Full wwPDB X-ray Structure Validation Report

Feb 1, 2016 – 11:53 AM GMT

PDB ID	:	3Q89
Title	:	Crystal structure of Staphylococcus aureus nucleoside diphosphate kinase complexed with CDP
Authors	:	Srivastava, S.K.; Rajasree, K.; Gopal, B.
Deposited on	:	2011-01-06
Resolution	:	2.90 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:

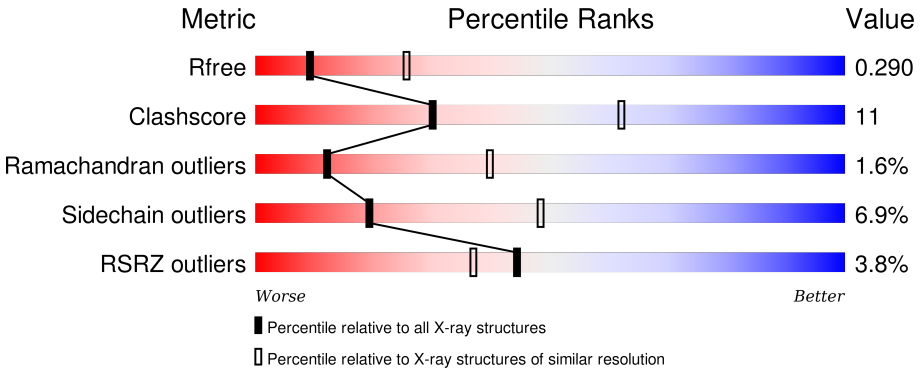
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.90 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	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	157	72% 20% 5%
1	B	157	72% 20% 5%
1	C	157	73% 20% 5%
1	D	157	66% 24% 5% 5%
1	E	157	65% 26% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	157	2% 73% 18% • 5%
1	G	157	10% 70% 20% • 5%
1	H	157	12% 73% 20% •• 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
3	CDP	E	158	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9291 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 Nucleoside diphosphate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	149	Total	C	N	O	S	0	0	0
			1153	726	201	221	5			
1	B	149	Total	C	N	O	S	0	0	0
			1161	731	202	223	5			
1	C	149	Total	C	N	O	S	0	0	0
			1161	731	202	223	5			
1	D	149	Total	C	N	O	S	0	0	0
			1137	713	199	220	5			
1	E	149	Total	C	N	O	S	0	0	0
			1161	731	202	223	5			
1	F	149	Total	C	N	O	S	0	0	0
			1133	712	200	216	5			
1	G	149	Total	C	N	O	S	0	0	0
			1122	701	199	217	5			
1	H	149	Total	C	N	O	S	0	0	0
			1139	714	200	220	5			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	150	LEU	-	EXPRESSION TAG	UNP Q5HFV4
A	151	GLU	-	EXPRESSION TAG	UNP Q5HFV4
A	152	HIS	-	EXPRESSION TAG	UNP Q5HFV4
A	153	HIS	-	EXPRESSION TAG	UNP Q5HFV4
A	154	HIS	-	EXPRESSION TAG	UNP Q5HFV4
A	155	HIS	-	EXPRESSION TAG	UNP Q5HFV4
A	156	HIS	-	EXPRESSION TAG	UNP Q5HFV4
A	157	HIS	-	EXPRESSION TAG	UNP Q5HFV4
B	150	LEU	-	EXPRESSION TAG	UNP Q5HFV4
B	151	GLU	-	EXPRESSION TAG	UNP Q5HFV4
B	152	HIS	-	EXPRESSION TAG	UNP Q5HFV4
B	153	HIS	-	EXPRESSION TAG	UNP Q5HFV4
B	154	HIS	-	EXPRESSION TAG	UNP Q5HFV4

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	155	HIS	-	EXPRESSION TAG	UNP Q5HFV4
B	156	HIS	-	EXPRESSION TAG	UNP Q5HFV4
B	157	HIS	-	EXPRESSION TAG	UNP Q5HFV4
C	150	LEU	-	EXPRESSION TAG	UNP Q5HFV4
C	151	GLU	-	EXPRESSION TAG	UNP Q5HFV4
C	152	HIS	-	EXPRESSION TAG	UNP Q5HFV4
C	153	HIS	-	EXPRESSION TAG	UNP Q5HFV4
C	154	HIS	-	EXPRESSION TAG	UNP Q5HFV4
C	155	HIS	-	EXPRESSION TAG	UNP Q5HFV4
C	156	HIS	-	EXPRESSION TAG	UNP Q5HFV4
C	157	HIS	-	EXPRESSION TAG	UNP Q5HFV4
D	150	LEU	-	EXPRESSION TAG	UNP Q5HFV4
D	151	GLU	-	EXPRESSION TAG	UNP Q5HFV4
D	152	HIS	-	EXPRESSION TAG	UNP Q5HFV4
D	153	HIS	-	EXPRESSION TAG	UNP Q5HFV4
D	154	HIS	-	EXPRESSION TAG	UNP Q5HFV4
D	155	HIS	-	EXPRESSION TAG	UNP Q5HFV4
D	156	HIS	-	EXPRESSION TAG	UNP Q5HFV4
D	157	HIS	-	EXPRESSION TAG	UNP Q5HFV4
E	150	LEU	-	EXPRESSION TAG	UNP Q5HFV4
E	151	GLU	-	EXPRESSION TAG	UNP Q5HFV4
E	152	HIS	-	EXPRESSION TAG	UNP Q5HFV4
E	153	HIS	-	EXPRESSION TAG	UNP Q5HFV4
E	154	HIS	-	EXPRESSION TAG	UNP Q5HFV4
E	155	HIS	-	EXPRESSION TAG	UNP Q5HFV4
E	156	HIS	-	EXPRESSION TAG	UNP Q5HFV4
E	157	HIS	-	EXPRESSION TAG	UNP Q5HFV4
F	150	LEU	-	EXPRESSION TAG	UNP Q5HFV4
F	151	GLU	-	EXPRESSION TAG	UNP Q5HFV4
F	152	HIS	-	EXPRESSION TAG	UNP Q5HFV4
F	153	HIS	-	EXPRESSION TAG	UNP Q5HFV4
F	154	HIS	-	EXPRESSION TAG	UNP Q5HFV4
F	155	HIS	-	EXPRESSION TAG	UNP Q5HFV4
F	156	HIS	-	EXPRESSION TAG	UNP Q5HFV4
F	157	HIS	-	EXPRESSION TAG	UNP Q5HFV4
G	150	LEU	-	EXPRESSION TAG	UNP Q5HFV4
G	151	GLU	-	EXPRESSION TAG	UNP Q5HFV4
G	152	HIS	-	EXPRESSION TAG	UNP Q5HFV4
G	153	HIS	-	EXPRESSION TAG	UNP Q5HFV4
G	154	HIS	-	EXPRESSION TAG	UNP Q5HFV4
G	155	HIS	-	EXPRESSION TAG	UNP Q5HFV4
G	156	HIS	-	EXPRESSION TAG	UNP Q5HFV4

Continued on next page...

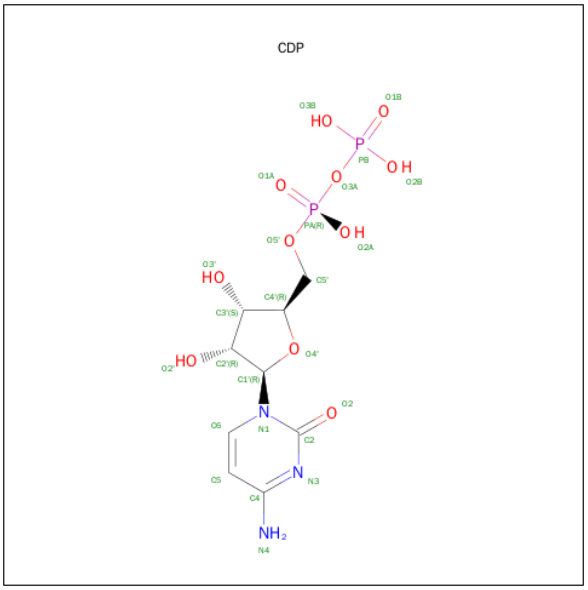
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	157	HIS	-	EXPRESSION TAG	UNP Q5HFV4
H	150	LEU	-	EXPRESSION TAG	UNP Q5HFV4
H	151	GLU	-	EXPRESSION TAG	UNP Q5HFV4
H	152	HIS	-	EXPRESSION TAG	UNP Q5HFV4
H	153	HIS	-	EXPRESSION TAG	UNP Q5HFV4
H	154	HIS	-	EXPRESSION TAG	UNP Q5HFV4
H	155	HIS	-	EXPRESSION TAG	UNP Q5HFV4
H	156	HIS	-	EXPRESSION TAG	UNP Q5HFV4
H	157	HIS	-	EXPRESSION TAG	UNP Q5HFV4

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Mg 1 1	0	0
2	E	1	Total Mg 1 1	0	0

- Molecule 3 is CYTIDINE-5'-DIPHOSPHATE (three-letter code: CDP) (formula: $C_9H_{15}N_3O_{11}P_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C N O P 25 9 3 11 2	0	0
3	E	1	Total C N O P 25 9 3 11 2	0	0

- Molecule 4 is water.

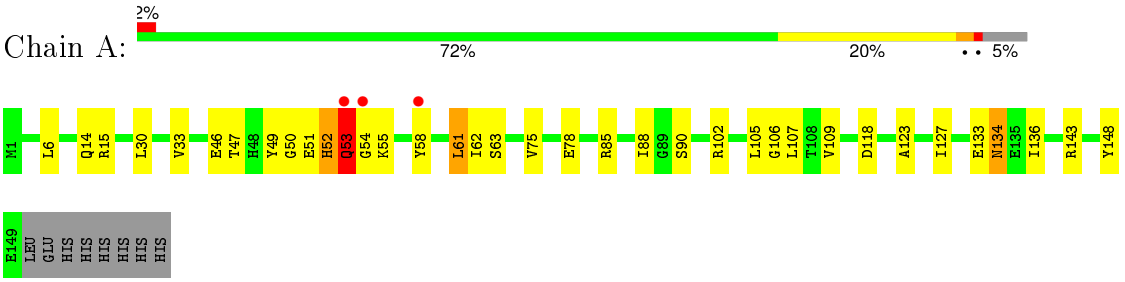
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	12	Total O 12 12	0	0
4	B	15	Total O 15 15	0	0
4	C	11	Total O 11 11	0	0
4	D	9	Total O 9 9	0	0
4	E	9	Total O 9 9	0	0
4	F	4	Total O 4 4	0	0
4	G	5	Total O 5 5	0	0
4	H	7	Total O 7 7	0	0

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.

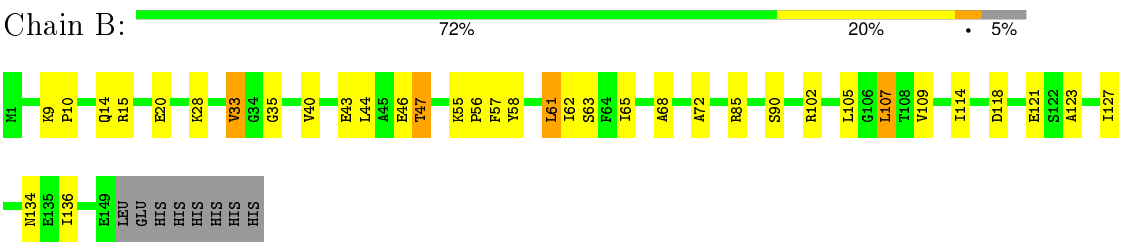
- Molecule 1: Nucleoside diphosphate kinase

Chain A:



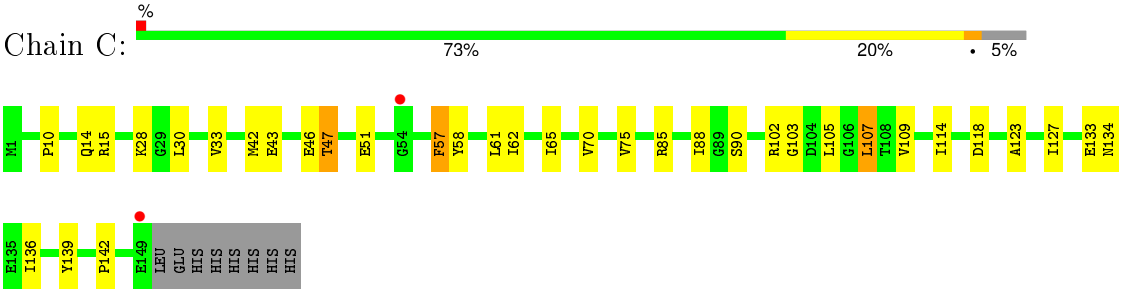
- Molecule 1: Nucleoside diphosphate kinase

Chain B:



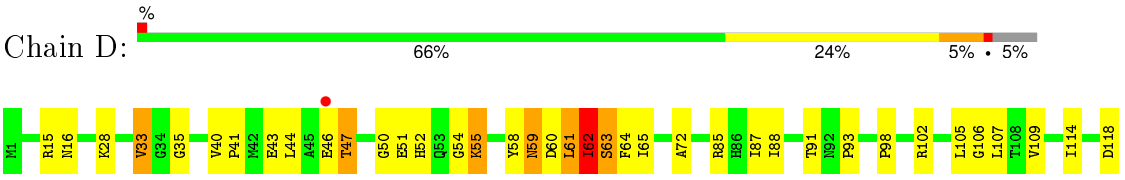
- Molecule 1: Nucleoside diphosphate kinase

Chain C:



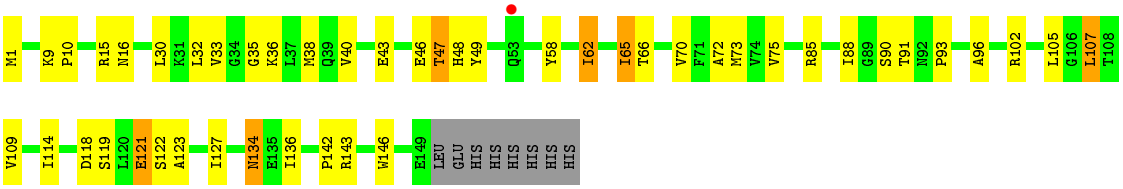
- Molecule 1: Nucleoside diphosphate kinase

Chain D:



• Molecule 1: Nucleoside diphosphate kinase

Chain E:

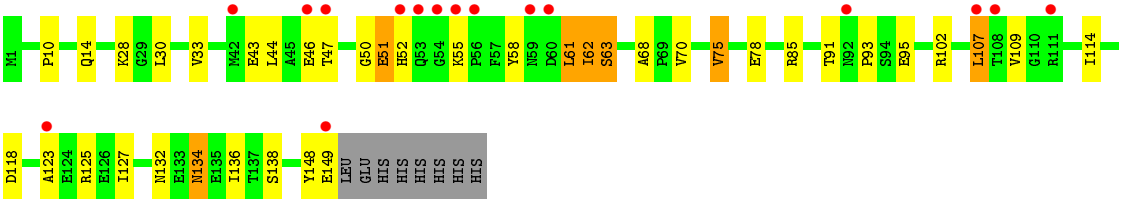


• Molecule 1: Nucleoside diphosphate kinase

Chain F:

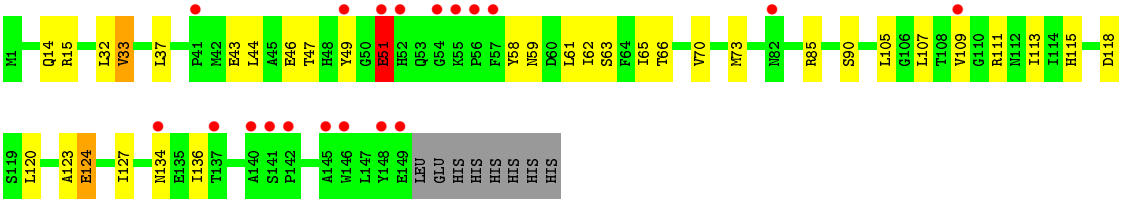
• Molecule 1: Nucleoside diphosphate kinase

Chain G:



• Molecule 1: Nucleoside diphosphate kinase

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	186.61Å 73.06Å 102.27Å 90.00° 108.23° 90.00°	Depositor
Resolution (Å)	34.19 – 2.90 33.15 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.8 (34.19-2.90) 98.9 (33.15-2.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	739.31 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.252 , 0.293 0.251 , 0.290	Depositor DCC
R_{free} test set	1473 reflections (5.36%)	DCC
Wilson B-factor (Å^2)	44.7	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 39.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 28959 reflections	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	9291	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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, 0.375 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, CDP

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	0.59	1/1176 (0.1%)	0.66	2/1593 (0.1%)
1	B	0.59	0/1184	0.63	0/1602
1	C	0.60	1/1184 (0.1%)	0.64	0/1602
1	D	0.64	1/1158 (0.1%)	0.69	2/1569 (0.1%)
1	E	0.61	0/1184	0.66	0/1602
1	F	0.61	1/1155 (0.1%)	0.66	0/1565
1	G	0.66	2/1144 (0.2%)	0.68	0/1549
1	H	0.66	0/1161	0.66	0/1574
All	All	0.62	6/9346 (0.1%)	0.66	4/12656 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	55	LYS	C-N	8.52	1.50	1.34
1	G	55	LYS	C-N	5.79	1.45	1.34
1	G	44	LEU	C-O	5.42	1.33	1.23
1	C	133	GLU	CG-CD	5.29	1.59	1.51
1	D	54	GLY	C-N	-5.25	1.22	1.34
1	F	133	GLU	C-O	5.06	1.32	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	54	GLY	C-N-CA	6.28	137.40	121.70
1	A	54	GLY	C-N-CA	5.35	135.08	121.70
1	A	55	LYS	CA-C-O	5.35	131.34	120.10
1	D	44	LEU	CA-CB-CG	5.28	127.44	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	55	LYS	Mainchain
1	D	60	ASP	Peptide

5.2 Too-close contacts (i)

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	1153	0	1130	20	0
1	B	1161	0	1145	20	0
1	C	1161	0	1145	24	0
1	D	1137	0	1104	34	0
1	E	1161	0	1145	33	0
1	F	1133	0	1100	25	0
1	G	1122	0	1063	22	1
1	H	1139	0	1101	26	1
2	B	1	0	0	0	0
2	E	1	0	0	0	0
3	B	25	0	12	1	0
3	E	25	0	12	11	0
4	A	12	0	0	0	0
4	B	15	0	0	1	0
4	C	11	0	0	3	0
4	D	9	0	0	3	0
4	E	9	0	0	0	0
4	F	4	0	0	1	0
4	G	5	0	0	2	0
4	H	7	0	0	6	0
All	All	9291	0	8957	201	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (201) 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)
3:E:158:CDP:H5'2	3:E:158:CDP:C6	1.40	1.56
3:E:158:CDP:C5'	3:E:158:CDP:H6	1.35	1.37
1:D:134:ASN:HB3	4:D:165:HOH:O	1.27	1.34
1:B:20:GLU:HB2	4:B:172:HOH:O	1.35	1.25
1:H:120:LEU:HD11	4:H:164:HOH:O	1.56	1.05
1:H:124:GLU:HB3	4:H:161:HOH:O	1.58	1.03
3:E:158:CDP:O1A	3:E:158:CDP:H4'	1.60	1.01
1:D:59:ASN:H	1:D:59:ASN:ND2	1.50	0.98
1:D:59:ASN:H	1:D:59:ASN:HD22	1.08	0.96
1:D:59:ASN:N	1:D:59:ASN:HD22	1.70	0.89
1:D:134:ASN:CB	4:D:165:HOH:O	1.96	0.88
1:F:128:ASN:O	4:F:158:HOH:O	1.90	0.88
1:H:49:TYR:CD2	1:H:61:LEU:HD11	2.14	0.82
1:D:59:ASN:N	1:D:59:ASN:ND2	2.28	0.82
3:E:158:CDP:C4'	3:E:158:CDP:O1A	2.30	0.80
1:C:57:PHE:HD1	1:C:58:TYR:N	1.79	0.80
1:A:15:ARG:NH1	1:A:105:LEU:O	2.16	0.78
1:C:103:GLY:O	1:D:28:LYS:HE3	1.83	0.78
1:D:106:GLY:O	1:F:28:LYS:NZ	2.17	0.77
1:C:43:GLU:O	1:C:47:THR:HG23	1.85	0.77
1:D:61:LEU:O	1:D:63:SER:N	2.19	0.75
3:E:158:CDP:C4'	3:E:158:CDP:O3A	2.30	0.74
1:H:49:TYR:CG	1:H:61:LEU:HD11	2.23	0.74
1:D:98:PRO:O	4:D:162:HOH:O	2.07	0.72
1:B:58:TYR:O	1:B:62:ILE:HG12	1.94	0.68
1:D:50:GLY:C	1:D:52:HIS:H	1.94	0.68
1:B:15:ARG:NH1	1:B:105:LEU:O	2.22	0.68
1:F:28:LYS:HD3	1:F:87:ILE:CG2	2.23	0.68
4:C:166:HOH:O	1:F:15:ARG:HD2	1.93	0.67
1:C:57:PHE:CD1	1:C:58:TYR:N	2.61	0.67
1:H:120:LEU:CD1	4:H:164:HOH:O	2.24	0.66
1:C:61:LEU:HD11	4:C:168:HOH:O	1.95	0.66
1:F:59:ASN:H	1:F:59:ASN:HD22	1.44	0.66
3:E:158:CDP:C5'	3:E:158:CDP:C6	2.29	0.66
1:A:49:TYR:CE2	1:A:61:LEU:HD22	2.30	0.66
1:D:50:GLY:O	1:D:52:HIS:N	2.28	0.65
1:C:15:ARG:NH1	1:C:105:LEU:O	2.26	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:65:ILE:HG23	1:H:66:THR:HG23	1.78	0.65
1:E:1:MET:N	1:G:95:GLU:OE2	2.30	0.65
1:A:143:ARG:HD3	1:D:16:ASN:HD21	1.63	0.63
3:E:158:CDP:O3A	3:E:158:CDP:H4'	1.85	0.62
1:H:115:HIS:ND1	4:H:162:HOH:O	2.31	0.62
1:F:28:LYS:O	1:F:28:LYS:HG3	2.00	0.62
1:E:65:ILE:O	1:E:65:ILE:HG23	1.98	0.61
1:F:28:LYS:HD3	1:F:87:ILE:HG21	1.83	0.61
1:A:123:ALA:O	1:A:127:ILE:HG13	2.02	0.60
1:C:57:PHE:HD1	1:C:57:PHE:C	2.05	0.59
1:E:91:THR:HG23	3:E:158:CDP:H3'	1.84	0.58
1:D:46:GLU:HG2	1:D:58:TYR:OH	2.03	0.58
1:E:15:ARG:NH1	1:E:105:LEU:O	2.31	0.57
1:C:57:PHE:C	1:C:57:PHE:CD1	2.77	0.57
1:H:15:ARG:NH1	1:H:105:LEU:O	2.29	0.56
1:H:49:TYR:CZ	1:H:61:LEU:HD21	2.40	0.56
1:E:30:LEU:HB3	1:E:75:VAL:HG13	1.87	0.56
1:A:50:GLY:O	1:A:53:GLN:HB2	2.06	0.55
1:F:134:ASN:H	1:F:134:ASN:HD22	1.55	0.55
1:H:46:GLU:HG2	1:H:58:TYR:OH	2.08	0.54
1:G:134:ASN:HB3	4:G:158:HOH:O	2.08	0.54
1:B:40:VAL:HG13	1:B:44:LEU:HD23	1.90	0.54
1:D:50:GLY:C	1:D:52:HIS:N	2.61	0.53
1:D:64:PHE:CD2	1:D:65:ILE:HD12	2.43	0.53
1:E:143:ARG:HD3	1:F:16:ASN:ND2	2.23	0.53
1:E:143:ARG:HD3	1:F:16:ASN:HD21	1.74	0.53
1:E:58:TYR:O	1:E:62:ILE:HD13	2.08	0.53
1:G:61:LEU:O	1:G:63:SER:N	2.41	0.53
1:D:33:VAL:HG13	1:D:136:ILE:HG23	1.91	0.52
1:A:143:ARG:HD3	1:D:16:ASN:ND2	2.24	0.52
1:F:15:ARG:NH1	1:F:105:LEU:O	2.28	0.52
1:D:58:TYR:CE2	1:D:62:ILE:HD11	2.46	0.51
1:E:40:VAL:HG12	1:E:66:THR:HG22	1.92	0.51
1:F:46:GLU:HG2	1:F:58:TYR:OH	2.10	0.51
1:E:48:HIS:HD2	1:E:49:TYR:CD2	2.28	0.51
1:H:85:ARG:HD2	1:H:118:ASP:HA	1.92	0.51
1:C:85:ARG:HD2	1:C:118:ASP:HA	1.94	0.50
1:B:46:GLU:HG2	1:B:58:TYR:OH	2.11	0.50
3:E:158:CDP:C4'	3:E:158:CDP:C6	2.92	0.50
1:E:46:GLU:HG2	1:E:58:TYR:OH	2.12	0.50
1:E:30:LEU:HD13	1:E:75:VAL:HG11	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:33:VAL:HG13	1:F:136:ILE:HG23	1.92	0.50
1:G:91:THR:O	1:G:93:PRO:HD3	2.12	0.50
1:G:46:GLU:HG2	1:G:58:TYR:OH	2.12	0.50
1:A:33:VAL:HG13	1:A:136:ILE:HG23	1.94	0.49
1:G:50:GLY:C	1:G:52:HIS:H	2.15	0.49
1:E:36:LYS:HE3	1:E:38:MET:SD	2.52	0.49
1:E:85:ARG:HD2	1:E:118:ASP:HA	1.94	0.49
1:D:85:ARG:HD2	1:D:118:ASP:HA	1.94	0.49
1:D:58:TYR:O	1:D:62:ILE:HD12	2.13	0.49
1:A:78:GLU:HB2	1:A:148:TYR:CE1	2.48	0.49
1:B:43:GLU:O	1:B:47:THR:HG23	2.12	0.49
1:A:88:ILE:O	1:A:102:ARG:HG3	2.13	0.49
1:E:33:VAL:HG13	1:E:136:ILE:HG23	1.94	0.48
1:F:50:GLY:O	1:F:52:HIS:N	2.47	0.48
1:D:149:GLU:OE2	1:D:149:GLU:C	2.52	0.48
1:D:58:TYR:CD2	1:D:62:ILE:HD11	2.49	0.47
1:A:30:LEU:HB3	1:A:75:VAL:CG1	2.44	0.47
1:H:33:VAL:HG13	1:H:136:ILE:HG23	1.96	0.47
1:H:15:ARG:HH11	1:H:113:ILE:HD11	1.80	0.47
1:G:85:ARG:HD2	1:G:118:ASP:HA	1.96	0.47
1:A:46:GLU:HG2	1:A:58:TYR:OH	2.14	0.47
1:G:28:LYS:HG3	1:G:28:LYS:O	2.14	0.47
1:F:32:LEU:HD11	1:F:73:MET:HG2	1.97	0.47
1:D:43:GLU:O	1:D:47:THR:HG23	2.13	0.47
1:H:115:HIS:CE1	4:H:162:HOH:O	2.67	0.47
1:G:102:ARG:NH2	1:G:114:ILE:O	2.48	0.47
1:C:33:VAL:HG13	1:C:136:ILE:HG23	1.96	0.47
1:D:58:TYR:O	1:D:62:ILE:CD1	2.63	0.47
1:A:85:ARG:HD2	1:A:118:ASP:HA	1.96	0.47
1:F:30:LEU:HB3	1:F:75:VAL:HG13	1.97	0.47
1:H:46:GLU:HG3	1:H:62:ILE:HD11	1.97	0.47
1:C:30:LEU:HB3	1:C:75:VAL:CG1	2.45	0.47
1:E:102:ARG:NH2	1:E:114:ILE:O	2.48	0.47
1:C:28:LYS:HG3	1:C:28:LYS:O	2.14	0.46
1:D:102:ARG:NH2	1:D:114:ILE:O	2.49	0.46
1:F:14:GLN:HA	1:F:14:GLN:OE1	2.16	0.46
1:B:9:LYS:NZ	3:B:158:CDP:O3'	2.48	0.46
1:F:85:ARG:HD2	1:F:118:ASP:HA	1.97	0.46
1:G:78:GLU:HB2	1:G:148:TYR:CE1	2.51	0.46
1:D:88:ILE:O	1:D:102:ARG:HG3	2.16	0.46
1:A:14:GLN:OE1	1:A:14:GLN:HA	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:158:CDP:H5'2	3:E:158:CDP:H6	0.44	0.46
1:G:14:GLN:HA	1:G:14:GLN:OE1	2.15	0.46
1:B:85:ARG:HD2	1:B:118:ASP:HA	1.97	0.46
1:E:32:LEU:HD11	1:E:73:MET:HG2	1.97	0.46
1:H:59:ASN:O	1:H:62:ILE:HG22	2.16	0.45
1:C:123:ALA:O	1:C:127:ILE:HG13	2.16	0.45
1:H:115:HIS:CG	4:H:162:HOH:O	2.68	0.45
1:A:30:LEU:HB3	1:A:75:VAL:HG12	1.98	0.45
1:D:123:ALA:O	1:D:127:ILE:HG13	2.16	0.45
1:G:10:PRO:HD3	1:G:70:VAL:HG12	1.99	0.45
1:G:33:VAL:HG13	1:G:136:ILE:HG23	1.98	0.45
1:C:139:TYR:HB2	4:C:159:HOH:O	2.16	0.45
1:H:14:GLN:HA	1:H:14:GLN:OE1	2.17	0.45
1:C:14:GLN:OE1	1:C:14:GLN:HA	2.17	0.45
1:E:65:ILE:O	1:E:65:ILE:CG2	2.62	0.45
1:B:33:VAL:HG13	1:B:136:ILE:HG23	1.98	0.45
1:B:57:PHE:O	1:B:61:LEU:HB2	2.17	0.45
1:F:107:LEU:HA	1:F:107:LEU:HD23	1.80	0.45
1:E:91:THR:O	1:E:93:PRO:HD3	2.16	0.45
1:G:107:LEU:HD23	1:G:107:LEU:HA	1.75	0.44
1:B:123:ALA:O	1:B:127:ILE:HG13	2.17	0.44
1:F:90:SER:OG	1:F:96:ALA:HA	2.16	0.44
1:A:106:GLY:O	1:B:28:LYS:HE3	2.17	0.44
1:H:61:LEU:O	1:H:61:LEU:HD13	2.18	0.44
1:G:134:ASN:H	1:G:134:ASN:HD22	1.65	0.44
1:C:142:PRO:HB3	1:E:142:PRO:O	2.17	0.44
1:B:55:LYS:HB3	1:B:56:PRO:HD2	2.00	0.44
1:C:46:GLU:HG2	1:C:58:TYR:OH	2.17	0.43
1:G:132:ASN:O	1:G:134:ASN:N	2.51	0.43
1:C:103:GLY:O	1:D:28:LYS:CE	2.61	0.43
1:G:10:PRO:HB3	1:G:68:ALA:HB3	2.00	0.43
1:G:30:LEU:HB3	1:G:75:VAL:HG13	2.00	0.43
1:C:62:ILE:HA	1:C:65:ILE:HG22	2.00	0.43
1:G:123:ALA:O	1:G:127:ILE:HG13	2.18	0.43
1:A:53:GLN:HE21	1:A:53:GLN:HB2	1.59	0.43
1:A:6:LEU:HD12	1:A:75:VAL:HG21	1.99	0.43
1:D:91:THR:O	1:D:93:PRO:HD3	2.19	0.43
1:E:33:VAL:CG1	1:E:136:ILE:HG23	2.48	0.43
1:C:102:ARG:NH2	1:C:114:ILE:O	2.52	0.43
1:E:88:ILE:O	1:E:102:ARG:HG3	2.19	0.43
1:B:14:GLN:HG3	1:E:146:TRP:CH2	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:9:LYS:NZ	3:E:158:CDP:O2'	2.52	0.42
1:G:125:ARG:NH2	4:G:160:HOH:O	2.31	0.42
1:F:36:LYS:HE3	1:F:38:MET:SD	2.59	0.42
1:B:10:PRO:HB3	1:B:68:ALA:HB3	2.01	0.42
1:B:55:LYS:HB3	1:B:56:PRO:CD	2.49	0.42
1:H:111:ARG:HD3	1:H:111:ARG:HA	1.91	0.42
1:D:15:ARG:NH1	1:D:105:LEU:O	2.33	0.42
1:E:43:GLU:O	1:E:47:THR:HG23	2.19	0.42
1:D:28:LYS:HD3	1:D:87:ILE:CG2	2.50	0.42
1:A:134:ASN:HD22	1:A:134:ASN:H	1.68	0.42
1:F:59:ASN:N	1:F:59:ASN:HD22	2.12	0.42
1:H:37:LEU:HD12	1:H:70:VAL:O	2.19	0.42
1:C:10:PRO:HD3	1:C:70:VAL:HG12	2.00	0.42
1:E:90:SER:OG	1:E:96:ALA:HA	2.20	0.42
1:C:107:LEU:HD23	1:C:107:LEU:HA	1.83	0.42
1:B:35:GLY:HA2	1:B:72:ALA:O	2.20	0.41
1:D:40:VAL:HA	1:D:41:PRO:HD3	1.89	0.41
1:B:102:ARG:NH2	1:B:114:ILE:O	2.53	0.41
1:D:35:GLY:HA2	1:D:72:ALA:O	2.19	0.41
1:E:121:GLU:HG3	1:E:122:SER:N	2.35	0.41
1:F:50:GLY:C	1:F:52:HIS:H	2.23	0.41
1:H:61:LEU:C	1:H:61:LEU:HD13	2.41	0.41
1:A:51:GLU:HG3	1:A:52:HIS:ND1	2.35	0.41
1:G:30:LEU:HD13	1:G:75:VAL:HG11	2.03	0.41
1:E:107:LEU:HA	1:E:107:LEU:HD23	1.79	0.41
1:E:16:ASN:HD21	1:F:143:ARG:HD3	1.86	0.41
1:E:123:ALA:O	1:E:127:ILE:HG13	2.19	0.41
1:H:32:LEU:HD11	1:H:73:MET:HG2	2.02	0.41
1:H:62:ILE:HA	1:H:62:ILE:HD12	1.89	0.41
1:G:61:LEU:O	1:G:62:ILE:C	2.60	0.41
1:C:88:ILE:O	1:C:102:ARG:HG3	2.21	0.41
1:E:35:GLY:HA2	1:E:72:ALA:O	2.21	0.41
1:F:31:LYS:HE3	1:F:31:LYS:HB2	1.94	0.41
1:B:107:LEU:HD23	1:B:107:LEU:HA	1.81	0.40
1:C:42:MET:SD	1:C:62:ILE:HG21	2.62	0.40
1:A:58:TYR:O	1:A:62:ILE:HG12	2.22	0.40
1:E:10:PRO:HD3	1:E:70:VAL:HG12	2.03	0.40
1:H:123:ALA:O	1:H:127:ILE:HG13	2.21	0.40
1:B:14:GLN:HA	1:B:14:GLN:OE1	2.21	0.40
1:E:134:ASN:H	1:E:134:ASN:HD22	1.70	0.40
1:H:51:GLU:H	1:H:51:GLU:HG3	1.55	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:149:GLU:OE2	1:H:111:ARG:NH1[4_556]	2.04	0.16

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	147/157 (94%)	138 (94%)	7 (5%)	2 (1%)	14 44
1	B	147/157 (94%)	138 (94%)	8 (5%)	1 (1%)	26 63
1	C	147/157 (94%)	139 (95%)	8 (5%)	0	100 100
1	D	147/157 (94%)	134 (91%)	7 (5%)	6 (4%)	3 14
1	E	147/157 (94%)	139 (95%)	8 (5%)	0	100 100
1	F	147/157 (94%)	136 (92%)	9 (6%)	2 (1%)	14 44
1	G	147/157 (94%)	132 (90%)	10 (7%)	5 (3%)	5 19
1	H	147/157 (94%)	135 (92%)	9 (6%)	3 (2%)	9 33
All	All	1176/1256 (94%)	1091 (93%)	66 (6%)	19 (2%)	12 40

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53	GLN
1	D	51	GLU
1	D	55	LYS
1	D	61	LEU
1	D	62	ILE
1	F	51	GLU
1	G	62	ILE
1	A	133	GLU
1	B	90	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	133	GLU
1	G	51	GLU
1	H	51	GLU
1	D	63	SER
1	G	43	GLU
1	G	61	LEU
1	G	63	SER
1	H	43	GLU
1	H	44	LEU
1	D	133	GLU

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	124/135 (92%)	115 (93%)	9 (7%)	17	45
1	B	126/135 (93%)	117 (93%)	9 (7%)	18	47
1	C	126/135 (93%)	119 (94%)	7 (6%)	26	60
1	D	120/135 (89%)	110 (92%)	10 (8%)	14	38
1	E	126/135 (93%)	118 (94%)	8 (6%)	22	54
1	F	119/135 (88%)	111 (93%)	8 (7%)	20	50
1	G	114/135 (84%)	107 (94%)	7 (6%)	23	56
1	H	120/135 (89%)	111 (92%)	9 (8%)	17	44
All	All	975/1080 (90%)	908 (93%)	67 (7%)	19	48

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	THR
1	A	52	HIS
1	A	53	GLN
1	A	61	LEU
1	A	63	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	90	SER
1	A	107	LEU
1	A	109	VAL
1	A	134	ASN
1	B	33	VAL
1	B	47	THR
1	B	61	LEU
1	B	63	SER
1	B	65	ILE
1	B	107	LEU
1	B	109	VAL
1	B	121	GLU
1	B	134	ASN
1	C	47	THR
1	C	51	GLU
1	C	57	PHE
1	C	90	SER
1	C	107	LEU
1	C	109	VAL
1	C	134	ASN
1	D	33	VAL
1	D	47	THR
1	D	59	ASN
1	D	62	ILE
1	D	107	LEU
1	D	109	VAL
1	D	119	SER
1	D	134	ASN
1	D	138	SER
1	D	149	GLU
1	E	47	THR
1	E	62	ILE
1	E	65	ILE
1	E	107	LEU
1	E	109	VAL
1	E	119	SER
1	E	121	GLU
1	E	134	ASN
1	F	44	LEU
1	F	47	THR
1	F	59	ASN
1	F	65	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	90	SER
1	F	107	LEU
1	F	109	VAL
1	F	134	ASN
1	G	47	THR
1	G	51	GLU
1	G	75	VAL
1	G	107	LEU
1	G	109	VAL
1	G	134	ASN
1	G	138	SER
1	H	33	VAL
1	H	47	THR
1	H	51	GLU
1	H	63	SER
1	H	90	SER
1	H	107	LEU
1	H	109	VAL
1	H	124	GLU
1	H	134	ASN

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	16	ASN
1	A	53	GLN
1	A	134	ASN
1	B	16	ASN
1	B	134	ASN
1	C	16	ASN
1	C	134	ASN
1	D	16	ASN
1	D	53	GLN
1	D	59	ASN
1	D	134	ASN
1	E	16	ASN
1	E	53	GLN
1	E	134	ASN
1	F	16	ASN
1	F	59	ASN
1	F	134	ASN
1	G	134	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	53	GLN
1	H	134	ASN

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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
3	CDP	B	158	2	19,26,26	2.28	7 (36%)	27,40,40	1.50	5 (18%)
3	CDP	E	158	2	19,26,26	1.42	3 (15%)	27,40,40	1.54	7 (25%)

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
3	CDP	B	158	2	-	0/12/32/32	0/2/2/2
3	CDP	E	158	2	-	0/12/32/32	0/2/2/2

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	158	CDP	C6-N1	-5.47	1.28	1.35
3	B	158	CDP	PB-O3B	-3.54	1.42	1.54
3	E	158	CDP	C6-N1	-3.42	1.31	1.35
3	B	158	CDP	C4-N3	-2.94	1.29	1.35
3	B	158	CDP	PB-O2B	-2.77	1.44	1.54
3	B	158	CDP	O4'-C4'	-2.75	1.38	1.45
3	B	158	CDP	PA-O2A	-2.53	1.44	1.54
3	B	158	CDP	PA-O1A	-2.24	1.43	1.51
3	E	158	CDP	PB-O3B	-2.18	1.46	1.54
3	E	158	CDP	PB-O2B	-2.13	1.47	1.54

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	158	CDP	O4'-C1'-N1	-3.40	100.91	108.08
3	E	158	CDP	PA-O3A-PB	-3.26	121.73	132.67
3	E	158	CDP	O3A-PA-O5'	-3.24	94.35	102.94
3	B	158	CDP	O4'-C4'-C3'	-2.80	99.50	105.15
3	B	158	CDP	O2'-C2'-C3'	-2.47	103.78	111.83
3	E	158	CDP	O3'-C3'-C2'	-2.35	104.19	111.83
3	B	158	CDP	C5-C6-N1	-2.29	114.98	120.58
3	E	158	CDP	C5-C4-N4	-2.12	118.06	121.31
3	E	158	CDP	O4'-C4'-C5'	-2.06	101.96	109.32
3	B	158	CDP	O2A-PA-O1A	2.01	123.41	112.53
3	E	158	CDP	O2B-PB-O1B	2.09	117.30	110.58
3	E	158	CDP	N4-C4-N3	2.16	120.44	116.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	158	CDP	1	0
3	E	158	CDP	11	0

5.7 Other polymers (i)

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	149/157 (94%)	0.02	3 (2%) 68 64	22, 34, 50, 57	0
1	B	149/157 (94%)	-0.05	0 100 100	19, 34, 49, 57	0
1	C	149/157 (94%)	-0.06	2 (1%) 79 78	22, 34, 50, 58	0
1	D	149/157 (94%)	-0.07	1 (0%) 89 88	21, 33, 47, 58	0
1	E	149/157 (94%)	-0.01	1 (0%) 89 88	21, 34, 50, 57	0
1	F	149/157 (94%)	0.03	3 (2%) 68 64	22, 33, 49, 57	0
1	G	149/157 (94%)	0.44	16 (10%) 8 4	22, 32, 49, 59	0
1	H	149/157 (94%)	0.72	19 (12%) 5 3	22, 33, 49, 60	0
All	All	1192/1256 (94%)	0.13	45 (3%) 44 37	19, 34, 50, 60	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	56	PRO	6.8
1	G	56	PRO	5.7
1	H	54	GLY	4.4
1	G	54	GLY	4.3
1	F	58	TYR	4.1
1	A	54	GLY	3.8
1	F	57	PHE	3.6
1	H	82	ASN	3.6
1	H	52	HIS	3.5
1	H	149	GLU	3.5
1	G	107	LEU	3.4
1	G	60	ASP	3.3
1	H	57	PHE	3.3
1	H	137	THR	3.1
1	H	148	TYR	2.9
1	G	59	ASN	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	108	THR	2.9
1	F	56	PRO	2.8
1	H	145	ALA	2.8
1	G	53	GLN	2.8
1	G	46	GLU	2.7
1	H	109	VAL	2.7
1	H	51	GLU	2.7
1	G	111	ARG	2.7
1	E	53	GLN	2.7
1	H	55	LYS	2.7
1	H	146	TRP	2.6
1	H	140	ALA	2.5
1	H	134	ASN	2.5
1	A	58	TYR	2.5
1	D	46	GLU	2.5
1	A	53	GLN	2.4
1	H	49	TYR	2.3
1	G	149	GLU	2.3
1	G	47	THR	2.3
1	C	149	GLU	2.2
1	G	123	ALA	2.2
1	H	41	PRO	2.2
1	H	142	PRO	2.2
1	G	52	HIS	2.2
1	G	55	LYS	2.1
1	C	54	GLY	2.1
1	G	42	MET	2.0
1	G	92	ASN	2.0
1	H	141	SER	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

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
3	CDP	E	158	25/25	0.88	0.22	0.14	20,20,20,20	0
3	CDP	B	158	25/25	0.96	0.12	-1.17	20,20,20,20	0
2	MG	E	159	1/1	0.83	0.13	-	38,38,38,38	0
2	MG	B	159	1/1	0.73	0.23	-	56,56,56,56	0

6.5 Other polymers

There are no such residues in this entry.