Full wwPDB X-ray Structure Validation Report ⓘ

Oct 22, 2024 – 01:12 pm BST

PDB ID	:	8R7T
Title	:	Crystal Structure of Cyclophilin TgCyp23 from Toxoplasma gondii in complex with Alisporivir (nonimmunosuppressive analogue of Cyclosporin)
Authors	:	Jimenez-Faraco, E.; Hermoso, J.A.
Deposited on	:	2023-11-27
Resolution	:	1.20 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

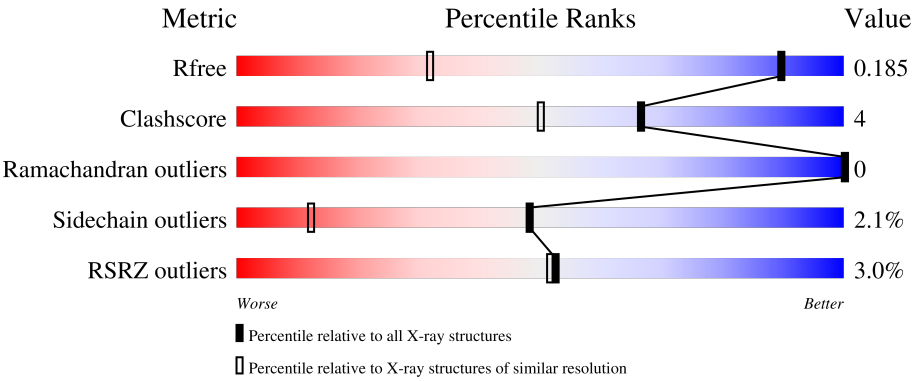
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 1.20 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}	164625	1079 (1.20-1.20)
Clashscore	180529	1183 (1.20-1.20)
Ramachandran outliers	177936	1146 (1.20-1.20)
Sidechain outliers	177891	1146 (1.20-1.20)
RSRZ outliers	164620	1078 (1.20-1.20)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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	213	2% 90% · 8%
1	B	213	3% 81% 12% · 7%
2	C	11	9% 18% 55% 27%
2	D	11	9% 45% 45%

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
2	MVA	C	4	-	X	-	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3922 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 Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	199	Total	C	N	O	S	0	9	0
			1585	1010	277	289	9			
1	A	197	Total	C	N	O	S	0	5	0
			1548	985	272	283	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP A0A7J6KAD1
B	0	HIS	-	expression tag	UNP A0A7J6KAD1
A	-1	GLY	-	expression tag	UNP A0A7J6KAD1
A	0	HIS	-	expression tag	UNP A0A7J6KAD1

- Molecule 2 is a protein called Alisporivir.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	11	Total	C	N	O	0	0	0
			86	63	11	12			
2	D	11	Total	C	N	O	0	0	0
			86	63	11	12			

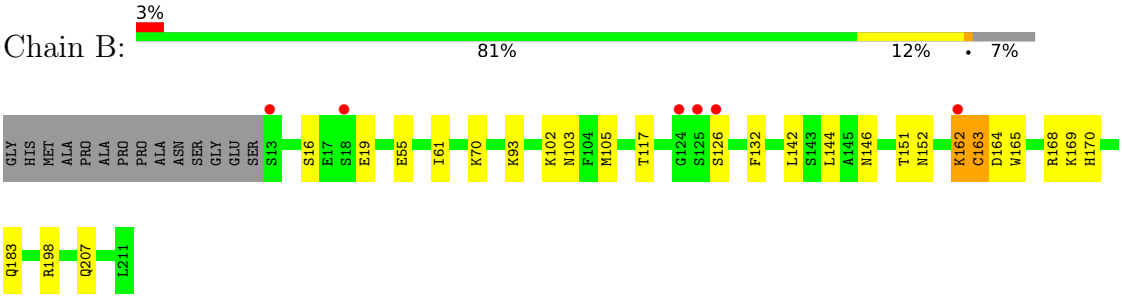
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	299	Total	O	0	0
			299	299		
3	A	296	Total	O	0	0
			296	296		
3	C	12	Total	O	0	0
			12	12		
3	D	10	Total	O	0	0
			10	10		

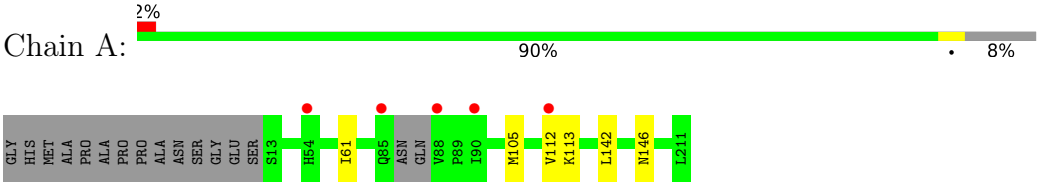
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

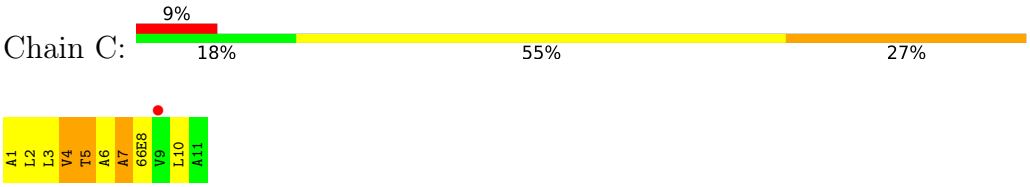
• Molecule 1: Peptidyl-prolyl cis-trans isomerase



• Molecule 1: Peptidyl-prolyl cis-trans isomerase



• Molecule 2: Alisporivir



• Molecule 2: Alisporivir

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	38.31Å 118.52Å 46.53Å 90.00° 103.53° 90.00°	Depositor
Resolution (Å)	42.27 – 1.20 42.27 – 1.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.27-1.20) 99.9 (42.27-1.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.62 (at 1.20Å)	Xtriage
Refinement program	REFMAC 5.8.0405, PHENIX 1.20.1	Depositor
R, R_{free}	0.164 , 0.179 0.172 , 0.185	Depositor DCC
R_{free} test set	6330 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	13.5	Xtriage
Anisotropy	0.365	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 30.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	3922	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.29% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 66E, DAL, BMT, 33X, MVA, MLE, ABA

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	0.37	0/1596	0.64	0/2149
1	B	0.35	0/1649	0.66	0/2221
2	C	3.21	0/10	2.40	0/11
2	D	2.94	0/10	2.60	0/11
All	All	0.43	0/3265	0.67	0/4392

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	1548	0	1537	3	0
1	B	1585	0	1591	17	0
2	C	86	0	100	3	0
2	D	86	0	100	4	0
3	A	296	0	0	0	0
3	B	299	0	0	2	0
3	C	12	0	0	0	0
3	D	10	0	0	0	0
All	All	3922	0	3328	24	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 4.

All (24) 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:144:LEU:O	1:B:170:HIS:HD2	1.85	0.59
1:B:61:ILE:HG21	1:B:142[B]:LEU:HD22	1.84	0.59
1:B:102:LYS:HE3	1:B:103:ASN:ND2	2.18	0.58
1:B:146:ASN:O	2:C:5:BMT:HA	2.03	0.58
1:B:93:LYS:HE3	1:B:207:GLN:HE22	1.70	0.56
1:A:146:ASN:O	2:D:5:BMT:HA	2.06	0.55
1:B:183:GLN:NE2	3:B:302:HOH:O	2.39	0.53
1:B:16:SER:OG	1:B:19:GLU:HG3	2.07	0.53
1:B:117:THR:HA	2:C:7:33X:HB1	1.92	0.51
1:B:163[A]:CYS:HA	1:B:165:TRP:CZ3	2.46	0.50
1:B:162:LYS:HZ3	1:B:164:ASP:HB2	1.79	0.47
1:B:170:HIS:HE1	3:B:526:HOH:O	1.97	0.47
1:B:126:SER:HA	1:B:152:ASN:O	2.15	0.46
2:D:9:VAL:HA	2:D:10:MLE:HN1	1.77	0.46
2:D:1:DAL:C	2:D:3:MLE:HN1	2.48	0.44
1:B:163[B]:CYS:HA	1:B:165:TRP:CZ3	2.53	0.44
1:A:112:VAL:HG12	1:A:113:LYS:HD3	1.99	0.44
2:C:4:MVA:HA	2:C:5:BMT:HN1	1.90	0.44
1:A:61:ILE:HG21	1:A:142:LEU:HD22	1.99	0.43
2:D:1:DAL:HA	2:D:2:MLE:HN1	1.63	0.43
1:B:70[A]:LYS:HB3	1:B:70[A]:LYS:HE2	1.85	0.42
1:B:126:SER:HB2	1:B:151:THR:HA	2.02	0.42
1:B:132:PHE:CG	1:B:168:ARG:HA	2.57	0.40
1:B:162:LYS:HD2	1:B:164:ASP:H	1.87	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	198/213 (93%)	195 (98%)	3 (2%)	0	100	100
1	B	207/213 (97%)	202 (98%)	5 (2%)	0	100	100
2	C	1/11 (9%)	1 (100%)	0	0	100	100
2	D	1/11 (9%)	1 (100%)	0	0	100	100
All	All	407/448 (91%)	399 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	170/176 (97%)	169 (99%)	1 (1%)	84	60
1	B	177/176 (101%)	170 (96%)	7 (4%)	27	3
2	C	1/1 (100%)	1 (100%)	0	100	100
2	D	1/1 (100%)	1 (100%)	0	100	100
All	All	349/354 (99%)	341 (98%)	8 (2%)	48	10

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	55	GLU
1	B	105	MET
1	B	162	LYS
1	B	163[A]	CYS
1	B	163[B]	CYS
1	B	169	LYS
1	B	198	ARG
1	A	105	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	103	ASN
1	B	170	HIS
1	B	183	GLN
1	B	207	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)

18 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
2	33X	D	7	2	4,5,6	2.54	3 (75%)	1,5,7	1.40	0
2	DAL	D	1	2	3,4,5	1.63	1 (33%)	2,4,6	1.16	0
2	33X	C	7	2	4,5,6	2.53	3 (75%)	1,5,7	0.82	0
2	ABA	C	6	2	4,5,6	1.74	1 (25%)	1,5,7	3.34	1 (100%)
2	MLE	D	3	2	7,8,9	1.89	3 (42%)	6,9,11	2.08	2 (33%)
2	MLE	C	3	2	7,8,9	2.45	6 (85%)	6,9,11	1.85	2 (33%)
2	MLE	D	2	2	7,8,9	2.04	3 (42%)	6,9,11	1.69	2 (33%)
2	BMT	D	5	2	11,12,13	2.81	7 (63%)	12,14,16	1.88	5 (41%)
2	DAL	C	1	2	3,4,5	1.81	1 (33%)	2,4,6	0.82	0
2	MLE	C	10	2	7,8,9	2.15	5 (71%)	6,9,11	2.32	2 (33%)
2	BMT	C	5	2	11,12,13	2.97	8 (72%)	12,14,16	1.89	4 (33%)
2	66E	D	8	2	7,8,9	2.67	4 (57%)	7,9,11	2.28	3 (42%)
2	MVA	D	4	2	6,7,8	2.18	4 (66%)	7,8,10	3.28	4 (57%)
2	MLE	D	10	2	7,8,9	2.20	5 (71%)	6,9,11	1.91	2 (33%)
2	MLE	C	2	2	7,8,9	2.48	4 (57%)	6,9,11	2.01	2 (33%)
2	66E	C	8	2	7,8,9	2.52	5 (71%)	7,9,11	2.49	3 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	ABA	D	6	2	4,5,6	1.71	1 (25%)	1,5,7	3.58	1 (100%)
2	MVA	C	4	2	6,7,8	2.64	5 (83%)	7,8,10	3.49	3 (42%)

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	33X	D	7	2	-	0/1/4/6	-
2	DAL	D	1	2	-	0/0/2/4	-
2	33X	C	7	2	-	0/1/4/6	-
2	ABA	C	6	2	-	0/3/4/6	-
2	MLE	D	3	2	-	0/5/8/10	-
2	MLE	C	3	2	-	0/5/8/10	-
2	MLE	D	2	2	-	0/5/8/10	-
2	BMT	D	5	2	-	1/13/16/18	-
2	DAL	C	1	2	-	0/0/2/4	-
2	MLE	C	10	2	-	0/5/8/10	-
2	BMT	C	5	2	-	1/13/16/18	-
2	66E	D	8	2	-	1/8/9/11	-
2	MVA	D	4	2	-	1/6/8/10	-
2	MLE	D	10	2	-	0/5/8/10	-
2	MLE	C	2	2	-	0/5/8/10	-
2	66E	C	8	2	-	1/8/9/11	-
2	ABA	D	6	2	-	0/3/4/6	-
2	MVA	C	4	2	-	2/6/8/10	-

All (69) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	5	BMT	CG2-CB	4.80	1.62	1.53
2	D	5	BMT	CG2-CB	4.73	1.61	1.53
2	D	8	66E	CB-CA	4.24	1.61	1.54
2	C	2	MLE	CA-N	4.17	1.54	1.47
2	C	5	BMT	CD2-CG2	4.08	1.60	1.54
2	C	4	MVA	CA-N	4.07	1.54	1.47
2	D	5	BMT	CD2-CG2	3.98	1.60	1.54
2	D	7	33X	CB-CA	3.72	1.62	1.51
2	C	5	BMT	CD2-CE	3.67	1.61	1.50
2	D	5	BMT	CD1-CG2	3.52	1.61	1.53
2	D	8	66E	CA-N	3.52	1.54	1.47

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	8	66E	CA-N	3.49	1.54	1.47
2	C	8	66E	CB-CA	3.45	1.60	1.54
2	C	5	BMT	CD1-CG2	3.42	1.61	1.53
2	D	5	BMT	CD2-CE	3.29	1.60	1.50
2	C	7	33X	CB-CA	3.26	1.60	1.51
2	C	3	MLE	CA-N	3.13	1.52	1.47
2	C	7	33X	CA-N	2.97	1.52	1.47
2	C	2	MLE	CN-N	2.96	1.54	1.46
2	C	3	MLE	CB-CA	2.94	1.63	1.54
2	D	4	MVA	CA-N	2.85	1.52	1.47
2	D	8	66E	CG1-CB	2.84	1.62	1.52
2	D	2	MLE	CA-N	2.77	1.52	1.47
2	C	3	MLE	CN-N	2.77	1.54	1.46
2	D	1	DAL	CB-CA	2.73	1.61	1.52
2	C	5	BMT	CN-N	2.69	1.54	1.46
2	C	5	BMT	CH-CZ	2.69	1.61	1.49
2	C	8	66E	CG1-CB	2.68	1.62	1.52
2	C	6	ABA	CB-CA	2.65	1.60	1.52
2	D	10	MLE	CB-CA	2.64	1.62	1.54
2	D	6	ABA	CB-CA	2.63	1.60	1.52
2	D	8	66E	CG2-CB	2.62	1.61	1.52
2	C	5	BMT	CA-N	2.61	1.52	1.47
2	D	5	BMT	CH-CZ	2.60	1.60	1.49
2	C	8	66E	CG2-CB	2.59	1.61	1.52
2	C	10	MLE	CA-N	2.58	1.52	1.47
2	D	10	MLE	CB-CG	2.57	1.63	1.52
2	C	4	MVA	CG2-CB	2.56	1.61	1.52
2	C	3	MLE	CB-CG	2.55	1.63	1.52
2	D	7	33X	CA-N	2.55	1.51	1.47
2	C	1	DAL	CB-CA	2.53	1.61	1.52
2	D	10	MLE	CA-N	2.49	1.51	1.47
2	C	4	MVA	CB-CA	2.48	1.58	1.54
2	C	4	MVA	CN-N	2.47	1.53	1.46
2	C	10	MLE	CN-N	2.47	1.53	1.46
2	D	4	MVA	CB-CA	2.44	1.58	1.54
2	C	7	33X	CM-N	2.42	1.53	1.46
2	C	10	MLE	CB-CA	2.41	1.61	1.54
2	D	2	MLE	CB-CG	2.41	1.62	1.52
2	C	10	MLE	CB-CG	2.40	1.62	1.52
2	D	4	MVA	CG2-CB	2.40	1.61	1.52
2	C	2	MLE	CB-CG	2.39	1.62	1.52
2	D	5	BMT	CA-N	2.36	1.51	1.47

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	7	33X	CM-N	2.35	1.53	1.46
2	D	5	BMT	CN-N	2.34	1.53	1.46
2	D	10	MLE	CN-N	2.34	1.53	1.46
2	D	3	MLE	CB-CA	2.32	1.61	1.54
2	C	8	66E	C2-C1	2.23	1.62	1.48
2	D	2	MLE	CN-N	2.22	1.52	1.46
2	D	3	MLE	CB-CG	2.21	1.62	1.52
2	D	3	MLE	CN-N	2.19	1.52	1.46
2	C	5	BMT	CB-CA	2.19	1.61	1.54
2	C	4	MVA	CG1-CB	2.17	1.60	1.52
2	C	3	MLE	CD1-CG	2.08	1.63	1.51
2	C	3	MLE	CD2-CG	2.04	1.62	1.51
2	C	2	MLE	CD2-CG	2.04	1.62	1.51
2	C	10	MLE	CD1-CG	2.01	1.62	1.51
2	D	4	MVA	CN-N	2.00	1.52	1.46
2	D	10	MLE	CD1-CG	2.00	1.62	1.51

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	4	MVA	CG2-CB-CA	-6.88	100.68	111.21
2	D	4	MVA	CG2-CB-CA	-6.11	101.86	111.21
2	C	8	66E	CG1-CB-CA	-5.28	103.12	111.21
2	D	4	MVA	CB-CA-C	-4.38	107.55	113.04
2	C	4	MVA	CB-CA-C	-4.25	107.72	113.04
2	C	4	MVA	C-CA-N	-4.08	97.23	110.88
2	C	10	MLE	CG-CB-CA	-3.88	105.65	115.34
2	D	8	66E	CG1-CB-CA	-3.59	105.71	111.21
2	D	6	ABA	CG-CB-CA	-3.58	105.22	113.42
2	C	2	MLE	CG-CB-CA	-3.48	106.66	115.34
2	D	8	66E	CG2-CB-CA	-3.48	105.89	111.21
2	C	10	MLE	CN-N-CA	3.42	124.29	113.64
2	D	3	MLE	CN-N-CA	3.40	124.22	113.64
2	C	2	MLE	CN-N-CA	3.35	124.06	113.64
2	C	3	MLE	CN-N-CA	3.35	124.06	113.64
2	D	10	MLE	CG-CB-CA	-3.34	107.00	115.34
2	C	6	ABA	CG-CB-CA	-3.34	105.78	113.42
2	D	3	MLE	CG-CB-CA	-3.30	107.10	115.34
2	D	8	66E	C-CA-N	-3.28	100.36	110.84
2	D	5	BMT	CG2-CB-CA	-3.28	105.89	113.78
2	D	2	MLE	CN-N-CA	3.10	123.29	113.64
2	C	5	BMT	CD2-CE-CZ	3.05	141.39	127.25

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	4	MVA	C-CA-N	-3.03	100.74	110.88
2	D	4	MVA	CG1-CB-CA	-2.99	106.63	111.21
2	C	8	66E	C-CA-N	-2.98	101.33	110.84
2	D	10	MLE	CN-N-CA	2.95	122.80	113.64
2	C	5	BMT	CG2-CD2-CE	-2.85	109.61	113.98
2	C	5	BMT	CG2-CB-CA	-2.78	107.09	113.78
2	D	5	BMT	CD2-CE-CZ	2.59	139.24	127.25
2	C	3	MLE	CG-CB-CA	-2.53	109.02	115.34
2	C	8	66E	CG2-CB-CA	-2.52	107.36	111.21
2	C	5	BMT	CH-CZ-CE	2.50	147.00	126.37
2	D	5	BMT	C-CA-N	-2.48	102.57	110.88
2	D	5	BMT	CB-CA-N	2.43	116.23	111.41
2	D	2	MLE	CG-CB-CA	-2.30	109.60	115.34
2	D	5	BMT	CH-CZ-CE	2.21	144.62	126.37

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	4	MVA	C-CA-CB-CG2
2	C	5	BMT	CB-CA-N-CN
2	D	5	BMT	CB-CA-N-CN
2	C	8	66E	CB-CA-N-C1
2	D	8	66E	CB-CA-N-C1
2	C	4	MVA	CB-CA-N-CN
2	D	4	MVA	CB-CA-N-CN

There are no ring outliers.

8 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	DAL	2	0
2	C	7	33X	1	0
2	D	3	MLE	1	0
2	D	2	MLE	1	0
2	D	5	BMT	1	0
2	C	5	BMT	2	0
2	D	10	MLE	1	0
2	C	4	MVA	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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

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	197/213 (92%)	0.05	5 (2%) 58 57	8, 15, 27, 41	5 (2%)
1	B	199/213 (93%)	0.10	6 (3%) 52 51	6, 14, 28, 38	9 (4%)
2	C	2/11 (18%)	1.95	1 (50%) 0 0	17, 17, 17, 20	0
2	D	2/11 (18%)	0.62	0 100 100	14, 14, 14, 15	0
All	All	400/448 (89%)	0.09	12 (3%) 52 51	6, 15, 27, 41	14 (3%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	88	VAL	4.4
1	B	125	SER	3.8
1	A	112	VAL	3.0
2	C	9	VAL	2.6
1	A	90	ILE	2.5
1	B	126	SER	2.5
1	B	124	GLY	2.5
1	B	18	SER	2.3
1	B	162	LYS	2.3
1	A	54[A]	HIS	2.2
1	A	85	GLN	2.1
1	B	13	SER	2.0

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

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. 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	B-factors(Å^2)	Q<0.9
2	MLE	C	2	9/10	0.94	0.10	16,17,21,25	0
2	MVA	C	4	8/9	0.94	0.09	11,12,14,15	0
2	ABA	C	6	6/7	0.94	0.08	11,12,12,14	0
2	DAL	D	1	5/6	0.95	0.08	12,12,13,15	0
2	33X	D	7	6/7	0.95	0.08	12,13,14,16	0
2	BMT	C	5	13/14	0.96	0.08	11,13,16,20	0
2	BMT	D	5	13/14	0.96	0.07	10,11,16,20	0
2	MLE	C	3	9/10	0.96	0.09	13,15,20,25	0
2	ABA	D	6	6/7	0.96	0.07	11,11,12,14	0
2	33X	C	7	6/7	0.96	0.08	12,14,15,15	0
2	DAL	C	1	5/6	0.96	0.09	17,17,18,21	0
2	66E	C	8	9/10	0.96	0.08	12,13,15,15	0
2	66E	D	8	9/10	0.96	0.08	12,13,17,19	0
2	MLE	D	10	9/10	0.96	0.09	12,14,18,20	0
2	MLE	D	3	9/10	0.97	0.06	9,10,13,15	0
2	MLE	D	2	9/10	0.97	0.07	10,11,14,14	0
2	MLE	C	10	9/10	0.97	0.10	15,17,23,26	0
2	MVA	D	4	8/9	0.97	0.06	9,10,10,10	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.