



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 03:08 PM UTC

PDB ID : 8R7U / pdb_00008r7u
Title : Crystal Structure of Cyclophilin TgCyp23 from Toxoplasma gondii in complex with dihydro Cyclosporin A
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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

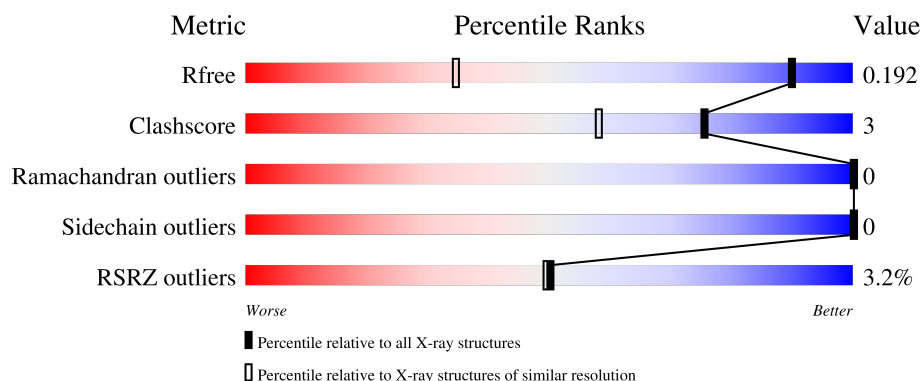
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	1216 (1.20-1.20)
Clashscore	190562	1265 (1.20-1.20)
Ramachandran outliers	187476	1226 (1.20-1.20)
Sidechain outliers	187428	1226 (1.20-1.20)
RSRZ outliers	180081	1214 (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 $\leq 5\%$. 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	213	4% 88% 5% 7%
1	B	213	% 88% 5% 7%
2	C	11	9% 55% 36%
2	D	11	18% 27% 45% 27%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3721 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	3	0
			1554	988	272	286	8			
1	A	199	Total	C	N	O	S	0	3	0
			1549	983	272	286	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 Dihydrocyclosporin A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	11	Total	C	N	O	0	0	0
			85	62	11	12			
2	D	11	Total	C	N	O	0	0	0
			85	62	11	12			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	223	Total	O	0	0
			223	223		
3	A	206	Total	O	0	0
			206	206		
3	C	12	Total	O	0	0
			12	12		
3	D	7	Total	O	0	0
			7	7		

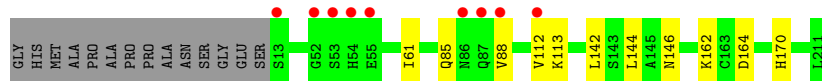
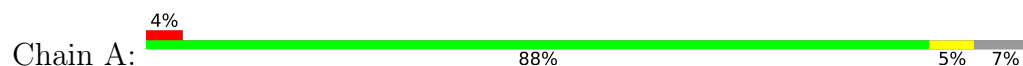
3 Residue-property plots [i](#)

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: Dihydrocyclosporin A



- Molecule 2: Dihydrocyclosporin A



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	38.35Å 118.11Å 47.46Å 90.00° 103.67° 90.00°	Depositor
Resolution (Å)	42.96 – 1.20 42.96 – 1.20	Depositor EDS
% Data completeness (in resolution range)	98.7 (42.96-1.20) 98.7 (42.96-1.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 1.20Å)	Xtriage
Refinement program	REFMAC 5.8.0405, PHENIX 1.20.1	Depositor
R, R_{free}	0.172 , 0.187 0.181 , 0.192	Depositor DCC
R_{free} test set	6380 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	16.0	Xtriage
Anisotropy	0.402	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 29.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3721	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.13% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: ABA, TMD, MVA, MLE, SAR, DAL

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	0.23	0/1594	0.53	0/2149
1	B	0.27	0/1602	0.55	0/2160
2	C	2.60	0/10	2.45	0/11
2	D	3.27	0/10	2.11	0/11
All	All	0.34	0/3216	0.56	0/4331

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	168	ARG	Sidechain

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	1549	0	1533	8	0
1	B	1554	0	1544	9	0
2	C	85	0	113	3	0
2	D	85	0	113	2	0
3	A	206	0	0	1	0
3	B	223	0	0	2	0
3	C	12	0	0	0	0
3	D	7	0	0	0	0
All	All	3721	0	3303	20	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 3.

All (20) 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:A:170:HIS:HE1	3:A:464:HOH:O	1.80	0.65
1:B:144:LEU:O	1:B:170:HIS:HD2	1.84	0.60
1:A:112:VAL:HG12	1:A:113:LYS:HE3	1.85	0.58
1:A:144:LEU:O	1:A:170:HIS:HD2	1.89	0.55
1:B:170:HIS:HE1	3:B:321:HOH:O	1.91	0.54
2:D:3:MLE:HD23	2:D:10:MLE:HB3	1.93	0.51
1:A:146:ASN:O	2:C:5:TMD:HA	2.12	0.50
1:B:61:ILE:HG21	1:B:142[A]:LEU:HD22	1.95	0.49
1:A:85:GLN:O	1:A:88:VAL:HG12	2.14	0.47
2:C:1:DAL:C	2:C:3:MLE:HN1	2.46	0.46
1:B:146:ASN:O	2:D:5:TMD:HA	2.16	0.45
2:C:9:VAL:HA	2:C:10:MLE:HN1	1.83	0.45
1:B:163:CYS:HA	1:B:165:TRP:CZ3	2.53	0.43
1:B:119:ARG:NH1	3:B:305:HOH:O	2.52	0.43
1:A:144:LEU:O	1:A:170:HIS:CD2	2.71	0.42
1:A:162:LYS:HE2	1:A:164:ASP:OD2	2.20	0.42
1:B:16:SER:H	1:B:19:GLU:CD	2.27	0.42
1:A:61:ILE:HG21	1:A:142:LEU:HD22	2.02	0.42
1:B:144:LEU:O	1:B:170:HIS:CD2	2.69	0.41
1:B:132:PHE:CG	1:B:168:ARG:HA	2.57	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	200/213 (94%)	197 (98%)	3 (2%)	0	100	100
1	B	201/213 (94%)	198 (98%)	3 (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	403/448 (90%)	397 (98%)	6 (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%)	170 (100%)	0	100	100
1	B	171/176 (97%)	171 (100%)	0	100	100
2	C	1/1 (100%)	1 (100%)	0	100	100
2	D	1/1 (100%)	1 (100%)	0	100	100
All	All	343/354 (97%)	343 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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	87	GLN
1	B	170	HIS
1	A	170	HIS
1	A	207	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	ABA	D	6	2	4,5,6	2.41	2 (50%)	1,5,7	1.42	0
2	MLE	C	2	2	7,8,9	2.99	4 (57%)	7,9,11	2.22	3 (42%)
2	MLE	D	3	2	7,8,9	3.95	5 (71%)	7,9,11	2.70	2 (28%)
2	TMD	D	5	2	11,12,13	2.72	6 (54%)	11,14,16	1.95	4 (36%)
2	SAR	D	7	2	3,4,5	2.32	2 (66%)	1,3,5	0.33	0
2	MLE	D	10	2	7,8,9	3.90	6 (85%)	7,9,11	1.09	1 (14%)
2	SAR	C	7	2	3,4,5	2.23	2 (66%)	1,3,5	0.63	0
2	MLE	D	2	2	7,8,9	4.05	6 (85%)	7,9,11	1.74	1 (14%)
2	MVA	C	4	2	6,7,8	2.28	5 (83%)	6,8,10	3.62	3 (50%)
2	DAL	D	1	2	3,4,5	1.73	0	2,4,6	0.56	0
2	TMD	C	5	2	11,12,13	2.71	6 (54%)	11,14,16	1.67	3 (27%)
2	MLE	D	8	2	7,8,9	3.30	6 (85%)	7,9,11	1.52	1 (14%)
2	MLE	C	10	2	7,8,9	3.27	5 (71%)	7,9,11	1.31	1 (14%)
2	ABA	C	6	2	4,5,6	2.38	1 (25%)	1,5,7	1.10	0
2	MVA	D	4	2	6,7,8	2.68	5 (83%)	6,8,10	3.17	3 (50%)
2	DAL	C	1	2	3,4,5	1.20	0	2,4,6	1.52	1 (50%)
2	MLE	C	8	2	7,8,9	3.42	6 (85%)	7,9,11	0.95	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MLE	C	3	2	7,8,9	3.45	4 (57%)	7,9,11	2.34	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	ABA	D	6	2	-	0/3/4/6	-
2	MLE	C	2	2	-	0/5/8/10	-
2	MLE	D	3	2	-	0/5/8/10	-
2	TMD	D	5	2	-	1/14/16/18	-
2	SAR	D	7	2	-	1/1/2/3	-
2	MLE	D	10	2	-	0/5/8/10	-
2	SAR	C	7	2	-	1/1/2/3	-
2	MLE	D	2	2	-	0/5/8/10	-
2	MVA	C	4	2	-	1/6/8/10	-
2	DAL	D	1	2	-	1/1/2/4	-
2	TMD	C	5	2	-	1/14/16/18	-
2	MLE	D	8	2	-	1/5/8/10	-
2	MLE	C	10	2	-	0/5/8/10	-
2	ABA	C	6	2	-	0/3/4/6	-
2	MVA	D	4	2	-	1/6/8/10	-
2	DAL	C	1	2	-	0/1/2/4	-
2	MLE	C	8	2	-	1/5/8/10	-
2	MLE	C	3	2	-	0/5/8/10	-

All (71) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	3	MLE	CB-CA	8.49	1.64	1.53
2	D	10	MLE	CB-CA	7.91	1.63	1.53
2	D	2	MLE	CB-CA	7.84	1.63	1.53
2	C	3	MLE	CB-CA	7.72	1.63	1.53
2	C	10	MLE	CB-CA	6.81	1.62	1.53
2	C	2	MLE	CB-CA	6.22	1.61	1.53
2	C	8	MLE	CB-CA	6.20	1.61	1.53
2	D	8	MLE	CB-CA	5.86	1.61	1.53
2	C	5	TMD	CG1-CB	5.19	1.62	1.53
2	D	5	TMD	CG1-CB	4.90	1.61	1.53
2	D	2	MLE	CA-N	4.74	1.55	1.47
2	C	8	MLE	CA-N	4.22	1.54	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	8	MLE	CA-N	4.04	1.54	1.47
2	C	6	ABA	CB-CA	3.76	1.63	1.53
2	D	6	ABA	CB-CA	3.74	1.63	1.53
2	D	4	MVA	CA-N	3.71	1.53	1.47
2	D	5	TMD	CN-N	3.54	1.55	1.46
2	D	5	TMD	CD2-CG1	3.53	1.62	1.53
2	D	3	MLE	CA-N	3.51	1.53	1.47
2	D	10	MLE	CA-N	3.51	1.53	1.47
2	C	5	TMD	CD2-CG1	3.40	1.61	1.53
2	D	10	MLE	CN-N	3.40	1.55	1.46
2	D	2	MLE	CN-N	3.39	1.55	1.46
2	D	7	SAR	CA-C	3.25	1.60	1.49
2	D	3	MLE	CN-N	3.13	1.54	1.46
2	C	5	TMD	CN-N	3.05	1.54	1.46
2	C	7	SAR	CA-C	3.04	1.60	1.49
2	D	2	MLE	CB-CG	3.02	1.65	1.52
2	D	5	TMD	CA-N	2.99	1.52	1.47
2	D	4	MVA	CN-N	2.97	1.54	1.46
2	C	5	TMD	CD1-CG1	2.94	1.61	1.54
2	D	8	MLE	CN-N	2.94	1.54	1.46
2	C	8	MLE	CN-N	2.87	1.53	1.46
2	C	4	MVA	CG1-CB	2.86	1.62	1.52
2	D	4	MVA	CG1-CB	2.83	1.62	1.52
2	D	10	MLE	CB-CG	2.82	1.64	1.52
2	C	8	MLE	CB-CG	2.70	1.63	1.52
2	C	10	MLE	CN-N	2.65	1.53	1.46
2	C	10	MLE	CB-CG	2.59	1.63	1.52
2	D	8	MLE	CB-CG	2.57	1.63	1.52
2	C	5	TMD	CA-N	2.56	1.51	1.47
2	D	5	TMD	CD1-CG1	2.56	1.60	1.54
2	C	5	TMD	CE-CD1	2.53	1.62	1.52
2	D	3	MLE	CB-CG	2.48	1.62	1.52
2	C	3	MLE	CA-N	2.45	1.51	1.47
2	C	4	MVA	CB-CA	2.43	1.58	1.54
2	C	3	MLE	CN-N	2.42	1.52	1.46
2	D	5	TMD	CE-CD1	2.42	1.62	1.52
2	D	4	MVA	CG2-CB	2.40	1.60	1.52
2	C	2	MLE	CN-N	2.40	1.52	1.46
2	C	4	MVA	CA-N	2.40	1.51	1.47
2	C	2	MLE	CA-N	2.37	1.51	1.47
2	C	10	MLE	CA-N	2.33	1.51	1.47
2	D	4	MVA	CB-CA	2.31	1.58	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3	MLE	CB-CG	2.31	1.62	1.52
2	C	2	MLE	CB-CG	2.30	1.62	1.52
2	C	4	MVA	CN-N	2.28	1.52	1.46
2	D	10	MLE	CD1-CG	2.27	1.63	1.51
2	C	7	SAR	CN-N	2.26	1.56	1.47
2	C	4	MVA	CG2-CB	2.25	1.60	1.52
2	C	10	MLE	CD1-CG	2.24	1.63	1.51
2	D	7	SAR	CN-N	2.23	1.55	1.47
2	D	2	MLE	CD2-CG	2.21	1.63	1.51
2	C	8	MLE	CD2-CG	2.13	1.62	1.51
2	D	6	ABA	CA-N	2.10	1.53	1.48
2	D	10	MLE	CD2-CG	2.09	1.62	1.51
2	D	8	MLE	CD1-CG	2.09	1.62	1.51
2	D	3	MLE	CD2-CG	2.07	1.62	1.51
2	D	8	MLE	CD2-CG	2.07	1.62	1.51
2	D	2	MLE	CD1-CG	2.05	1.62	1.51
2	C	8	MLE	CD1-CG	2.04	1.62	1.51

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	4	MVA	CG1-CB-CA	-6.53	101.21	111.18
2	D	4	MVA	CG1-CB-CA	-6.22	101.68	111.18
2	D	3	MLE	CB-CA-N	-5.31	102.53	110.59
2	C	4	MVA	CB-CA-C	-5.12	106.35	112.96
2	D	3	MLE	CN-N-CA	4.18	126.18	113.70
2	D	2	MLE	CN-N-CA	4.05	125.81	113.70
2	C	3	MLE	CB-CA-N	-3.82	104.80	110.59
2	D	4	MVA	CB-CA-C	-3.78	108.08	112.96
2	D	5	TMD	CD1-CG1-CB	-3.73	105.57	111.51
2	C	3	MLE	CN-N-CA	3.59	124.42	113.70
2	C	2	MLE	CB-CA-C	-3.57	105.50	110.99
2	C	2	MLE	CN-N-CA	3.33	123.65	113.70
2	D	8	MLE	CN-N-CA	3.33	123.64	113.70
2	D	5	TMD	CB-CA-N	3.21	117.88	111.27
2	C	2	MLE	CB-CA-N	-3.13	105.84	110.59
2	C	4	MVA	CG2-CB-CA	-3.00	106.59	111.18
2	C	10	MLE	CN-N-CA	2.96	122.54	113.70
2	C	5	TMD	CD1-CG1-CB	-2.90	106.89	111.51
2	C	5	TMD	CB-CA-N	2.67	116.77	111.27
2	C	3	MLE	CB-CA-C	-2.63	106.95	110.99
2	D	4	MVA	CG2-CB-CA	-2.60	107.20	111.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	5	TMD	CG1-CB-CA	-2.52	107.02	113.28
2	D	5	TMD	CG1-CB-CA	-2.52	107.03	113.28
2	D	10	MLE	CN-N-CA	2.45	121.03	113.70
2	C	1	DAL	CB-CA-N	-2.10	102.72	110.02
2	C	8	MLE	CN-N-CA	2.04	119.81	113.70
2	D	5	TMD	OG2-CB-CA	-2.01	104.98	109.24

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	DAL	O-C-CA-CB
2	C	4	MVA	C-CA-CB-CG1
2	D	4	MVA	C-CA-CB-CG1
2	D	5	TMD	CB-CA-N-CN
2	D	7	SAR	C-CA-N-CN
2	C	8	MLE	O-C-CA-CB
2	D	8	MLE	O-C-CA-CB
2	C	5	TMD	CB-CA-N-CN
2	C	7	SAR	C-CA-N-CN

There are no ring outliers.

7 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	3	MLE	1	0
2	D	5	TMD	1	0
2	D	10	MLE	1	0
2	C	5	TMD	1	0
2	C	10	MLE	1	0
2	C	1	DAL	1	0
2	C	3	MLE	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 [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	199/213 (93%)	0.33	9 (4%) 38 39	10, 21, 38, 70	3 (1%)
1	B	199/213 (93%)	0.18	2 (1%) 79 82	8, 18, 31, 43	3 (1%)
2	C	2/11 (18%)	1.07	0 100 100	18, 18, 18, 20	0
2	D	2/11 (18%)	2.88	2 (100%) 0 0	25, 25, 25, 27	0
All	All	402/448 (89%)	0.27	13 (3%) 50 49	8, 20, 35, 70	6 (1%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	88	VAL	3.6
1	A	87	GLN	3.4
1	A	52	GLY	3.3
2	D	9	VAL	3.3
1	B	87	GLN	3.2
1	B	86	ASN	3.2
1	A	54	HIS	3.2
1	A	13	SER	2.8
1	A	86	ASN	2.8
2	D	11	ALA	2.5
1	A	53	SER	2.3
1	A	55	GLU	2.2
1	A	112	VAL	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [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. 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	B-factors($\text{\AA}^2$)	Q<0.9
2	SAR	C	7	5/6	0.91	0.12	20,21,21,22	0
2	MLE	D	2	9/10	0.92	0.13	19,22,26,29	0
2	ABA	C	6	6/7	0.92	0.11	17,19,19,23	0
2	DAL	D	1	5/6	0.92	0.12	20,21,26,26	0
2	ABA	D	6	6/7	0.94	0.09	16,16,18,20	0
2	SAR	D	7	5/6	0.94	0.09	17,18,19,22	0
2	MLE	D	10	9/10	0.94	0.10	19,23,25,25	0
2	MLE	C	8	9/10	0.95	0.10	17,21,27,30	0
2	DAL	C	1	5/6	0.95	0.09	14,14,16,16	0
2	MLE	D	3	9/10	0.96	0.09	17,19,24,25	0
2	MLE	D	8	9/10	0.96	0.08	18,19,26,28	0
2	MLE	C	10	9/10	0.96	0.09	17,17,21,23	0
2	MVA	C	4	8/9	0.96	0.07	12,13,14,14	0
2	TMD	C	5	13/14	0.97	0.07	14,15,20,22	0
2	TMD	D	5	13/14	0.97	0.07	16,17,21,21	0
2	MLE	C	2	9/10	0.97	0.06	11,13,15,15	0
2	MLE	C	3	9/10	0.97	0.06	12,13,16,16	0
2	MVA	D	4	8/9	0.97	0.07	15,16,17,19	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.