



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:35 AM GMT

PDB ID : 2AZ3
Title : Structure of a halophilic nucleoside diphosphate kinase from Halobacterium salinarum in complex with CDP
Authors : Besir, H.; Zeth, K.; Bracher, A.; Heider, U.; Ishibashi, M.; Tokunaga, M.; Oesterhelt, D.
Deposited on : 2005-09-09
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

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

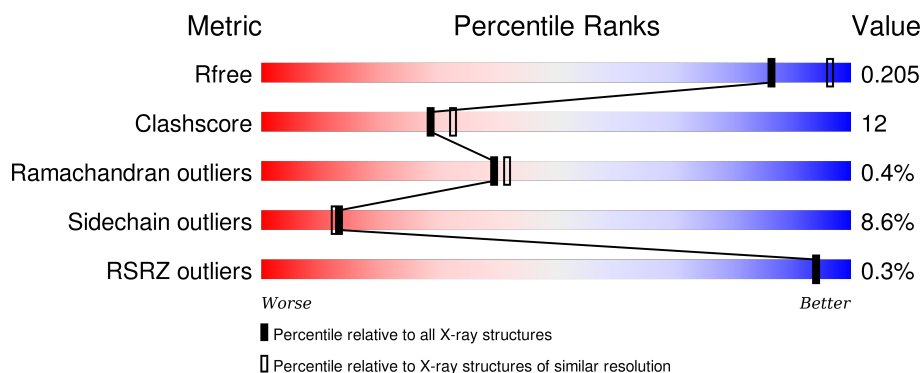
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	164	<div> <div>66%</div> <div>22%</div> <div>•</div> <div>7%</div> </div>
1	B	164	<div> <div>66%</div> <div>23%</div> <div>•</div> <div>8%</div> </div>
1	C	164	<div> <div>67%</div> <div>21%</div> <div>5%</div> <div>7%</div> </div>
1	D	164	<div> <div>70%</div> <div>18%</div> <div>5%</div> <div>7%</div> </div>
1	E	164	<div> <div>68%</div> <div>20%</div> <div>5%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	164	
1	G	164	
1	H	164	
1	I	164	

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	G	1700	-	-	-	X
3	CDP	I	1900	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11117 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	152	Total	C	N	O	S	0	0	0
			1188	741	205	237	5			
1	B	151	Total	C	N	O	S	0	0	0
			1191	743	205	238	5			
1	C	153	Total	C	N	O	S	0	0	0
			1206	752	209	240	5			
1	D	152	Total	C	N	O	S	0	0	0
			1192	744	206	237	5			
1	E	152	Total	C	N	O	S	0	0	0
			1188	742	206	235	5			
1	F	152	Total	C	N	O	S	0	0	0
			1201	749	208	239	5			
1	G	152	Total	C	N	O	S	0	1	0
			1206	753	212	236	5			
1	H	152	Total	C	N	O	S	0	1	0
			1195	745	209	236	5			
1	I	151	Total	C	N	O	S	0	0	0
			1183	739	205	234	5			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	CLONING ARTIFACT	UNP P61136
A	-1	SER	-	CLONING ARTIFACT	UNP P61136
A	0	HIS	-	CLONING ARTIFACT	UNP P61136
B	-2	GLY	-	CLONING ARTIFACT	UNP P61136
B	-1	SER	-	CLONING ARTIFACT	UNP P61136
B	0	HIS	-	CLONING ARTIFACT	UNP P61136
C	-2	GLY	-	CLONING ARTIFACT	UNP P61136
C	-1	SER	-	CLONING ARTIFACT	UNP P61136
C	0	HIS	-	CLONING ARTIFACT	UNP P61136
D	-2	GLY	-	CLONING ARTIFACT	UNP P61136
D	-1	SER	-	CLONING ARTIFACT	UNP P61136

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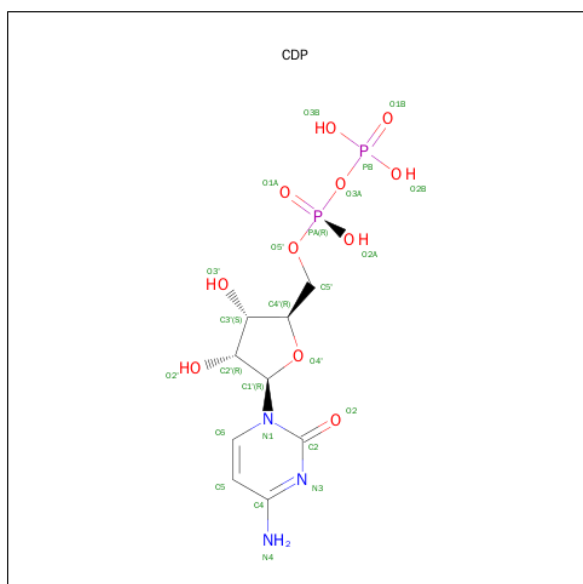
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Chain	Residue	Modelled	Actual	Comment	Reference
D	0	HIS	-	CLONING ARTIFACT	UNP P61136
E	-2	GLY	-	CLONING ARTIFACT	UNP P61136
E	-1	SER	-	CLONING ARTIFACT	UNP P61136
E	0	HIS	-	CLONING ARTIFACT	UNP P61136
F	-2	GLY	-	CLONING ARTIFACT	UNP P61136
F	-1	SER	-	CLONING ARTIFACT	UNP P61136
F	0	HIS	-	CLONING ARTIFACT	UNP P61136
G	-2	GLY	-	CLONING ARTIFACT	UNP P61136
G	-1	SER	-	CLONING ARTIFACT	UNP P61136
G	0	HIS	-	CLONING ARTIFACT	UNP P61136
H	-2	GLY	-	CLONING ARTIFACT	UNP P61136
H	-1	SER	-	CLONING ARTIFACT	UNP P61136
H	0	HIS	-	CLONING ARTIFACT	UNP P61136
I	-2	GLY	-	CLONING ARTIFACT	UNP P61136
I	-1	SER	-	CLONING ARTIFACT	UNP P61136
I	0	HIS	-	CLONING ARTIFACT	UNP P61136

- 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	A	1	Total Mg 1 1	0	0

- Molecule 3 is CYTIDINE-5'-DIPHOSPHATE (three-letter code: CDP) (formula: C₉H₁₅N₃O₁₁P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 25	C 9	N 3	O 11	P 2	0	0
3	B	1	Total 25	C 9	N 3	O 11	P 2	0	0
3	C	1	Total 25	C 9	N 3	O 11	P 2	0	0
3	D	1	Total 25	C 9	N 3	O 11	P 2	0	0
3	E	1	Total 25	C 9	N 3	O 11	P 2	0	0
3	F	1	Total 25	C 9	N 3	O 11	P 2	0	0
3	G	1	Total 25	C 9	N 3	O 11	P 2	0	0
3	H	1	Total 25	C 9	N 3	O 11	P 2	0	0
3	I	1	Total 25	C 9	N 3	O 11	P 2	0	0

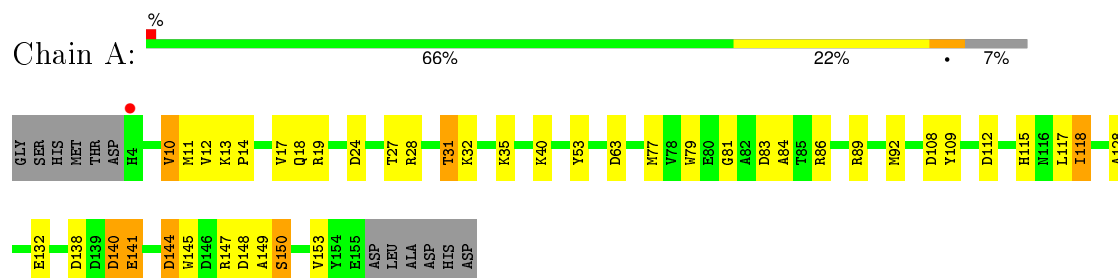
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	25	Total 25	O 25	0	0
4	B	19	Total 19	O 19	0	0
4	C	19	Total 19	O 19	0	0
4	D	15	Total 15	O 15	0	0
4	E	12	Total 12	O 12	0	0
4	F	13	Total 13	O 13	0	0
4	G	11	Total 11	O 11	0	0
4	H	17	Total 17	O 17	0	0
4	I	9	Total 9	O 9	0	0

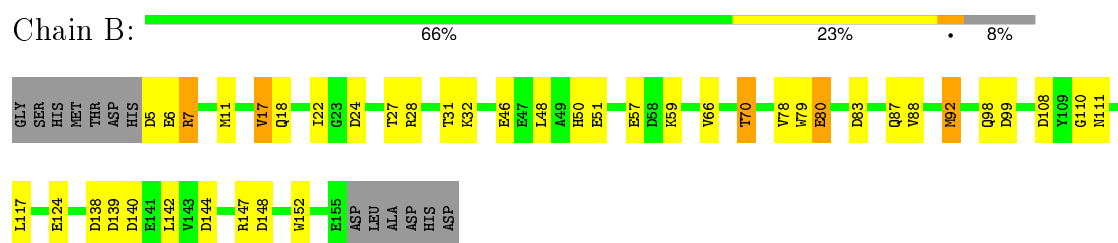
3 Residue-property plots [i](#)

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.

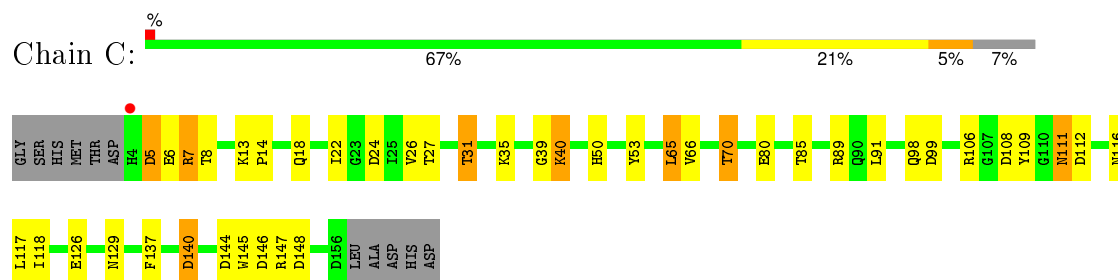
- Molecule 1: Nucleoside diphosphate kinase



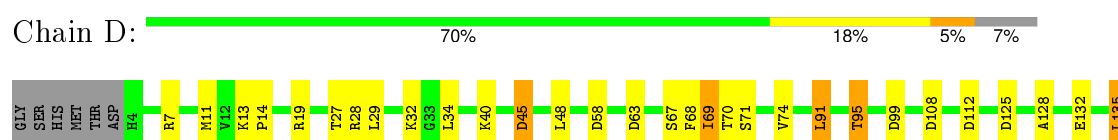
- Molecule 1: Nucleoside diphosphate kinase



- Molecule 1: Nucleoside diphosphate kinase



- Molecule 1: Nucleoside diphosphate kinase





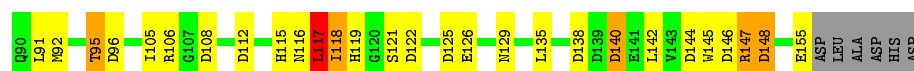
• Molecule 1: Nucleoside diphosphate kinase

Chain E: 68% 20% 5% 7%



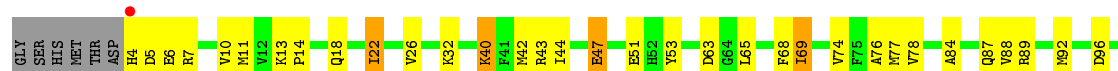
• Molecule 1: Nucleoside diphosphate kinase

Chain F: 54% 34% 7% 7%



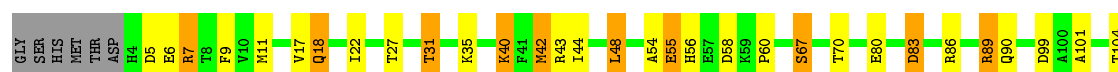
• Molecule 1: Nucleoside diphosphate kinase

Chain G: 60% 28% 7% 7%



• Molecule 1: Nucleoside diphosphate kinase

Chain H: 66% 20% 7% 7%



• Molecule 1: Nucleoside diphosphate kinase

Chain I: 63% 26% 8% 8%



V88	R89	Q90	L91	M92	T95	P102	D108	Y109	G110	H111	D112	L113	G114	H115	I133	A134	L135	F136	F137	E141	D144	D148	F155	ASP	LEU	ALA	ASP	HIS	ASP
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4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	124.37Å 71.52Å 157.99Å 90.00° 95.53° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 157.25 – 2.20	Depositor EDS
% Data completeness (in resolution range)	80.4 (20.00-2.20) 80.3 (157.25-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.80 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.200 , 0.271 0.206 , 0.205	Depositor DCC
R_{free} test set	2853 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	39.7	Xtriage
Anisotropy	0.126	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 37.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	1 of 70397 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11117	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 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	1.12	4/1214 (0.3%)	1.21	11/1643 (0.7%)
1	B	1.10	3/1217 (0.2%)	1.30	15/1645 (0.9%)
1	C	1.07	1/1233 (0.1%)	1.14	8/1667 (0.5%)
1	D	0.95	0/1218	1.15	13/1647 (0.8%)
1	E	0.94	0/1214	1.16	10/1642 (0.6%)
1	F	0.97	0/1228	1.19	14/1660 (0.8%)
1	G	0.92	1/1233 (0.1%)	1.12	11/1666 (0.7%)
1	H	0.90	0/1221	1.10	7/1652 (0.4%)
1	I	0.96	0/1209	1.09	5/1635 (0.3%)
All	All	1.00	9/10987 (0.1%)	1.16	94/14857 (0.6%)

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	B	0	1
1	E	0	1
1	G	0	1
1	H	0	1
All	All	0	4

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	92	MET	SD-CE	-6.82	1.39	1.77
1	A	12	VAL	CB-CG2	6.35	1.66	1.52
1	B	5	ASP	CB-CG	6.22	1.64	1.51
1	B	17	VAL	CB-CG2	-6.04	1.40	1.52
1	C	111	ASN	CB-CG	-5.79	1.37	1.51

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	28	ARG	NE-CZ-NH2	-9.86	115.37	120.30
1	A	24	ASP	CB-CG-OD2	9.56	126.90	118.30
1	D	140	ASP	CB-CG-OD2	9.21	126.58	118.30
1	E	148	ASP	CB-CG-OD2	9.00	126.40	118.30
1	C	140	ASP	CB-CG-OD2	8.72	126.15	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	110	GLY	Peptide
1	E	116	ASN	Peptide
1	G	110	GLY	Peptide
1	H	116	ASN	Peptide

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	1188	0	1090	22	0
1	B	1191	0	1103	17	0
1	C	1206	0	1112	35	0
1	D	1192	0	1101	24	0
1	E	1188	0	1097	24	0
1	F	1201	0	1110	42	0
1	G	1206	0	1118	43	0
1	H	1195	0	1098	28	0
1	I	1183	0	1095	40	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	25	0	12	0	0
3	B	25	0	12	0	0
3	C	25	0	12	3	0
3	D	25	0	12	2	0
3	E	25	0	12	2	0
3	F	25	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	25	0	12	1	0
3	H	25	0	12	0	0
3	I	25	0	12	0	0
4	A	25	0	0	0	0
4	B	19	0	0	1	0
4	C	19	0	0	3	0
4	D	15	0	0	1	0
4	E	12	0	0	0	0
4	F	13	0	0	1	0
4	G	11	0	0	0	0
4	H	17	0	0	0	0
4	I	9	0	0	0	0
All	All	11117	0	10032	242	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 12.

The worst 5 of 242 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:G:40:LYS:NZ	1:G:141:GLU:OE2	2.00	0.94
1:I:11:MET:CE	1:I:69:ILE:HD11	1.99	0.92
1:F:148:ASP:H	1:G:18:GLN:HE22	1.16	0.91
1:F:148:ASP:H	1:G:18:GLN:NE2	1.67	0.91
1:C:98:GLN:HG2	1:C:111:ASN:HB2	1.56	0.86

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	150/164 (92%)	143 (95%)	6 (4%)	1 (1%)	26	25
1	B	149/164 (91%)	144 (97%)	5 (3%)	0	100	100
1	C	151/164 (92%)	146 (97%)	5 (3%)	0	100	100
1	D	150/164 (92%)	143 (95%)	7 (5%)	0	100	100
1	E	150/164 (92%)	147 (98%)	2 (1%)	1 (1%)	26	25
1	F	150/164 (92%)	144 (96%)	5 (3%)	1 (1%)	26	25
1	G	151/164 (92%)	147 (97%)	4 (3%)	0	100	100
1	H	151/164 (92%)	144 (95%)	5 (3%)	2 (1%)	15	11
1	I	149/164 (91%)	142 (95%)	6 (4%)	1 (1%)	26	25
All	All	1351/1476 (92%)	1300 (96%)	45 (3%)	6 (0%)	39	42

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	55	GLU
1	E	117	LEU
1	I	58	ASP
1	A	150	SER
1	H	60	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	120/133 (90%)	113 (94%)	7 (6%)	25	28
1	B	122/133 (92%)	112 (92%)	10 (8%)	14	13
1	C	123/133 (92%)	111 (90%)	12 (10%)	10	9
1	D	121/133 (91%)	111 (92%)	10 (8%)	14	13
1	E	120/133 (90%)	110 (92%)	10 (8%)	14	13
1	F	123/133 (92%)	108 (88%)	15 (12%)	6	5
1	G	122/133 (92%)	112 (92%)	10 (8%)	14	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	120/133 (90%)	110 (92%)	10 (8%)	14	13
1	I	120/133 (90%)	110 (92%)	10 (8%)	14	13
All	All	1091/1197 (91%)	997 (91%)	94 (9%)	13	12

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	69	ILE
1	F	46	GLU
1	I	51	GLU
1	E	70	THR
1	E	139	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	50	HIS
1	G	18	GLN
1	H	90	GLN
1	D	50	HIS
1	F	18	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	A	1100	2	19,26,26	1.36	3 (15%)	27,40,40	1.37	2 (7%)
3	CDP	B	1200	2	19,26,26	1.23	2 (10%)	27,40,40	1.55	6 (22%)
3	CDP	C	1300	-	19,26,26	1.23	3 (15%)	27,40,40	1.47	5 (18%)
3	CDP	D	1400	-	19,26,26	1.22	2 (10%)	27,40,40	1.69	4 (14%)
3	CDP	E	1500	-	19,26,26	1.24	2 (10%)	27,40,40	1.62	4 (14%)
3	CDP	F	1600	-	19,26,26	1.23	2 (10%)	27,40,40	1.67	5 (18%)
3	CDP	G	1700	-	19,26,26	1.40	3 (15%)	27,40,40	1.63	6 (22%)
3	CDP	H	1800	-	19,26,26	1.27	3 (15%)	27,40,40	1.58	3 (11%)
3	CDP	I	1900	-	19,26,26	1.17	2 (10%)	27,40,40	1.36	2 (7%)

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	A	1100	2	-	0/12/32/32	0/2/2/2
3	CDP	B	1200	2	-	0/12/32/32	0/2/2/2
3	CDP	C	1300	-	-	0/12/32/32	0/2/2/2
3	CDP	D	1400	-	-	0/12/32/32	0/2/2/2
3	CDP	E	1500	-	-	0/12/32/32	0/2/2/2
3	CDP	F	1600	-	-	0/12/32/32	0/2/2/2
3	CDP	G	1700	-	-	0/12/32/32	0/2/2/2
3	CDP	H	1800	-	-	0/12/32/32	0/2/2/2
3	CDP	I	1900	-	-	0/12/32/32	0/2/2/2

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1300	CDP	C6-N1	-2.18	1.32	1.35
3	A	1100	CDP	PB-O3B	2.04	1.62	1.54
3	B	1200	CDP	O4'-C1'	2.39	1.44	1.41
3	H	1800	CDP	O4'-C1'	2.40	1.44	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1200	CDP	PB-O1B	2.42	1.59	1.51

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	1500	CDP	PA-O3A-PB	-3.94	119.46	132.67
3	D	1400	CDP	PA-O3A-PB	-3.43	121.17	132.67
3	D	1400	CDP	C5-C4-N3	-3.09	117.91	121.80
3	G	1700	CDP	PA-O3A-PB	-2.91	122.91	132.67
3	C	1300	CDP	O2'-C2'-C3'	-2.86	102.52	111.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1300	CDP	3	0
3	D	1400	CDP	2	0
3	E	1500	CDP	2	0
3	G	1700	CDP	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	152/164 (92%)	-0.30	1 (0%) 89 88	23, 31, 48, 50	0
1	B	151/164 (92%)	-0.31	0 100 100	24, 32, 48, 55	0
1	C	153/164 (93%)	-0.26	1 (0%) 89 88	24, 32, 49, 57	0
1	D	152/164 (92%)	-0.21	0 100 100	29, 39, 52, 55	0
1	E	152/164 (92%)	-0.18	0 100 100	29, 41, 52, 57	0
1	F	152/164 (92%)	-0.23	1 (0%) 89 88	28, 39, 52, 63	0
1	G	152/164 (92%)	-0.16	1 (0%) 89 88	31, 41, 59, 68	0
1	H	152/164 (92%)	-0.16	0 100 100	32, 41, 57, 62	0
1	I	151/164 (92%)	-0.19	0 100 100	32, 41, 57, 61	0
All	All	1367/1476 (92%)	-0.22	4 (0%) 94 94	23, 38, 54, 68	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	4	HIS	4.3
1	G	4	HIS	4.0
1	A	4	HIS	2.2
1	C	4	HIS	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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
3	CDP	G	1700	25/25	0.84	0.22	3.29	75,78,86,86	0
3	CDP	I	1900	25/25	0.88	0.19	2.30	81,82,88,89	0
3	CDP	D	1400	25/25	0.92	0.13	0.21	46,52,57,60	0
3	CDP	B	1200	25/25	0.97	0.11	-0.45	29,37,48,52	0
3	CDP	A	1100	25/25	0.96	0.11	-0.55	33,40,54,57	0
3	CDP	C	1300	25/25	0.97	0.11	-0.56	34,39,49,50	0
3	CDP	H	1800	25/25	0.90	0.12	-0.68	59,65,73,73	0
3	CDP	F	1600	25/25	0.93	0.11	-0.75	45,52,58,60	0
3	CDP	E	1500	25/25	0.93	0.10	-1.17	43,53,55,57	0
2	MG	A	201	1/1	0.94	0.14	-	43,43,43,43	0
2	MG	B	202	1/1	0.91	0.09	-	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.