WORLDWIDE PDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 10:29 PM GMT

PDB ID	:	1TW3
Title	:	Crystal structure of Carminomycin-4-O-methyltransferase (DnrK) in complex with S-adenosyl-L-homocystein (SAH) and 4-methoxy-e-rhodomycin T (M-ET)
Authors	:	Jansson, A.; Koskiniemi, H.; Mantsala, P.; Niemi, J.; Schneider, G.
Deposited on	:	2004-06-30
Resolution	:	2.35 Å(reported)

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

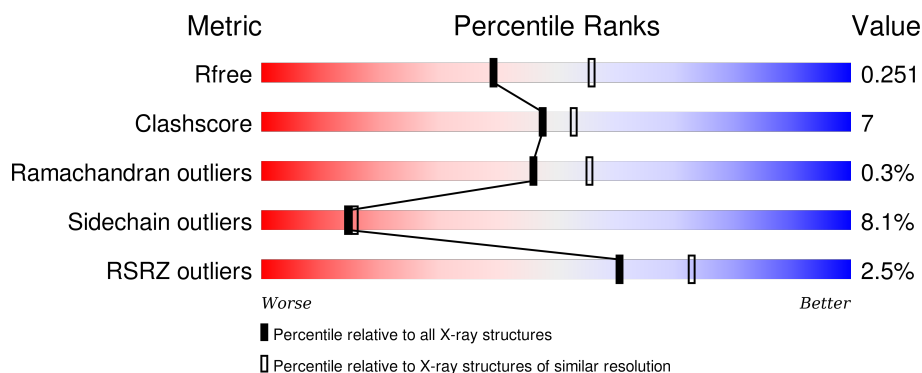|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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:
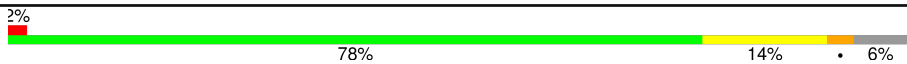*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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	Percentile Ranks	Value
Rfree		0.251
Clashscore		7
Ramachandran outliers		0.3%
Sidechain outliers		8.1%
RSRZ outliers		2.5%

Worse *Better*

▮ Percentile relative to all X-ray structures
❑ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1352 (2.38-2.34)
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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	360	2% · 78% · 14% · 6%
1	B	360	3% · 76% · 16% · 6%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5742 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 Carminomycin 4-O-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total 2627	C 1661	N 470	O 491	S 5	0	0	0
1	B	340	Total 2627	C 1661	N 470	O 491	S 5	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	CLONING ARTIFACT	UNP Q06528
A	-3	SER	-	CLONING ARTIFACT	UNP Q06528
A	-2	PRO	-	CLONING ARTIFACT	UNP Q06528
A	-1	ASN	-	CLONING ARTIFACT	UNP Q06528
A	0	SER	-	CLONING ARTIFACT	UNP Q06528
B	-4	GLY	-	CLONING ARTIFACT	UNP Q06528
B	-3	SER	-	CLONING ARTIFACT	UNP Q06528
B	-2	PRO	-	CLONING ARTIFACT	UNP Q06528
B	-1	ASN	-	CLONING ARTIFACT	UNP Q06528
B	0	SER	-	CLONING ARTIFACT	UNP Q06528

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 3 is METHYL (4R)-2-ETHYL-2,5,12-TRIHYDROXY-7-METHOXY-6,11-DIOX O-4-{[2,3,6-TRIDEOXY-3-(DIMETHYLAMINO)-BETA-D-RIBO-HEXOPYRANOSYL] OXY}-1H,2H,3H,4H,6H,11H-TETRACENE-1-CARBOXYLATE (three-letter code: ERT) (formula: $C_{31}H_{37}NO_{11}$).
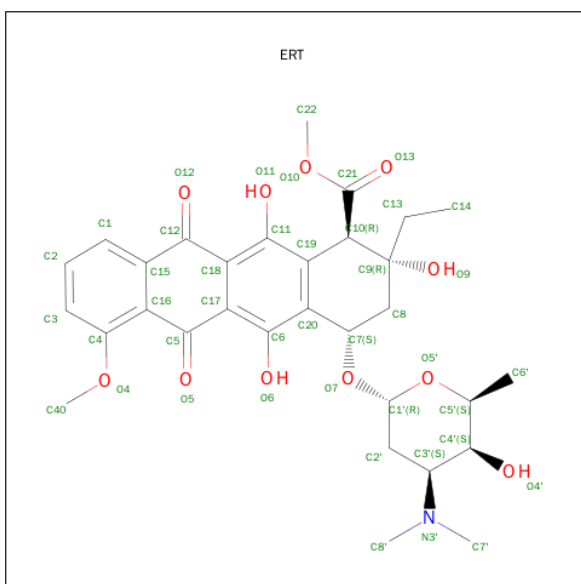
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			43	31	1	11		
3	B	1	Total	C	N	O	0	0
			43	31	1	11		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	212	Total	O	0	0
			212	212		
4	B	138	Total	O	0	0
			138	138		

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: Carminomycin 4-O-methyltransferase
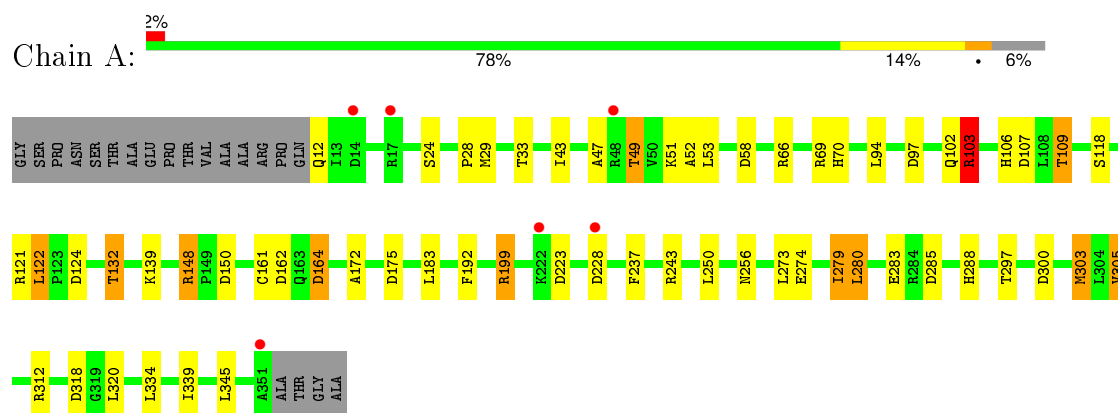
- Molecule 1: Carminomycin 4-O-methyltransferase
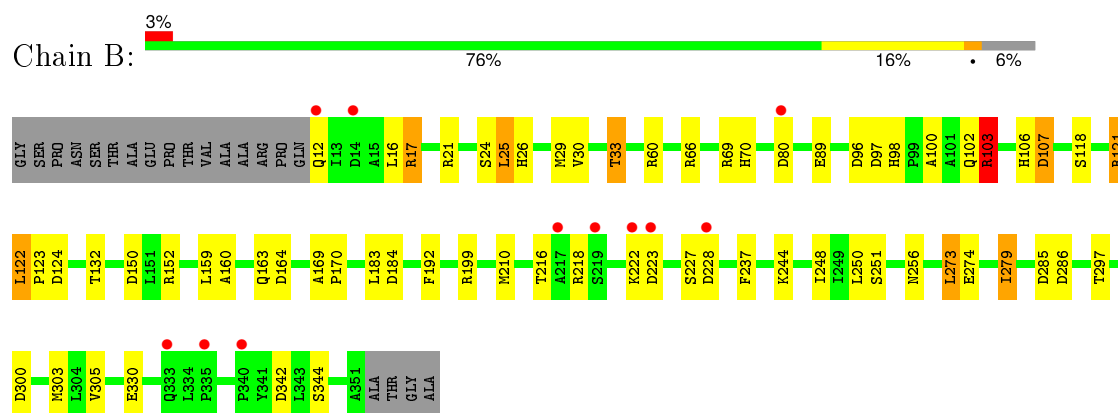
4　Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	210.69Å　53.13Å　83.07Å 90.00°　105.03°　90.00°	Depositor
Resolution (Å)	35.00　–　2.35 32.37　–　2.35	Depositor EDS
% Data completeness (in resolution range)	95.6 (35.00-2.35) 95.6 (32.37-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$<I/\sigma(I)>$ [1]	5.65 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, R_{free}	0.193　,　0.244 0.205　,　0.251	Depositor DCC
R_{free} test set	1829 reflections (5.39%)	DCC
Wilson B-factor (Å^2)	25.3	Xtriage
Anisotropy	0.074	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 37.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$<|L|> = 0.50, <L^2> = 0.34$	Xtriage
Outliers	0 of 35785 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5742	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.76% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ERT, SAH

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	0.49	1/2681 (0.0%)	0.89	14/3654 (0.4%)
1	B	0.45	1/2681 (0.0%)	0.94	15/3654 (0.4%)
All	All	0.47	2/5362 (0.0%)	0.92	29/7308 (0.4%)

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	1	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	12	GLN	N-CA	5.34	1.57	1.46
1	A	303	MET	SD-CE	-5.29	1.48	1.77

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	12	GLN	N-CA-CB	20.74	147.93	110.60
1	A	97	ASP	CB-CG-OD2	7.89	125.41	118.30
1	B	223	ASP	CB-CG-OD2	7.71	125.24	118.30
1	B	107	ASP	CB-CG-OD2	7.64	125.17	118.30
1	A	103	ARG	NE-CZ-NH2	-7.58	116.51	120.30
1	A	162	ASP	CB-CG-OD2	7.43	124.99	118.30
1	B	80	ASP	CB-CG-OD2	7.15	124.74	118.30
1	B	97	ASP	CB-CG-OD2	6.77	124.39	118.30
1	A	223	ASP	CB-CG-OD2	6.32	123.99	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	103	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	B	164	ASP	CB-CG-OD2	5.87	123.58	118.30
1	A	103	ARG	NE-CZ-NH1	5.75	123.17	120.30
1	B	96	ASP	CB-CG-OD2	5.67	123.40	118.30
1	A	124	ASP	CB-CG-OD2	5.67	123.40	118.30
1	A	69	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	B	342	ASP	CB-CG-OD2	5.62	123.35	118.30
1	A	318	ASP	CB-CG-OD2	5.58	123.32	118.30
1	A	148	ARG	NE-CZ-NH2	-5.55	117.53	120.30
1	B	228	ASP	CB-CG-OD2	5.55	123.29	118.30
1	B	12	GLN	N-CA-C	-5.44	96.31	111.00
1	B	69	ARG	NE-CZ-NH1	5.33	122.97	120.30
1	A	150	ASP	CB-CG-OD2	5.31	123.08	118.30
1	A	164	ASP	CB-CG-OD2	5.30	123.07	118.30
1	A	175	ASP	CB-CG-OD2	5.26	123.04	118.30
1	B	103	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	A	228	ASP	CB-CG-OD2	5.14	122.93	118.30
1	B	124	ASP	CB-CG-OD2	5.14	122.92	118.30
1	B	150	ASP	CB-CG-OD2	5.02	122.82	118.30
1	A	69	ARG	NE-CZ-NH1	5.00	122.80	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	12	GLN	CA

There are no planarity outliers.

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	2627	0	2624	40	3
1	B	2627	0	2624	41	0
2	A	26	0	19	3	0
2	B	26	0	18	5	0
3	A	43	0	35	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	43	0	35	4	0
4	A	212	0	0	6	3
4	B	138	0	0	5	0
All	All	5742	0	5355	79	3

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 7.

All (79) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:ARG:O	1:B:222:LYS:HG3	1.79	0.83
1:A:33:THR:HG21	1:B:122:LEU:HB3	1.66	0.77
1:A:29:MET:O	1:A:33:THR:HG23	1.85	0.77
2:B:1635:SAH:SD	3:B:1600:ERT:C40	2.75	0.74
1:B:256:ASN:HD22	1:B:303:MET:HE2	1.54	0.72
1:B:118:SER:O	1:B:132:THR:HG21	1.94	0.68
1:A:118:SER:O	1:A:132:THR:HG21	1.94	0.67
2:B:1635:SAH:SD	3:B:1600:ERT:H401	2.37	0.65
1:B:256:ASN:HD22	1:B:303:MET:CE	2.10	0.64
2:A:635:SAH:SD	3:A:600:ERT:C40	2.85	0.64
1:B:17:ARG:O	1:B:21:ARG:HG3	2.02	0.59
1:A:49:THR:HG23	1:A:52:ALA:H	1.67	0.59
1:A:103:ARG:NH2	1:A:107:ASP:OD1	2.36	0.58
1:A:122:LEU:HB3	1:B:33:THR:HG21	1.86	0.57
1:A:312:ARG:HD2	1:A:320:LEU:HD22	1.85	0.57
1:A:118:SER:CB	1:A:305:VAL:HG13	2.35	0.56
1:A:12:GLN:NE2	1:B:98:HIS:NE2	2.54	0.56
1:B:103:ARG:NH2	1:B:107:ASP:OD1	2.38	0.55
1:A:172:ALA:HA	1:A:199:ARG:NH1	2.22	0.55
1:A:102:GLN:O	1:A:106:HIS:HD2	1.91	0.54
1:B:250:LEU:HD12	1:B:279:ILE:CD1	2.38	0.54
1:A:256:ASN:HA	1:A:303:MET:CE	2.37	0.54
1:B:256:ASN:HA	1:B:303:MET:CE	2.38	0.54
3:B:1600:ERT:O4'	3:B:1600:ERT:H7'3	2.09	0.53
1:A:256:ASN:HD22	1:A:303:MET:CE	2.21	0.53
1:B:29:MET:O	1:B:33:THR:HG23	2.08	0.53
2:B:1635:SAH:SD	3:B:1600:ERT:H402	2.49	0.53
1:B:210:MET:HE2	2:B:1635:SAH:C8	2.40	0.52
1:A:118:SER:HB3	1:A:305:VAL:HG13	1.92	0.51
2:A:635:SAH:SD	3:A:600:ERT:H403	2.50	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:LEU:HD23	1:A:280:LEU:N	2.25	0.51
1:A:66:ARG:HD2	1:B:300:ASP:OD2	2.11	0.50
1:B:248:ILE:HD12	1:B:273:LEU:HD13	1.93	0.50
1:A:300:ASP:OD2	1:B:66:ARG:HD2	2.10	0.50
1:B:250:LEU:HD12	1:B:279:ILE:HD12	1.94	0.50
1:A:297:THR:OG1	1:B:70:HIS:HD2	1.95	0.49
4:A:644:HOH:O	1:B:106:HIS:HE1	1.93	0.49
1:A:66:ARG:HD3	4:B:1662:HOH:O	2.12	0.49
1:B:160:ALA:O	1:B:163:GLN:HB2	2.12	0.49
1:A:118:SER:HB2	1:A:305:VAL:HG13	1.95	0.48
1:B:102:GLN:O	1:B:106:HIS:HD2	1.97	0.48
1:B:256:ASN:ND2	1:B:303:MET:CE	2.76	0.47
1:A:107:ASP:OD2	1:A:109:THR:HB	2.15	0.47
1:A:161:CYS:SG	4:A:835:HOH:O	2.27	0.47
1:A:279:ILE:C	1:A:280:LEU:HD23	2.34	0.47
1:B:26:HIS:O	1:B:30:VAL:HG23	2.15	0.47
1:A:256:ASN:HD22	1:A:303:MET:HE2	1.81	0.46
1:A:139:LYS:HE3	4:A:842:HOH:O	2.16	0.46
4:A:781:HOH:O	1:B:66:ARG:HD3	2.15	0.45
1:A:274:GLU:HG2	4:A:682:HOH:O	2.16	0.45
1:A:164:ASP:HB2	4:A:841:HOH:O	2.17	0.45
1:A:94:LEU:O	1:A:103:ARG:HG3	2.17	0.45
1:B:152:ARG:HH12	1:B:210:MET:HE3	1.81	0.45
1:A:288:HIS:HE1	4:B:1653:HOH:O	2.00	0.45
1:B:256:ASN:ND2	1:B:303:MET:HE1	2.32	0.44
1:A:256:ASN:HA	1:A:303:MET:HE2	2.00	0.44
1:A:256:ASN:ND2	1:A:303:MET:HE1	2.32	0.44
1:A:70:HIS:HD2	1:B:297:THR:OG1	2.00	0.44
1:B:122:LEU:N	1:B:123:PRO:CD	2.81	0.44
1:B:251:SER:O	2:B:1635:SAH:N	2.51	0.43
1:B:98:HIS:HD1	1:B:100:ALA:H	1.65	0.43
1:B:222:LYS:HG2	1:B:227:SER:OG	2.18	0.43
1:B:118:SER:HB3	1:B:132:THR:CG2	2.48	0.43
1:B:29:MET:O	1:B:33:THR:CG2	2.66	0.43
1:A:312:ARG:HD2	1:A:320:LEU:CD2	2.49	0.43
1:A:43:ILE:HA	1:A:47:ALA:O	2.19	0.43
1:A:43:ILE:HG13	1:A:53:LEU:HD21	2.02	0.42
1:B:184:ASP:OD2	4:B:1645:HOH:O	2.21	0.42
1:B:121:ARG:HB2	1:B:132:THR:OG1	2.19	0.42
1:A:106:HIS:HE1	4:B:1641:HOH:O	2.03	0.42
1:B:89:GLU:CD	1:B:89:GLU:H	2.23	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:ASP:OD1	1:A:58:ASP:O	2.38	0.41
1:B:169:ALA:N	1:B:170:PRO:HD2	2.36	0.41
1:B:60:ARG:HD2	4:B:1717:HOH:O	2.19	0.41
1:A:300:ASP:OD2	1:B:66:ARG:CD	2.68	0.41
1:B:152:ARG:HH12	1:B:210:MET:CE	2.33	0.41
1:A:28:PRO:HB2	1:B:25:LEU:HD13	2.01	0.40
2:A:635:SAH:SD	3:A:600:ERT:H401	2.61	0.40
1:A:250:LEU:HD12	1:A:279:ILE:HD12	2.04	0.40

All (3) 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:A:58:ASP:OD1	4:A:836:HOH:O[2_656]	1.40	0.80
1:A:58:ASP:OD2	4:A:802:HOH:O[2_656]	1.90	0.30
1:A:58:ASP:CG	4:A:836:HOH:O[2_656]	2.13	0.07

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	338/360 (94%)	334 (99%)	3 (1%)	1 (0%)	46	55
1	B	338/360 (94%)	327 (97%)	10 (3%)	1 (0%)	46	55
All	All	676/720 (94%)	661 (98%)	13 (2%)	2 (0%)	46	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	283	GLU
1	B	286	ASP

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	272/285 (95%)	250 (92%)	22 (8%)	15	16
1	B	272/285 (95%)	250 (92%)	22 (8%)	15	16
All	All	544/570 (95%)	500 (92%)	44 (8%)	15	16

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	SER
1	A	49	THR
1	A	51	LYS
1	A	103	ARG
1	A	109	THR
1	A	121	ARG
1	A	122	LEU
1	A	132	THR
1	A	148	ARG
1	A	183	LEU
1	A	192	PHE
1	A	199	ARG
1	A	237	PHE
1	A	243	ARG
1	A	273	LEU
1	A	279	ILE
1	A	280	LEU
1	A	285	ASP
1	A	305	VAL
1	A	334	LEU
1	A	339	ILE
1	A	345	LEU
1	B	16	LEU
1	B	17	ARG
1	B	24	SER
1	B	25	LEU
1	B	33	THR

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Mol	Chain	Res	Type
1	B	103	ARG
1	B	121	ARG
1	B	122	LEU
1	B	159	LEU
1	B	183	LEU
1	B	192	PHE
1	B	199	ARG
1	B	216	THR
1	B	237	PHE
1	B	244	LYS
1	B	273	LEU
1	B	274	GLU
1	B	279	ILE
1	B	285	ASP
1	B	305	VAL
1	B	330	GLU
1	B	344	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	26	HIS
1	A	70	HIS
1	A	102	GLN
1	A	106	HIS
1	A	163	GLN
1	A	181	HIS
1	A	256	ASN
1	A	282	HIS
1	A	288	HIS
1	B	70	HIS
1	B	106	HIS
1	B	163	GLN
1	B	181	HIS
1	B	256	ASN
1	B	282	HIS
1	B	333	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)

4 ligands are modelled in this entry.

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	ERT	A	600	-	45,47,47	2.20	8 (17%)	61,73,73	3.17	11 (18%)
2	SAH	A	635	-	20,28,28	3.02	5 (25%)	19,40,40	5.52	8 (42%)
3	ERT	B	1600	-	45,47,47	2.17	8 (17%)	61,73,73	2.55	14 (22%)
2	SAH	B	1635	-	20,28,28	3.03	4 (20%)	19,40,40	5.23	10 (52%)

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	ERT	A	600	-	-	0/19/70/70	0/5/5/5
2	SAH	A	635	-	-	0/7/31/31	0/3/3/3
3	ERT	B	1600	-	-	0/19/70/70	0/5/5/5
2	SAH	B	1635	-	-	0/7/31/31	0/3/3/3

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	635	SAH	C5'-SD	-6.64	1.68	1.81
2	B	1635	SAH	C5'-SD	-6.47	1.68	1.81
3	B	1600	ERT	C8'-N3'	-5.26	1.26	1.46
3	A	600	ERT	O11-C11	-5.13	1.25	1.37
3	A	600	ERT	C7'-N3'	-5.10	1.27	1.46
3	B	1600	ERT	O11-C11	-5.03	1.25	1.37
3	B	1600	ERT	C7'-N3'	-5.01	1.27	1.46
3	A	600	ERT	C8'-N3'	-4.99	1.27	1.46
3	A	600	ERT	C15-C12	-3.77	1.40	1.48
2	A	635	SAH	CG-SD	-3.64	1.67	1.81
3	B	1600	ERT	C15-C12	-3.49	1.40	1.48
2	B	1635	SAH	CG-SD	-3.33	1.68	1.81
3	A	600	ERT	C18-C12	-2.69	1.41	1.47
3	B	1600	ERT	C18-C12	-2.58	1.41	1.47
2	A	635	SAH	O4'-C1'	2.33	1.44	1.41
3	A	600	ERT	C17-C18	2.82	1.47	1.41
3	B	1600	ERT	C17-C18	3.22	1.48	1.41
3	A	600	ERT	O10-C21	3.94	1.43	1.33
3	B	1600	ERT	O10-C21	3.98	1.43	1.33
2	A	635	SAH	C2-N1	6.77	1.46	1.33
2	B	1635	SAH	C2-N1	7.11	1.47	1.33
2	A	635	SAH	C2-N3	7.96	1.46	1.32
2	B	1635	SAH	C2-N3	8.43	1.47	1.32
3	B	1600	ERT	O13-C21	8.55	1.42	1.21
3	A	600	ERT	O13-C21	8.61	1.43	1.21

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	635	SAH	N3-C2-N1	-21.50	112.44	128.89
2	B	1635	SAH	N3-C2-N1	-19.29	114.13	128.89
2	A	635	SAH	C4-C5-N7	-4.44	105.39	109.48
3	B	1600	ERT	O13-C21-C10	-4.39	117.50	124.82
3	A	600	ERT	O4-C4-C3	-3.73	118.06	124.35
2	B	1635	SAH	C4-C5-N7	-3.22	106.52	109.48
3	A	600	ERT	C2'-C3'-N3'	-3.01	106.79	115.70
3	B	1600	ERT	O10-C21-O13	-2.52	118.58	123.79
3	B	1600	ERT	C4-C16-C5	-2.51	118.94	122.34
2	A	635	SAH	C1'-N9-C4	-2.38	123.35	126.94
3	B	1600	ERT	C2'-C3'-N3'	-2.34	108.78	115.70
3	A	600	ERT	C13-C9-C8	-2.30	105.23	110.93
2	B	1635	SAH	C5'-C4'-C3'	-2.09	109.56	114.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1600	ERT	C2'-C3'-C4'	2.09	113.07	110.03
3	B	1600	ERT	O4-C4-C16	2.10	119.05	115.78
2	B	1635	SAH	C2'-C3'-C4'	2.11	106.95	102.61
3	A	600	ERT	C15-C16-C4	2.11	120.45	118.13
2	B	1635	SAH	C5'-SD-CG	2.12	108.76	102.41
3	B	1600	ERT	C8-C7-C20	2.16	116.20	111.07
2	A	635	SAH	C2'-C3'-C4'	2.19	107.12	102.61
3	A	600	ERT	C15-C12-C18	2.34	122.00	117.99
3	B	1600	ERT	C8'-N3'-C7'	2.47	118.25	110.43
2	A	635	SAH	O4'-C4'-C5'	2.50	115.66	108.85
3	A	600	ERT	C8'-N3'-C7'	2.60	118.63	110.43
2	B	1635	SAH	N6-C6-N1	2.60	124.79	119.20
3	B	1600	ERT	C15-C12-C18	2.67	122.56	117.99
3	B	1600	ERT	C15-C16-C4	3.00	121.43	118.13
2	B	1635	SAH	C1'-N9-C4	3.04	131.52	126.94
3	B	1600	ERT	C7'-N3'-C3'	3.59	123.46	113.09
2	B	1635	SAH	C2-N1-C6	3.78	125.52	118.77
3	A	600	ERT	C8'-N3'-C3'	3.80	124.08	113.09
2	B	1635	SAH	C2'-C1'-N9	3.90	120.24	114.29
3	A	600	ERT	O4-C4-C16	3.92	121.88	115.78
3	B	1600	ERT	C40-O4-C4	3.97	123.57	117.54
3	A	600	ERT	O10-C21-C10	4.05	118.09	111.17
2	A	635	SAH	C5'-SD-CG	4.38	115.56	102.41
2	A	635	SAH	O4'-C1'-N9	4.57	117.66	108.10
2	A	635	SAH	C2-N1-C6	5.06	127.81	118.77
3	A	600	ERT	C40-O4-C4	5.32	125.62	117.54
3	B	1600	ERT	O10-C21-C10	7.44	123.89	111.17
2	B	1635	SAH	O4'-C1'-N9	8.27	125.42	108.10
3	B	1600	ERT	C20-C19-C10	13.93	119.02	113.15
3	A	600	ERT	C20-C19-C10	21.11	122.04	113.15

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	600	ERT	3	0
2	A	635	SAH	3	0
3	B	1600	ERT	4	0
2	B	1635	SAH	5	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	340/360 (94%)	0.01	6 (1%)	71	81	18, 26, 37, 48	0
1	B	340/360 (94%)	0.19	11 (3%)	51	64	18, 32, 45, 59	0
All	All	680/720 (94%)	0.10	17 (2%)	61	73	18, 28, 42, 59	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	12	GLN	4.1
1	B	222	LYS	3.8
1	B	228	ASP	3.5
1	B	340	PRO	2.9
1	A	14	ASP	2.8
1	B	217	ALA	2.6
1	A	222	LYS	2.5
1	A	351	ALA	2.3
1	B	80	ASP	2.3
1	A	17	ARG	2.3
1	B	219	SER	2.3
1	B	333	GLN	2.3
1	B	14	ASP	2.2
1	B	335	PRO	2.2
1	A	48	ARG	2.1
1	A	228	ASP	2.1
1	B	223	ASP	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	ERT	A	600	43/43	0.94	0.16	0.67	23,29,32,34	0
2	SAH	A	635	26/26	0.95	0.14	0.42	20,26,28,28	0
3	ERT	B	1600	43/43	0.92	0.14	-0.21	32,41,48,50	0
2	SAH	B	1635	26/26	0.94	0.12	-0.50	25,28,30,31	0

6.5 Other polymers (i)

There are no such residues in this entry.