1:F:43:ARG:HB2	2.28	0.48
1:D:18:GLU:HG2	4:D:904:HOH:O	2.13	0.48
1:E:246:ILE:HD12	1:E:285:ALA:O	2.14	0.48
1:F:9:ILE:HG22	1:F:70:LEU:HD21	1.95	0.48
1:B:167:PRO:HB2	1:B:171:LEU:HD13	1.96	0.48
1:B:124:GLN:O	1:B:127:VAL:HG13	2.14	0.48
1:B:255:PHE:CE2	1:B:259:LEU:HD22	2.48	0.48
1:E:296:ARG:HB3	4:E:358:HOH:O	2.13	0.47
1:E:244:ARG:O	1:E:285:ALA:HA	2.14	0.47
1:E:140:ILE:CD1	1:E:256:ARG:HG3	2.43	0.47
1:E:270:ALA:O	1:E:274:ARG:HG3	2.15	0.47
1:D:18:GLU:CG	4:D:904:HOH:O	2.62	0.47
1:A:281:ALA:O	1:A:284:ILE:HG22	2.13	0.47
1:B:53:ILE:HD13	1:B:140:ILE:HD13	1.96	0.47
1:E:93:ARG:HB2	1:E:93:ARG:HE	1.55	0.47
1:E:244:ARG:HD3	1:E:285:ALA:HB1	1.96	0.46
1:F:18:GLU:HG2	4:F:873:HOH:O	2.14	0.46
1:E:282:LEU:HD13	1:E:294:PRO:HG3	1.97	0.46
1:B:81:ARG:HG3	1:B:81:ARG:HH11	1.80	0.46
1:B:43:ARG:H	1:B:43:ARG:HG3	1.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:298:GLU:O	1:E:302:ARG:HG2	2.16	0.46
1:F:43:ARG:HH11	1:F:43:ARG:HB2	1.81	0.46
1:A:32:LEU:HD21	1:D:25:ILE:CD1	2.46	0.46
1:E:274:ARG:HG3	1:E:274:ARG:NH1	2.08	0.46
1:D:282:LEU:HD13	1:D:294:PRO:HG3	1.97	0.46
1:E:153:THR:HG22	1:E:185:LEU:CD1	2.45	0.45
1:A:104:MET:CB	1:D:15:MET:HE3	2.46	0.45
1:B:116:ALA:HB1	1:E:15[A]:MET:HG2	1.95	0.45
1:E:300:ASP:OD1	1:E:311:PRO:HG2	2.17	0.45
1:A:253:ASP:OD2	2:A:501:AMP:O3P	2.35	0.45
1:C:44:ARG:NH1	1:C:44:ARG:CB	2.63	0.45
1:A:268:ASP:OD2	1:A:270:ALA:HB3	2.17	0.45
1:D:303:PHE:CD2	1:D:311:PRO:HD3	2.51	0.45
1:E:73:VAL:HG22	1:E:99:TYR:HA	1.99	0.45
1:E:274:ARG:NH1	1:E:274:ARG:CG	2.63	0.45
1:B:119:PRO:HB2	1:B:123[A]:MET:HG2	1.97	0.45
1:E:146:PHE:CD1	1:E:173:LEU:HB3	2.52	0.44
1:E:153:THR:HG22	1:E:185:LEU:HD12	1.99	0.44
1:E:202:LYS:HE3	1:E:202:LYS:HB2	1.72	0.44
1:D:283:LYS:NZ	1:D:288:GLY:O	2.46	0.44
1:F:230:HIS:C	1:F:232:ASP:N	2.71	0.44
1:F:124:GLN:O	1:F:127:VAL:HG22	2.18	0.44
1:E:274:ARG:HD3	1:E:307:PHE:CG	2.52	0.44
1:A:137:LYS:HD3	4:A:889:HOH:O	2.17	0.44
1:B:9:ILE:HG22	1:B:70:LEU:HD21	1.98	0.44
1:A:274:ARG:HH11	1:A:274:ARG:HG3	1.83	0.43
1:A:258:GLY:HA3	1:A:276:ALA:HA	2.00	0.43
1:C:23:GLU:HA	4:C:734:HOH:O	2.19	0.43
1:A:5:ILE:HD12	1:A:64:ALA:HB1	1.99	0.43
1:D:165:PHE:CZ	1:D:167:PRO:HB3	2.54	0.43
1:F:218:ILE:HD13	1:F:259:LEU:HD21	2.01	0.43
1:C:143:PRO:HD3	1:C:166:ASP:O	2.19	0.43
1:C:126:HIS:HB2	1:C:151:GLN:OE1	2.18	0.43
4:B:868:HOH:O	1:E:38:LEU:HD21	2.18	0.43
1:C:271:THR:HG21	1:C:311:PRO:HB3	2.00	0.43
1:A:137:LYS:CD	4:A:889:HOH:O	2.66	0.42
1:F:163:PHE:HE1	1:F:165:PHE:HB2	1.84	0.42
1:D:230:HIS:CG	1:D:230:HIS:O	2.72	0.42
1:F:211:ALA:HB3	1:F:229:ARG:HH11	1.84	0.42
1:A:158:GLN:HG3	4:E:729:HOH:O	2.20	0.42
1:D:253:ASP:OD2	2:D:501:AMP:O1P	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:256:ARG:CG	1:D:256:ARG:NH1	2.78	0.42
1:F:151:GLN:HG2	4:F:950:HOH:O	2.18	0.42
1:B:33:ILE:CD1	1:E:112:ASN:HB3	2.35	0.42
1:F:189:ILE:HG23	1:F:217:LEU:HA	2.02	0.42
1:B:22:ARG:NH2	1:E:29:GLN:O	2.53	0.42
1:E:67:MET:SD	1:E:128:ASN:HB3	2.59	0.42
1:C:44:ARG:NH1	1:C:44:ARG:CG	2.78	0.42
1:E:119:PRO:HB2	1:E:123:MET:HG2	2.00	0.42
1:A:40:PRO:O	1:D:118:HIS:CD2	2.73	0.42
1:C:243:GLU:OE2	1:C:244:ARG:NH2	2.53	0.41
1:F:218:ILE:HA	1:F:227:THR:O	2.20	0.41
1:A:119:PRO:HB2	1:A:123[A]:MET:HG2	2.02	0.41
1:F:26:LEU:HA	1:F:27:PRO:HD2	1.84	0.41
1:C:22:ARG:NH2	1:F:27:PRO:O	2.53	0.41
1:E:231:ARG:CB	1:E:231:ARG:HH11	2.32	0.41
1:A:189:ILE:HG23	1:A:217:LEU:HA	2.02	0.41
1:F:310:ARG:HD3	1:F:310:ARG:H	1.85	0.41
1:A:227:THR:HG23	1:A:234:THR:HG23	2.01	0.41
1:B:304:GLU:OE1	1:B:310:ARG:HD3	2.19	0.41
1:A:244:ARG:HG3	1:A:244:ARG:NH2	2.35	0.41
1:F:20:ARG:NH1	1:F:110:ASP:OD1	2.44	0.41
1:A:261:TYR:CZ	1:A:296:ARG:NH2	2.87	0.41
1:F:42:MET:O	1:F:43:ARG:HG3	2.21	0.41
1:D:168:GLY:HA2	1:D:195:GLU:CD	2.41	0.41
1:D:81:ARG:HH12	1:D:290:GLN:HB3	1.85	0.41
1:F:256:ARG:HG3	1:F:256:ARG:HH11	1.85	0.41
1:F:189:ILE:HG22	1:F:214:VAL:HG21	2.03	0.41
1:B:261:TYR:CZ	1:B:265:HIS:CE1	3.09	0.41
1:F:22:ARG:NH1	1:F:110:ASP:OD2	2.54	0.41
1:C:194:TYR:HA	1:F:29:GLN:HG2	2.02	0.41
1:E:304:GLU:HB2	1:E:310:ARG:HG2	2.03	0.41
1:B:189[A]:ILE:HG23	1:B:217:LEU:CD1	2.51	0.41
1:F:150:VAL:O	1:F:153:THR:HB	2.21	0.41
1:C:95:LEU:HA	1:C:96:PRO:HD2	1.88	0.41
1:D:33:ILE:HD11	1:D:35:LEU:HD22	2.03	0.41
1:F:119:PRO:HB2	1:F:123[A]:MET:SD	2.61	0.41
1:E:216:ALA:HA	1:E:229:ARG:O	2.21	0.41
1:B:278:LEU:O	1:B:282:LEU:HG	2.21	0.40
1:C:6:CYS:HB3	1:C:152:HIS:CD2	2.57	0.40
1:E:76:GLN:HB2	1:E:77:PRO:HD3	2.03	0.40
1:B:120:GLY:O	1:B:123[B]:MET:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:GLU:HA	1:A:158:GLN:HG2	2.03	0.40
1:B:5:ILE:HD12	1:B:54:ALA:HA	2.04	0.40
1:B:259:LEU:HA	1:B:259:LEU:HD12	1.88	0.40
1:C:44:ARG:NH1	1:C:44:ARG:HB3	2.22	0.40
1:B:73:VAL:HG21	1:B:99:TYR:CD2	2.57	0.40
1:F:244:ARG:HG3	1:F:246:ILE:HG12	2.03	0.40
1:F:281:ALA:O	1:F:284:ILE:HG22	2.22	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	309/320 (97%)	301 (97%)	7 (2%)	1 (0%)	46	41
1	B	310/320 (97%)	302 (97%)	6 (2%)	2 (1%)	30	22
1	C	309/320 (97%)	300 (97%)	8 (3%)	1 (0%)	46	41
1	D	308/320 (96%)	297 (96%)	10 (3%)	1 (0%)	46	41
1	E	310/320 (97%)	304 (98%)	6 (2%)	0	100	100
1	F	309/320 (97%)	301 (97%)	8 (3%)	0	100	100
All	All	1855/1920 (97%)	1805 (97%)	45 (2%)	5 (0%)	46	41

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	231	ARG
1	B	40	PRO
1	B	42	MET
1	C	120	GLY
1	A	168	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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	241/249 (97%)	220 (91%)	21 (9%)	13 7
1	B	242/249 (97%)	220 (91%)	22 (9%)	12 6
1	C	241/249 (97%)	222 (92%)	19 (8%)	15 9
1	D	240/249 (96%)	222 (92%)	18 (8%)	17 11
1	E	242/249 (97%)	224 (93%)	18 (7%)	17 11
1	F	241/249 (97%)	224 (93%)	17 (7%)	18 12
All	All	1447/1494 (97%)	1332 (92%)	115 (8%)	15 9

All (115) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ASP
1	A	38	LEU
1	A	41	THR
1	A	42	MET
1	A	78	TYR
1	A	87	LEU
1	A	98	THR
1	A	104	MET
1	A	189	ILE
1	A	198	LEU
1	A	230	HIS
1	A	231	ARG
1	A	232	ASP
1	A	241	ARG
1	A	244	ARG
1	A	248	PRO
1	A	259	LEU
1	A	264	GLU
1	A	283	LYS
1	A	292	TYR
1	A	310	ARG
1	B	22	ARG

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Mol	Chain	Res	Type
1	B	33	ILE
1	B	38	LEU
1	B	39	VAL
1	B	41	THR
1	B	43	ARG
1	B	78	TYR
1	B	87	LEU
1	B	93	ARG
1	B	106	THR
1	B	118	HIS
1	B	135	ASP
1	B	151	GLN
1	B	153	THR
1	B	158	GLN
1	B	171	LEU
1	B	173	LEU
1	B	231	ARG
1	B	232	ASP
1	B	241	ARG
1	B	268	ASP
1	B	283	LYS
1	C	25	ILE
1	C	42	MET
1	C	44	ARG
1	C	78	TYR
1	C	98	THR
1	C	104	MET
1	C	107	THR
1	C	109	LEU
1	C	135	ASP
1	C	171	LEU
1	C	188	TYR
1	C	189	ILE
1	C	231	ARG
1	C	243	GLU
1	C	246	ILE
1	C	277	SER
1	C	283	LYS
1	C	292	TYR
1	C	296	ARG
1	D	33	ILE
1	D	35	LEU

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Mol	Chain	Res	Type
1	D	41	THR
1	D	42	MET
1	D	43	ARG
1	D	44	ARG
1	D	78	TYR
1	D	95	LEU
1	D	102	GLN
1	D	104	MET
1	D	107	THR
1	D	158	GLN
1	D	171	LEU
1	D	173	LEU
1	D	189	ILE
1	D	256	ARG
1	D	283	LYS
1	D	292	TYR
1	E	41	THR
1	E	43	ARG
1	E	44	ARG
1	E	78	TYR
1	E	93	ARG
1	E	104	MET
1	E	109	LEU
1	E	171	LEU
1	E	173	LEU
1	E	181	ARG
1	E	197	LYS
1	E	231	ARG
1	E	235	GLU
1	E	244	ARG
1	E	256	ARG
1	E	274	ARG
1	E	283	LYS
1	E	310	ARG
1	F	18	GLU
1	F	25	ILE
1	F	28	ASP
1	F	38	LEU
1	F	42	MET
1	F	44	ARG
1	F	78	TYR
1	F	87	LEU

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Mol	Chain	Res	Type
1	F	104	MET
1	F	158	GLN
1	F	171	LEU
1	F	227	THR
1	F	268	ASP
1	F	283	LYS
1	F	292	TYR
1	F	304	GLU
1	F	310	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	ASN
1	B	112	ASN
1	B	124	GLN
1	B	128	ASN
1	B	151	GLN
1	B	224	HIS
1	B	236	GLN
1	C	13	ASN
1	C	29	GLN
1	C	224	HIS
1	C	236	GLN
1	D	29	GLN
1	D	236	GLN
1	E	118	HIS
1	E	124	GLN
1	E	236	GLN
1	F	34	ASN
1	F	128	ASN
1	F	230	HIS
1	F	236	GLN

5.3.3 RNA

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 19 ligands modelled in this entry, 7 are monoatomic - leaving 12 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	AMP	A	501	3	20,25,25	0.95	1 (5%)	22,38,38	2.21	6 (27%)
2	AMP	A	502	-	20,25,25	1.04	1 (5%)	22,38,38	2.54	5 (22%)
2	AMP	B	501	3	20,25,25	0.98	1 (5%)	22,38,38	2.15	4 (18%)
2	AMP	B	502	-	20,25,25	1.07	1 (5%)	22,38,38	2.19	3 (13%)
2	AMP	C	501	3	20,25,25	1.01	1 (5%)	22,38,38	1.93	4 (18%)
2	AMP	C	502	-	20,25,25	1.09	1 (5%)	22,38,38	2.56	4 (18%)
2	AMP	D	501	3	20,25,25	1.11	1 (5%)	22,38,38	1.85	3 (13%)
2	AMP	D	502	-	20,25,25	1.09	1 (5%)	22,38,38	2.48	3 (13%)
2	AMP	E	501	3	20,25,25	0.95	1 (5%)	22,38,38	1.90	3 (13%)
2	AMP	E	502	-	20,25,25	0.97	1 (5%)	22,38,38	2.27	4 (18%)
2	AMP	F	501	3	20,25,25	1.00	1 (5%)	22,38,38	2.08	4 (18%)
2	AMP	F	502	-	20,25,25	1.00	1 (5%)	22,38,38	2.43	5 (22%)

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	AMP	A	501	3	-	0/6/26/26	0/3/3/3
2	AMP	A	502	-	-	0/6/26/26	0/3/3/3
2	AMP	B	501	3	-	0/6/26/26	0/3/3/3
2	AMP	B	502	-	-	0/6/26/26	0/3/3/3
2	AMP	C	501	3	-	0/6/26/26	0/3/3/3
2	AMP	C	502	-	-	0/6/26/26	0/3/3/3
2	AMP	D	501	3	-	0/6/26/26	0/3/3/3
2	AMP	D	502	-	-	0/6/26/26	0/3/3/3
2	AMP	E	501	3	-	0/6/26/26	0/3/3/3
2	AMP	E	502	-	-	0/6/26/26	0/3/3/3
2	AMP	F	501	3	-	0/6/26/26	0/3/3/3
2	AMP	F	502	-	-	0/6/26/26	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	AMP	C5-C4	2.71	1.46	1.40
2	C	501	AMP	C5-C4	2.72	1.46	1.40
2	B	501	AMP	C5-C4	2.73	1.46	1.40
2	E	501	AMP	C5-C4	2.79	1.46	1.40
2	F	501	AMP	C5-C4	2.79	1.46	1.40
2	A	502	AMP	C5-C4	2.94	1.47	1.40
2	E	502	AMP	C5-C4	2.98	1.47	1.40
2	B	502	AMP	C5-C4	3.04	1.47	1.40
2	C	502	AMP	C5-C4	3.07	1.47	1.40
2	D	502	AMP	C5-C4	3.17	1.47	1.40
2	F	502	AMP	C5-C4	3.18	1.47	1.40
2	D	501	AMP	C5-C4	3.33	1.48	1.40

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	502	AMP	N3-C2-N1	-8.49	122.39	128.89
2	A	502	AMP	N3-C2-N1	-8.22	122.60	128.89
2	B	501	AMP	N3-C2-N1	-8.17	122.64	128.89
2	D	502	AMP	N3-C2-N1	-8.14	122.66	128.89
2	A	501	AMP	N3-C2-N1	-8.07	122.71	128.89
2	E	502	AMP	N3-C2-N1	-7.98	122.78	128.89
2	F	502	AMP	N3-C2-N1	-7.41	123.22	128.89
2	F	501	AMP	N3-C2-N1	-7.32	123.29	128.89
2	D	501	AMP	N3-C2-N1	-7.10	123.46	128.89
2	C	501	AMP	N3-C2-N1	-7.04	123.50	128.89
2	B	502	AMP	N3-C2-N1	-7.01	123.53	128.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	502	AMP	C2'-C1'-N9	-6.70	104.05	114.29
2	D	502	AMP	C2'-C1'-N9	-6.41	104.49	114.29
2	A	502	AMP	C2'-C1'-N9	-6.31	104.64	114.29
2	F	502	AMP	C2'-C1'-N9	-6.22	104.78	114.29
2	E	501	AMP	N3-C2-N1	-6.08	124.24	128.89
2	B	502	AMP	C2'-C1'-N9	-5.83	105.38	114.29
2	E	502	AMP	C2'-C1'-N9	-4.42	107.54	114.29
2	E	501	AMP	C4'-O4'-C1'	-3.22	106.18	109.72
2	E	502	AMP	C4-C5-N7	-3.15	106.58	109.48
2	D	502	AMP	C4-C5-N7	-3.12	106.61	109.48
2	D	501	AMP	C4-C5-N7	-2.85	106.86	109.48
2	B	501	AMP	C4-C5-N7	-2.82	106.89	109.48
2	A	502	AMP	C4-C5-N7	-2.81	106.89	109.48
2	F	502	AMP	C4-C5-N7	-2.80	106.91	109.48
2	E	501	AMP	C4-C5-N7	-2.65	107.04	109.48
2	A	502	AMP	C1'-N9-C4	-2.60	123.02	126.94
2	C	502	AMP	C4-C5-N7	-2.60	107.09	109.48
2	F	501	AMP	O4'-C1'-N9	-2.49	102.89	108.10
2	A	501	AMP	O4'-C1'-N9	-2.38	103.11	108.10
2	C	501	AMP	C4-C5-N7	-2.32	107.34	109.48
2	F	501	AMP	C4-C5-N7	-2.26	107.40	109.48
2	A	501	AMP	C4'-O4'-C1'	-2.23	107.26	109.72
2	B	502	AMP	C4-C5-N7	-2.21	107.45	109.48
2	B	501	AMP	O5'-P-O1P	-2.03	101.97	107.14
2	F	502	AMP	C1'-N9-C4	-2.03	123.88	126.94
2	D	501	AMP	O3P-P-O2P	2.01	115.04	107.38
2	B	501	AMP	C2-N1-C6	2.06	122.44	118.77
2	C	501	AMP	O3P-P-O2P	2.07	115.28	107.38
2	A	502	AMP	O3P-P-O2P	2.08	115.30	107.38
2	A	501	AMP	N6-C6-N1	2.08	123.67	119.20
2	C	501	AMP	C2-N1-C6	2.08	122.49	118.77
2	C	502	AMP	C2-N1-C6	2.14	122.59	118.77
2	E	502	AMP	O3P-P-O2P	2.23	115.86	107.38
2	A	501	AMP	C2-N1-C6	2.27	122.82	118.77
2	F	502	AMP	C2-N1-C6	2.52	123.28	118.77
2	A	501	AMP	C2'-C1'-N9	2.54	118.17	114.29
2	F	501	AMP	C2'-C1'-N9	2.97	118.83	114.29

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	AMP	1	0
2	D	501	AMP	1	0
2	E	501	AMP	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, 95^{th} 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	310/320 (96%)	-0.37	3 (0%) 84 84	14, 21, 32, 38	0
1	B	310/320 (96%)	-0.37	0 100 100	12, 20, 29, 34	0
1	C	310/320 (96%)	-0.38	0 100 100	11, 23, 32, 42	0
1	D	310/320 (96%)	-0.39	0 100 100	15, 23, 33, 39	0
1	E	310/320 (96%)	-0.30	2 (0%) 90 90	11, 20, 32, 39	0
1	F	310/320 (96%)	-0.32	2 (0%) 90 90	14, 24, 34, 44	0
All	All	1860/1920 (96%)	-0.36	7 (0%) 93 93	11, 22, 32, 44	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	231	ARG	5.0
1	A	232	ASP	4.2
1	F	232	ASP	3.3
1	A	230	HIS	3.1
1	F	231	ARG	2.6
1	E	233	GLY	2.0
1	E	210	ILE	2.0

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, 95^{th} 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
2	AMP	E	501	23/23	0.98	0.09	0.49	11,14,20,21	0
2	AMP	A	502	23/23	0.98	0.10	0.25	14,19,22,23	0
2	AMP	A	501	23/23	0.98	0.09	0.17	9,13,19,21	0
2	AMP	F	502	23/23	0.98	0.09	0.09	14,18,20,20	0
2	AMP	B	502	23/23	0.98	0.10	0.05	11,14,17,18	0
2	AMP	C	501	23/23	0.99	0.09	-0.05	13,15,21,23	0
2	AMP	D	502	23/23	0.98	0.10	-0.09	15,20,21,22	0
2	AMP	B	501	23/23	0.98	0.09	-0.16	13,15,18,19	0
2	AMP	D	501	23/23	0.98	0.09	-0.36	12,15,23,24	0
2	AMP	E	502	23/23	0.98	0.09	-0.40	18,20,21,21	0
2	AMP	F	501	23/23	0.98	0.08	-0.46	10,12,19,20	0
2	AMP	C	502	23/23	0.98	0.09	-0.47	16,22,23,24	0
3	MG	D	503	1/1	0.99	0.07	-0.78	19,19,19,19	0
3	MG	C	503	1/1	0.98	0.07	-0.95	22,22,22,22	0
3	MG	E	503	1/1	0.98	0.07	-1.01	17,17,17,17	0
3	MG	F	503	1/1	0.99	0.05	-1.93	22,22,22,22	0
3	MG	B	503	1/1	0.99	0.05	-2.49	13,13,13,13	0
3	MG	A	503	1/1	0.98	0.05	-3.07	21,21,21,21	0
3	MG	D	313	1/1	0.93	0.08	-	35,35,35,35	0

6.5 Other polymers

There are no such residues in this entry.