



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 04:12 AM GMT

PDB ID : 2A27
Title : Human DRP-1 kinase, W305S S308A D40 mutant, crystal form with 8 monomers in the asymmetric unit
Authors : Kursula, P.; Lehmann, F.; Shani, G.; Kimchi, A.; Wilmanns, M.
Deposited on : 2005-06-22
Resolution : 3.00 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

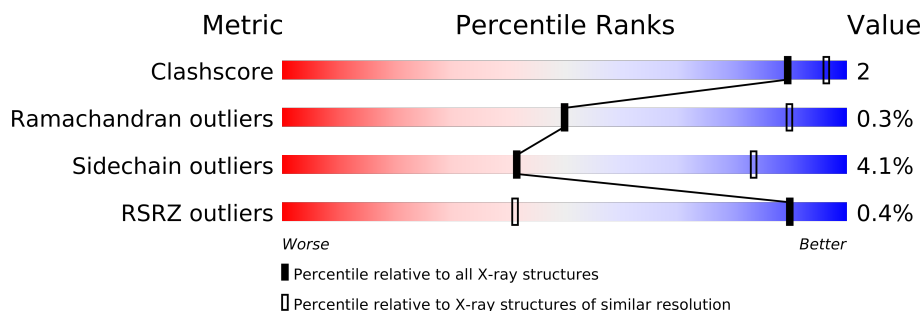
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.00 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))
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)
RSRZ outliers	66119	1217 (3.00-3.00)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	321	
1	B	321	
1	C	321	
1	D	321	
1	E	321	
1	F	321	
1	G	321	
1	H	321	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	DTT	D	1004	-	X
2	DTT	F	1007	-	X
2	DTT	G	1006	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
2	DTT	H	1008	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20003 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Death-associated protein kinase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	0	0	0
			2478	1584	425	465	4			
1	B	303	Total	C	N	O	S	0	0	0
			2467	1578	421	464	4			
1	C	303	Total	C	N	O	S	0	0	0
			2467	1578	421	464	4			
1	D	304	Total	C	N	O	S	0	0	0
			2478	1584	425	465	4			
1	E	303	Total	C	N	O	S	0	0	0
			2467	1578	421	464	4			
1	F	303	Total	C	N	O	S	0	0	0
			2467	1578	421	464	4			
1	G	303	Total	C	N	O	S	0	0	0
			2467	1578	421	464	4			
1	H	304	Total	C	N	O	S	0	0	0
			2472	1581	422	465	4			

There are 24 discrepancies between the modelled and reference sequences:

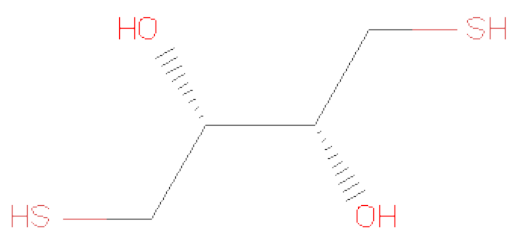
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	CLONING ARTIFACT	UNP Q9UIK4
A	305	SER	TRP	ENGINEERED	UNP Q9UIK4
A	308	ALA	SER	ENGINEERED	UNP Q9UIK4
B	0	GLY	-	CLONING ARTIFACT	UNP Q9UIK4
B	305	SER	TRP	ENGINEERED	UNP Q9UIK4
B	308	ALA	SER	ENGINEERED	UNP Q9UIK4
C	0	GLY	-	CLONING ARTIFACT	UNP Q9UIK4
C	305	SER	TRP	ENGINEERED	UNP Q9UIK4
C	308	ALA	SER	ENGINEERED	UNP Q9UIK4
D	0	GLY	-	CLONING ARTIFACT	UNP Q9UIK4
D	305	SER	TRP	ENGINEERED	UNP Q9UIK4
D	308	ALA	SER	ENGINEERED	UNP Q9UIK4
E	0	GLY	-	CLONING ARTIFACT	UNP Q9UIK4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	305	SER	TRP	ENGINEERED	UNP Q9UIK4
E	308	ALA	SER	ENGINEERED	UNP Q9UIK4
F	0	GLY	-	CLONING ARTIFACT	UNP Q9UIK4
F	305	SER	TRP	ENGINEERED	UNP Q9UIK4
F	308	ALA	SER	ENGINEERED	UNP Q9UIK4
G	0	GLY	-	CLONING ARTIFACT	UNP Q9UIK4
G	305	SER	TRP	ENGINEERED	UNP Q9UIK4
G	308	ALA	SER	ENGINEERED	UNP Q9UIK4
H	0	GLY	-	CLONING ARTIFACT	UNP Q9UIK4
H	305	SER	TRP	ENGINEERED	UNP Q9UIK4
H	308	ALA	SER	ENGINEERED	UNP Q9UIK4

- Molecule 2 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (three-letter code: DTT) (formula: $C_4H_{10}O_2S_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			8	4	2	2		
2	B	1	Total	C	O	S	0	0
			8	4	2	2		
2	C	1	Total	C	O	S	0	0
			8	4	2	2		
2	E	1	Total	C	O	S	0	0
			8	4	2	2		
2	D	1	Total	C	O	S	0	0
			8	4	2	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	G	1	Total	C	O	S	0	0
			8	4	2	2		
2	F	1	Total	C	O	S	0	0
			8	4	2	2		
2	H	1	Total	C	O	S	0	0
			8	4	2	2		

- Molecule 3 is water.

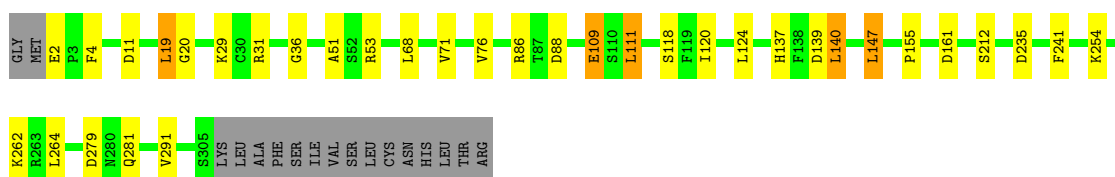
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	37	Total	O	0	0
			37	37		
3	B	55	Total	O	0	0
			55	55		
3	C	44	Total	O	0	0
			44	44		
3	D	17	Total	O	0	0
			17	17		
3	E	9	Total	O	0	0
			9	9		
3	F	3	Total	O	0	0
			3	3		
3	G	5	Total	O	0	0
			5	5		
3	H	6	Total	O	0	0
			6	6		

3 Residue-property plots

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: Death-associated protein kinase 2

Chain A:



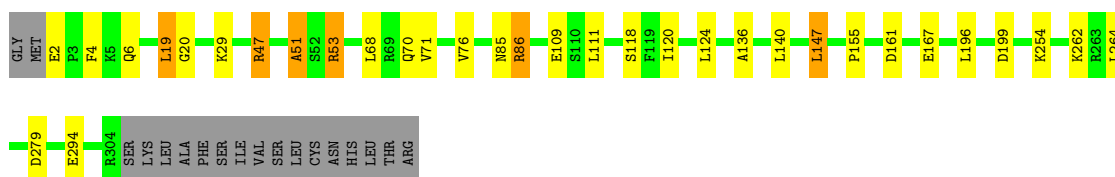
- Molecule 1: Death-associated protein kinase 2

Chain B:



- Molecule 1: Death-associated protein kinase 2

Chain C:



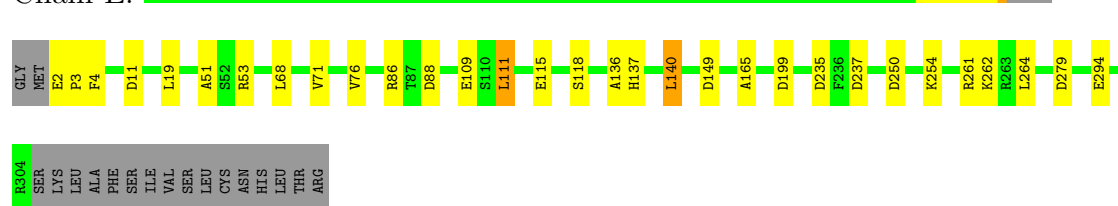
- Molecule 1: Death-associated protein kinase 2

Chain D:



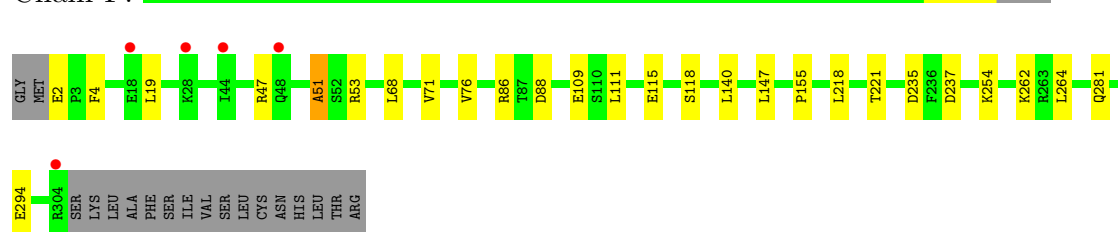
- Molecule 1: Death-associated protein kinase 2

Chain E:



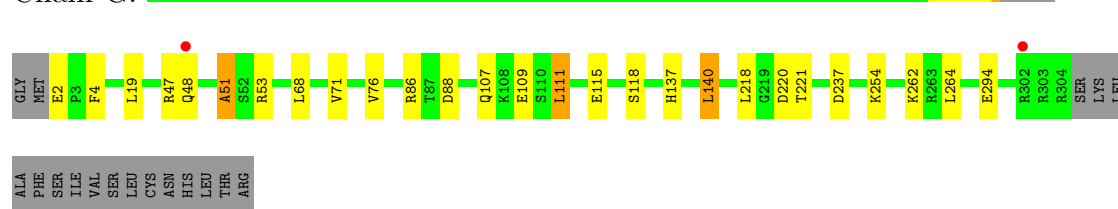
- Molecule 1: Death-associated protein kinase 2

Chain F:



- Molecule 1: Death-associated protein kinase 2

Chain G:



- Molecule 1: Death-associated protein kinase 2

Chain H:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	159.12Å 113.35Å 247.31Å 90.00° 95.09° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 33.46 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-3.00) 99.8 (33.46-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 3.00Å)	Xtriage
Refinement program	REFMAC 5.2.0000	Depositor
R, R_{free}	0.217 , 0.238 0.221 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	70.4	Xtriage
Anisotropy	0.581	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 121.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 87689 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	20003	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.58	0/2525	0.77	5/3405 (0.1%)
1	B	0.65	0/2514	0.79	5/3391 (0.1%)
1	C	0.49	0/2514	0.74	2/3391 (0.1%)
1	D	0.42	0/2525	0.71	5/3405 (0.1%)
1	E	0.38	0/2514	0.70	10/3391 (0.3%)
1	F	0.35	0/2514	0.67	3/3391 (0.1%)
1	G	0.34	0/2514	0.69	2/3391 (0.1%)
1	H	0.34	0/2519	0.68	6/3398 (0.2%)
All	All	0.46	0/20139	0.72	38/27163 (0.1%)

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	A	0	2
1	B	0	2
1	C	0	2
1	D	0	2
1	E	0	2
1	F	0	2
1	G	0	2
1	H	0	2
All	All	0	16

There are no bond length outliers.

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	279	ASP	CB-CG-OD2	7.67	125.21	118.30
1	A	235	ASP	CB-CG-OD2	6.34	124.00	118.30
1	B	235	ASP	CB-CG-OD2	6.32	123.98	118.30
1	B	88	ASP	CB-CG-OD2	5.88	123.59	118.30
1	D	279	ASP	CB-CG-OD2	5.85	123.57	118.30

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2	GLU	Peptide
1	A	51	ALA	Peptide
1	B	2	GLU	Peptide
1	B	51	ALA	Peptide
1	C	2	GLU	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2478	0	2489	13	0
1	B	2467	0	2476	12	0
1	C	2467	0	2476	12	0
1	D	2478	0	2489	16	0
1	E	2467	0	2476	6	0
1	F	2467	0	2476	9	0
1	G	2467	0	2476	15	0
1	H	2472	0	2478	9	0
2	A	8	0	8	2	0
2	B	8	0	8	0	0
2	C	8	0	8	0	0
2	D	8	0	10	0	0
2	E	8	0	8	1	0
2	F	8	0	10	1	0
2	G	8	0	10	1	0
2	H	8	0	10	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	37	0	0	1	0
3	B	55	0	0	3	0
3	C	44	0	0	1	0
3	D	17	0	0	1	0
3	E	9	0	0	0	0
3	F	3	0	0	0	0
3	G	5	0	0	0	0
3	H	6	0	0	1	0
All	All	20003	0	19908	89	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

The worst 5 of 89 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:1001:DTT:S1	2:A:1001:DTT:S4	2.30	1.29
2:E:1005:DTT:S1	2:E:1005:DTT:S4	2.33	1.25
2:H:1008:DTT:HS1	2:H:1008:DTT:HS2	1.21	0.86
2:H:1008:DTT:S1	2:H:1008:DTT:S4	2.83	0.76
1:D:51:ALA:HB3	1:G:218:LEU:HD21	1.72	0.72

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	302/321 (94%)	287 (95%)	13 (4%)	2 (1%)	30	78
1	B	301/321 (94%)	287 (95%)	13 (4%)	1 (0%)	50	90
1	C	301/321 (94%)	287 (95%)	12 (4%)	2 (1%)	30	78
1	D	302/321 (94%)	288 (95%)	13 (4%)	1 (0%)	50	90
1	E	301/321 (94%)	289 (96%)	12 (4%)	0	100	100
1	F	301/321 (94%)	291 (97%)	10 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	301/321 (94%)	293 (97%)	8 (3%)	0	100	100
1	H	302/321 (94%)	290 (96%)	11 (4%)	1 (0%)	50	90
All	All	2411/2568 (94%)	2312 (96%)	92 (4%)	7 (0%)	50	90

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	4	PHE
1	A	161	ASP
1	C	161	ASP
1	A	20	GLY
1	C	20	GLY

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	272/288 (94%)	261 (96%)	11 (4%)	42	84
1	B	271/288 (94%)	261 (96%)	10 (4%)	45	86
1	C	271/288 (94%)	258 (95%)	13 (5%)	35	79
1	D	272/288 (94%)	261 (96%)	11 (4%)	42	84
1	E	271/288 (94%)	261 (96%)	10 (4%)	45	86
1	F	271/288 (94%)	260 (96%)	11 (4%)	41	83
1	G	271/288 (94%)	259 (96%)	12 (4%)	39	82
1	H	271/288 (94%)	260 (96%)	11 (4%)	41	83
All	All	2170/2304 (94%)	2081 (96%)	89 (4%)	41	83

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	109	GLU
1	E	109	GLU
1	H	107	GLN
1	D	111	LEU

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Mol	Chain	Res	Type
1	E	19	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	223	GLN
1	E	85	ASN
1	H	6	GLN
1	E	23	GLN
1	E	144	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

8 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	$\# Z > 2$
2	DTT	A	1001	-	7,7,7	0.62	0	8,8,8	1.38	2 (25%)
2	DTT	B	1002	-	7,7,7	0.71	0	8,8,8	1.14	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	DTT	C	1003	-	7,7,7	0.66	0	8,8,8	0.88	0
2	DTT	D	1004	-	7,7,7	0.86	0	8,8,8	1.61	2 (25%)
2	DTT	E	1005	-	7,7,7	0.60	0	8,8,8	1.34	1 (12%)
2	DTT	F	1007	-	7,7,7	0.68	0	8,8,8	0.91	0
2	DTT	G	1006	-	7,7,7	0.64	0	8,8,8	0.74	0
2	DTT	H	1008	-	7,7,7	0.65	0	8,8,8	0.64	0

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	DTT	A	1001	-	1/1/2/2	0/8/8/8	0/0/0/0
2	DTT	B	1002	-	1/1/2/2	0/8/8/8	0/0/0/0
2	DTT	C	1003	-	1/1/2/2	0/8/8/8	0/0/0/0
2	DTT	D	1004	-	1/1/2/2	0/8/8/8	0/0/0/0
2	DTT	E	1005	-	1/1/2/2	0/8/8/8	0/0/0/0
2	DTT	F	1007	-	1/1/2/2	0/8/8/8	0/0/0/0
2	DTT	G	1006	-	1/1/2/2	0/8/8/8	0/0/0/0
2	DTT	H	1008	-	1/1/2/2	0/8/8/8	0/0/0/0

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1004	DTT	C2-C1-S1	-3.00	109.94	114.66
2	A	1001	DTT	C3-C4-S4	-2.54	110.66	114.66
2	D	1004	DTT	C4-C3-C2	2.45	118.67	113.07
2	E	1005	DTT	C3-C4-S4	-2.23	111.14	114.66
2	A	1001	DTT	O3-C3-C4	-2.11	105.91	109.87

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1001	DTT	C3
2	B	1002	DTT	C3
2	E	1005	DTT	C3
2	H	1008	DTT	C3
2	D	1004	DTT	C3

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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, 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	304/321 (94%)	-0.21	0	100 100	94, 99, 104, 121	0
1	B	303/321 (94%)	-0.21	0	100 100	94, 99, 104, 113	0
1	C	303/321 (94%)	-0.19	0	100 100	94, 99, 103, 111	0
1	D	304/321 (94%)	-0.09	1 (0%)	91 48	95, 99, 103, 112	0
1	E	303/321 (94%)	-0.03	0	100 100	94, 99, 103, 109	0
1	F	303/321 (94%)	0.10	5 (1%)	67 15	96, 99, 103, 106	0
1	G	303/321 (94%)	0.02	2 (0%)	84 28	95, 99, 103, 106	0
1	H	304/321 (94%)	0.01	1 (0%)	91 48	95, 99, 103, 111	0
All	All	2427/2568 (94%)	-0.08	9 (0%)	90 41	94, 99, 103, 121	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	48	GLN	3.9
1	G	302	ARG	2.7
1	F	28	LYS	2.7
1	H	83	TYR	2.7
1	F	44	ILE	2.5

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

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

6.3 Carbohydrates ⓘ

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	DTT	G	1006	8/8	0.40	4.87	134,136,137,139	0
2	DTT	H	1008	8/8	0.36	2.88	136,137,138,140	0
2	DTT	F	1007	8/8	0.29	2.67	123,124,125,125	0
2	DTT	D	1004	8/8	0.27	2.01	114,117,118,119	0
2	DTT	A	1001	8/8	0.26	1.61	93,96,97,98	0
2	DTT	B	1002	8/8	0.20	0.61	72,73,74,75	0
2	DTT	C	1003	8/8	0.21	0.19	74,79,81,81	0
2	DTT	E	1005	8/8	0.23	-0.02	102,103,104,104	0

6.5 Other polymers ⓘ

There are no such residues in this entry.